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CURRENT DEVELOPMENTS AND THEMATIC REVIEWS IN AGRICULTURE, FORESTRY AND AQUACULTURE

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Prof. İsmet Daşdemir, PhD.
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CHAPTER 1

Cucurbit Virus Diseases: Epidemiology, Diagnosis, Integrated Management and Breeding for Virus Resistance

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1. Importance of virus diseases in cucurbits

The Cucurbitaceae includes economically important crops such as cucumber, melon, watermelon, and squash. Successive plantings, weed hosts, and protected cultivation can maintain susceptible hosts throughout the year, helping to sustain inoculum, particularly for vector-borne viruses. Seed and transplant trade can also move seed-associated or readily mechanically transmitted viruses into new production areas (Lecoq and Desbiez, 2012; Jones and Naidu, 2019; Jones, 2021; Desbiez, 2020). Economic losses depend not only on the virus involved but also on the timing of infection, host genotype, environmental conditions, mixed infections, and vector pressure.

Immunity, resistance, and tolerance should be distinguished in resistance studies. Immunity refers to the failure of infection to become established, resistance refers to reduced virus accumulation or systemic spread, and tolerance refers to limited symptom expression and yield loss despite a comparable viral load. Phenotyping should therefore combine symptom scores with virus detection or titre measurements, appropriate controls, and adequate biological replication (Martín-Hernández and Picó, 2021; Kang et al., 2005). Management priorities depend on the transmission route. For non-persistently aphid-transmitted viruses such as ZYMV and WMV, insecticides alone are insufficient. Seed health and sanitation are central to CGMMV management, whitefly management is critical for ToLCNDV, and seed, substrate, and root-zone hygiene are priorities for MNSV (Desbiez and Lecoq, 1997; Dombrovsky et al., 2017; Moriones et al., 2017).

2. Major viruses of cucurbit crops

Table 1. Comparison of eight major cucurbit viruses

Agent	Genus / family	Genome	Main transmission routes	Main hosts	Critical point in diagnosis and management
ZYMV	*Potyvirus / Potyviridae*	+ssRNA	Aphid-borne, non-persistent. Mechanical inoculation is possible experimentally.	Squash, cucumber, melon, watermelon	Transmission can occur during brief aphid stylet penetration. Insecticide-based protection alone is often insufficient.
WMV	*Potyvirus / Potyviridae*	+ssRNA	Aphid-borne, non-persistent. Mechanical inoculation is possible experimentally.	Melon, watermelon, cucumber, squash	Isolate diversity should be considered in diagnosis and resistance screening. Because WMV is transmitted non-persistently by aphids, insecticide-based vector control alone may not prevent primary infection.

Agent	Genus / family	Genome	Main transmission routes	Main hosts	Critical point in diagnosis and management
CMV	*Cucumovirus / Bromoviridae*	Tripartite +ssRNA	Aphid-borne, non-persistent; seed association occurs in some hosts.	Very broad host range, including major cucurbit species	Symptoms are variable. Weed reservoirs and mixed infections should be considered.
CGMMV	*Tobamovirus / Virgaviridae*	+ssRNA	Seed-associated; contact, tools, grafting, and nutrient solution.	Cucumber, melon, watermelon, squash	High environmental stability. Seed contamination, seedling infection, and infectivity should be assessed separately.
CABYV	*Polerovirus / Solemoviridae*	+ssRNA	Aphid-borne, persistent-circulative.	Melon, cucumber, squash, watermelon	Phloem-limited. Vascular tissue should be sampled, and yellowing should be distinguished from nutrient deficiency.
SqMV	*Comovirus / Secoviridae*	Bipartite +ssRNA	Seed and chrysomelid leaf beetles. Mechanical inoculation is possible experimentally.	Primarily squash and melon	Seed lots and primary infection foci are important. Symptom-based screening should be confirmed in the laboratory.
MNSV	*Gammacarmovirus / Tombusviridae*	+ssRNA	Seed-associated; soil and root-zone spread via *Olpidium bornovanus*; irrigation water.	Primarily melon; also several other cucurbits	Seed, substrate, irrigation water, and the fungal vector should be considered together. *nsv* resistance should be tested against multiple isolates.
ToLCNDV	*Begomovirus / Geminiviridae*	Bipartite ssDNA comprising DNA-A and DNA-B	*Bemisia tabaci, persistent-circulative.*	Squash, melon, cucumber; watermelon with some isolates	Seedlings should be protected from whiteflies, and resistance should be tested against different isolates.

References: ZYMV, Desbiez and Lecoq (1997); WMV, Desbiez et al. (2007), Pérez-de-Castro et al. (2019), Agaoua et al. (2022), and López-Martín et al. (2024); CMV, Jacquemond (2012); CGMMV, Dombrovsky et al. (2017); CABYV, Lecoq et al. (1992); SqMV, Martín-Hernández and Picó (2021); MNSV, Campbell et al. (1996); ToLCNDV, Moriones et al. (2017).

2.1. Zucchini yellow mosaic virus (ZYMV)

ZYMV is a positive-sense single-stranded RNA virus in the genus *Potyvirus*, family *Potyviridae*. It can cause mosaic, vein clearing, leaf deformation, and fruit

distortion in squash, cucumber, melon, and watermelon. Because it is transmitted non-persistently by aphids, acquisition and inoculation can occur during brief feeding contacts. Insecticides alone therefore provide limited protection against primary infection, and management should combine reduction of inoculum sources, reflective mulches, mineral oil applications, and resistant cultivars (Desbiez and Lecoq, 1997; Gal-On, 2007). In cucumber, the recessive *zym* region derived from A192-18 was mapped to chromosome 6, with a VPS4-like gene identified as a strong candidate (Amano et al., 2013). The presence of distinct haplotypes encoding the same protein in TMG-1 and Dina-1, together with the limited discriminatory power of the CAP marker in a Turkish germplasm panel, shows that markers should be validated in the target germplasm before routine use (Ramírez-Madera and Havey, 2017; Coşkun et al., 2024).

2.2. Watermelon mosaic virus (WMV)

WMV belongs to the family *Potyviridae* and is transmitted non-persistently by aphids. It can cause mosaic, leaf deformation, and stunting in melon, watermelon, cucumber, and squash. Genetic and serological diversity in the Mediterranean basin makes isolate selection an important consideration in both diagnosis and resistance testing (Desbiez et al., 2007). In TGR-1551-derived material, the *wmv1551* region was fine-mapped and the P30R substitution in CmVPS4 was shown to be directly associated with resistance (Pérez-de-Castro et al., 2019; Agaoua et al., 2022). P30R was not detected in another TGR-1551-derived material, where MELO3C021395/MED33A was proposed as an alternative candidate (López-Martín et al., 2024). The identity of the donor material, the target allele, and the WMV isolate used for phenotyping should therefore be confirmed before the resistance is incorporated into a breeding programme.

2.3. Cucumber mosaic virus (CMV)

CMV is a tripartite positive-sense RNA virus in the genus *Cucumovirus*, family *Bromoviridae*, with an exceptionally broad host range. It is transmitted non-persistently by aphids, and weeds and other cultivated hosts can serve as important reservoirs. Mosaic, leaf deformation, stunting, and fruit quality losses vary with isolate, genotype, and environmental conditions (Jacquemond, 2012). In cucumber, the *cmv6.1* QTL on chromosome 6 explains roughly one-third of the phenotypic variation, whereas in melon PI 161375, *cmv1* acts together with additional QTLs (Shi et al., 2018; Guiu-Aragonés et al., 2014). *cmv1* has been associated with natural variation in CmVPS41 and limits the transition of CMV to systemic infection. For this reason, locally inoculated and systemic tissues should be sampled separately during resistance phenotyping (Giner et al., 2017; Pascual et al., 2019).

2.4. Cucumber green mottle mosaic virus (CGMMV)

CGMMV is a positive-sense RNA virus in the genus *Tobamovirus*, family *Virgaviridae*, and is highly stable in the environment. In protected cultivation, hands, knives, grafting equipment, strings, crates, plant residues, and nutrient solution can all contribute to mechanical spread. Detection of viral RNA in seed does not necessarily indicate embryo infection or predict the rate of transmission to seedlings. The virus is most often associated with the seed coat, perisperm, and endosperm (Dombrovsky et al., 2017; Liu et al., 2014; Sui et al., 2019; Gea-Caballero and Aranda, 2026).

Management should combine clean mother plants, seed-lot testing with adequate sample sizes, separation of production units, and effective sanitation after organic debris has been removed. A reduction in RT-qPCR signal after disinfection does not by itself demonstrate complete loss of infectivity (Reingold et al., 2015; Reingold et al., 2016). Sources of partial resistance have been reported in cucumber, while two complementary recessive genes, *cgmmv-1* and *cgmmv-2*, have been described in the melon material 'Chang Bougi'. Because resistance can vary with isolate and environment, symptom expression, virus accumulation, systemic spread, and, where possible, fruit quality should be evaluated together (Sugiyama et al., 2006; Sugiyama et al., 2007; Crespo et al., 2018; Ruiz et al., 2021).

2.5. Cucurbit aphid-borne yellows virus (CABYV)

CABYV is a phloem-limited RNA virus in the genus *Polerovirus*, family *Solemoviridae*. It is transmitted persistently and circulatively by aphids, particularly *Aphis gossypii* and *Myzus persicae*. Interveinal yellowing can be confused with nutrient deficiency or natural senescence (Lecoq et al., 1992). In melon PI 124112, resistance has been associated with two complementary recessive genes, *cab-1* and *cab-2* (Dogimont et al., 1996; Dogimont et al., 1997). In TGR-1551, a dominant major gene together with modifier loci has been proposed, and reduced systemic virus accumulation and reduced efficiency of aphid-mediated inoculation have been reported (Kassem et al., 2015). The two sources therefore provide complementary genetic mechanisms for breeding.

2.6. Squash mosaic virus (SqMV)

SqMV is a bipartite positive-sense single-stranded RNA (+ssRNA) virus in the genus *Comovirus*, family *Secoviridae*. It can cause mosaic, blistering, and deformation in squash and melon. In natural epidemics, infected seed and chrysomelid leaf beetles of the genera *Acalymma* and *Diabrotica* are important routes of spread (Martín-Hernández and Picó, 2021; Desbiez, 2020). Because the genetics of resistance is less well resolved than for ZYMV or CMV, reliable evaluation of candidate material requires repeated phenotyping with standardized isolates, and infection should be confirmed by ELISA or RT-PCR.

2.7. Melon necrotic spot virus (MNSV)

MNSV is an RNA virus in the genus *Gammacarmovirus*, family *Tombusviridae*. It can cause necrosis of leaves, stems, and roots, vascular browning, wilting, and collapse, particularly in melon. Because seed-associated transmission can develop into root infection in the presence of *Olpidium bornovanus* zoospores, seed, substrate, the root zone, and irrigation water should be considered together (Campbell et al., 1996; Martín-Hernández and Picó, 2021). In Türkiye, MNSV was confirmed in summer squash samples from Adana-Pozantı in 2013 by DAS-ELISA and RT-PCR (Koç et al., 2014). Recessive *nsv* resistance in melon is associated with an *eIF4E* allele. The occurrence of resistance-breaking isolates means that resistance requires verification against multiple isolates (Nieto et al., 2006; Díaz et al., 2004).

2.8. Tomato leaf curl New Delhi virus (ToLCNDV)

ToLCNDV is a bipartite ssDNA virus in the genus *Begomovirus*, family *Geminiviridae*, with DNA-A and DNA-B components, and is transmitted by *Bemisia tabaci* in a persistent-circulative manner. The ToLCNDV-ES strain has become an important cucurbit pathogen in the Mediterranean basin, where mosaic, leaf curling, stunting, and reduced fruit set have been reported in squash, melon, and cucumber (Fortes et al., 2016; Moriones et al., 2017; Ruiz et al., 2017). Management relies on protected, whitefly-free transplants, weed and crop-residue management, early removal of infected plants, and the use of resistant cultivars. In cucumber, distinct sources of ToLCNDV resistance have been described. In accession CGN23089, resistance is predominantly recessive and is associated with a QTL on chromosome 2 (Sáez et al., 2021). In accession No. 44, Cy-1 on chromosome 1 and cy-2 on chromosome 2 are major-effect QTLs, acting dominantly and recessively, respectively. Fine mapping narrowed the Cy-1 region to 209 kb, and VIGS provided functional support for CsRDR3 as the gene underlying Cy-1 resistance, although the causal polymorphism has not yet been conclusively identified (Koeda et al., 2024).

2.9. Other important semipersistently transmitted whitefly-borne viruses

CYSDV, CCYV, and BPYV belong to the genus *Crinivirus* in the family *Closteroviridae*, whereas CVYV belongs to the genus *Ipomovirus* in the family *Potyviridae*. CYSDV, CCYV, and CVYV are transmitted mainly by *Bemisia tabaci*, while BPYV is transmitted primarily by *Trialeurodes vaporariorum*. CYSDV, CCYV, and BPYV typically cause interveinal yellowing on older leaves and yield loss, whereas CVYV is associated with vein yellowing, mosaic, and reduced fruit quality (Lecoq and Desbiez, 2012; Desbiez, 2020). Because these symptoms overlap with one another and with nutritional disorders, visual diagnosis is not sufficient and should be supported by virus-specific serological or molecular tests. In semipersistent transmission, whiteflies retain the virus longer than in non-persistent transmission. Management should therefore

emphasize whitefly exclusion in transplant production, the use of healthy whitefly-free transplants, weed control, and suppression of vector populations early in crop development (Ng and Falk, 2006; Lecoq and Desbiez, 2012).

2.10. Other important aphid-borne potyviruses

PRSV-W and MWMV are potyviruses that can cause mosaic, leaf deformation, stunting, and fruit disorders in cucurbits. Both are transmitted non-persistently by aphids, and their symptoms can overlap with those caused by ZYMV and WMV. Serological or molecular confirmation is therefore required. Management should combine reduction of infected crop and weed sources, limitation of early vector entry, reflective surfaces, and validated sources of resistance (Lecoq and Desbiez, 2012; De Moya-Ruiz et al., 2023).

2.11. Selected studies on cucurbit viruses in Türkiye

Studies from Türkiye span different years, hosts, and sampling strategies, so reported frequencies should not be extrapolated directly to the country as a whole. Selected studies are summarized in Table 2. These studies were selected to illustrate geographic, epidemiological, and viral diversity rather than to provide a systematic estimate of national virus prevalence. Molecular subgroups in ZYMV and WMV, contrasting phylogenetic patterns in CABYV, and regional records of MNSV and ToLCNDV all support the use of current local isolates in diagnostic panels and resistance testing (Topkaya et al., 2019; Topkaya and Desbiez, 2020; Fidan et al., 2023; Morca et al., 2025). Surveys in Kırşehir and Eskişehir have also highlighted the importance of mixed infections and regional differences in virus composition (Karabıyık and Yeşil, 2021; Çandar et al., 2026).

Table 2. Selected studies of cucurbit viruses in Türkiye and the epidemiological information they provide

Region / study	Material and methods	Main finding	Interpretation
Adana-Pozantı, Koç et al. (2014)	Forty-nine leaf samples from summer squash in 2013; DAS-ELISA and MNSV-specific RT-PCR	Three samples were MNSV-positive by DAS-ELISA and were confirmed by specific RT-PCR.	Documents MNSV in squash in Türkiye and supports its inclusion in regional diagnostic panels.
Ankara-Antalya, Topkaya et al. (2019)	221 samples collected between 2009 and 2014; DAS-ELISA for six viruses; CP-gene sequencing of 45 ZYMV isolates	Most Turkish ZYMV isolates belonged to subgroup A1, while three Antalya isolates belonged to A4.	Diagnostic primers and resistance tests should account for local isolate diversity.

Region / study	Material and methods	Main finding	Interpretation
Antalya, Ankara, Burdur, Tokat, and historical collections, Topkaya and Desbiez (2020)	Symptomatic cucurbit samples; RT-PCR and CP-gene sequencing of 15 CABYV isolates	Turkish samples showed phylogenetic affinities with Mediterranean/European-African and Asian groups.	CABYV should not be treated as a single uniform local population.
Eskişehir, Karabıyık and Yeşil (2021)	164 plant samples collected in 2019; DAS-ELISA for seven viruses	CABYV, WMV, ZYMV, CMV, PRSV-W, and SqMV were detected among symptomatic samples.	Reported frequencies should be interpreted in the context of symptom-based sampling and a single growing season.
Antalya, Fidan et al. (2023)	PCR and sequencing from eight adjacent greenhouses in 2019, followed by surveys in 2020-2021	ToLCNDV was reported for the first time and was not redetected in approximately 84 subsequent suspect samples.	A limited outbreak record that illustrates the value of early detection, destruction, and sanitation.
Western Black Sea-Central Anatolia, Morca et al. (2025)	Complete CP-gene sequences of 19 WMV isolates from four cucurbit species	Eight isolates belonged to the emerging group and 11 to the classic group. A small additional phylogroup was also reported.	Breeding and diagnostic validation based on a single WMV isolate may be inadequate.
Kırşehir, Çandar et al. (2026)	149 samples showing virus-like symptoms in 2023; DAS-ELISA for five viruses	CMV, Tomato spotted wilt virus (TSWV), and Tomato mosaic virus (ToMV) were prominent, and mixed infections were frequent.	Shows that regional virus composition is not limited to the classical cucurbit viruses.

Taken together, the available data indicate that a fixed, narrow testing panel is unlikely to be sufficient across Türkiye. Molecular subgroups of ZYMV and WMV, distinct phylogenetic patterns in CABYV, detection of MNSV in different cucurbit hosts and regions, the limited but quarantine-relevant record of ToLCNDV, and the prominence of viruses not usually regarded as core cucurbit pathogens in Kırşehir all argue for survey designs that are updated according to host, vector, production system, and current regional findings. Multi-year surveys that include asymptomatic as well as symptomatic plants would provide more comparable data at the national scale.

3. Virus-host-vector relationships

Epidemics of cucurbit viruses arise from interactions among primary inoculum, vector behaviour, infection timing, the spatial distribution of hosts, and environmental conditions. Non-persistent, semipersistent, persistent-circulative, mechanical or seed-associated, and soil-borne vector-assisted transmission each require different management strategies (Ng and Falk, 2006; Whitfield et al.,

2015; Campbell et al., 1996). In ZYMV, WMV, and CMV, aphids can transmit virus during brief stylet penetration, so killing the vector with an insecticide does not necessarily prevent the first inoculation event. Reflective mulches, mineral oil applications, planting-date adjustment, and reduction of early inoculum sources are therefore important.

Transmission mode directly affects the timing and emphasis of vector management. With non-persistently transmitted viruses, an aphid can acquire the virus during a brief plant contact and transmit it soon afterwards without the virus entering the vector's circulatory system. In semipersistent transmission, the virus is retained longer in the mouthparts and foregut. In persistent-circulative transmission, the virus passes from the digestive tract through the haemocoel to the salivary glands, allowing the vector to remain infective for a longer period (Ng and Falk, 2006; Whitfield et al., 2015). Management should therefore focus on reducing initial contacts for non-persistent viruses and on suppressing vector populations and viruliferous vector entry for persistent-circulative viruses.

For CABYV and ToLCNDV, the persistent-circulative relationship makes reduction of vector populations and viruliferous vector entry more directly relevant to disease suppression. In CGMMV, mechanical contact and production equipment are central, whereas seed and leaf beetles are important for SqMV, and seed transmission together with *Olpidium bornovanus*-associated root infection is important for MNSV. Contact points along the production chain, shared irrigation or drainage systems, and contact between suspect and healthy lots should therefore be incorporated into the management plan.

Virus infection can alter vector behaviour in some pathosystems. CMV-infected plants, for example, may attract aphids while becoming less suitable for prolonged feeding (Mauck et al., 2010). In melon, the *Vat* locus confers resistance to *Aphis gossypii* colonization and to virus inoculation mediated by this aphid, but it does not provide broad virus resistance after mechanical inoculation (Dogimont et al., 2014; Boissot et al., 2016). Because mixed infections can alter symptom severity and virus accumulation, candidate resistant material should be challenged first with standardized isolates and then with representative regional isolates and, where relevant, common mixed infections.

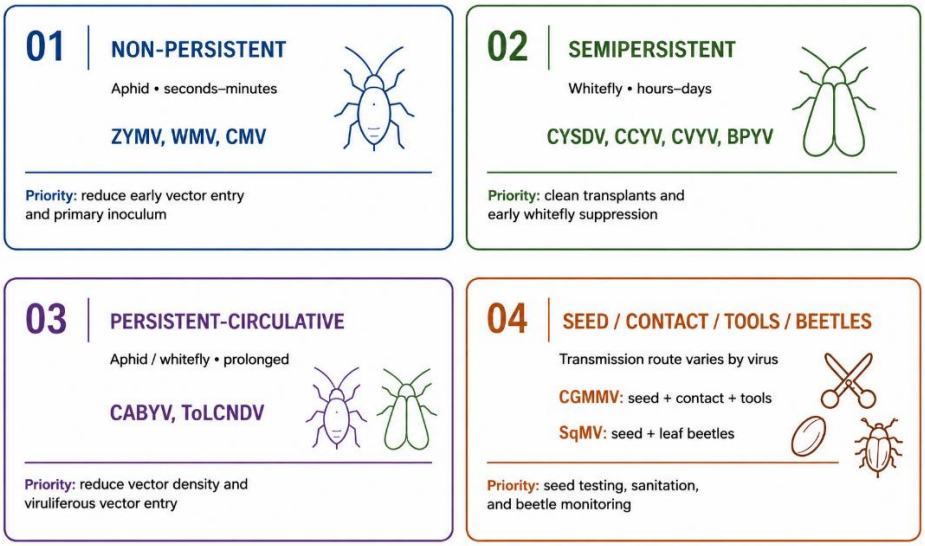


Figure 1. Selected major transmission and spread pathways of cucurbit viruses and corresponding management priorities. Representative viruses and vectors are indicated for each transmission category. MNSV represents an additional seed-associated and root-zone transmission pathway involving *Olpidium bornovanus*.

4. Virus diagnosis, sampling, and molecular confirmation

The diagnostic method should be chosen according to the purpose of the investigation. Field surveys, detection of low prevalence in a seed lot, comparison of viral load in breeding material, and discovery of an unknown agent do not require the same analytical approach. Method selection should consider sample type, target prevalence, analytical sensitivity and specificity, and the consequences of false results for plant-health decisions (Boonham et al., 2014).

Table 3. Main diagnostic methods for cucurbit viruses, their applications, and limitations

Method	Primary target	Strength	Main limitation	Appropriate use
Symptoms and field records	Plant phenotype	Rapid, inexpensive, and provides epidemiological context	Low specificity; latent infection and environmental effects	Sampling, disease-severity scoring, and tolerance assessment
DAS-ELISA	Viral protein	Low per-sample cost for large sample sets	Dependent on antibody quality and virus titre; possible cross-reaction	Surveys of known viruses and preliminary screening in breeding programme
RT-PCR / PCR	Target RNA or DNA region	High specificity; amplicons can be sequenced	Primer mismatch and contamination; usually qualitative presence/absence output	Pathogen confirmation and isolate characterization

Method	Primary target	Strength	Main limitation	Appropriate use
RT-qPCR / qPCR	Target nucleic acid and quantity	High sensitivity and broad dynamic range	Requires standardization and normalization; does not demonstrate infectivity on its own	Low-titre infections, seed health, and viral-load comparisons
LAMP	Multi-region target amplification	Rapid at constant temperature and suitable for on-site use	Primer design, product contamination, and visual interpretation	Rapid preliminary screening where infrastructure is limited
Reverse-transcription droplet digital PCR / droplet digital PCR (RT-ddPCR / ddPCR)	Absolute nucleic-acid copy number	Low-copy quantification without a standard curve	Cost, instrumentation, droplet quality, and threshold optimization	Reference material and confirmation of low-titre samples
HTS	Total viral sequences / virome	Target-independent discovery and detection of mixed infections	Cost, bioinformatics, biological interpretation, and need for targeted confirmation	Novel or divergent viruses and unexplained disease syndromes

References: Boonham et al. (2014), Villamor et al. (2019), Massart et al. (2022), and Huggett et al. (2013).

Symptom recording is rapid and inexpensive, but its specificity is limited. Latent infection, environmental conditions, and similar physiological disorders can lead to misinterpretation. DAS-ELISA is well suited to routine screening of large sample numbers, although its performance depends on antibody quality and virus titre (Clark and Adams, 1977). RT-PCR or PCR provides high specificity for pathogen confirmation and allows amplicons to be sequenced, but sequence variation at primer-binding sites can produce false-negative results in genetically diverse virus populations.

RT-qPCR and qPCR are useful for detecting low-titre infections and comparing viral loads. Quantitative interpretation should account for extraction efficiency, inhibitors, amplification efficiency, standard curves, and normalization. Reporting of quantitative PCR assays should also follow MIQE principles, including adequate description of primers, amplification efficiency, controls, normalization procedures, and assay performance (Bustin et al., 2009). Detection of viral nucleic acid does not by itself demonstrate the presence of infectious virions. In CGMMV, PMA pretreatment can improve this distinction indirectly (Torre et al., 2020; Chai et al., 2022). RT-ddPCR and ddPCR allow low copy numbers to be quantified without a standard curve, but threshold setting, controls, and limits of quantification should be reported explicitly (Huggett et al., 2013).

LAMP and RT-LAMP provide rapid amplification at a constant temperature and are useful for on-site testing, although primer design and amplicon contamination remain important limitations (Notomi et al., 2000; Li et al., 2013). HTS can detect novel or divergent viruses and mixed infections without a predefined target, but bioinformatic interpretation and target-specific confirmation remain necessary (Adams et al., 2009; Villamor et al., 2019; Massart et al., 2022). Sampling error is an important source of uncertainty regardless of the analytical method. Vascular tissue should be prioritized for phloem-limited viruses, young leaves for newly established systemic infections, and an appropriate pooling strategy should be used for seed lots.

Diagnosis of cucurbit viruses is best approached in stages. First, observed symptoms, production conditions, and crop history should be used to define an appropriate sampling strategy. Viruses expected in the region or host can then be tested with specific ELISA, PCR, or RT-PCR assays. When laboratory results do not match the symptoms or epidemiological context, or when the cause remains unexplained, broader molecular methods or high-throughput sequencing can be used. Reports should specify the genomic target, sample type, positive and negative controls, and whether the method demonstrates only the presence of viral nucleic acid or can also provide information relevant to infectivity.

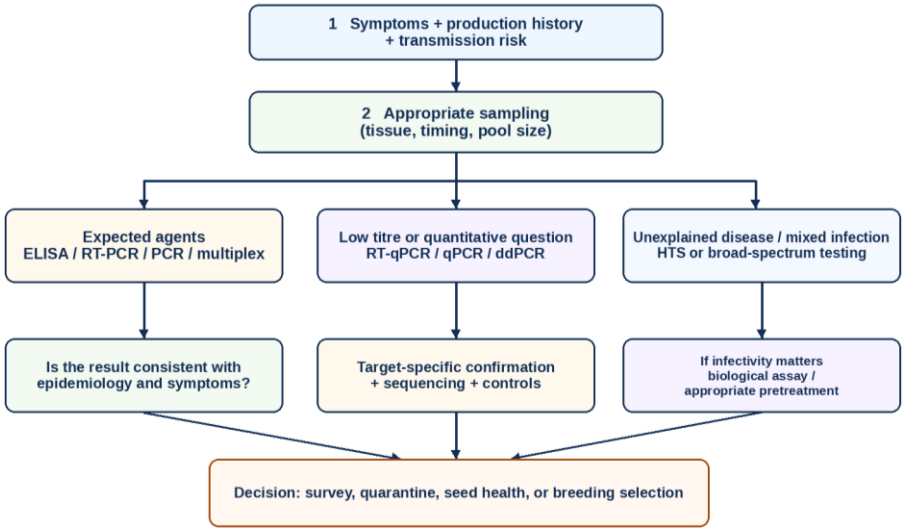


Figure 2. Stepwise diagnostic workflow for cucurbit viruses, from sampling to confirmation.

5. Virus resistance in cucurbit genetic resources

Resistance screening should include commercial cultivars, landraces, older commercial material, breeding lines, wild relatives, and germplasm maintained in gene banks. Resistance information recorded in passport data should not be treated as sufficient on its own. Within-accession heterogeneity, mixing during seed regeneration, differences among virus isolates, and variation in earlier

phenotyping protocols can all alter the observed response, so resistance should be reconfirmed before a material is used as a donor (Martín-Hernández and Picó, 2021).

Initial screening of large germplasm collections should be conducted under sufficient infection pressure and include susceptible controls. Genotypes selected as resistant should then be retested with larger plant numbers, in independent experiments, and against different virus isolates. Symptom severity should be interpreted together with virus detection and, where possible, viral titre so that plants remaining uninfected because inoculation failed are not misclassified as resistant. The breeding value of a genotype should be judged from the inheritance of resistance, the range of isolates controlled, agronomic performance, fruit quality, and the feasibility of transferring the resistance into commercial material.

Representative sources include cucumber TMG-1, melon PI 414723, and watermelon PI 595203 for ZYMV; PI 124112 and TGR-1551 for CABYV; lines carrying *nsv*/*eIF4E* for MNSV; and resistant *Cucurbita moschata*, melon, and cucumber materials for ToLCNDV (Park et al., 2004; Guner et al., 2018; Dogimont et al., 1997; Kassem et al., 2015; Nieto et al., 2006; Sáez et al., 2016; Sáez et al., 2021). Passport information, seed lot, selfing generation, virus isolate, and inoculation protocol should be recorded for donor material. Linkage drag and undesirable agronomic traits should be monitored during introgression. Backcrossing, marker-assisted background selection, and gene pyramiding can be used to move resistance into a commercial genetic background.

6. Resistance genes and QTLs

Virus resistance can be conferred by dominant NLR genes, recessive alleles of host factors required by the virus, or quantitative QTLs that partially reduce virus accumulation or disease severity (Kang et al., 2005; Nicaise, 2014). A functionally validated gene, a strong candidate gene, and a linked QTL do not represent the same level of evidence. Table 4A summarizes major-effect resistance genes, candidate genes, and loci supported by strong genetic or functional evidence, whereas Table 4B lists regions associated with partial resistance, vector-related resistance, and candidates requiring further validation.

Table 4A. Major-effect virus-resistance genes, candidate genes, and loci with strong genetic or functional support in cucurbits

Host	Virus	Source	Gene / QTL and inheritance	Breeding note
Cucumber	ZYMV	A192-18	*zym, Chr. 6; VPS4-like strong candidate; recessive*	The dCAPS assay should be validated for source and haplotype (Amano et al., 2013; Ramírez-Madera and Havey, 2017).
Cucumber	WMV	02245	*wmv02245, Chr. 6; single recessive major-effect locus*	Linked marker transferability requires validation across breeding pools, and the locus should be tested against different WMV isolates (Tian et al., 2016).
Melon	ZYMV	PI 414723	*Zym-1 plus additional loci; dominant/oligogenic*	Because resistance is isolate-dependent, results from a single isolate should not be generalized (Pitrat and Lecoq, 1984; Adler-Berke et al., 2021).
Watermelon	ZYMV	PI 595203	*zym-FL, recessive*	Should be monitored independently of WMV resistance (Guner et al., 2018; Xu et al., 2004).
Melon	WMV	Defined TGR-1551 research material	*wmv1551 / CmVPS4, P30R, recessive*	P30R was absent from another TGR-1551 material. Donor identity should be confirmed molecularly (Pérez-de-Castro et al., 2019; Agaoua et al., 2022; López-Martín et al., 2024).
Cucumber	CMV	02245	*cmv6.1, Chr. 6; quantitative, major effect*	Does not confer immunity on its own. Environmental and genetic-background validation is required (Shi et al., 2018).
Melon	CMV	PI 161375	*cmv1 / CmVPS41 plus additional QTLs; recessive*	Local multiplication and systemic movement should be assessed separately (Guiu-Aragonés et al., 2014; Giner et al., 2017; Pascual et al., 2019).
Melon	MNSV	PI 161375, 'Gulfstream', and other *nsv*-carrying lines	*nsv / eIF4E, recessive*	Effective against many isolates, but the material should also be tested against resistance-breaking isolates (Nieto et al., 2006; Díaz et al., 2004).
Melon	CABYV	PI 124112	*cab-1 and cab-2; two complementary recessive genes*	Both loci must be present in the same plant (Dogimont et al., 1997).

Host	Virus	Source	Gene / QTL and inheritance	Breeding note
Melon	CABYV	TGR-1551	Dominant major gene plus modifiers	Can be combined with the PI 124112 resistance genes to strengthen resistance within the same genotype (Kassem et al., 2015).
Cucumber	ToLCNDV	No. 44	*Cy-1/CsRDR3*, Chr. 1, dominant major-effect locus; *cy-2*, Chr. 2, recessive major-effect QTL	CsRDR3 is functionally supported by VIGS and a codominant marker is available. The causal polymorphism remains unresolved, and the gene underlying cy-2 remains to be identified (Koeda et al., 2024).

Table 4B. Partial-resistance regions, vector-related resistance, and candidate loci requiring further validation in cucurbits

Host	Virus / trait	Source	Gene / QTL and evidence	Breeding note
Melon	Aphid-transmitted viruses	*Vat lines*	*Vat, CC-NBS-LRR; resistance to Aphis gossypii*	Not a general form of virus resistance after mechanical inoculation. Aphid clone matters (Dogimont et al., 2014; Boissot et al., 2016).
Cucumber	CGMMV	Diverse germplasm	Quantitative regions on Chr. 5 and 2; partial resistance	Symptoms, titre, systemic movement, and fruit quality should be assessed together (Crespo et al., 2018; Monnot et al., 2022).
Melon	CGMMV	'Chang Bougi'	*cgmmv-1* and *cgmmv-2*; two complementary recessive genes against isolate CGMMV-SH	Because resistance varies with isolate and environment, it should be reconfirmed using different CGMMV isolates (Sugiyama et al., 2006; Sugiyama et al., 2007; Ruiz et al., 2021).
Cucurbita moschata	ToLCNDV	Nigerian germplasm	Major recessive QTL on Chr. 8	*A valuable donor for Cucurbita breeding (Sáez et al., 2016; Sáez et al., 2020).*
Melon	ToLCNDV	WM-7	Major QTL on Chr. 11 with modifiers on Chr. 2 and 12	The model should not be transferred directly to PI 414723 (Sáez et al., 2017).
Melon	ToLCNDV	PI 414723	Overlapping QTLs on Chr. 11 with support from Chr. 2	Donor identity, isolate, and genetic background should be verified (Pérez-Moro et al., 2024).
Melon	WMV	P30R-negative TGR-1551-derived RIL	*MELO3C021395/MED33A; transcriptome- and variant-based candidate*	Functional validation is required. CmVPS4 has not been completely excluded (López-Martín et al., 2024).

6.1. Resistance to ZYMV

In cucumber, the recessive *zym* region derived from A192-18 has been narrowed on chromosome 6, and a VPS4-like gene is a strong candidate. Validation of the dCAPS marker across relevant haplotypes is necessary before routine breeding use (Amano et al., 2013; Ramírez-Madera and Havey, 2017). In the panel studied by Coşkun et al. (2024), the CAP marker alone explained approximately 42-44% of phenotypic variation, while a model combining significant markers explained a larger proportion. Because no independent validation population was available, these results should not be interpreted as direct predictive accuracy. ZYMV resistance in sources such as melon PI 414723 and watermelon PI 595203 follows different genetic models, and a single universal resistance allele should not be assumed across cucurbit species (Pitrat and Lecoq, 1984; Guner et al., 2018; Shrestha et al., 2021).

6.2. Resistance to WMV

In cucumber, WMV resistance in line 02245 has been associated with the recessive major-effect locus *wmv02245* on chromosome 6 (Tian et al., 2016). In melon, TGR-1551-derived resistance was mapped to linkage group XI/chromosome 11, and the *wmv1551* region was fine-mapped. A functional effect of the CmVPS4-P30R substitution was demonstrated in one TGR-1551-derived material (Palomares-Rius et al., 2011; Pérez-de-Castro et al., 2019; Agaoua et al., 2022). P30R was absent from another TGR-1551-derived material, in which MELO3C021395/MED33A was proposed as an alternative candidate. Thus, the same material name does not guarantee that the same resistance allele is present (López-Martín et al., 2024).

6.3. Resistance to CMV

In cucumber, *cmv6.1* on chromosome 6 is a quantitative and environmentally responsive component of CMV resistance (Shi et al., 2018). In melon PI 161375, *cmv1* acts together with additional QTLs. *cmv1* has been linked to natural variation in CmVPS41 and restricts CMV movement across the bundle sheath-phloem boundary into systemic tissues (Guiu-Aragonés et al., 2014; Giner et al., 2017; Pascual et al., 2019). This mechanism makes separate sampling of inoculated and systemic leaves important for accurate phenotyping.

6.4. CABYV and vector-related resistance

In melon, CABYV resistance is controlled by two complementary recessive genes, *cab-1* and *cab-2*, in PI 124112, whereas TGR-1551 carries a dominant major gene with modifier loci (Dogimont et al., 1997; Kassem et al., 2015). *Vat* represents a different mechanism. It confers resistance to *Aphis gossypii* colonization and to virus inoculation mediated by this vector, but it does not provide broad virus resistance after mechanical inoculation (Dogimont et al.,

2014; Boissot et al., 2016). Plant-intrinsic virus resistance and vector-related resistance therefore represent distinct phenotypes.

6.5. Resistance to CGMMV

Broad-spectrum complete resistance to CGMMV remains uncommon. Quantitative resistance regions have been reported on chromosomes 5 and 2 in cucumber germplasm, while two complementary recessive genes, *cgmmv-1* and *cgmmv-2*, have been described in melon 'Chang Bougi' (Crespo et al., 2018; Monnot et al., 2022; Sugiyama et al., 2006; Sugiyama et al., 2007). Because isolate and environmental effects can be substantial, phenotyping should not rely only on early foliar symptoms. A robust phenotyping scheme should integrate virus accumulation, systemic spread, plant growth, and, where possible, fruit quality (Ruiz et al., 2021).

6.6. Resistance to ToLCNDV

Resistance to ToLCNDV maps to different chromosomal regions in different cucurbit species. A major recessive QTL has been reported on chromosome 8 in *Cucurbita moschata*. In melon WM-7, a major QTL occurs on chromosome 11 with modifiers on chromosomes 2 and 12, while PI 414723 carries overlapping QTLs on chromosome 11 with additional support from chromosome 2 (Sáez et al., 2017; Sáez et al., 2020; Pérez-Moro et al., 2024). In cucumber, Sáez et al. (2021) identified highly resistant Indian accessions and mapped the predominantly recessive resistance of CGN23089 to a QTL on chromosome 2. A distinct resistance source, accession No. 44, was characterized by Koeda et al. (2024), who identified the major QTL Cy-1 on chromosome 1 and the recessive major QTL cy-2 on chromosome 2. Cy-1 acts dominantly and was fine-mapped to a 209-kb region containing CsRDR3. VIGS of CsRDR3 compromised resistance, providing functional evidence that this gene underlies Cy-1, although the specific causal polymorphism remains unresolved.

More recently, the cucumber accession ABS.PE.045 was identified as highly resistant to the aggressive cucumber isolate ToLCNDV-CsES. Bulk-segregant analysis combined with RNA-seq identified resistance-associated intervals on chromosomes 1, 2, 6, and 7. CsRDR3 and CsHSFA2 were supported as candidates within the chromosome 1 and 2 regions, respectively, while CsaV3_7G022160 was proposed as a candidate for the newly identified chromosome 7 QTL (Donaire et al., 2026).

6.7. Resistance to MNSV

In melon, the recessive *nsv* locus has been functionally identified as an *eIF4E* allele (Nieto et al., 2006). This form of resistance is based on natural variation in a host factor used by the virus. However, isolates such as MNSV-264 can overcome *nsv* resistance (Díaz et al., 2004). Donor material and markers should therefore be validated together with phenotyping against isolates that represent

geographic and genetic diversity, including assessment of symptoms, root infection, and virus accumulation.

7. Marker-assisted selection and genomic breeding approaches

The value of a marker in marker-assisted selection depends on its genetic proximity to the resistance gene or region and on its ability to classify genotypes correctly across different genetic backgrounds. SNPs or indels shown to be directly responsible for resistance are among the most reliable markers for identifying the target allele. When the underlying genetic change is not known, markers closely linked to the target gene or locus reduce the risk of misclassification caused by recombination. More distant RAPD, AFLP, or SSR markers may show a strong association in the discovery population but should be revalidated in other germplasm before routine use (Collard and Mackill, 2008). Results from the ZYMV-cucumber dCAPS/CAP system illustrate this need for transferability testing (Amano et al., 2013; Ramírez-Madera and Havey, 2017; Coşkun et al., 2024).

KASP, HRM, and targeted amplicon assays are suitable for high-throughput genotyping of variants that directly determine resistance or lie very close to the target gene. Fine-mapping of the *Cy-1* region with KASP and HRM markers and development of a codominant assay based on an indel in the CsRDR3 promoter provide one example (Koeda et al., 2024). GWAS can exploit recombination accumulated across genetically diverse individuals to refine resistance-associated genomic regions. Population structure, relatedness, allele frequency, and correction for multiple testing must nevertheless be handled appropriately (Monnot et al., 2022).

Genomic selection can be useful for quantitative traits influenced by many loci, but reliable prediction requires a sufficiently large reference set that represents the target breeding material and has both genotypic and phenotypic data (Crossa et al., 2017). In GWAS conducted under natural epidemic conditions, virus presence and titre, vector density, and plant developmental stage should be recorded together. This helps distinguish true genetic resistance from plants that remain healthy simply because they were not exposed to infection (Monnot et al., 2025). When several resistance genes or loci are combined in one genotype, the aim should not be to maximize gene number alone, but to combine mechanisms that interfere with different stages of infection. Such combinations should be phenotypically validated for interactions among genes, possible effects on plant growth and yield, and the breadth of resistance across virus isolates.

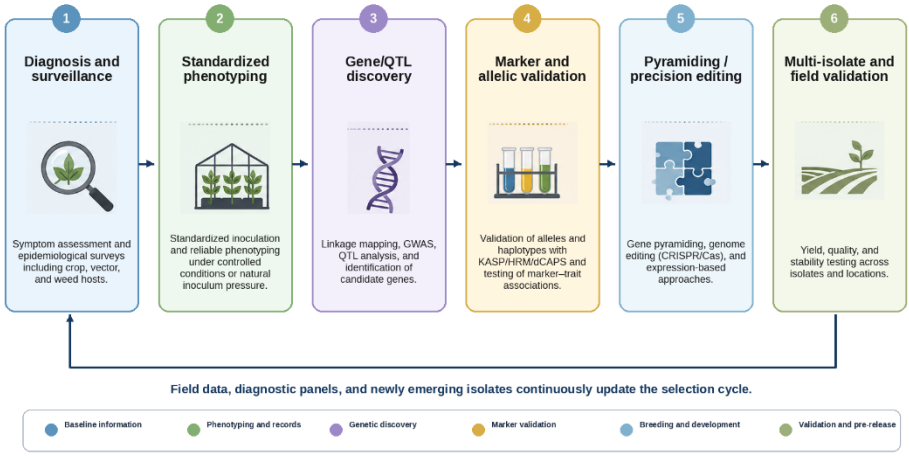


Figure 3. Evidence-based development and validation cycle for breeding virus resistance in cucurbits.

8. Host defence mechanisms and transcriptomic responses to virus infection

Plant antiviral defence is a multilayered system involving pattern recognition, hormone signalling, reactive oxygen species, regulation of cell walls and plasmodesmata, RNA silencing, protein turnover, and NLR-mediated recognition (Jones and Dangl, 2006; Mandadi and Scholthof, 2013). Viral double-stranded RNA intermediates are processed into small RNAs by Dicer-like proteins, and ARGONAUTE proteins use these small RNAs to guide the recognition of viral RNA. Viral suppressors of RNA silencing can interfere with several steps in this pathway (Ding and Voinnet, 2007; Pumplin and Voinnet, 2013).

Studies of CGMMV have linked resistance with miRNA profiles, salicylic-acid signalling, flavonoid metabolism, and the functions of AGO1 and AGO5 (Liu et al., 2015; Liu et al., 2023a; Liu et al., 2023b). In WMV-resistant melon, early transcriptomic responses have highlighted genes involved in defence, vesicle trafficking, hormone signalling, and RNA metabolism (González-Ibeas et al., 2012; López-Martín et al., 2024). RNA-seq studies of ToLCNDV resistance have likewise identified candidates associated with RNA silencing, DNA methylation, and the cell cycle (Sáez et al., 2022).

The recurring identification of CmVPS41, CmVPS4, and the VPS4-like candidate in the *zym* region across different cucurbit-virus systems suggests that intracellular vesicle trafficking is an important component of virus infection and resistance (Amano et al., 2013; Giner et al., 2017; Agaoua et al., 2022). However, a change in gene expression after infection does not by itself show that the gene

determines resistance. Resistant and susceptible genotypes should be compared within the same experimental design, mock-inoculated controls should be included, and sampling times should represent different stages of infection. Viral titre and gene expression should be measured within the same sampling framework. Strong evidence for a candidate gene requires transcriptomic data to be supported by genetic mapping and functional approaches such as VIGS, CRISPR, overexpression, or complementation, followed by confirmation in independent experiments.

9. CRISPR/Cas and RNA-based approaches to virus resistance

New resistance strategies either target the viral genome directly or modify host factors required for infection. CRISPR/Cas9 editing of *eIF4E* in cucumber generated resistance to several potyviruses in subsequent generations that no longer carried the transgene (Chandrasekaran et al., 2016). In melon, *eIF4E* editing was accompanied by male sterility, illustrating the pleiotropic consequences that can follow complete loss of gene function (Pechar et al., 2022). Precise edits that mimic naturally resistant alleles may therefore offer better control than complete knockout approaches.

Cas9 targeting of geminivirus DNA has reduced viral DNA accumulation in model systems, but direct field validation in cucurbit-ToLCNDV systems remains limited (Ali et al., 2015; Ali et al., 2016). Cas13a and Cas13d can target RNA viruses and have shown antiviral activity in model plants (Aman et al., 2018; Mahas et al., 2019). For both approaches, target-sequence diversity, viral changes within the target region, off-target effects, and genetic background are important considerations during validation.

In non-transgenic RNAi approaches, dsRNA can be applied directly to plants. Rapid degradation under field conditions limits persistence, although clay nanosheet carriers have extended the duration of protection and exogenous dsRNA has reduced aphid-mediated virus transmission in experimental systems (Mitter et al., 2017; Worrall et al., 2019). Application rate, conservation of the target sequence among isolates, carrier cost, effects on non-target organisms, and regulatory requirements all need to be considered for field use. Development should proceed from molecular efficacy to testing across diverse isolates and genetic backgrounds, followed by evaluation of yield, quality, and performance under natural epidemic conditions.

Table 5. Evidence level and major development risks of next-generation resistance approaches

Approach	Target	Current evidence	Advantage	Development risk / required validation
Loss of function in a host gene	*A host factor used by the virus, such as eIF4E*	Broad *potyvirus* resistance in cucumber; male sterility reported in melon	Transgene-free plants can be selected in subsequent generations; potential for broad-spectrum resistance	Pleiotropy, isoform compensation, yield, and reproductive performance
Precise allelic editing	Interaction surface defined by a natural resistance allele	Natural VPS and *eIF4E* variants provide design templates, but direct editing evidence remains limited	Greater chance of preserving essential host-gene function	Resistance-associated amino-acid change and performance across genetic backgrounds must be validated
Cas9 targeting of viral DNA	Genomes of DNA viruses such as ToLCNDV	Reduced viral DNA in model plant-geminivirus systems; no direct field evidence in cucurbits	Directly targets the viral sequence	Viral change within the target sequence, multiplex targeting, off-target effects, and continuous Cas expression
Cas13 targeting of viral RNA	RNA viruses such as ZYMV, WMV, and CGMMV	Suppression of RNA viruses in model plants; no direct field evidence for these cucurbit viruses	Targets viral RNA without introducing double-strand breaks into the host DNA genome	Guide compatibility, isolate diversity, tissue expression, and field validation
Exogenous dsRNA / carrier	Conserved viral RNA sequences	Extended protection with clay carriers and reduced aphid-mediated transmission in model systems	No genome modification required and can be redesigned	UV and rain stability, dose, cost, non-target assessment, and regulation

References: Chandrasekaran et al. (2016), Ali et al. (2015, 2016), Aman et al. (2018), Mahas et al. (2019), Mitter et al. (2017), Worrall et al. (2019), and Pechar et al. (2022).

10. Integrated management and future perspectives

Integrated management of cucurbit viruses requires clean planting material, reliable diagnosis, sanitation, vector management, and genetic resistance to be used together rather than as isolated measures. The relative importance of each component depends on the virus's transmission biology. An effective programme should therefore begin with accurate identification of the target virus, recognition

of likely inoculum sources within and around the production area, and assessment of the main routes by which the virus can spread.

Surveillance and diagnosis form the basis of this process. Sampling only symptomatic plants can miss asymptomatic infections, so both symptomatic and asymptomatic material should be included when the objective is to describe virus occurrence. Viruses expected in the region can be screened with specific ELISA, PCR, or RT-PCR assays. When laboratory results do not explain the observed disease, high-throughput sequencing can be used to investigate a broader range of agents (Villamor et al., 2019; Massart et al., 2022). Sampling time, tissue type, and the analytical characteristics of the method should be considered when diagnostic results are translated into production decisions.

Management priorities should be matched to transmission biology. For non-persistently aphid-transmitted viruses such as ZYMV, WMV, and CMV, management should emphasize reduction of primary inoculum and early vector contact rather than reliance on insecticides alone. Persistent-circulative viruses such as CABYV and ToLCNDV require greater emphasis on healthy transplants, vector exclusion, and suppression of viruliferous vector populations. By contrast, CGMMV and MNSV require rigorous attention to seed health and production-system hygiene, with sanitation being particularly important for CGMMV and root-zone, substrate, and irrigation-water management for MNSV (Ng and Falk, 2006; Lecoq and Desbiez, 2012; Dombrovsky et al., 2017; Moriones et al., 2017; Campbell et al., 1996).

Genetic resistance is an important component of integrated management. Combining resistance genes in the same genotype may provide greater durability, particularly when the genes interfere with different stages of infection. Marker confirmation alone is not sufficient, however. Virus isolate, inoculation method, plant age, sampling time, symptom severity, and virus accumulation should be evaluated together. Clear reporting of these factors also makes resistance results more comparable across studies.

Genome editing, genomic prediction, and RNA-based applications offer additional routes for developing virus resistance, but their value still depends on reliable phenotyping. Effects should be validated across virus isolates and genetic backgrounds and assessed for plant growth, yield, and fruit quality (Pechar et al., 2022; Coşkun et al., 2024). Climate-driven changes in vector development and movement, the length of production seasons, and continuity of susceptible hosts should also be considered in future risk assessments (Trebicki, 2020).

Table 6. Comparison of management priorities across major cucurbit virus groups

Virus / group	Primary inoculum	Main spread	Priority measures	Common mistake
ZYMV, WMV, CMV, PRSV-W, MWMV	Infected crops and weeds	Aphids, non-persistent	Early inoculum-source management, reflective mulch/mineral oils, resistant cultivars, current diagnostics	Assuming insecticides alone will stop primary infection
CABYV	Infected cucurbits and weeds	Aphids, persistent-circulative	Healthy transplants, reduced vector density and viruliferous vector entry, diagnosis from vascular tissue	Attributing yellowing only to nutrient deficiency
CYSDV, CCYV, CVYV	Infected transplants, crop plants, and weeds	*Bemisia tabaci, semipersistent*	Healthy whitefly-free transplants, exclusion barriers, early whitefly suppression, specific testing	Treating similar yellowing symptoms as evidence of a single pathogen
BPYV	Infected greenhouse plants and weeds	*Trialeurodes vaporariorum, semipersistent*	Greenhouse whitefly management, healthy transplants, molecular confirmation from phloem-rich tissue	*Assuming transmission by Bemisia tabaci*
ToLCNDV	Infected transplants and host plants	*Bemisia tabaci, persistent-circulative*	Protect the seedling stage, early removal of infected plants, weed management, resistance and isolate validation	Treating whitefly suppression as sufficient on its own
CGMMV	Contaminated seed, transplants, residues, surfaces, and solution	Contact, tools, grafting, water/solution	Seed-lot testing, clean mother plants, removal of organic debris, validated disinfection, compartmentalization	Treating PCR negativity or surface disinfection as an absolute guarantee
MNSV	Contaminated seed, infected root residues, substrate, and water	Seed-associated transmission and *Olpidium bornovanus*-mediated soil/root spread	Tested seed, clean substrate, irrigation-water hygiene, resistant cultivars, and multi-isolate validation	Relying only on leaf samples or insect-vector control
SqMV	Contaminated seed and infected plants	Seed and leaf beetles	Mother-plant and seed-lot testing, volunteer-plant management, beetle monitoring, laboratory confirmation	Focusing only on aphid control

References: ZYMV/WMV/CMV/PRSV-W/MWMV, Lecoq and Desbiez (2012) and De Moya-Ruiz et al. (2023); CABYV, Lecoq et al. (1992); CYSDV/CCYV/CVYV/BPYV, Lecoq and Desbiez (2012) and Ng and Falk (2006); ToLCNDV, Moriones et al. (2017);

CGMMV, Dombrovsky et al. (2017); MNSV, Campbell et al. (1996); SqMV, Martín-Hernández and Picó (2021).

11. Conclusion

Sustainable management of cucurbit viruses depends on combining accurate sampling and diagnosis, a clean seed and transplant chain, transmission-specific vector management, effective sanitation, and validated genetic resistance. Genome editing and RNA-based strategies can complement this framework, but before agricultural deployment their performance should be tested across virus isolates and evaluated for agronomic performance and effectiveness under natural field conditions.

References

Adams, I.P., Glover, R.H., Monger, W.A. et al. (2009). Next-generation sequencing and metagenomic analysis: a universal diagnostic tool in plant virology. Molecular Plant Pathology, 10, 537–545.

Adler-Berke, N., Goldenberg, Y., Brotman, Y. et al. (2021). The melon Zym locus conferring resistance to ZYMV: high-resolution mapping and candidate gene identification. Agronomy, 11, 2427.

Agaoua, A., Guiu-Aragonés, C., Fernández-Muñoz, R. et al. (2022). A single substitution in vacuolar protein sorting 4 is responsible for resistance to Watermelon mosaic virus in melon. Journal of Experimental Botany, 73, 4008–4021.

Ali, Z., Abulfaraj, A., Idris, A. et al. (2015). CRISPR/Cas9-mediated viral interference in plants. Genome Biology, 16, 238.

Ali, Z., Ali, S., Tashkandi, M. et al. (2016). CRISPR/Cas9-mediated immunity to geminiviruses: differential interference and evasion. Scientific Reports, 6, 26912.

Aman, R., Ali, Z., Butt, H. et al. (2018). RNA virus interference via CRISPR/Cas13a system in plants. Genome Biology, 19, 1.

Amano, M., Mochizuki, A., Kawagoe, Y. et al. (2013). High-resolution mapping of zym, a recessive gene for Zucchini yellow mosaic virus resistance in cucumber. Theoretical and Applied Genetics, 126, 2983–2993.

Boissot, N., Thomas, S., Chovelon, V. et al. (2016). Vat, an amazing gene conferring resistance to aphids and viruses they carry: from molecular structure to field effects. Frontiers in Plant Science, 7, 1420.

Boonham, N., Kreuze, J., Winter, S. et al. (2014). Methods in virus diagnostics: from ELISA to next generation sequencing. Virus Research, 186, 20–31.

Bustin, S.A., Benes, V., Garson, J.A. et al. (2009). The MIQE guidelines: Minimum information for publication of quantitative real-time PCR experiments. *Clinical Chemistry*, 55, 611–622.

Campbell, R.N., Wipf-Scheibel, C. and Lecoq, H. (1996). Vector-assisted seed transmission of Melon necrotic spot virus in melon. Phytopathology, 86, 1294–1298.

Çandar, A., Aydın, A., Şavkan, A.N., Güngör, R. and Başak, H. (2026). Detection and Incidence of Cucurbit Viruses in Kırşehir Province, Türkiye. Plant Protection Bulletin, 66, 26–38.

Chai, A., Wang, Q., Kang, H. et al. (2022). Rapid quantification of infectious cucumber green mottle mosaic virus in watermelon tissues by PMA coupled with RT-qPCR. Viruses, 14, 2046.

Chandrasekaran, J., Brumin, M., Wolf, D. et al. (2016). Development of broad virus resistance in non-transgenic cucumber using CRISPR/Cas9 technology. Molecular Plant Pathology, 17, 1140–1153.

Clark, M.F. and Adams, A.N. (1977). Characteristics of the microplate method of enzyme-linked immunosorbent assay for the detection of plant viruses. Journal of General Virology, 34, 475–483.

Collard, B.C.Y. and Mackill, D.J. (2008). Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philosophical Transactions of the Royal Society B, 363, 557–572.

Coşkun, Ö.F., Gökbulut, T., Fidan, H. et al. (2024). Genome-wide analysis of cucumber (Cucumis sativus L.) lines to identify zucchini yellow mosaic virus resistance loci. Bangladesh Journal of Botany, 53, 895–902.

Crespo, O., Janssen, D., Robles, C. et al. (2018). Resistance to cucumber green mottle mosaic virus in Cucumis sativus. Euphytica, 214, 201.

Crossa, J., Pérez-Rodríguez, P., Cuevas, J. et al. (2017). Genomic selection in plant breeding: methods, models, and perspectives. Trends in Plant Science, 22, 961–975.

De Moya-Ruiz, C., Rabadán, P., Juárez, M. and Gómez, P. (2023). Occurrence, distribution, and management of aphid-transmitted viruses in cucurbit crops in Spain. Pathogens, 12, 422.

Desbiez, C. (2020). The never-ending story of cucurbits and viruses. Acta Horticulturae, 1294, 173–191.

Desbiez, C. and Lecoq, H. (1997). Zucchini yellow mosaic virus. Plant Pathology, 46, 809–829.

Desbiez, C., Costa, C., Wipf-Scheibel, C. et al. (2007). Serological and molecular variability of Watermelon mosaic virus (genus Potyvirus). Archives of Virology, 152, 775–781.

Díaz, J.A., Nieto, C., Moriones, E., Truniger, V. and Aranda, M.A. (2004). Molecular characterization of a Melon necrotic spot virus strain that overcomes resistance in melon and nonhost plants. Molecular Plant-Microbe Interactions, 17, 668–675.

Ding, S.-W. and Voinnet, O. (2007). Antiviral immunity directed by small RNAs. Cell, 130, 413–426.

Dogimont, C., Bussemakers, A., Martin, J. et al. (1997). Two complementary recessive genes conferring resistance to Cucurbit aphid-borne yellows luteovirus in an Indian melon line (Cucumis melo L.). Euphytica, 96, 391–395.

Dogimont, C., Chovelon, V., Pauquet, J. et al. (2014). The Vat locus encodes for a CC-NBS-LRR protein that confers resistance to Aphis gossypii infestation and A. gossypii-mediated virus resistance. The Plant Journal, 80, 993–1004.

Dogimont, C., Slama, S., Martin, J. et al. (1996). Sources of resistance to Cucurbit aphid-borne yellows luteovirus in a melon germ plasm collection. Plant Disease, 80, 1379–1382.

Dombrovsky, A., Tran-Nguyen, L.T.T. and Jones, R.A.C. (2017). Cucumber green mottle mosaic virus: rapidly increasing global distribution, etiology, epidemiology, and management. Annual Review of Phytopathology, 55, 231–256.

Donaire, L., Gómez-Aix, C., Bretó, P. et al. (2026). Identification and characterization of a cucumber accession resistant to tomato leaf curl New Delhi virus. *Annals of Applied Biology*, 188, 182–194.

Fidan, H., Yildiz, K., Sarikaya, P. and Calis, O. (2023). First report of Tomato leaf curl New Delhi virus in Türkiye. New Disease Reports, 47, e12180.

Fortes, I.M., Sánchez-Campos, S., Fiallo-Olivé, E. et al. (2016). A novel strain of Tomato leaf curl New Delhi virus has spread to the Mediterranean basin. Viruses, 8, 307.

Gal-On, A. (2007). Zucchini yellow mosaic virus: insect transmission and pathogenicity—the tails of two proteins. Molecular Plant Pathology, 8, 139–150.

Gea-Caballero, E. and Aranda, M.A. (2026). Cucumber green mottle mosaic virus: A persistent seed-borne threat to cucurbits. Annals of Applied Biology, 189, e70136.

Giner, A., Pascual, L., Bourgeois, M. et al. (2017). A mutation in the melon Vacuolar Protein Sorting 41 prevents systemic infection of Cucumber mosaic virus. Scientific Reports, 7, 10471.

González-Ibeas, D., Cañizares, J. and Aranda, M.A. (2012). Microarray analysis shows that recessive resistance to Watermelon mosaic virus in melon is associated with the induction of defense response genes. Molecular Plant-Microbe Interactions, 25, 107–118.

Guiu-Aragonés, C., Monforte, A.J., Saladié, M. et al. (2014). The complex resistance to Cucumber mosaic cucumovirus in the melon accession PI 161375 is governed by one gene and at least two quantitative trait loci. Molecular Breeding, 34, 351–362.

Guner, N., Rivera-Burgos, L.A. and Wehner, T.C. (2018). Inheritance of resistance to Zucchini yellow mosaic virus in watermelon. HortScience, 53, 1115–1118.

Huggett, J.F., Foy, C.A., Benes, V. et al. (2013). The digital MIQE guidelines: Minimum Information for Publication of Quantitative Digital PCR Experiments. Clinical Chemistry, 59, 892–902.

Jacquemond, M. (2012). Cucumber mosaic virus. Advances in Virus Research, 84, 439–504.

Jones, J.D.G. and Dangl, J.L. (2006). The plant immune system. Nature, 444, 323–329.

Jones, R.A.C. (2021). Global plant virus disease pandemics and epidemics. Plants, 10, 233.

Jones, R.A.C. and Naidu, R.A. (2019). Global dimensions of plant virus diseases: current status and future perspectives. Annual Review of Virology, 6, 387–409.

Kang, B.-C., Yeam, I. and Jahn, M.M. (2005). Genetics of plant virus resistance. Annual Review of Phytopathology, 43, 581–621.

Karabıyık, M. and Yeşil, S. (2021). Eskişehir ili kabakgil ekim alanlarında görülen virüs hastalıklarının belirlenmesi. Ege Üniversitesi Ziraat Fakültesi Dergisi, 58, 589–598.

Kassem, M.A., Gosálvez, B., Garzo, E. et al. (2015). Resistance to Cucurbit aphid-borne yellows virus in melon accession TGR-1551. Phytopathology, 105, 1389–1396.

Koç, G., Fıdan, H. and Baloğlu, S. (2014). Melon necrotic spot virus (MNSV), a newly reported virus diseases for Turkey in squash species. The Journal of Turkish Phytopathology, 43(1–2–3), 1–6.

Koeda, S., Yamamoto, C., Yamamoto, H. et al. (2024). Cy-1, a major QTL for Tomato leaf curl New Delhi virus resistance, harbors a gene encoding a DFDGD-class RNA-dependent RNA polymerase in cucumber (Cucumis sativus). BMC Plant Biology, 24, 879.

Lecoq, H. and Desbiez, C. (2012). Viruses of cucurbit crops in the Mediterranean region: an ever-changing picture. Advances in Virus Research, 84, 67–126.

Lecoq, H., Bourdin, D., Wipf-Scheibel, C. et al. (1992). A new yellowing disease of cucurbits caused by a luteovirus, Cucurbit aphid-borne yellows virus. Plant Pathology, 41, 749–761.

Li, J., Wei, Q., Liu, Y. et al. (2013). One-step reverse transcription loop-mediated isothermal amplification for the rapid detection of Cucumber green mottle mosaic virus. Journal of Virological Methods, 193, 583–588.

Liu, H.-W., Luo, L.-X., Li, J.-Q. et al. (2014). Pollen and seed transmission of Cucumber green mottle mosaic virus in cucumber. Plant Pathology, 63, 72–77.

Liu, H.-W., Luo, L.-X., Liang, C.-Q. et al. (2015). High-throughput sequencing identifies novel and conserved cucumber (Cucumis sativus L.) microRNAs in response to Cucumber green mottle mosaic virus infection. PLOS ONE, 10, e0129002.

Liu, M., Kang, B., Wu, H. et al. (2023a). Transcriptomic and metabolic profiling of watermelon uncovers the role of salicylic acid and flavonoids in the resistance to cucumber green mottle mosaic virus. Journal of Experimental Botany, 74, 5218–5235.

Liu, M., Wu, H., Hong, N. et al. (2023b). Argonaute 1 and 5 proteins play crucial roles in the defence against cucumber green mottle mosaic virus in watermelon. Molecular Plant Pathology, 24, 961–972.

López-Martín, M., Montero-Pau, J., Ylla, G. et al. (2024). Insights into the early transcriptomic response against Watermelon mosaic virus in melon. BMC Plant Biology, 24, 58.

Mahas, A., Aman, R. and Mahfouz, M. (2019). CRISPR-Cas13d mediates robust RNA virus interference in plants. Genome Biology, 20, 263.

Mandadi, K.K. and Scholthof, K.-B.G. (2013). Plant immune responses against viruses: how does a virus cause disease? The Plant Cell, 25, 1489–1505.

Martín-Hernández, A.M. and Picó, B. (2021). Natural resistances to viruses in cucurbits. Agronomy, 11, 23.

Massart, S., Candresse, T., Gil, J. et al. (2022). Guidelines for the reliable use of high throughput sequencing technologies to detect plant pathogens and pests. Peer Community Journal, 2, e62.

Mauck, K.E., De Moraes, C.M. and Mescher, M.C. (2010). Deceptive chemical signals induced by a plant virus attract insect vectors to inferior hosts. Proceedings of the National Academy of Sciences USA, 107, 3600–3605.

Mitter, N., Worrall, E.A., Robinson, K.E. et al. (2017). Clay nanosheets for topical delivery of RNAi for sustained protection against plant viruses. Nature Plants, 3, 16207.

Monnot, S., Cantet, M., Mary-Huard, T. et al. (2022). Unravelling cucumber resistance to several viruses via genome-wide association studies highlighted resistance hotspots and new QTLs. Horticulture Research, 9, uhac184.

Monnot, S., Ravineau, A., Coindre, E. et al. (2025). Genome-wide association studies to assess genetic factors controlling cucumber resistance to CABYV and CMV in crop fields and the attractiveness for their Aphis gossypii vector. Horticulture Research, 12, uhaf016.

Morca, A.F., Coşkan, S., Öncü, F. et al. (2025). Genetic diversity and phylogenetic analysis of Watermelon mosaic virus in Türkiye: insights into emerging and classic populations. Current Microbiology, 82, 298.

Moriones, E., Praveen, S. and Chakraborty, S. (2017). Tomato leaf curl New Delhi virus: an emerging virus complex threatening vegetable and fiber crops. Viruses, 9, 264.

Ng, J.C.K. and Falk, B.W. (2006). Virus-vector interactions mediating nonpersistent and semipersistent transmission of plant viruses. Annual Review of Phytopathology, 44, 183–212.

Nicaise, V. (2014). Crop immunity against viruses: outcomes and future challenges. Frontiers in Plant Science, 5, 660.

Nieto, C., Morales, M., Orjeda, G. et al. (2006). An eIF4E allele confers resistance to an uncapped and non-polyadenylated RNA virus in melon. The Plant Journal, 48, 452–462.

Notomi, T., Okayama, H., Masubuchi, H. et al. (2000). Loop-mediated isothermal amplification of DNA. Nucleic Acids Research, 28, e63.

Palomares-Rius, F.J., Viruel, M.A., Yuste-Lisbona, F.J. et al. (2011). Simple sequence repeat markers linked to QTL for resistance to Watermelon mosaic virus in melon. Theoretical and Applied Genetics, 123, 1207–1214.

Park, Y., Katzir, N., Brotman, Y. et al. (2004). Comparative mapping of ZYMV resistances in cucumber (Cucumis sativus L.) and melon (Cucumis melo L.). Theoretical and Applied Genetics, 109, 707–712.

Pascual, L., Yan, J., Pujol, M. et al. (2019). CmVPS41 is a general gatekeeper for resistance to Cucumber mosaic virus phloem entry in melon. Frontiers in Plant Science, 10, 1219.

Pechar, G.S., Donaire, L., Gosálvez, B. et al. (2022). Editing of melon eIF4E associates with virus resistance and male sterility. Plant Biotechnology Journal, 20, 2006–2022.

Pérez-de-Castro, A., Esteras, C., Alfaro-Fernández, A. et al. (2019). Fine mapping of wmv1551, a resistance gene to Watermelon mosaic virus in melon. Molecular Breeding, 39, 93.

Pérez-Moro, C., Sáez, C., Sifres, A. et al. (2024). Genetic dissection of ToLCNDV resistance in resistant sources of Cucumis melo. International Journal of Molecular Sciences, 25, 8880.

Pitrat, M. and Lecoq, H. (1984). Inheritance of Zucchini yellow mosaic virus resistance in Cucumis melo L. Euphytica, 33, 57–61.

Pumplin, N. and Voinnet, O. (2013). RNA silencing suppression by plant pathogens: defence, counter-defence and counter-counter-defence. Nature Reviews Microbiology, 11, 745–760.

Ramírez-Madera, A.O. and Havey, M.J. (2017). Different haplotypes encode the same protein for independent sources of Zucchini yellow mosaic virus resistance in cucumber. HortScience, 52, 1040–1042.

Reingold, V., Lachman, O., Belausov, E. et al. (2016). Epidemiological study of Cucumber green mottle mosaic virus in greenhouses enables reduction of disease damage in cucurbit production. Annals of Applied Biology, 168, 29–40.

Reingold, V., Lachman, O., Blaosov, E. et al. (2015). Seed disinfection treatments do not sufficiently eliminate the infectivity of Cucumber green mottle mosaic virus (CGMMV) on cucurbit seeds. Plant Pathology, 64, 245–255.

Ruiz, L., López, C., Picó, B. and Janssen, D. (2021). Resistance to Cucumber green mottle mosaic virus in Cucumis melo. Plants, 10, 1077.

Ruiz, L., Simón, A., Velasco, L. et al. (2017). Biological characterization of Tomato leaf curl New Delhi virus from Spain. Plant Pathology, 66, 376–382.

Sáez, C., Ambrosio, L.G.M., Miguel, S.M. et al. (2021). Resistant sources and genetic control of resistance to Tomato leaf curl New Delhi virus in cucumber. Microorganisms, 9, 913.

Sáez, C., Esteras, C., Martínez, C. et al. (2017). Resistance to Tomato leaf curl New Delhi virus in melon is controlled by a major QTL located in chromosome 11. Plant Cell Reports, 36, 1571–1584.

Sáez, C., Flores-León, A., Montero-Pau, J. et al. (2022). RNA-Seq transcriptome analysis provides candidate genes for resistance to Tomato leaf curl New Delhi virus in melon. Frontiers in Plant Science, 12, 798858.

Sáez, C., Martínez, C., Ferriol, M. et al. (2016). Resistance to Tomato leaf curl New Delhi virus in Cucurbita spp. Annals of Applied Biology, 169, 91–105.

Sáez, C., Martínez, C., Montero-Pau, J. et al. (2020). A major QTL located in chromosome 8 of Cucurbita moschata is responsible for resistance to Tomato leaf curl New Delhi virus. Frontiers in Plant Science, 11, 207.

Shi, L., Yang, Y., Xie, Q. et al. (2018). Inheritance and QTL mapping of Cucumber mosaic virus resistance in cucumber. PLOS ONE, 13, e0200571.

Shrestha, S., Michael, V.N., Fu, Y. et al. (2021). Genetic loci associated with resistance to Zucchini yellow mosaic virus in squash. Plants, 10, 1935.

Sugiyama, M., Ohara, T. and Sakata, Y. (2006). A new source of resistance to Cucumber green mottle mosaic virus in melon. Journal of the Japanese Society for Horticultural Science, 75, 469–475.

Sugiyama, M., Ohara, T. and Sakata, Y. (2007). Inheritance of resistance to Cucumber green mottle mosaic virus in Cucumis melo L. ‘Chang Bougi’. Journal of the Japanese Society for Horticultural Science, 76, 316–318.

Sui, X., Li, R., Shamimuzzaman, M. et al. (2019). Understanding the transmissibility of Cucumber green mottle mosaic virus in watermelon seeds and seed health assays. Plant Disease, 103, 1126–1131.

Tian, G., Miao, H., Yang, Y. et al. (2016). Genetic analysis and fine mapping of Watermelon mosaic virus resistance gene in cucumber. Molecular Breeding, 36, 131.

Topkaya, Ş. and Desbiez, C. (2020). Molecular characterization of Cucurbit aphid-borne yellows virus (CABYV) affecting cucurbits in Turkey. Zemdirbyste-Agriculture, 107, 353–358.

Topkaya, Ş., Desbiez, C. and Ertunç, F. (2019). Presence of cucurbit viruses in Ankara and Antalya province and molecular characterization of coat protein gene of Zucchini yellow mosaic virus Turkish isolates. Fresenius Environmental Bulletin, 28, 2442–2449.

Torre, C., Agüero, J., Gómez-Aix, C. et al. (2020). Comparison of DAS-ELISA and qRT-PCR for the detection of cucurbit viruses in seeds. Annals of Applied Biology, 176, 158–169.

Trebicki, P. (2020). Climate change and plant virus epidemiology. Virus Research, 286, 198059.

Villamor, D.E.V., Ho, T., Al Rwahnih, M. et al. (2019). High throughput sequencing for plant virus detection and discovery. Phytopathology, 109, 716–725.

Whitfield, A.E., Falk, B.W. and Rotenberg, D. (2015). Insect vector-mediated transmission of plant viruses. Virology, 479–480, 278–289.

Worrall, E.A., Bravo-Cazar, A., Nilon, A.T. et al. (2019). Exogenous application of RNAi-inducing double-stranded RNA inhibits aphid-mediated transmission of a plant virus. Frontiers in Plant Science, 10, 265.

Xu, Y., Kang, D., Shi, Z. et al. (2004). Inheritance of resistance to Zucchini yellow mosaic virus and Watermelon mosaic virus in watermelon. Journal of Heredity, 95, 498–502.

CHAPTER 2

The Biology of Silage Fermentation and Silage Additives

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Introduction

Silage is a feed material obtained by fermenting plant products with high moisture content under oxygen-free (anaerobic) conditions using lactic acid bacteria (LAB). This process is called "ensiling," while the structure in which it is carried out is referred to as a "silo" (McDonald, 1981; Filya, 2005). The primary goal in silage production is to preserve the nutritional value of green fodder and ensure it can be stored for long periods without spoiling. The ensiling process begins with the natural epiphytic microflora in the plant, particularly LAB, fermenting water-soluble carbohydrates (WSC) to produce lactic acid (LA). This acid production causes a rapid drop in pH, inactivates aerobic microorganisms, and stops the activity of proteolytic enzymes, thereby preserving the feed material (Muck and Pitt, 1994; Filya, 2003).

The primary goal of the ensiling process is to preserve the product under anaerobic conditions and at a low pH level. Anaerobic environments promote the growth of LAB while inhibiting the growth of aerobic microorganisms, yeasts, and molds. The rapid decrease in pH limits protein degradation by inactivating plant proteases and stops the activity of unwanted microorganisms (Muck, 1996).

Practically speaking, anaerobic conditions are created by chopping material with the appropriate dry matter (DM) content into suitable lengths, filling the silo quickly, ensuring sufficient compaction, and sealing the silo airtight. Otherwise, aerobic activity develops in the areas of the silage that come into contact with air, which leads to spoilage and a decrease in feed value.

The second key objective in ensiling is to limit the activity of undesirable microorganisms such as *Clostridium* and *Enterobacter* bacteria. In silage without additives, this effect is achieved by LABs naturally present in the plant fermenting WSCs, particularly producing LA. The organic acids formed suppress the growth of unwanted microorganisms by lowering the pH. The critical pH value depends on the DM content of the material, and this value must be lower as the moisture content increases. In addition, legumes with high buffering capacity are more difficult to ensile than grasses (McDonald, 1981).

The management of these biochemical processes can be optimized through the use of appropriate silage additives. Additives are used to guide fermentation, accelerate pH reduction, reduce nutrient loss, and increase aerobic stability. The selection and application of appropriate additives play a critical role in maintaining silage quality and ensuring sustainable animal performance.

Biochemical Foundations of Silage Fermentation

Silage fermentation is a complex biochemical process achieved by subjecting plant material with high moisture content to microbial fermentation under oxygen-free conditions. The primary goal in this process is to preserve the nutritional value of the feed material and ensure it can be stored for a long time

without spoiling. During ensiling, the epiphytic microflora naturally present in the plant, particularly LAB, ferments WSCs to produce LA. The resulting LA causes the pH to drop rapidly, thereby inhibiting the growth of aerobic microorganisms (McDonald, 1981; Filya, 2003). The biochemistry of silage fermentation is shaped by microbial dynamics, fermentation stages, the resulting organic acid profile, and the interaction of environmental factors affecting these processes.

Stages of Silage Fermentation

Silage fermentation is a dynamic process that begins with the filling of the silo with silage material and continues to the feeding stage. This process involves four main stages: aerobic, fermentation, stability, and feed-out, depending on microbial activity and environmental conditions (Wilkinson and Davies, 2013).

1. Aerobic Stage

The aerobic stage takes place during the time between harvesting the crop and closing the silo. This stage occurs both in the field and inside the silo and directly affects silage quality (Rooke and Hatfield, 2003). The material taken into the silo initially contains a certain amount of oxygen (O_2) and the pH of the environment is approximately 6.0–6.5. Under these conditions, plant respiration and proteolytic activity occur simultaneously. The respiratory process produces carbon dioxide (CO_2), water (H_2O), and heat through the oxidation of carbohydrates; the breakdown of proteins results in compounds such as ammonia (NH_3) (Muck, 1988; McAllister and Hristov, 2000; Filya, 2005). These lead to DM losses and temperature increases. Silo temperatures reaching excessively high values such as 45–50 °C indicate oxygen leakage or insufficient compaction (Holmes, 2006; Borreani et al., 2017). Therefore, the ensiling process must be completed quickly, the material must be well compacted, and it must be sealed airtight.

2. Fermentation Stage

During this stage, once the oxygen in the silo is depleted, anaerobic conditions develop, and the fermentation process begins to be controlled by anaerobic microflora. Lactic acid bacteria produce organic acids by utilizing the carbohydrates present in plants. Among these acids, LA is the most dominant (Pahlow et al., 2003; Knický, 2005). Lactic acid production rapidly lowers silage pH, thereby suppressing other microorganisms (enterobacteria, yeasts, bacilli, and *Clostridium* species) that compete with LAB. This competition is based on differences in acid tolerance among microorganisms. LAB becomes dominant in the later stages of the fermentation process because it exhibits high resistance to low pH conditions (Pahlow et al., 2003). As fermentation progresses, the LAB population increases, more lactic acid is produced, and the pH value drops to 4.0-4.2. This pH level inhibits the growth of other bacteria and causes fermentation

to end naturally. Throughout the process, gases (CO_2) and some side products are also formed along with organic acids (Knicky, 2005). Fermentation is usually completed within 1 week; however, it can take up to 1 month depending on the plant species, WSC content, DM ratio, and silage conditions (Pahlow et al., 2003).

3. Stable Stage

Once the fermentation process is complete, the stable period begins as long as the silo remains airtight. Microbial activity is extremely low during this period; only acid-tolerant enzymes continue their activity to a limited extent. These enzymes cause gradual hydrolysis of structural and storage carbohydrates in an acidic environment, thereby providing a carbohydrate reserve that reduces energy losses during long-term storage (Pahlow et al., 2003). In addition, some protease enzymes can cause decomposition reactions that may lead to the formation of NH_3 from complex nitrogen compounds. However, low pH significantly limits these processes. The LAB population gradually decreases due to the low pH of the environment and the inhibitory effect of fermentation products. Some species, such as *Lactobacillus buchneri* (LB), can increase aerobic stability by producing acetic acid, exhibiting limited activity even at low pH (Keleş, 2009). Some acid-resistant yeast types and *Clostridium* spores can also live inactively during this period. Theoretically, the stable period can continue indefinitely under suitable conditions; however, in practice, most silage is consumed until the following harvest season (Pahlow et al., 2003).

4. Feeding Stage

When the silo is opened, the feeding stage begins and during this stage the silage comes into contact with O_2 again. Oxygen entering the silage surface and approximately 1 meter deep causes aerobic microorganisms (especially yeast, mold, and acetic acid bacteria) to multiply rapidly (Honig, 1991). These microorganisms are particularly prevalent in corn and grain silage. With the presence of air, yeasts consume LA, the pH rises, and the aerobic spoilage process begins. This situation causes the silage to heat up, leading to LA loss and a decrease in energy and nutritional value (Honig and Woolford, 1980). These losses occurring on the silo surface can reach very large proportions in a short time. In fact, a loss of 30–50 g KM kg^{-1} in a single day can be equivalent to the loss that could occur in an airtight silo over several months. For this reason, during the feeding period, it is recommended that the silage surface be cut evenly, opened in amounts appropriate to the daily consumption rate, air contact be minimized, and protective additives be used if necessary.

The silage production process consists of the interaction of four successive biochemical and microbiological phases. Keeping the aerobic stage short,

supporting LAB activity during the fermentation stage, maintaining airtightness during the stabile stage, and limiting oxygen contact during the feeding stage are fundamental principles for obtaining high-quality, nutrient-rich, and long-lasting silage.

Silage Microbiology

Silage fermentation is initiated by microorganisms naturally present on plant material. This epiphytic microflora consists mainly of LAB, yeast, mold, enterobacteria, and *Clostridium* species (Pahlow et al., 2003). Among these, the LAB group is the most important group of microorganisms that determines the stability and quality of silage.

Lactic acid bacteria lower the pH of the environment by fermenting carbohydrates and producing acid. These bacteria are generally divided into two types as homofermentative and heterofermentative (Muck et al., 2018). Homofermentative LAB (*Lactobacillus plantarum, Pediococcus pentosaceus*, and *Enterococcus faecium*) primarily convert glucose into LA and rapidly lower the pH due to their high acid production capacity during the fermentation process. Heterofermentative LAB (*Lactobacillus brevis, Lactobacillus buchneri*, and *Leuconostoc mesenteroides*) produce both LA and acetic acid, ethanol, and CO_2 from glucose. While these bacteria slow down fermentation, species such as *L. buchneri* increase aerobic stability, thereby extending the shelf life of silage after opening (Kleinschmit et al., 2005; Keleş, 2009).

Aerobic microorganisms (yeast, mold, and aerobic bacteria species) become active in the presence of O_2, consuming carbohydrates and LA, leading to an increase in temperature and spoilage. Therefore, the rapid establishment of anaerobic conditions is a prerequisite for successful biochemical fermentation (Muck, 2010).

The Biochemical Role of Silage Microflora and Its Effects on Quality

Silage microflora is the fundamental biological element that determines the direction, speed, and quality of the silage fermentation process. These microorganisms include LAB, yeasts, molds, enterobacteria, *Clostridia* species, and other auxiliary microorganisms. Preserving the nutritional value of silage, preventing energy losses, and increasing aerobic stability are directly related to the composition and activity of this microflora (Filya, 2005).

Biochemical fermentation is based on the conversion of plant carbohydrates into organic acids by microorganisms. The main component that rapidly lowers the pH of silage is LA, and this acid is an indicator of LAB activity. Homofermentative LAB species (e.g., *Lactobacillus plantarum, Pediococcus pentosaceus*) convert glucose almost entirely into LA, while heterofermentative species (*Lactobacillus brevis, Leuconostoc mesenteroides*) produce products such as acetic acid, ethanol, and CO_2 in addition to LA (Muck, 2010). Lactic acid

production lowers the pH of the environment to 4.0–4.2, preventing the growth of unwanted microorganisms. This situation ensures both the stabilization of fermentation and the preservation of nutrients. Acetic acid production increases, particularly due to the activity of heterofermentative bacteria, and enhances the aerobic stability of silage. However, excessive acetic acid production can negatively affect feed consumption. Therefore, a balanced presence of homofermentative and heterofermentative LAB species is desirable (McDonald et al., 1991). Additionally, some LAB types provide natural protection against pathogenic bacteria through combinations of bacteriocins and organic acids. These biochemical processes preserve quality not only by lowering pH, but also through antimicrobial effects.

Yeasts are microorganisms that can metabolize both sugars and organic acids during fermentation. Yeasts belonging to the *Saccharomyces* and *Candida genera*, in particular, break down LA under aerobic conditions, causing the silage to reheat and the pH to rise (Jonsson and Pahlow, 1984). This process is known as "aerobic spoilage" and leads to energy loss, mold growth, and the formation of mycotoxins. For this reason, it is crucial to compress the silage, ensure it is airtight, and consume it quickly after opening.

Enterobacteria are facultative anaerobic bacteria that are particularly active during the early stages of fermentation. These bacteria ferment carbohydrates while also breaking down proteins to produce NH_3 and biogenic amines. These biochemical events increase the buffer capacity of the silage and delay the drop in pH (Woolford, 1984). As a result, LAB activity decreases and the nutritional value of silage declines. Therefore, preventing soil contamination in harvested material and maintaining a dry matter content of around 30–35% limits enterobacterial growth (McDonald, 1981).

Clostridia species are among the most important microorganisms that impair silage quality. These bacteria become active especially in silage with low dry matter content. Species such as *Clostridium butyricum* increase pH by converting LA to butyric acid, causing energy loss. Additionally, proteolytic *Clostridia* species break down amino acids to produce NH_3, amines, and foul-smelling compounds. This situation both reduces feed consumption by animals and compromises the microbiological safety of silage (Keleş, 2009). To maintain the biochemical stability of silage, measures to prevent *Clostridia* growth—rapid pH drop, appropriate dry matter content, and an airtight environment—are critical.

Molds, especially species belonging to the *Penicillium, Aspergillus*, and *Fusarium genera*, grow under aerobic conditions and can cause mycotoxin production in the surface layers of silage. These toxins accumulate in milk and meat products, endangering animal health (Oldenburg, 1991). The biochemical activity of molds releases energy through carbohydrate and lipid oxidation, which causes silage temperature to rise and leads to nutrient loss. Therefore, sealing

techniques that minimize contact with air and antifungal additives are important for silage quality.

Epiphytic microflora, i.e., microorganisms naturally found on plant surfaces, form the initial microbiome for fermentation. The composition of this microflora varies depending on the plant species, climatic conditions, and harvest time (Kaya and Polat, 2010; Kızılsimsek et al., 2016). In many cases, since the epiphytic LAB population is low, the use of inoculants (especially LAB-based preparations) is recommended for high-quality fermentation (Filya, 2005). These inoculants rapidly lower the pH in the early stages of fermentation, thereby suppressing the growth of both *Clostridia* and enterobacteria.

In conclusion, the biochemical role of silage microflora is not solely limited to organic acid production. These microorganisms directly affect many quality parameters such as protein preservation, energy stability, antimicrobial activity, and aerobic resistance. Good silage management should promote LAB dominance while limiting the growth of harmful microorganisms. This results in silage that is both highly nutritious and stable over a long period of time.

Factors Affecting Silage Quality

Silage quality is directly related to the efficiency of the fermentation process, nutrient preservation, and digestibility of the feed for animals. The factors affecting this quality are determined by both the initial characteristics of the silage material and the techniques applied during the ensiling process. Plant type and variety are fundamental elements that determine the chemical and physical structure of the silage. For example, corn silage is rich in starch, while alfalfa or trefoil silage has a higher protein content. The plant growth stage also directly affects protein and carbohydrate content; plants harvested early generally have higher protein and lower fiber content, while mature plants have higher DM and fiber content (Filya, 2005).

The DM content of products to be ensiled is important both for the quality of the silage and for the development of lactic acid bacteria. Depending on the chemical properties of the material, the optimum DM content is generally accepted as 30–35%. High DM content makes it difficult to compress the silage and leads to the formation of air pockets. This situation triggers aerobic spoilage and promotes the growth of yeast and mold by limiting the development of LAB populations. Materials with low DM, however, make it difficult to prevent *Clostridial* fermentation. In addition, an increase in silo water and intense fermentation result in the heating of the silage. The sugar content of silage is also critically important; if there is insufficient sugar, LAB proliferation slows down and the pH decline is delayed. This situation leads to increased activity of enterobacteria and *Clostridia*. Therefore, it is necessary to determine the optimal levels of DM and sugar to ensure silage quality and stability. This balance both

controls fermentation and reduces nutrient losses (McDonald, 1981; Keleş, 2009; Muck, 1988, 2010).

The breakdown process is one of the critical stages of silage production, ensuring that the plants to be ensiled are broken down into homogeneous and suitable sizes (0.8–2.5 cm). This process allows the plant to mix evenly with the additives and enables the silage to be effectively compressed. Plants with high or low DM content should be processed in smaller pieces, while plants with low DM or high quality should be processed in larger pieces; otherwise, an increase in silage moisture and nutrient losses will occur. Particle size is important in terms of compaction efficiency and air insulation; finely crushed material reduces air voids, promoting anaerobic conditions. Proper compaction and covering of silage are fundamental practices in preventing aerobic spoilage; inadequate compaction or improper covering creates an environment for development of surface molds and yeasts (Woolford, 1984).

Climate and environmental conditions are also important factors affecting silage quality. Hot and humid environments can accelerate aerobic spoilage, especially after the silo is opened. Cold environments, on the other hand, slow down fermentation and delay the growth of LAB populations. The temperature, humidity, and air circulation of the storage location play a decisive role in maintaining silage quality (Filya, 2005).

One of the key factors affecting silage fermentation is the composition and density of the microorganism population naturally present on the plant surface prior to ensiling. Lactic acid bacteria play a key role in directing fermentation, causing a rapid drop in pH and creating the desired anaerobic conditions. Conversely, high levels of yeast and mold cause the consumption of organic acids and accelerate aerobic spoilage. The structure of epiphytic microflora is affected by factors such as plant species, maturity stage, climatic conditions, and harvesting method. Therefore, the initial microorganism load plays a decisive role in silage quality, stability, and nutritional value (Karadağoğlu and Özdüven, 2019; Romero et al., 2021).

The interaction of all these factors determines the nutritional value, fermentation efficiency, and aerobic stability of silage. Therefore, keeping these factors under control before using silage additives increases the effectiveness of the additives and ensures that high-quality silage is obtained.

Silage Additives

Silage fermentation is a complex process that converts plant material into a stable feed form rich in organic acids as a result of microbial activity in an oxygen-free environment (Muck et al., 2018). This process is determined by many factors, such as plant species, pre-harvest conditions, DM level, buffer capacity, microbial population structure, and ensiling techniques applied. In

recent years, the number of studies conducted on the role and application methods of silage additives to ensure the sustainability of silage nutritional value and minimize losses during the fermentation process has increased significantly (Muck et al., 2018; Kung et al., 2018; Bai et al., 2020).

An effective additive should promote LA production to ensure a rapid drop in pH, minimize DM and energy losses, increase aerobic stability, and suppress the growth of undesirable microorganisms. This improves both the hygienic quality of the silage and animal performance, thereby ensuring an economic return on the additive costs (Muck et al., 2018; Bai et al., 2020).

Silage fermentation is a complex process that converts plant material into a stable feed form rich in organic acids as a result of microbial activity in an oxygen-free environment. This process is influenced by many factors, such as plant species, pre-harvest conditions, DM content, buffer capacity, microbial flora, and the ensiling techniques applied. Research on the effectiveness and application methods of additives to preserve the nutritional value of silage and reduce fermentation losses has increased rapidly in recent years (Yitbarek and Tamir, 2014). An effective additive supports LA production, causing the pH to drop rapidly, reducing DM and energy losses, improving aerobic stability, and inhibiting the growth of undesirable microorganisms. This improves the hygienic quality of silage and enhances animal performance (milk yield and composition, live weight gain, body condition, and reproduction); the investment in the additive provides economic benefits to the producer through the resulting increase in yield (Getabalew et al. 2022). Silage additives are classified into three main groups based on their effects on the fermentation process: fermentation stimulants, fermentation inhibitors, and absorbent substances (Table 1). This classification aims to optimize fermentation, preserve the nutritional value of silage, and increase animal productivity.

Table 1. Classification, functions, and examples of silage additives

Additive	Function	Examples
Fermentation Stimulants	Accelerates the pH decrease by increasing lactic acid production and optimizes fermentation	Microbial inoculants (Lactobacillus, Pediococcus, Enterococcus), enzymes (cellulase, hemicellulase, amylase), fermentable carbohydrate sources (molasses, sugar beet pulp, grains)
Fermentation Inhibitors	Prevents the growth of unwanted microorganisms and keeps fermentation under control	Organic acids (formic, propionic, acetic acid), chemical preservatives (formaldehyde, sodium nitrite, sodium metabisulfite), food additives (urea, ammonia, grains, minerals
Absorbents	Balances moisture in silage with low dry matter content	Hay, grain, bentonite, polyacrylamide

Fermentation-Stimulating Additives

The most commonly used additives in practice to optimize silage fermentation are LAB inoculants, cell wall-degrading enzymes, and easily fermentable carbohydrate sources.

Lactic Acid Bacteria Inoculants

Silage fermentation is a process based on the conversion of plant material into organic acids through microbial activity under anaerobic conditions. During this process, LAB are the primary group of microorganisms that determine the rate and direction of fermentation and the microbiological quality of the silage. Lactic acid bacteria are generally classified into two main groups: homofermentative and heterofermentative, and the contributions of both groups to silage quality are based on different mechanisms (McDonald et al., 1991; Muck, 2013).

The most common homofermentative LAB used as silage inoculants are *Lactobacillus plantarum, Pediococcus pentosaceus*, and *Enterococcus faecium* (Zheng et al., 2020). Homofermentative LAB convert WSCs largely into a single product, LA. This feature allows for a rapid decrease in silage pH during the early stages of fermentation (Okeye et al., 2023). The rapid decrease in pH limits the activity of *Clostridium* spp., enterobacteria, and proteolytic microorganisms. Studies have shown that homofermentative LAB inoculants improve silage fermentation; specifically, they reduce pH, acetic acid, and ammonia nitrogen (NH_3-N) levels while increasing LA concentration (Muck and Kung, 1997; Keleş,

2009; Zhao et al., 2021). These changes reflect the fermentation characteristics desired in high-quality silage. In addition, the dominance of homofermentative LAB in the fermentation process enables more effective use of existing WSCs, increasing the possibility of producing silage of acceptable quality even in materials with relatively low WSC content (Oliveira et al., 2017; Muck et al., 2018). When silage is opened and exposed to air, yeasts that can oxidize LA multiply rapidly, causing the silage temperature to rise and the pH to increase again. This increase in pH creates a favorable environment for aerobic bacteria and molds, accelerating the aerobic degradation process (Kung et al., 2018). On the other hand, recent studies have shown that the use of homofermentative LAB cannot sufficiently maintain the aerobic stability of silage in all cases and that silage may therefore be more prone to spoilage after opening. To increase aerobic stability, the use of heterofermentative LAB strains such as *Lactobacillus buchneri*, *L. hilgardii*, and *L. fermentum* is recommended. Heterofermentative LAB ferments soluble carbohydrates found in plants not only into LA, but also into acetic acid and 1,2-propanediol. The resulting acetic acid exhibits a stronger antifungal effect against yeast and mold, thereby increasing the silage's resistance to spoilage after opening (Kung and Shaver, 2001; Oude Elferink et al., 2001; Dunière et al., 2015; Muck et al. 2018). Studies aimed at improving aerobic stability in silage, particularly *Lactobacillus buchneri* within heterofermentative LAB, have shown that it significantly improves the aerobic stability of silage both in laboratory (Weinberg et al., 1999; Driehuis et al., 1999; Ranjit and Kung, 2000) and field conditions (Mari et al., 2009; Kristensen et al., 2010; Tabacco et al., 2011) significantly improved the aerobic stability of silage. Some studies report that heterofermentative fermentation may increase dry matter losses and reduce feed intake due to increased acetic acid production (Ranjit and Kung, 2000; Taylor and Kung, 2002; Kleinschmit and Kung, 2006); however, it is noted that this situation may not always be evident under practical conditions and is generally not confirmed by large-scale studies (Kristensen et al., 2010). In this regard, combination inoculants using both homofermentative and heterofermentative LAB have gained importance in current applications. In combinations, homofermentative strains improve fermentation quality by causing a rapid pH drop at the start of fermentation, while heterofermentative strains delay spoilage by maintaining aerobic stability after the silage is opened. Indeed, it has been reported that inoculant combinations containing *L. plantarum* and *L. buchneri* enable more efficient utilization of WSCs present in the plant during the fermentation process, thereby reducing DM losses and protein degradation while also increasing the aerobic stability of silage (Filya, 2003; Jin et al., 2024). This demonstrates that the combined use of heterofermentative and homofermentative LAB creates a synergistic effect in terms of both fermentation quality and the durability of silage after opening.

Enzymes

Enzymes are protein-based molecules that accelerate biochemical reactions, and enzyme complexes that break down polysaccharides (cellulose and hemicellulose) and starch, which form the plant cell wall, are widely used as additives in silage. The use of proteases as silage additives is not recommended. This is because these enzymes have been reported to excessively break down protein fractions, thereby increasing the soluble nitrogen content in the rumen and elevating unwanted NH_3 formation (Getabalew et al., 2022).

There are two main purposes for using fiber-degrading enzymes in silage. The first is to increase the amount of soluble sugar in silage by breaking down part of the cellulose and hemicellulose. These sugars are rapidly utilized by LAB, increasing LA production and causing the silage pH to drop more quickly. This makes fermentation more efficient, reduces DM and protein losses, and limits NH_3 formation. The second purpose is to improve the digestibility of silage. Partial breakdown of the cell wall allows fiber fractions to be more easily digested by rumen microorganisms. This increases the digestibility of organic matter and can positively affect the animal's feed intake (Oladosu et al., 2016). In recent years, it has been demonstrated that the use of enzymes in combination with LAB inoculants produces a synergistic effect. Enzymes partially break down the cell wall, releasing fermentable carbohydrates, while LAB rapidly converts these sugars into lactic acid, accelerating the fermentation process and supporting the pH decrease. It has been reported that LAB and LAB + enzyme applications in rye silage reduce Neutral Detergent Fiber (NDF), Acid Detergent Fiber (ADF), and cellulose levels, while increasing DM digestibility and metabolizable energy values (Uğurlu et al., 2022). Studies conducted on sunflower and triticale silage similarly show that enzyme-supported inoculants lower pH, increase LA levels, improve aerobic stability, and enhance digestibility (Özdüven et al., 2009; Özdüven et al., 2010). When enzyme and LAB combinations are used, the breakdown of plant cell walls is facilitated, and the amount of soluble carbohydrates increases. This situation enables the fermentation process to proceed more quickly and efficiently. It also improves the aerobic stability of the silage and increases its digestibility by animals. For this reason, these contributions are considered an important biotechnological tool that enhances silage quality during the ensiling process, particularly for feed materials with high fiber content (Li et al., 2024).

Carbohydrate Sources

The effectiveness of silage fermentation largely depends on the level of WSCs present in the silage material. Lactic acid bacteria produce lactic acid by using these carbohydrates during fermentation, thereby causing the pH of the silage to drop rapidly. However, especially in products that are deficient in WSC, such as legume feed crops, it is difficult for natural fermentation to occur at a sufficient

level. For this reason, various carbohydrate sources are added to increase the ensilability of these products. The main carbohydrate sources used in silage include molasses, various sugars, grain kernels, whey, beet and citrus pulp, and potatoes (Filya 2005).

Molasses is a byproduct of the sugarcane (*Saccharum officinarum* L.) and sugar beet (*Beta vulgaris* L.) processing industries and is a cheap energy source with a high WSC content. Molasses obtained from sugar beets contains approximately 70-75% DM and 45-50% WSC (mostly sucrose) (Palmonari et al. 2020). The primary purpose of using molasses as a silage additive is to provide a fermentable carbohydrate source for LAB, thereby supporting a faster start to LA fermentation and a quicker drop in pH. It is recommended to add 20-60 kg of molasses per 1 ton of fresh material (Kaiser, 2004). On the other hand, cereal grains such as barley, wheat, oats, sorghum, and corn can also be used to provide carbohydrates; however, these grains must be crushed or ground. Otherwise, fermentation activity decreases and the grains are excreted in the animal's feces without being digested. The recommended usage amount for crushed grain is 40–50 kg per ton. Cheese whey, containing approximately 4–5% lactose, supports fermentation by providing additional carbohydrate content and can be added to silage material at a rate of 15–20 kg per ton. Additionally, dried beet pulp and citrus pulp are used to increase DM in products with high water content. Potatoes, whether fresh or cooked, are another carbohydrate source that can be ensiled either alone or mixed with legumes (Filya 2005).

Fermentation-Inhibiting Additives

The addition of acidic or alkaline additives to silage material is applied to control the fermentation process and limit the growth of undesirable microorganisms. In silage production, acidic and alkaline additives are used to direct fermentation and control spoilage microorganisms.

Organic Acids

Acid additives rapidly lower silage pH, limiting the growth of undesirable microflora; alkaline additives, on the other hand, raise pH, slowing down fermentation. However, the activity of LAB does not completely cease, and the fermentation process continues with a different pH profile depending on the type of additive. In the past, inorganic acids such as sulfuric and hydrochloric acid have been used to lower the pH in silage. However, the weak antimicrobial effects of these substances, their abrasive properties, and the safety risks they pose during use have significantly reduced their popularity today. Current approaches favor organic acids and their salts in terms of both safety and fermentation efficiency. The most commonly used organic acids in practice are formic acid and propionic acid. Formic acid-based additives in silage production control fermentation by lowering pH, reduce the excessive fermentation of WSCs, and reduce proteolysis (Conaghan et al., 2011; Seppälä et al., 2016). Additives containing propionic acid

are effective in improving aerobic stability (Kung et al., 2004). It has been reported that the application of additive mixtures containing formic and propionic acids reduces DM losses in silage, lowers yeast and ethanol levels, and reduces the risk of aerobic spoilage after silo opening (Nadeau et al., 2013). Since acid-based additives are offered as commercial products with different properties and formulations, it is important to follow the manufacturer's recommendations when applying them.

Ammonia and Urea

Alkali compounds are also used as silage additives, including urea, anhydrous NH_3, bi-urea, and sodium hydroxide (NaOH). Although the effects of these additives on silage fermentation are generally based on similar mechanisms, the most common and applicable additive in practice is urea (Keleş, 2017). Urea is one of the main non-protein nitrogen (NPN) sources used to increase crude protein content during the ensiling of corn, sorghum, and other grains. In silage, urea is hydrolyzed into NH_3 and water by the naturally occurring urease enzyme in plants. The resulting NH_3 has a strong alkaline effect and increases the pH of the silage, reducing the growth of yeast and mold. This mechanism contributes to the increased aerobic stability of silage with added urea and to the increased aerobic stability after opening. Additionally, urea application may increase the digestibility of DM and crude cellulose due to the breakdown of plant cell wall complexes; however, it has been reported that this increase does not lead to a significant improvement in performance indicators such as milk yield or live weight gain (Kung et al., 2003; Yitbarek and Tamir, 2014). Urea application is typically around 2–3 kg per ton of fresh material in practice, and excessive use may increase the risk of NH_3 toxicity. Homogeneous distribution of the additive is important; otherwise, localized NH_3 concentrations in the silage mass may pose a poisoning risk to animals (Filya 2005).

Absorbents

Absorbents are additives used to bind excess moisture in silage materials with high water content (80-90%) in order to increase the DM level of the silage. In this context, materials such as barley, wheat straw, dry sugar beet pulp, certain polymers, and bentonite can be considered as absorbents. The use of absorbent agents increases the DM content of silage and reduces silo water losses, thereby preventing nutrient and energy losses. Especially in situations where adequate drying cannot be achieved due to environmental conditions, the use of absorbents is of great importance for optimizing the ensiling process. Dry beet pulp and molasses beet pulp reduce silage moisture and improve fermentation quality without negatively affecting the energy and protein composition of the silage, thanks to their high DM content and suitable nutritional values (Jones and Jones, 1996). Grain kernels increase DM and the energy density of silage, but due to their low WSCs content, they do not provide an extra fermentable substrate for

LAB (Yitbarek and Tamir, 2014). Hay, on the other hand, has a high absorptive effect but can reduce the nutritional value of silage when used in high quantities (Jones and Jones, 1996).

Conclusion

Silage fermentation is a fundamental bio conservation process that aims to stabilize plant material through the production of organic acids under anaerobic conditions. The success of this process is directly related to the initial DM level, plant composition, epiphytic microflora, and the accuracy of the ensiling technique. The rapid activation of LAB and the early drop in pH are one of the main mechanisms that determine the microbiological and nutritional quality of silage by inhibiting the growth of undesirable microorganisms.

Silage additives are an important tool in directing fermentation and reducing quality losses. Microbial inoculants increase lactic acid production by supporting LAB activity, reducing proteolysis and dry matter losses. Organic acids improve aerobic stability, particularly after silo opening, by controlling pH decline and reducing yeast and mold-related spoilage. Alkaline additives such as urea and ammonia can reduce yeast and mold activity in addition to providing a NPN source; however, it should be noted that fermentation may slow down due to an increase in pH, and the application rate must be carefully monitored. Absorbent additives reduce silo water losses by binding excess moisture in DM content materials and support more balanced fermentation. Enzyme additives (cellulase and hemicellulase) increase the amount of soluble carbohydrates by breaking down cell wall carbohydrates, thereby providing additional substrate for LAB, which can enhance both fermentation efficiency and the digestibility of nutrients.

However, additives (regardless of their group) cannot replace proper silage practices. Ensuring sufficient DM levels, rapid filling of the silo, effective compaction, and complete elimination of air contact are fundamental conditions for additives to be effective. The choice of additives should be made considering the characteristics of the silage material, operational capabilities, economic evaluation, and the targeted feeding strategy.

In conclusion, the scientifically based and controlled use of additives, when applied in conjunction with proper ensiling techniques, improves silage quality, reduces feed losses, and positively impacts animal performance. This approach constitutes one of the fundamental components of sustainable and efficient feed management.

References

Bai, J., Xu, D., Xie, D., Wang, M., Li, Z., & Guo, X. (2020). Effects of antibacterial peptide-producing *Bacillus subtilis* and *Lactobacillus buchneri* on fermentation, aerobic stability, and microbial community of alfalfa silage. *Bioresource Technology, 315*, 123881.

Borreani, G., Tabacco, E., Schmidt, R. J., Holmes, B. J., & Muck, R. E. (2018). Silage review: Factors affecting dry matter and quality losses in silages. *Journal of Dairy Science, 101*, 3952–3979.

Conaghan, P., O'Kiely, P., & O'Mara, F. P. (2011). Possibilities of increasing the residual water-soluble carbohydrate concentration and aerobic stability of low dry-matter perennial ryegrass silage through additive and cultivar use. *Grass and Forage Science, 67*, 177–198.

Driehuis, F., Oude Elferink, S. J. W. H., & Spoelstra, S. F. (1999). Anaerobic lactic acid degradation during ensilage of whole-crop maize inoculated with *Lactobacillus buchneri* inhibits yeast growth and improves aerobic stability. *Journal of Applied Microbiology, 87*(4), 583–594.

Dunière, L., Jin, L., Smiley, B., Qi, M., Rutherford, W., Wang, Y., & McAllister, T. (2015). Impact of adding *Saccharomyces* strains on fermentation, aerobic stability, nutritive value, and select lactobacilli populations in corn silage. *Journal of Animal Science, 93*, 2322–2335.

Filya, İ. (2003). The effect of *Lactobacillus buchneri* and *Lactobacillus plantarum* on the fermentation, aerobic stability, and ruminal degradability of low dry matter corn and sorghum silages. *Journal of Dairy Science, 86*, 3575–3581.

Filya, İ. (2005). *Silaj yapımı, teknolojisi ve kullanımı*. Süt Hayvancılığı Eğitim Merkezi Yayınları, Hayvancılık Serisi: 8, Karacabey, Bursa.

Getabalew, M., Mindaye, A., & Alemneh, T. (2022). Silage and enzyme additives as animal feed and animals response. *Archives of Animal Husbandry & Dairy Science, 2*(4).

Holmes, B. J. (2006). Density in silage storage. In *Silage for dairy farms: Growing, harvesting, storing and feeding* (NRAES-181). Natural Resource, Agriculture and Engineering Service.

Honig, H. (1991). Reducing losses during storage and unloading of silage. In G. Pahlow & H. Honig (Eds.), *Forage conservation towards 2000* (Sonderheft 123, pp. 116–128). Landbauforschung Volkenrode.

Honig, H., & Woolford, M. K. (1980). Changes in silage on exposure to air. In C. Thomas (Ed.), *Forage conservation in the 80s* (Occasional Symposium No. 11, pp. 76–87). British Grassland Society.

Jonsson, A., & Pahlow, G. (1984). Systematic classification and biochemical characterization of yeasts growing in grass silage inoculated with *Lactobacillus* cultures. *Animal Research and Development, 20*, 7–22.

Kaiser, A. G. (2004). Silage additives. In A. G. Kaiser, J. W. Piltz, H. M. Burns, & N. W. Griffiths (Eds.), *Successful silage* (Chapter 7). Dairy Australia & New South Wales Department of Primary Industries.

Kaya, Ö., & Polat, C. (2010). Tekirdağ ili koşullarında I. ve II. ürün olarak yetiştirilen bazı mısır çeşitlerinin silaj fermantasyon özellikleri ve yem değerinin belirlenmesi. *Tekirdağ Ziraat Fakültesi Dergisi, 7*(3), 129–136.

Karadağoğlu, Ö., & Özdüven, M. L. (2019). Bazı tritikale çeşitlerinde farklı olgunlaşma dönemlerinin silolamada fermantasyon özellikleri ve yem değeri üzerine etkileri. *Journal of Turkish Veterinary Medical Society, 90*(2), 132–142.

Keles, G. (2009). *Homofermantatif ve heterofermantatif laktik asit bakterilerinin mısır silajının kimyasal kompozisyonu ile Konya merinosu toklularda performansa etkileri* (Doktora tezi). Selçuk Üniversitesi.

Keles, G. (2017). Silaj katkıları. *Türkiye Klinikleri Journal of Animal Nutrition & Nutritional Diseases–Special Topics, 3*(3), 171–180.

Kleinschmit, D. H., & Kung, L., Jr. (2006). A meta-analysis of the effects of *Lactobacillus buchneri* on the fermentation and aerobic stability of corn and grass and small-grain silages. *Journal of Dairy Science, 89*(10), 4005–4013.

Kleinschmit, D. H., Schmidt, R. J., & Kung, L., Jr. (2005). The effects of various antifungal additives on the fermentation and aerobic stability of corn silage. *Journal of Dairy Science, 88*(6), 2130–2139.

Knický, M. (2005). *Possibilities to improve silage conservation: Effects of crop, ensiling technology and additives* (Doctoral thesis). Sveriges Lantbruksuniversitet.

Kristensen, N. B., Sloth, K. H., Højberg, O., Spliid, N. H., Jensen, C., & Thøgersen, R. (2010). Effects of microbial inoculants on corn silage fermentation, microbial contents, aerobic stability, and milk production under field conditions. *Journal of Dairy Science, 93*, 3764–3774.

Kung, L., Jr., Savage, R. M., da Silva, E. B., Polukis, S. A., Smith, M. L., Johnson, A. C. B., & Miller, M. A. (2021). The effects of air stress during storage and low packing density on the fermentation and aerobic stability of corn silage inoculated with *Lactobacillus buchneri* 40788. *Journal of Dairy Science, 104*(4), 4206–4222.

Kung, L., Jr., Shaver, R. D., Grant, R. J., & Schmidt, R. J. (2018). Silage review: Interpretation of chemical, microbial, and organoleptic components of silage. *Journal of Dairy Science, 101*, 4020–4033.

Kung, L., Jr., Taylor, C. C., Lynch, M. P., & Neylon, J. M. (2003). The effect of treating alfalfa with *Lactobacillus buchneri* 40788 on silage fermentation, aerobic stability, and nutritive value for lactating dairy cows. *Journal of Dairy Science, 86*, 336–343.

Kung, L., & Shaver, R. (2001). How good is your silage making? *Hoard's Dairyman, 146*.

Kung, L., Jr., Myers, C. L., Neylon, J. M., Taylor, C. C., Lazartic, J., Mills, J. A., & Whiter, A. G. (2004). The effects of buffered propionic acid-based additives alone or combined with microbial inoculation on the fermentation of high moisture corn and whole-crop barley. *Journal of Dairy Science, 87*(4), 1310–1316.

Li, M., Hassan, F. U., Akhtar, M. U., Peng, L., Xie, F., Deng, Q., … Yang, C. (2024). Fibrolytic enzymes and lactic acid bacteria improve the ensiling characteristics of ramie and elephant grass mixed silage. *Agriculture, 14*(10), 1746.

Mari, L. J., Schmidt, R. J., Nussio, L. G., Hallada, C. M., & Kung, L., Jr. (2009). An evaluation of *Lactobacillus buchneri* 40788 to alter fermentation and improve the aerobic stability of corn silage in farm silos. *Journal of Dairy Science, 92*, 1174–1176.

McAllister, T. A., & Hristov, A. N. (2000). The fundamentals of making good quality silage. *Advances in Dairy Technology, 12*, 381–399.

McDonald, P. (1981). *The biochemistry of silage*. John Wiley & Sons.

McDonald, P., Henderson, A. R., & Heron, S. J. E. (1991). *The biochemistry of silage*. Chalcombe Publications.

Muck, R. E. (1988). Factors influencing silage quality and their implications for management. *Journal of Dairy Science, 71*(11), 2992–3002.

Muck, R. E. (1996). *A lactic acid bacteria strain to improve aerobic stability of silages*. US Dairy Forage Research Center, 42–43.

Muck, R. E. (1996). Silage inoculation: Inoculation of silage and its effects on silage quality. *Dairy Forage Center–Informational Conference, 43*, 51.

Muck, R. E. (2010). Silage microbiology and its control through additives. *Revista Brasileira de Zootecnia, 39*, 183–191.

Muck, R. E., & Kung, L., Jr. (1997). Effects of silage additives on ensiling. In *Silage: Field to feedbunk* (pp. 187–199). Northeast Regional Agricultural Engineering Service.

Muck, R. E., Nadeau, E. M. G., McAllister, T. A., Contreras-Govea, F. E., Santos, M. C., & Kung, L., Jr. (2018). Silage review: Recent advances and future uses of silage additives. *Journal of Dairy Science, 101*, 3980–4000.

Nadeau, E., Hallin, O., Auerbach, H., Jakobsson, J., & Arnesson, A. (2013). Quality of baled grass–clover silage as affected by additives and harvest methods. In D. L. Michalk, G. D. Millar, W. B. Badgery, & K. M. Broadfoot (Eds.), *Proceedings of the 22nd International Grassland Congress* (pp. 744–745). New South Wales Department of Primary Industry.

Okoye, C. O., Wei, Z., Jiang, H., Wu, Y., Wang, Y., Gao, L., & Jiang, J. (2023). Metagenomics analysis reveals lactic acid bacteria performance in alfalfa silage. *Journal of Animal Science, 101*, skad163.

Oladosu, Y., Rafii, M. Y., Abdullah, N., Magaji, U., Hussin, G., Ramli, A., et al. (2016). Fermentation quality and additives: A case of rice straw silage. *BioMed Research International, 2016*, 1–14.

Oldenburg, E. (1991). Mycotoxins in conserved forages. *Landbauforschung Völkenrode, Sonderheft, 123*, 191–205.

Oliveira, A. S., Weinberg, Z. G., Ogunade, I. M., Cervantes, A. A., Arriola, K. G., Jiang, Y., & Adesogan, A. T. (2017). Meta-analysis of lactic acid bacteria inoculation effects on silage fermentation and cow performance. *Journal of Dairy Science, 100*(6), 4587–4603.

Oude Elferink, S. J. W. H., Krooneman, J., Gottschal, J. C., Spoelstra, S. F., Faber, F., & Driehuis, F. (2001). Anaerobic conversion of lactic acid by *Lactobacillus buchneri*. *Applied and Environmental Microbiology, 67*, 125–132.

Özdüven, M. L., Koç, F., Polat, C., & Coşkuntuna, L. (2009). The effects of lactic acid bacteria and enzyme mixture inoculants on fermentation and nutrient digestibility of sunflower silage. *Kafkas Üniversitesi Veteriner Fakültesi Dergisi, 15*, 195–199.

Özdüven, M. L., Kurşun Önal, Z., & Koç, F. (2010). The effects of bacterial inoculants and/or enzymes on the fermentation, aerobic stability and in vitro dry and organic matter digestibility characteristics of triticale silages. *Kafkas Üniversitesi Veteriner Fakültesi Dergisi, 16*(5), 751–756.

Pahlow, G., Muck, R. E., Driehuis, F., Oude Elferink, S. J. W. H., & Spoelstra, S. F. (2003). Microbiology of ensiling. In *Silage science and technology* (pp. 31–94). American Society of Agronomy.

Palmonari, A., Cavallini, D., Sniffen, C. J., Fernandes, L., Holder, P., Fagioli, L., Fusaro, I., Biagi, G., Formigoni, A., & Mammi, L. (2020). Characterization of molasses chemical composition. *Journal of Dairy Science, 103*(7), 6244–6249.

Ranjit, N. K., & Kung, L., Jr. (2000). Effects of *Lactobacillus buchneri* and *Lactobacillus plantarum* on corn silage fermentation and stability. *Journal of Dairy Science, 83*, 526–535.

Romero, J. J., Park, J., Joo, Y., Zhao, Y., Killerby, M., Reyes, D. C., et al. (2021). A combination of *Lactobacillus buchneri* and *Pediococcus pentosaceus* extended aerobic stability of corn hybrids ensiled at low dry matter. *Journal of Animal Science, 99*(8), 1–16.

Rooke, J. A., & Hatfield, R. D. (2003). Biochemistry of ensiling. In D. R. Buxton, R. E. Muck, & H. J. Harrison (Eds.), *Silage science and technology* (Agronomy Series No. 42, pp. 95–139). American Society of Agronomy.

Seppälä, A., Heikkilä, T., Mäki, M., & Rinne, M. (2016). Effects of additives on grass silages and TMR. *Grass and Forage Science*.

Tabacco, E., Piano, S., Revello-Chion, A., & Borreani, G. (2011). Effect of *Lactobacillus buchneri* strains on corn silage aerobic stability under farm conditions. *Journal of Dairy Science, 94*, 5589–5598.

Taylor, C. C., & Kung, L., Jr. (2002). Effect of *Lactobacillus buchneri* 40788 on high-moisture corn fermentation. *Journal of Dairy Science, 85*, 1526–1532.

Uğurlu, S., Okuyucu, B., & Özdüven, M. L. (2022). The effects of bacterial inoculants on rye silages. *Turkish Journal of Agriculture–Food Science and Technology, 10*(3), 426–433.

Weinberg, Z. G., Szakacs, G., Ashbell, G., & Hen, Y. (1999). Effect of lactic acid bacteria on wheat and sorghum silages. *Journal of Industrial Microbiology & Biotechnology, 23*, 218–222.

Wilkinson, J. M., & Davies, D. R. (2013). The aerobic stability of silage: Key findings and recent developments. *Grass and Forage Science, 68*(1), 1–19.

Woolford, M. K. (1984). *The silage fermentation*. Marcel Dekker.

Xu, J.-Y., Na, B.-B., Liu, S., Chen, C., Sun, H., & Zheng, Y.-L. (2021). Silage of lactic acid bacteria and its application. *Biotechnology Bulletin, 5*, 39–47.

Yitbarek, M., & Tamir, B. (2014). Silage additives: Review. *Open Journal of Applied Sciences, 4*, 258–274.

Zhao, J., Tao, X., Wang, S., Li, J., & Shao, T. (2021). Effect of sorbic acid on rice straw silage. *Journal of Applied Microbiology, 130*, 1456–1465.

Zheng, J., Wittouck, S., Salvetti, E., Franz, C. M. A. P., Harris, H. M. B., Mattarelli, P., et al. (2020). A taxonomic note on *Lactobacillus*. *International Journal of Systematic and Evolutionary Microbiology, 70*, 2782–2858.

CHAPTER 3

UAV and Drone Technologies for Agricultural Field Monitoring and Assessment of Plant Health

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1. INTRODUCTION

Agriculture is fundamentally a production system characterized by spatial heterogeneity. Within even a small field, it is quite plausible for various parameters such as biomass, nutrient level, water availability, disease levels, weed pressure, and yield potential to display considerable variation across the field. Traditionally, management is done without taking account of the variation that exists - treating the field almost like a production unit where input application levels are more or less similar. For example, application of irrigation, fertilizers, pesticides and other farm inputs at roughly uniform rates. In this way, differences in the needs of the crop in varying parts of the same area are not accounted for. Precision agriculture solves this problem through the idea of pairing input requirements (for crops) and their availability in different (temporal and spatial) periods. This requires that the farmers must depend on very good sources and in-depth data concerning the crops and soil conditions (Maes & Steppe, 2019; Tsouros et al., 2019a, 2019b).

Remote sensing is among the primary sources for such data. For large-scale monitoring or at regional scales, satellite imagery is the most practical tool. However, satellite sensors can be limited by their resolution, the ability to revisit areas at the right time, cloud cover and the availability of suitable observations at the key crop development phases. In these ways, the use of UAVs is very different from that of satellites. They are able to take very high-resolution pictures quickly as and when needed, and usually only over very small areas. With their ability to provide both high spatial and temporal resolutions along with a set of optical and thermal sensors, it is no wonder that UAVs have become one of the main tools for accurately monitoring crops today (Maes & Steppe, 2019; Tsouros et al., 2019a, 2019b).

UAVs have also evolved in their function thanks to advances in artificial intelligence. They no longer need be just flying cameras! A present-day UAV system can be viewed as a complete automated sensing device which connects everything: image taking, image processing, machine-learning analysis, geospatial mapping, and decision support. Through optical (RGB, multispectral, hyperspectral), thermal image and LiDAR sensors, it is possible to obtain different types of information complementary to each other. Additionally, machine learning methods can extract hidden patterns or relations from such a mass of data to finally produce a map of the crop's physical properties (disease, weeds, stress, biomass, etc.) or agronomic characteristics. The overall procedure therefore, starting from planning the work and getting the data, up to the calibration of the equipment, photogrammetric processing, image analysis, AI interpretation, geospatial mapping and eventually making the decision of the intervention.

2. UAV PLATFORMS AND THEIR AGRICULTURAL APPLICATIONS

Words like "UAV" or "drone" may be sometimes used interchangeably with "unmanned aircraft system (UAS)", albeit these two are different things describing different parts of a general system.

Agro-monitoring is among these uses of the UAV system where a UAV with other accessories such as flight controller and a remote-control interface will make up the major parts whereas positioning equipment like GNSS/GPS, imaging sensors, communication tools, the ground-control unit, and software to process and interpret the collected data will be the accessories of the system as well. Platform selection should be made considering the factors such as the area under cultivation, the shape of the land/terrain, number of days the task will be done/ the period of the task, sensor carrying capacity, the desired spatial resolution, and the type/purpose of the task. For example, multirotor unmanned aerial vehicles are preferred for small and irregular-shaped fields because they are capable of vertical take/off and landing, floating, and hovering.

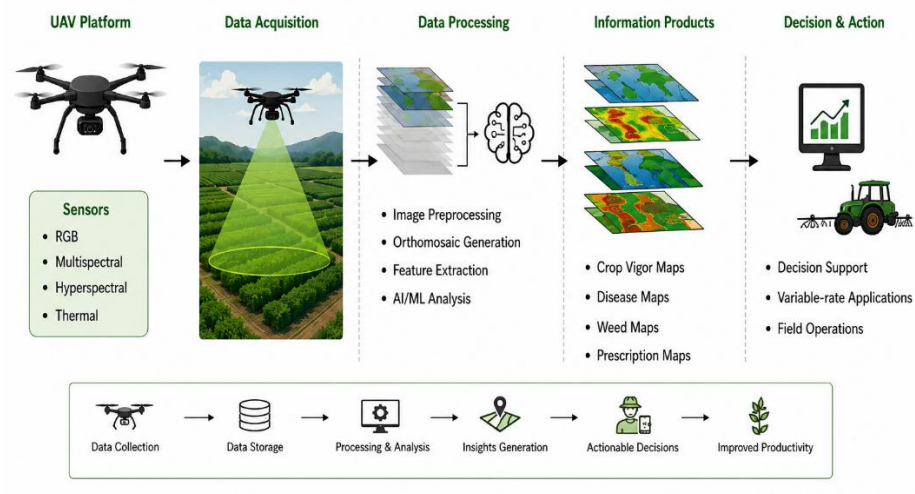


Figure 1. General architecture of UAV-based agricultural monitoring.

On the other hand, a fixed-wing aircraft will be the best UAV platform if we want to monitor an extensive area because the design of forward-flight gives these platforms a longer time of endurance and greater area coverage compared to a hovering flight. However, they are not able to hover and also require appropriate launching and landing equipment. The vertical take-off and landing (VTOL) type of hybrid systems integrate features of the two types of flying structures while single-rotor and heavy-lift multirotor platforms are able to be equipped with and carry even more massive, bulky, heavy or specialized sensors. Table 1 highlights the general strengths of each of these types of UAVs that make them well-suited to their respective applications.

Table 1. Comparison of UAV platforms used in agricultural applications.

UAV Platform	Typical Flight Time	Payload Capacity	Main Advantages	Main Limitations	Recommended Agricultural Applications
Multirotor UAV	20–45 min	Low–medium	High maneuverability; precise flight control; suitable for small and irregular fields	Limited endurance; relatively low coverage per flight	Crop monitoring, disease detection, weed mapping, field scouting, precision spraying
Fixed-wing UAV	45–120+ min	Medium	Long endurance; high area coverage; efficient flight	Cannot hover; less suitable for small/irregular fields; more complex operation	Large-scale crop monitoring, vegetation mapping, biomass estimation, stress assessment
Hybrid VTOL UAV	45–120 min	Medium	Combines VTOL flexibility with fixed-wing endurance and coverage	Higher cost and system complexity	Large-field monitoring, regional crop surveillance, multispectral mapping
Single-rotor UAV	30–90 min	Medium–high	Higher payload capacity and endurance than many multirotors	More complex mechanics; higher operational risk	Heavy sensor payloads, specialized mapping, experimental agricultural applications
Heavy-lift multirotor	15–40 min	High	Can carry spraying systems and heavy multisensor payloads	Shorter endurance; high energy consumption	Precision spraying, liquid application, multisensor crop monitoring

3. MISSION PLANNING AND IMAGE ACQUISITION

The quality of agricultural information derived from UAVs is mainly determined by how the mission is designed. The flight altitude, speed, image overlap, camera angle, acquisition time, illumination, sensor settings, ground sampling distance (GSD), and weather conditions ought to have been decided before the data collection phase itself. GSD is the measure of the ground area reflected by one image pixel. Generally, a lower flight altitude would decrease the GSD and thus enhance the details of the spatial information, but it also means the amount of area covered per flight is smaller as well as the number of images and consequently the amount of data that needs processing, which can be significant. That being said, mission planning essentially constitutes the weighing of spatial resolution against field extent together with flight time and one's data management demands, i.e., handling and storing a lot of images (Tsouros et al., 2019a, 2019b).

For photogrammetric reconstruction, image overlapping is no less significant. Forward overlap as well as side overlap are what give visual information that software relies on to detect features at the same spot across adjacent images and so to generate the 3D geometry of a scene. If there is not enough overlap in two images a result could be that holes appear in reconstruction, some parts become

slightly misaligned or one can see the effects of the original image grid in the final image, or even a totally missing area. Excessive overlapping on the other hand leads to more images produced which also makes the software processing time longer. Therefore, there is no universal solution since the level of overlap depends on the type of camera, how high is the altitude at which one is flying, the speed of the aircraft, the terrain, type of the planting/crop and lighting conditions (Tsouros et al., 2019a, 2019b).

4. UAV SENSOR TECHNOLOGIES FOR CROP MONITORING

4.1 RGB, Multispectral, Hyperspectral, and Thermal Imaging

To most people, RGB sensors of drones remain one of the few affordable sources for aerial data since they are very cheap compared to other types, widely sold and the camera is simple to operate. Besides, these sensors can deliver a high spatial resolution photo. RGB sensors can be used to map crops, count plants, evaluate the canopy, check for visible signs of diseases and identify weeds. The major drawback of these sensors is that they can only detect what is within the visible range and thus might miss out on the changes in the physiological state that have taken place prior to symptoms showing. If one is able to detect physiological changes using the visible spectrum only it would be difficult. Hence, the use of multispectral sensors. Multispectral sensors capture different light wavelengths such as blue, green, red, red-edge and near-infrared. The information collected in the different spectral bands will provide great results as input for indices of plant health and crop vigour measurement, nutrient status analysis, and stress evaluation besides the usual vegetation indices.

We call "hyperspectral" sensors those that are sensitive to many and often contiguous narrow spectral bands. In that way, through each pixel, a very comprehensive spectroreflectometric signature is produced which in turn can open the door to detecting even tiny distinctions at the biochemical and structural levels of plants and have been used for detecting diseases, assessing of nutrients, identifying water stress, weed differentiation, and even classification of different species. The problem is that these advantages come along a lot of challenges: a big data size, higher costs, more laborious processing, and greater sensitivity to acquisition and calibration factors (Maes and Steppe, 2019; Mensah et al., 2024). Thermal imaging sensors offer an added layer of data by measuring emitted thermal heat radiation, typically in the longwave infrared region. Since surface temperature is linked to transpiration and thus water status, the use of thermographic imagery can give a great insight into the state of water and the heat-stress of the crop, but one needs however to be mindful of external factors which are solar radiation, wind, atmospheric conditions, canopy arrangement, emissivity of the surface, and sensor calibration.

Table 2. Comparison of major UAV sensors used in agricultural monitoring.

Sensor Type	Approximate Spectral Range	Major Advantages	Main Limitations	Typical Agricultural Applications
RGB	400–700 nm	Low cost; easy operation; high spatial resolution; widely available	Limited spectral information; weak sensitivity to some physiological changes	Crop stand assessment, plant counting, canopy cover, weed detection, disease symptom detection
Multispectral	Approximately 450–900 nm	Vegetation-sensitive spectral information; suitable for vegetation indices; manageable data volume	Fewer bands than hyperspectral sensors; calibration required	Crop vigor assessment, biomass estimation, nutrient/stress monitoring, disease detection, yield estimation
Hyperspectral	Approximately 400–1000+ nm; system dependent	Detailed spectral signatures; high sensitivity to biochemical and physiological changes	High data volume; expensive; computationally demanding; sensitive to illumination and calibration	Early disease detection, nutrient status, biochemical characterization, stress discrimination
Thermal	Approximately 8–14 μm for common LWIR systems	Measures canopy temperature; useful for water and heat stress	Sensitive to environmental conditions, emissivity and atmospheric effects; often lower spatial resolution	Water-stress detection, irrigation management, heat-stress assessment, disease-related thermal anomalies

5. VEGETATION INDICES AND PLANT-HEALTH INTERPRETATION

By vegetation indices, the spectral data is turned into numeric values that are connected with plant state in some way. Of the many indices, normalized difference vegetation index (NDVI) has become almost synonymous with plant vigor because it reflects the differential capability between red and near-infrared reflections (R and NIR respectively) and hence can serve as a proxy measure of plant productivity. There are other indices such as NDRE, GNDVI, SAVI, EVI, NDWI, GCI, and MSI that have been suggested or used to highlight certain characteristics like those of the pigments, the condition of the plants as a whole, the effect of the soil as the background, moisture and/or water content, etc. (Figure 2 and Table 3). The choice of an index should be driven by the biological question and the characteristics of the crop and acquisition system rather than by popularity alone (Maes & Steppe, 2019).

NDVI is calculated as follows: $(NIR - Red) / (NIR + Red)$

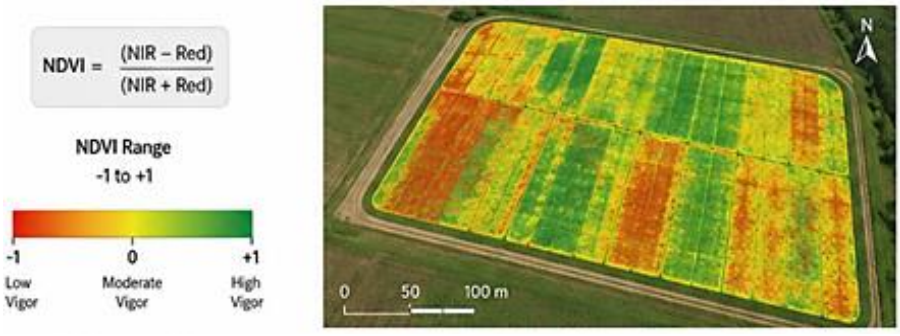


Figure 2. NDVI-based crop vigor mapping.

Generally higher NDVI is linked with healthy and actively growing vegetation and lower NDVI can be attributed to disease, lack of rainfall, nutrient scarcity, poor emergence, senescence, physical injury or bare soil. Thus NDVI isn't a specific measure for a disease. Remote sensing offers more accurate results if vegetation indices are combined with observations taken in the field and environmental or agronomical data (Chakhvashvili et al., 2024; Maes & Steppe, 2019).

Table 3. Common vegetation indices and their agricultural applications**.**

Vegetation Index	**Formula**	**Main Spectral Bands**	**Primary Sensitivity**	**Typical Agricultural Applications**
NDVI	(NIR − Red) / (NIR + Red)	Red, NIR	Vegetation vigor and chlorophyll-related response	Crop vigor mapping, biomass assessment, stress detection, yield estimation
NDRE	(NIR − Red Edge) / (NIR + Red Edge)	Red Edge, NIR	Chlorophyll content and canopy condition	Nitrogen-status assessment, late-season crop monitoring, stress detection
GNDVI	(NIR − Green) / (NIR + Green)	Green, NIR	Chlorophyll and leaf structure	Crop vigor monitoring, nitrogen assessment, biomass estimation
SAVI	(1 + L)(NIR − Red) / (NIR + Red + L)	Red, NIR	Vegetation response with reduced soil-background influence	Sparse vegetation, early crop stages, soil-exposed fields
EVI	G × (NIR − Red) / (NIR + C_1Red − C_2Blue + L)	Blue, Red, NIR	Vegetation density and canopy structure	Dense crop canopies, biomass estimation, crop-

Vegetation Index	Formula	Main Spectral Bands	Primary Sensitivity	Typical Agricultural Applications
				condition assessment
NDWI	(NIR − SWIR) / (NIR + SWIR)	NIR, SWIR	Leaf/canopy water content	Water-stress monitoring, irrigation management, drought assessment
GCI	NIR / Green − 1	Green, NIR	Leaf chlorophyll concentration	Nitrogen management, chlorophyll estimation, nutritional assessment
MSI	SWIR / NIR	SWIR, NIR	Vegetation water stress	Drought monitoring, irrigation decision support, plant-water-status assessment

Normalized Difference Red Edge Index (NDRE), Green Normalized Difference Vegetation Index (GNDVI), Soil-Adjusted Vegetation Index (SAVI), Enhanced Vegetation Index (EVI), Normalized Difference Water Index (NDWI), Green Chlorophyll Index (GCI), and Moisture Stress Index (MSI).

6. REMOTE SENSING FOR PLANT-HEALTH ASSESSMENT

Remote sensing can give insights into different aspects of a plant's well being by measuring various aspects of the plant. For example it can assess reflectance of the plant canopy, temperature, biomass, plant height, various spectral indices, properties related to the chlorophyll, and water content. Therefore, plant-health assessment is a stepwise process from sensors to an agronomic diagnosis through indicators and physiological interpretation. This is an incredibly important distinction as it is possible for different causes to result in very similar responses in remote-sensing. Reduced vegetation vigor could potentially result from a variety of diseases or even a combination of different diseases, drought, nutrient deficiency, insect damage, or herbicide injury (Chakhvashvili et al., 2024; Maes & Steppe, 2019).

Therefore, reliable disease detection using UAV monitoring needs to be closely linked with ground-truth studies. Examples of the ground-truth measurements could be, the number and seriousness of disease cases, weeds present and weed number identification, chlorophyll levels, leaf moisture, soil moisture levels, and harvested quantity. When remote-sensing (UAV derived) data with field-based observations are connected at their geographic location, it can result into better understanding of the underlying process of the crop development and serve as an important basis for the design, as well as the verification phases, of the machine learning models.

7. UAV-BASED CROP DISEASE DETECTION AND EARLY WARNING

Disease detection is one of the most promising applications of UAV technology because pathogens can alter leaf color, canopy structure, leaf area, chlorophyll status, water relations, temperature, and spectral reflectance. UAV imagery can therefore support rapid assessment over large areas while repeated flights make it possible to examine disease development through time (Chin et al., 2023; Shahi et al., 2023).

The best spatial scale for you is dependent upon the type of problem that you, as a manager, want. Leaf-by-leaf observations are concerned with looking at different kinds of lesions, at the plant level one will find diseased plants and at the plot level a diseased plant is defined by being at least partly diseased. At the field level maps show where disease has spread the most in a given area. UAVs can give very detailed information for plot as well as field levels. Diseases may be measured as the share of plants that are affected whereas disease severity refers to the proportion of disease in the plant. UAV-derived estimates of severity based on color of canopy, vegetation index, canopy texture, leaf surface temperature, or density of plant as well as a deep-learning model could be calibrated on a ground-truth measurements to make accurate disease severity prediction (Chin et al., 2023). A single photograph is not a good reference compared with a time series of UAV images for disease control and prevention. One example is when a vegetation index is falling slowly together with weather favoring pathogens a field scout would be directed to focus on this field where as the final diagnosis will have to be verified with biology.

8. UAV-BASED WEED DETECTION AND CROP–WEED DISCRIMINATION

Use of Unmanned Aerial Vehicles (UAVs) for weed monitoring includes determination of the weed occurrence location, weed distribution density, identification of the dominant species in cases that is a problem species of the time, and changes of weed pressure from time to time and from place to place. This information is of great use in managing weeds in a site-specific way, i.e., by directing attention and treatment to areas with a higher level of weed pressure (Maes & Steppe, 2019; Pérez-Ortiz et al., 2015). The biggest challenge, however, is that crops and weeds are both vegetations that have a green color, especially during early growth phases, making crop and weed discrimination quite tricky. Thus, even though a vegetation index detects vegetation it still fails to reliably separate crop species from their wilder kin (Figure 3).

It is possible to effectively distinguish a crop from the weed based on plant shapes, leaf arrangement, presence of crop rows, texture differences at the

canopy, spectral signature, height, and temporal development. Computer vision-based identification methods have demonstrated the benefit of image classification in the recognition of weeds and crops, and multiband (multispectral) and hyperspectral sensors can give more details when the physical appearance of a plant is not clear enough (Lottes et al., 2017a, 2017b; Mensah et al., 2024; Sa et al., 2018). The weed map, which is the outcome of processing data from weed monitoring and weed mapping, can be represented as a georeferenced, weed density map with low-, moderate and high-pressure areas identified on it. This weed map could then be converted into an agrochemical control map showing prescription doses required for site-specific weed management.

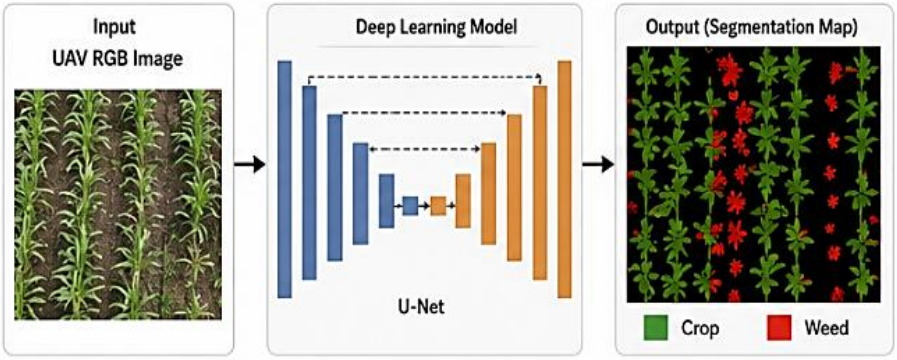


Figure 3. Deep-learning-based crop–weed semantic segmentation.

9. IMAGE PREPROCESSING, ORTHOMOSAICS, AND GEOREFERENCING

In most cases, the original image of an UAV that records the scene as it is does not require analysis unless it first undergoes a number of image processing operations. Workflow of image analysis varies depending on sensor type and objective. Common steps include assessing the image's quality, radiometric calibration, geometric correction, image registration, noise filtering, orthorectification, mosaicking, spectrally normalization, and identifying of vegetation (Tsouros et al., 2019a, 2019b).Radiometric calibration plays a vital role in multispectral and hyperspectral imaging; one has to understand that raw values must be associated with reflectance measurements to ensure proper interpretation.

Without proper calibration, it's really difficult to tell if the variation seen between two images is because of lighting or because of differences in the fields. To make things right and prevent mistakes, illumination and environmental parameters such as light availability, cloudiness, shadows, wind, water vapor concentration, rainfall events etc. should be logged as far as it's practical to do so to be able to standardize these conditions later on. Besides that an acquisition of

a single image by a flying robot will only provide limited coverage of the field hence multiple overlapping photos will have to be photogrammetrically combined into a large-scale image, i.e an orthomosaic. Such orthomosaic is quite a convenient way of making a spatially integrated image that can be used for analysis and mapping at the farm level (Sa et al., 2018; Tsouros et al., 2019a, 2019b).

Positioning UAV images onto an exact map with geographic coordinates is called georeferencing and becomes a necessity for integrating or comparing data across different flights or other data sources in GIS/disease map/weed maps/treatment maps/agro-machinery operations etc. GPS-derived data can provide approximate positions, while RTK, PPK, or accurately measured ground control points (GCPs) can provide accurate positioning data. Geographical precision level required would depend upon the nature of the operation. For field inspection purposes, absolute positioning down to the centimetre may not be necessary. Whereas, for repetitive spatial analysis and precision maps of treatments, higher accuracy of positioning should certainly be adopted (Tsousros et al., 2019).

10. GIS INTEGRATION, SPATIAL MAPPING, AND TEMPORAL CHANGE DETECTION

If UAV data is used alone, its value in agriculture may be limited. The data from the UAV can provide a very detailed view of the field, but it will only be useful for farming decisions if it is connected to a wider source of information, such as a soil map or weather data.

The integration of the UAV data and GIS provides farmers with the opportunity to create decision-making tools for spatial analysis and management. For example, they could merge field boundaries, digital soil maps, information about yields, irrigation maps, the records of fertilizer application, weather data, the tracks of machines, and the locations where weeds and diseases were found previously, with UAV photos for more accurate field planning (Maes & Steppe, 2019; Tsouros et al., 2019).

With the ability to integrate all these features, users can, for instance, pinpoint repeatedly infected areas, check weed pressure against crop density, and correlate what they see at the moment they see it with past management and environmental conditions. Such integration allows users to identify recurring disease zones, compare weed pressure with crop density, and relate current observations to previous management and environmental conditions.

Furthermore, multiple UAV flights enable the detection of changes over time. Observations at various dates can show decline, development of disease, symptoms of drought, changes caused by harvesting, or mechanical damage, For example, the change in NDVI between two observation dates can be represented

as ΔNDVI = NDVI(t2) − NDVI(t1). Temporal data should still be looked at with reference to how consistent the data collection was because differences in illumination, changes in sensor configuration, recalibrations, or flight parameters could otherwise be taken as signs of biological change (Chakhvashvili et al., 2024; Maes & Steppe, 2019).

11. MULTISENSOR MONITORING OF CROP STRESS

Certainly, no one sensor gives an all-inclusive picture of the actual condition of a plant. While RGB images give detailed morphological characteristics and visual symptoms, multispectral images offer photosensitive vegetation measurements. Hyperspectral imaging allows for very accurate color separation, and infrared images can give information related to the temperature of the canopy and the water situation. Therefore, it will usually be possible to obtain better understanding by using several observations at the same time. This is especially the case with the symptoms of disease, drought, deficiency of nutrients, etc., that give nearly similar visual or spectral responses (Chakhvashvili et al., 2024; Maes & Steppe, 2019).

The idea is the same when applied to individual cases. Nitrogen deficiency, for instance, can cause variations in chlorophyll levels, a change in the color of the leaves, and canopy reflectivity, and these are the sorts of factors which spectral reflectance can help evaluate. Crop type, stage of growth, canopy pattern, soil background, and weather conditions can all affect these interactions so, in order to trust UAV-derived data, it's necessary to check field measurements first before drawing conclusions directly from physiological measurements.

12. CROP PHENOTYPING AND YIELD ESTIMATION

The utilization of UAVs for high-throughput crop phenotyping has become a regular practice and one of their main attractions is the opportunity of making repeated aerial observations that measure, in a non-invasive way, the height of individual plants, the canopy size, biomass-related traits, flowering, lodging, plant density, and rate of growth (Sankaran et al., 2015). To this day, the 3D imaging technique remains one of the best means of getting the information on plant height. As a result, UAV systems are not only very efficient in crop protection applications but also valuable for breeding and cultivar evaluation. Likewise, these kinds of data obtained through 3D reconstruction can equally be applied to yield estimation where predictors may include crop vegetation, canopy cover, vegetation indices, plant height, flowering intensity, biomass, and thermal characteristics. As yield is a combination of different factors that develop throughout the growing season, it goes without saying that, on a general level, multi-temporal UAV observations would (Maes & Steppe, 2019; Sankaran et al., 2015).

13. ARTIFICIAL INTELLIGENCE AND DEEP LEARNING FOR UAV IMAGERY

Artificial intelligence can be incorporated into the UAV system workflow in various ways. An object-detection algorithm can pinpoint the location of plants, weeds, trees, or infected spots; classification is a machine learning algorithm that will label them as crop, weed, disease, or stress; semantic segmentation can help in clearly defining and marking the boundaries of the plants and disease spots; and finally, one can rely on regression models for estimating disease severity, biomass, nutrient levels, or productivity; and also, on predictive models for forecasting disease or stress risk (Chin et al., 2023; Shahi et al., 2023). These techniques together change UAVs from just a tool for observation to a smart one that can recognize, quantify, predict and even advise on the next steps.

Deep-learning techniques are very beneficial in interpreting complicated agricultural pictures, as they can learn from the data and not depend on feature designs by hand. Convolutional Neural Networks (CNNs), U-Net, SegNet, Faster R-CNN, You Only Look Once (YOLO), Mask R-CNN, and those based on a transformer structure are some examples of the deep-learning architectures used for the analysis of agricultural images. Precision management has a high degree of dependency on semantic segmentation since knowing just that there are weeds is of little value compared with knowing exactly where they are (Lottes et al., 2017a, 2017b; Milioto et al., 2017; Sa et al., 2018).

BIG aerial orthomosaics have also led to a new trend in deep learning by combining them with the multispectral data. The WeedMap system, for example, created a semantic weed map with aerial multispectral images and deep neural networks, clearly showing how the shift from individual-level image classification has resulted in large-scale mapping (Sa et al., 2018). In practice, UAVs form the observational layer and AI the interpretative layer, after which GIS will map the predictions as spatial units of management.

14. FROM UAV IMAGERY TO PRESCRIPTION MAPS AND SITE-SPECIFIC CROP PROTECTION

Only the real value of the UAV operational system gets demonstrated if the information obtained from such equipment can be turned into an agricultural plan. Monitoring the situation by taking images of a farm through aircrafts (like UAVs) will give insight to what kind of weeds and their distribution and density are like to help create better zones of management and allow for the targeted Variable Rate Technology (VAT) application. Disease diagnosis based on UAV-derived images. You can combine the images and other environmental factors as input variables in your disease prediction model to identify high-risk areas, measure the disease severity, determine the areas of treatment, and finally prioritize the actions you should take for intervention (Maes & Steppe, 2019; Pérez-Ortiz et al., 2015).

The role of UAVs in monitoring and UAVs for applying herbicides must be different. The main responsibility of a monitoring UAV is to detect through sensors such as red, green, blue (RGB), multispectral, hyperspectral, thermal that information that is of interest for a farmer. However, a spraying UAV is just a carrier vehicle that moves spraying gear in agricultural production. Even though it is possible that these two tasks are being completed independently they could still work in synergy if a monitoring UAV supplies images to AI. AI then analyzes the images and prescribes what treatments are needed which could be sent directly to a spraying UAV which would apply the treatment as prescribed. This kind of system can help save unnecessary herbicide application and still effectively and accurately treat disease.

15. DATA QUALITY, GROUND TRUTH, VALIDATION, AND MODEL RELIABILITY

Even when an AI algorithm is very complicated it is going to make wrong predictions if the data given in is incorrect. UAV images which appear blurred due to motion, not much overlapping images and low-quality images taken in different light conditions, sensor saturation causing the images to look washed out or overly bright areas, radiometric calibration errors (that is, the way the sensor measures different light intensities being off), georeferencing errors which mean that the real position of places on the images is incorrect, and other factors leading for inconsistencies in the data collection will all be propagated through to the results of the analytics and finally undermine the trustworthiness of the produced maps. The data quality control procedures should be an integral part of the data analysis, and to do the same job again one has to ensure consistency in the time of flight, altitude, the type and setup of the sensor, the calibration procedures, and the processing of the data, if only the results of the comparison will be trustworthy (Chakhvashvili et al., 2024; Tsouros et al., 2019a, 2019b).

Ground truth is of equal importance because UAV observations provide the means of assessing biological condition only indirectly. Field observations should form an integral and systematic component of the data, with the location of the field samples properly indicated in reference to the spatial locations of the UAV data. The disease incidence, severity, weed density, species identity, chlorophyll, water status, soil moisture, and yield may act as reference variables depending on the objective of the study. Without solid ground truth, even apparently a good model performance may not be easy or clear explanation of the results and may not give any indication to the field usefulness of the technique. To do this, the way we assess the accuracy of a model has to be aligned with the purpose of the analysis (Chin et al., 2023; Maes & Steppe, 2019).

Classification is one of the types of accuracy assessment which includes calculating accuracy, precision, recall, F1-score, and using of the confusion matrix; segmentation can be evaluated using of IoU, Dice coefficient and pixel

accuracy; regression is one of accuracy assessments that can also benefit from the metrics of R^2, RMSE, and MAE; spatial mapping has its own set of requirements such as positional accuracy, area agreement, and spatial consistency. A model may have high pixel-level accuracy but still be giving inadequate spatial localization which would be a real problem if the system is going to be used for precision interventions. The reproducibility of a study also necessitates the thorough documentation of UAV specifications, sensor features, flight parameters, acquisition dates, environmental conditions, calibration, ground-truth procedures, data processing, statistical evaluation.

16. CHALLENGES IN UAV-BASED DISEASE AND WEED DETECTION

Detecting disease is difficult, among other reasons: different diseases can produce very similar symptoms, early disease signs might be barely visible, abiotic factors can show signs similar to that of diseases, canopy structure may conceal infected leaves, and UAV captures can lack spatial detail required for resolving tiny lesions at higher altitudes. All these issues are just some of the reasons that automated disease detection systems must be verified and validated in the field rather than being viewed as error-proof diagnostic tools (Chin et al., 2023; Shahi et al., 2023). Detecting weed species has many overlapping features with diseases yet is also a separate area that brings its own challenges. Early weed seeds may look and appear very similar to the crop seedlings both in the morphological and the spectrophotometric aspects.

As the growth stages of crop and weed plants are usually intermingled, occlusions happen quite often, especially with high-density crops like grass in the case of maize and the broadleaf weeds in wheat. The complexity of field is increased when a variety of weed species are present as well as when plant morphology changes with the development. The bare soil and shadows areas are additional segmentation challenges. Therefore, all these conditions must be taken into account for training ML models and the necessity of the training datasets to be comprehensive, the field validation needs to be independent has been reinforced (Mensah et al., 2024; Pérez-Ortiz et al., 2016).

17. ECONOMIC AND ENVIRONMENTAL CONSIDERATIONS

Implementing UAV technology for monitoring purposes must not only take into account the technical features and capabilities of the equipment but also the economic value of using them. Cost drivers are likely to be related mainly to the type of aircraft used, sensors, batteries, software solutions, pilot training, data storage, cloud computing, upkeep, and regulatory compliance. Benefits such as reducing scouting labor, avoiding unnecessary field visits, the possibility of making disease diagnostics earlier, increasing the efficiency of water use, and decreasing the amount of chemical input while at the same time improving the quality of crops and management are some potential advantages. The economic

viability of UAV technology would then be influenced by at least the crop price (value of the crop to be grown), the land area, the frequency of monitoring, and the agricultural management system in which UAV is to be incorporated as a tool (Tsouros et al., 2019a, 2019b).

Environmental gains are also conditional - not an automatic feature. For instance, by making use of the UAV for precision agriculture, the amount of inputs and fuel used, and the number of times people or machines walk over the field, are all reduced so the environment may be protected. If UAVs actually lead to significantly more accurate farm management decisions, then its environmental role will be based less on the quantity of images produced and most on the impact of these images on the quality and targeting of decisions at the farm level. Therefore, the environmental worth of this technology is largely conditioned on not how much imagery one collects with UAVs but on whether those images help one to make better quality and targeted farm decisions (Maes & Steppe, 2019; Tsouros et al., 2019a, 2019b).

18. AUTONOMOUS MONITORING, EDGE COMPUTING, AND MULTIMODAL SYSTEMS

In order to achieve greater autonomy, UAVs are likely to evolve into highly intelligent autonomous systems. A smart monitoring system for example might accept a field boundary as input, generate a route, execute the mission, analyze the data, pick up on irregular areas, make risk maps, and possibly suggest further investigations. Flexible scanning might be a technique which enables a UAV to spend more time on an area which initial analysis indicated some unusual crop or weed conditions. By such approaches, UAVs will no longer be passive tools for gathering data but turn into an active tool for monitoring (Tsouros et al., 2019a, 2019b).

Edge computation that happens either in real time or quasi- real time could reduce the gap between when the image is captured and when it is understood. On the UAV itself or in proximity to it the computer will execute operations as preprocessing, object detection, segmentation, or anomaly detection while or just after the flight. Based on these detections a system might redirect the UAV to a spot that is urgent, and gather more imagery with a very refined resolution. In addition to that, the development of multimodal systems is expected, as such system are designed to integrate various sources of information, namely: RGB, multispectral, hyperspectral, thermal, and structural data for a more accurate and comprehensive assessment of the plant health status (Chakhvashvili et al., 2024; Maes & Steppe, 2019).

Another potential development direction would be agricultural digital twins. Basically, in simple words, a digital twin is a living digital picture of an actual field that gets updated regularly based on observations such as crop growth, structure, disease, weed infestation, and other spatial patterns. With time such

representations might help to carry out scenario analyses before management measures are put into effect. Also, the combination of aerial and ground platforms can bring significant advantages since although UAVs are very good at capturing images from the air covering large areas, ground robots can move towards individual plants for a detailed inspection or targeted action (Liebisch et al., 2017).

19. HUMAN EXPERTISE, STANDARDIZATION, REGULATION AND DATA GOVERNANCE

Even as the degree of automation is increasing, farmers and agronomists should be in the loop and play a significant role. Crop history, past disease outbreaks, practices of irrigation and fertilization, use of pesticide, weed flora, and varieties are examples of context provided by farming experts which may not be directly observable in images. To sum up, a cooperative model in which unmanned aircraft capture observations, artificial intelligence aids in interpretation, verification in the field finds biological patterns, and experts take over to decide upon management is the model most suitable for the farmer, according to studies (Maes & Steppe, 2019).

Nevertheless, the use of a standard methodology is important as differences in the types of drones, sensors, flying altitude, time of data collection, image processing software, vegetation indices, vegetation indices, and methods of ground-truth verification may have been made such that no direct comparison can been done. The experimental design needs to incorporate the regulatory aspects such as pilot licensing, aircraft documentation, altitude limitations, airspace restrictions, and visual-line-of-sight provisions, etc. as specified by the governing bodies (Tsouros et al., 2019a, 2019b).

20. PROPOSED UAV-BASED PLANT-HEALTH MONITORING FRAMEWORK

A working UAV-basedplant-health monitoring system would consist mainly of a chain of operations including mission planning, data acquisition, calibration, photogrammetry, modeling and reconstruction, image analysis, artificial intelligence, geospatial mapping, anddecision support. From planning to execution, all of these processes will work together to identify and address the different problems a farmer has to deal with. This will lead to a very detailed plant-health management system, allowing the farmer to monitor his crops more accurately and take the right steps at the right time.

Metric data such as orthomosaics, elevation maps, and point cloud scans are produced during the radiometric and photogrammetric processes. Image processing techniques can be used to retrieve a variety of features from a single aerial photo including vegetation indexes, texture, canopy features, etc. AI tools on the other, side will be able to detect pests and weeds, identify affected area,

analyze disease spread, perform crop health assessment, and forecast the situation. The result of these operations will be transformed into disease maps, weed maps, stress maps, or even prescription maps via GIS tools.

As the technology and methodology advance, disease observation via UAVs will be more efficient. It is expected that a few flights using multispectral sensors and/or the UAVs' cameras can capture sufficient information to determine areas with anomalies. The field is then visited to investigate further. These disease locations that are actually found will be recorded in the software and linked to the relevant UAV pixels or objects. That way, spectral, textural, spatial, and field observation variables will enable models to learn better. Similarly, multispectral and RGB images can feed a segmenting model to identify which areas are crop, which are weeds, and where is the soil. The weed pixels identified on the map can then be regrouped to define management zones. These cases reveal how UAVs are being integrated for monitoring with field data and crop protection practices being tailored for the site.

21. FROM UAV MONITORING TO AUTONOMOUS PRECISION AGRICULTURE

Farmers should remember that one of UAV technology's main advantages is making them the eyes above their land. Besides giving them a chance to replace scouting by walking the fields (and possibly risking getting tired or injured), an ongoing agricultural information system based on UAVs can be developed and used for years. This type ofsystem would automatically sense the status of crops, crop pattern interpretation will be done with the help of AI, and it will be transformed into spatial information by GIS tools, which will allow decision-making by prioritizing, for instance, different field areas. With those interventions having been made, an inspection by the farm equipment can show whether or not they have succeeded and that information can become an input for the next iteration of the sequence (Maes & Steppe, 2019; Tsouros et al., 2019a, 2019b).

The picture that is drawn in this way makes it clear where and how the contribution of drones can support farmers. Collecting maximum amount of data from imagery should be considered just as a small part of a larger picture, but replacing farmers' knowledge with an automaton labeling system is not in the game. Rather, collecting the right information at the right time and space scale and being able to make a recommendation of the next farming steps after understanding the current crop situation as per the environmental and soil conditions is the goal. Of course, these types of interpretations could lead to very different crop management decisions as the same vegetation response might have different biological causes.

22. CONCLUSION

Agriculturalists have embraced the use of unmanned aerial systems as a means of getting around the limitations that conventional methods of monitoring agricultural activities pose to them.It is because these machines deliver high-resolution images at very short notice besides which one can easily combine them with other types of data collection devices that most agricultural producers will rely on UAVs from then on. In essence, drones help farm producers turn fields into datasets by capturing spatial variations across the land which would otherwise be difficult and time-consuming for a single person to do at a glance. The primary value of UAVs and drones lies in their ability to provide a means for agriculturalists to carry out crop monitoring, identify plant diseases, produce maps of weed infested areas, assess crop stress levels, perform crop phenotyping, and predict yields. The RGB camera is a great source of clear images that anyone can afford. Multispectral sensors add more levels of color so it becomes easier to get the data about vegetation and the health condition of plants. Hyperspectral systems are a level above and provide a full spectrum of light for a detailed analysis, and finally, thermal sensors measure temperature and moisture and help to understand these factors that are so crucial for plant growth (Chin et al., 2023; Maes & Steppe, 2019; Mensah et al., 2024).

The application of artificial intelligence has allowed drones to go from simply gathering images to actively interpreting the scenes and even making decisions that have a spatial element, all thanks to integrating GIS, prescription maps, and precision machinery. The use of such output has made drones a possible site-specific crop protection tool; however, the system's performance depends on several things before and after the image is taken like mission sensors setup, image processing including georeferencing, ground hat are representative of the ground truth, appropriate statistical validation methods, and agronomic interpretation.

Next-generation machines will likely include various types of sensors, mission planning that is done autonomously, computing near the device so that one does not rely on the cloud so much, having a digital twins concept - this is like an exact replica, and finally having a collaboration of aerial and ground robots. At the same time, farming and field people will have a bigger role in interpretation in general and being the ones accountable to the decisions. Therefore, the most efficient way is not total automation but a fully-integrated system with UAVs, AI-based analysis, geospatial data, field trials, and the wisdom of an expert in the area. If all these components work hand in hand in this system, then the last result will be a better understanding of a crop and its requirements leading to faster, better decisions.

DECLARATION OF AI USE

AI-based tools were used to assist in the creation and design of some figures presented in this chapter. The authors take full responsibility for the scientific content, accuracy, and interpretation of the presented materials.

REFERENCES

Berni, J. A. J., Zarco-Tejada, P. J., Sepulcre-Cantó, G., Fereres, E., & Villalobos, F. (2009). Mapping canopy conductance and CWSI in olive orchards using high resolution thermal remote sensing imagery. *Remote Sensing of Environment, 113*(11), 2380–2388. doi:10.1016/j.rse.2009.06.018

Borra-Serrano, I., Peña, J. M., Torres-Sánchez, J., Mesas-Carrascosa, F. J., & López-Granados, F. (2015). Spatial quality evaluation of resampled unmanned aerial vehicle-imagery for weed mapping. *Sensors, 15*(8), 19688–19708. doi:10.3390/s150819688

Chakhvashvili, E., Machwitz, M., Antala, M., Rozenstein, O., Prikaziuk, E., Schlerf, M., ... Naethe, P. (2024). Crop stress detection from UAVs: Best practices and lessons learned for exploiting sensor synergies. *Precision Agriculture, 25*(5), 2614–2642. doi:10.1007/s11119-024-10168-3

Chin, R., Catal, C., & Kassahun, A. (2023). Plant disease detection using drones in precision agriculture. *Precision Agriculture, 24*(5), 1663–1682. doi:10.1007/s11119-023-10014-y

Eyili, M., & Kaya Altop, E. (2024). Weed detection in lettuce fields via image processing. In *Current studies on agriculture, forest and aquatic products* (pp. 299–341). Iksad Publications.

Liebisch, F., Popovic, M., Pfeifer, J., Khanna, R., Lottes, P., Stachniss, C., Pretto, A., Sa, I., Nieto, J., Siegwart, R., & Walter, A. (2017). Automatic UAV-based field inspection campaigns for weeding in row crops. In *Proceedings of the 10th EARSeL SIG Imaging Spectroscopy Workshop*.

Lottes, P., Hörferlin, M., Sander, S., & Stachniss, C. (2017a). Effective vision-based classification for separating sugar beets and weeds for precision farming. *Journal of Field Robotics, 34*(6), 1160–1178. doi:10.1002/rob.21675

Lottes, P., Khanna, R., Pfeifer, J., Siegwart, R., & Stachniss, C. (2017b). UAV-based crop and weed classification for smart farming. In *2017 IEEE International Conference on Robotics and Automation (ICRA)* (pp. 3024–3031). IEEE. doi:10.1109/ICRA.2017.7989347

Maes, W. H., & Steppe, K. (2019). Perspectives for remote sensing with unmanned aerial vehicles in precision agriculture. *Trends in Plant Science, 24*(2), 152–164. doi:10.1016/j.tplants.2018.11.007

Mensah, B., Rai, N., Betitame, K., & Sun, X. (2024). Advances in weed identification using hyperspectral imaging: A comprehensive review of platform sensors and deep learning techniques. *Journal of Agriculture and Food Research, 18*, 101388. doi:10.1016/j.jafr.2024.101388

Milioto, A., Lottes, P., & Stachniss, C. (2017). Real-time blob-wise sugar beets vs. weeds classification for monitoring fields using convolutional neural

networks. *ISPRS Annals of the Photogrammetry, Remote Sensing and Spatial Information Sciences, IV-2/W3*, 41–48. doi:10.5194/isprs-annals-IV-2-W3-41-2017

Pérez-Ortiz, M., Peña, J. M., Gutiérrez, P. A., Torres-Sánchez, J., Hervás-Martínez, C., & López-Granados, F. (2015). A semi-supervised system for weed mapping in sunflower crops using unmanned aerial vehicles and a crop row detection method. *Applied Soft Computing, 37*, 533–544. doi:10.1016/j.asoc.2015.08.027

Pérez-Ortiz, M., Peña, J. M., Gutiérrez, P. A., Torres-Sánchez, J., Hervás-Martínez, C., & López-Granados, F. (2016). Selecting patterns and features for between- and within-crop-row weed mapping using UAV-imagery. *Expert Systems with Applications, 47*, 85–94. doi:10.1016/j.eswa.2015.10.043

Sa, I., Popović, M., Khanna, R., Chen, Z., Lottes, P., Liebisch, F., Nieto, J., Stachniss, C., Walter, A., & Siegwart, R. (2018). WeedMap: A large-scale semantic weed mapping framework using aerial multispectral imaging and deep neural network for precision farming. *Remote Sensing, 10*(9), 1423. doi:10.3390/rs10091423

Sankaran, S., Khot, L. R., Espinoza, C. Z., Jarolmasjed, S., Sathuvalli, V. R., Vandemark, G. J., Miklas, P. N., Carter, A. H., Pumphrey, M. O., Knowles, N. R. N., & Pavek, M. J. (2015). Low-altitude, high-resolution aerial imaging systems for row and field crop phenotyping: A review. *European Journal of Agronomy, 70*, 112–123. doi:10.1016/j.eja.2015.07.004

Shahi, T. B., Xu, C.-Y., Neupane, A., & Guo, W. (2023). Recent advances in crop disease detection using UAV and deep learning techniques. *Remote Sensing, 15*(9), 2450. doi:10.3390/rs15092450

Torres-Sánchez, J., López-Granados, F., & Peña, J. M. (2015). An automatic object-based method for optimal thresholding in UAV images: Application for vegetation detection in herbaceous crops. *Computers and Electronics in Agriculture, 114*, 43–52. doi:10.1016/j.compag.2015.03.019

Tsouros, D. C., Bibi, S., & Sarigiannidis, P. G. (2019a). A review on UAV-based applications for precision agriculture. *Information, 10*(11), 349. doi:10.3390/info10110349

Tsouros, D. C., Triantafyllou, A., Bibi, S., & Sarigiannidis, P. G. (2019b). Data acquisition and analysis methods in UAV-based applications for precision agriculture. In *2019 15th International Conference on Distributed Computing in Sensor Systems (DCOSS)* (pp. 377–384). IEEE. doi:10.1109/DCOSS.2019.00080

CHAPTER 4

Canker Stain Disease of Plane Trees in a Changing Climate: From Global Origins to Its Emergence in Türkiye

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1. Introduction: Climate Change and Forest Ecosystems

Forest ecosystems worldwide are undergoing profound structural and functional changes in response to a rapidly changing climate (Trumbore et al., 2015; McDowell et al., 2020). Rising temperatures, shifts in precipitation regimes, prolonged droughts, and the increasing frequency and intensity of extreme weather events are altering the environmental conditions under which trees grow, reproduce, and maintain their physiological functions (Hanson and Weltzin, 2000; Bréda et al., 2006; Rennenberg et al., 2006; Özden and Erbay, 2017; Singh, 2024) These pressures are not restricted to natural forests. Urban and peri-urban trees may experience particularly complex combinations of stress because regional climatic changes interact with the urban heat-island effect, restricted rooting space, soil compaction, limited water availability, pollution, and recurrent mechanical disturbance. One increasingly important consequence of these environmental changes is their potential to modify interactions between trees and their pathogens (Pandey and Ghosh, 2023; Pakhira et al., 2024). Climate-related stress can influence host physiology and defence, while changing temperature and moisture regimes may alter pathogen development, distribution, and opportunities for establishment (Sutherst et al., 2011; Finch et al., 2021; Priya et al., 2024). Nevertheless, the importance of climate varies considerably among individual pathosystems, and climatic stress should not automatically be interpreted as the primary cause of disease emergence. In many tree diseases, pathogen introduction, host susceptibility, human activities, and management practices remain equally or more important determinants of disease development (Boyd et al., 2013; Potter and Urquhart, 2017). This distinction is particularly relevant to canker stain disease of plane trees, caused by the ascomycete fungus *Ceratocystis platani* (Panconesi, 1999; Harrington, 2013). The pathogen is an aggressive wound invader capable of colonizing the vascular tissues of susceptible Platanus species and causing progressive crown decline and mortality. Its epidemiology is strongly associated with wounds and human-mediated dispersal, particularly through pruning, construction-related root injuries, contaminated equipment, and the handling of infected woody material. Even relatively small wounds can provide infection courts, after which the pathogen may rapidly colonize the underlying conducting tissues. Thus, the contemporary threat posed by canker stain should be considered within a broader framework in which pathogen introduction and spread, urban tree management, host susceptibility, and changing environmental conditions interact (Tubby and Pérez-Sierra, 2015; Moricca et al., 2018; This chapter therefore examines the historical emergence and geographical expansion of canker stain, its infection biology and characteristic symptoms, its particular significance for urban and

riparian plane trees, and the potential relevance of a changing climate to the future vulnerability of Platanus populations.

2. Canker Stain Disease: Origin and Historical Spread

The history of canker stain disease is a striking example of how a tree pathogen can move from its presumed native range to become an international threat to both urban landscapes and natural ecosystems (Garbelotto, 2008). *Ceratocystis platani* is considered native to the southeastern United States, where it is thought to have been associated with Platanus populations long before the disease was formally described. Symptoms consistent with canker stain were observed in urban plane trees as early as the 1920s, while the first confirmed report was made in Pennsylvania in 1935. During the following decades, destructive outbreaks appeared in several cities of the eastern United States, providing the foundation for the early pathological and epidemiological descriptions of the disease and its subsequent taxonomic characterization (Walter, 1946; Walter et al. 1952). These North American outbreaks revealed a pattern that would later become familiar in Europe: apparently healthy mature plane trees developing progressive crown decline and eventually dying after infection, with disease spread frequently associated with wounds and human activities (Walter et al., 1952; Panconesi, 1999).

The geographical history of the disease changed dramatically during the Second World War. C. *platani* is believed to have crossed the Atlantic in infected wood used for packaging military equipment and other materials transported from North America to Europe (Panconesi, 1999; Engelbrecht, 2004). Early European disease centres appeared around important Mediterranean ports and transportation hubs, including Naples, Livorno, Syracuse and Marseille, supporting the hypothesis of wartime introduction through contaminated wood (Panconesi, 1999). From these early introduction points, canker stain gradually established itself in Mediterranean Europe. Italy became one of the principal centres of the epidemic, and the disease eventually caused severe losses in urban plane-tree populations (Panconesi, 1999; Tsopelas et al., 2017). One of the clearest historical examples occurred at Forte dei Marmi, where approximately 90% of the surveyed plane trees became infected and died between 1972 and 1991 (Panconesi, 1999). From Italy and other established foci, the disease was subsequently recorded elsewhere in southern and central Europe. Its arrival in Greece marked an especially important stage in this expansion because the pathogen was no longer threatening primarily planted London planes (Platanus X acerifolia) in cities and avenues; it had reached natural populations of Oriental plane (*P. orientalis*) (Ocasio-Morales et al., 2007).

In Greece, canker stain was first detected in the southwestern Peloponnese in 2003 and subsequently confirmed as *C. platani*. Diseased *P. orientalis* displayed extensive cankers, characteristic dark bluish-black staining of the underlying wood, crown decline and mortality (Tsopelas and Angelopoulos, 2004; EFSA Panel on Plant Health, 2016; Tsopelas et al., 2017). Genetic evidence indicated that the Greek population was closely related to populations already established in Italy, France and Switzerland, supporting the interpretation that the pathogen reached Greece through its continuing European expansion rather than through a separate introduction directly from North America (Ocasio-Morales et al., 2007). The establishment of the disease in natural riparian *P. orientalis* forests demonstrated that canker stain had developed from a predominantly urban tree-health problem into a broader ecological threat.

3. The Arrival of Canker Stain in Türkiye

Türkiye represents a particularly important point in this eastward progression because *P. orientalis* is not merely an ornamental tree. It is a native and ecologically important component of riparian vegetation and, at the same time, one of the country's culturally significant trees, widely planted along streets and avenues and in parks, gardens and historic landscapes (Çakar, 2012; Kamer Aksoy, 2022).



Figure 1. Symptoms of stain canker caused by *Ceratocystis platani* on *Platanus* spp., showing characteristic longitudinal reddish-brown to dark necrotic staining of the bark and underlying sapwood, exposed discoloured wood following bark removal, and bark cracking and necrosis associated with disease progression (Source: URL-1).

The arrival of *C. platani* therefore created a potential threat to both managed urban trees and naturally occurring plane-tree populations. The first major warning came from Istanbul. Unusual decline and mortality of plane trees had been noticed during the early 2010s, and the disease was briefly reported in 2011, although the causal agent was not fully characterized at that stage. Definitive evidence followed surveys conducted in August 2016 in parks and along major

avenues on the European side of the city. Laboratory investigations based on fungal morphology, molecular identification and pathogenicity testing confirmed *C. platani* on both *P.* x *acerifolia* and *P. orientalis* (Lehtijärvi et al., 2018; Beram ve Akyol, 2024).



Figure 2. Symptoms associated with *Ceratocystis platani* infection in *Platanus* trees along Çırağan Avenue, Beşiktaş, İstanbul, Türkiye, showing internal wood discoloration and decay in a cross-section (left) and pronounced canker formation with abnormal bark proliferation on the trunk (right) (Source: URL-2).

The scale of the Istanbul findings was concerning of 976 plane trees examined, 26.5% were symptomatic and 5.6% were already dead. Disease occurrence was particularly associated with sites where interventions such as pruning, topping and the removal of infected trees had taken place (Lehtijärvi et al., 2018). These observations mirrored the epidemiological pattern already documented in Europe and North America and demonstrated how management activities can unintentionally facilitate transmission when wounds are created or contaminated equipment is moved between trees. For several years, Istanbul represented the principal documented focus of canker stain in Türkiye. This picture changed with the detection of *C. platani* on *P. orientalis* in Denizli Province. Beram and Akyol (2024) confirmed the pathogen using complementary diagnostic approaches, including real-time PCR and ITS sequence analysis. The Denizli record is particularly important because it demonstrates that the known occurrence of *C. platani* in Türkiye is not restricted to Istanbul. Rather than proving continuous geographic spread between the two locations, however, this finding should be interpreted cautiously as evidence of a broader known distribution within the country. The historical journey of canker stain can therefore be followed across almost a century: from its presumed native range in southeastern North America, through wartime introduction into Europe, expansion across Italy and the Mediterranean, establishment in natural P. *orientalis* populations in Greece, and finally confirmed occurrence in Istanbul and Denizli in Türkiye. What began as

a destructive disease of urban plane trees in North America has consequently developed into a transcontinental plant-health concern affecting ornamental, historical and naturally occurring Platanus populations. This progression also provides an important lesson for interpreting the disease today: its geographical expansion has been driven primarily by pathogen introduction, movement of infected material and human-mediated transmission, while the possible influence of contemporary climatic change should be considered as an interacting environmental factor rather than the original cause of its spread.

4. Biology, Taxonomy and Disease Development of Ceratocystis platani

Ceratocystis platani (J.M. Walter) Engelbr. & T.C. Harr., the causal agent of canker stain of plane trees, is an ascomycetous fungus belonging to the class Sordariomycetes, order Microascales, and family Ceratocystidaceae. The disease is also referred to as blue stain canker or plane canker and is regarded as one of the most destructive vascular diseases affecting *Platanus* spp. (Panconesi, 1981; Tsopelas et al., 2017). The taxonomic identity of the pathogen has changed considerably since its first description. Walter (1946) initially described the fungus as *Endoconidiophora fimbriata* f. sp. *platani*, after which it was transferred to Ceratocystis and subsequently treated as *C. fimbriata* f. sp. *platani* (Bakshi, 1950; Hunt, 1956; May and Palmer, 1959). Molecular and phylogenetic studies later demonstrated that the plane-tree pathogen constitutes a distinct lineage within the *C. fimbriata* species complex, leading to its recognition as *C. platani* (Engelbrecht et al., 2004; Engelbrecht and Harrington, 2005). Biologically, the pathogen is notable for its ability to infect and kill vigorous as well as physiologically stressed plane trees. Infection is primarily associated with wounds because intact bark provides an effective barrier against penetration. Pruning cuts, broken branches, trunk injuries and damaged roots consequently represent important infection courts. This wound-dependent biology is particularly relevant in cities, where pruning, road and pavement construction, excavation, mowing and other mechanical disturbances frequently injure trees and create opportunities for infection (Harrington, 2013). Following entry, the fungus establishes rapidly in the exposed tissues and colonizes the functional sapwood. Reproductive development can also occur quickly, with asexual structures reported within a few days and sexual structures approximately a week after infection. Mycelial growth then extends longitudinally and radially through the xylem. Under favourable conditions, longitudinal colonization may reach approximately 2-2.5 m per year, and moderately sized infected trees may die within two or three growing seasons, whereas disease development in large, mature trees may extend over a longer period (Panconesi, 1999). In addition to direct infection through wounds, the pathogen can pass between adjacent trees

through root contacts or natural root grafts. Contaminated water may facilitate local dissemination, and insects, including ambrosia beetles, have been proposed as potential contributors to pathogen movement. In urban and intensively managed environments, however, infected woody material, sawdust and contaminated pruning or felling equipment are particularly important pathways by which viable inoculum can be transferred to newly wounded trees.

The principal pathological effect of *C. platani* results from progressive colonization and dysfunction of the water-conducting xylem rather than from superficial bark damage alone. As the fungus advances through the sapwood, infected vascular tissues become necrotic and lose their conductive capacity. Host defence responses, including the formation of tyloses and deposition of gums within vessels, may restrict pathogen movement locally but simultaneously contribute to hydraulic blockage (Pilotti et al., 2016). Progressive loss of functional xylem ultimately produces water stress in the crown, so external symptoms may become conspicuous only after substantial internal colonization has already occurred. Early crown symptoms include reduced shoot growth, small or chlorotic leaves and localized foliage wilting, followed by reddish-brown discoloration of leaves, progressive canopy thinning and branch dieback. Advanced infections may cause rapid death of individual branches or entire crown sectors, and severely affected trees may fail to produce foliage in the following growing season. Disease progression is sometimes less abrupt in large mature trees, where crown deterioration may develop gradually over several years. Stem symptoms provide particularly useful diagnostic evidence. Elongated cankers develop along affected trunks and branches, accompanied by hazel-brown to reddish or wine-coloured bark discoloration; as necrosis progresses, the bark may crack and separate into irregular plates. Removal of symptomatic bark typically reveals one of the most characteristic signs of the disease: longitudinal reddish-brown, dark brown or blue-black staining extending through the underlying sapwood. The combination of vascular staining, elongated cankers and progressive crown decline can therefore provide a strong field indication of canker stain, although symptom-based diagnosis alone is insufficient for definitive pathogen identification. Similar crown decline, bark necrosis or wood discoloration may be produced by other biotic and abiotic stresses; consequently, suspected infections should be confirmed by isolation of the pathogen or species-specific molecular diagnostic methods. From a disease-development perspective, canker stain can thus be viewed as a sequence beginning with wound-mediated infection, followed by rapid xylem colonization, progressive loss of hydraulic function, expression of crown and stem symptoms and, ultimately, mortality. This capacity to invade the vascular system of otherwise vigorous trees, together with efficient transmission through root connections and human activities, explains

why *C. platani* can cause extensive losses in mature urban and natural Platanus populations (Panconesi, 1972, 1979).

5. Urban Susceptibility and Disease Management in Canker Stain

The widespread use of *Platanus* spp. in European and Mediterranean cities has unintentionally created favourable conditions for the establishment of canker stain. Plane trees have traditionally been selected for streets, parks and boulevards because of their rapid development, expansive crowns, effective shade provision and ability to persist under demanding urban conditions (Lara et al., 2020; Sanusi and Livesley, 2020; Yin et al., 2024). Consequently, many cities contain long avenues and large public spaces dominated by closely spaced plane trees, providing *Ceratocystis platani* with a substantial and spatially continuous host population. Their vulnerability is further increased by the frequency of mechanical disturbance associated with urban infrastructure and tree maintenance. Pruning, accidental branch breakage, excavation, road and pavement works, utility installation, mowing and vehicle damage can expose living tissues on stems and roots, thereby creating infection courts for the pathogen (Czaja et al., 2020). Importantly, disease occurrence does not necessarily indicate that the affected tree was previously unhealthy; *C. platani* can establish in vigorous trees when inoculum is introduced into suitable wounds. Urban environmental constraints, including compacted or sealed soils, restricted rooting volume, limited water availability, high temperatures and atmospheric pollution, may nevertheless influence the capacity of infected trees to withstand progressive loss of functional vascular tissue. Increasing heat and drought associated with climate change could reinforce these pressures, but should be regarded as factors modifying tree condition and disease consequences rather than as direct causes of infection.

The spatial configuration and intensive management of urban trees can further accelerate local disease expansion (Özden, 2023). Arboricultural operations are particularly relevant because cutting an infected tree can contaminate saws and other equipment with fungal propagules. Subsequent use of the same equipment on another plane tree may simultaneously create a new wound and introduce inoculum into susceptible tissue. Sanitation felling presents an additional challenge (Özden et al., 2021): although removing diseased trees is necessary to reduce infection sources, the operation itself can generate contaminated sawdust, wood fragments and other residues that facilitate local dissemination if they are not carefully contained (Panconesi, 1999). Transport of infected timber and pruning residues may similarly move the pathogen beyond the original outbreak site. Disease spread is not restricted to above-ground activities. In regularly spaced avenues and mature urban plantings, neighbouring root systems may

overlap and form natural grafts, enabling *C. platani* to pass directly from an infected tree into an adjacent host. Thus, rapid outbreak development may result from several interacting pathways rather than a single dispersal mechanism, particularly where susceptible trees occur continuously along streets or within parks. Management must therefore focus primarily on exclusion, early detection and containment, since advanced vascular colonization cannot readily be reversed. Avoiding preventable injuries is one of the most effective measures: trunks and structural roots should be protected during construction, excavation, pavement repair and routine landscape maintenance, while pruning should be limited to necessary operations and conducted according to appropriate phytosanitary procedures. Equipment that has contacted a potentially infected tree should be cleaned and disinfected before being transferred to another Platanus. Surveillance is equally important, especially in locations where the disease has previously occurred. Crown thinning, reduced foliage, premature discoloration, localized branch mortality, bark necrosis and elongated cankers can indicate infection, while dark reddish-brown to bluish staining of the underlying sapwood provides particularly important diagnostic evidence. However, because similar symptoms may result from other pathogens or environmental stresses, visual assessment should be followed by laboratory confirmation using fungal isolation and/or appropriate molecular diagnostic techniques before definitive identification.

Once *C. platani* is confirmed, management should extend beyond the visibly diseased individual. Infected trees and contaminated woody material require removal, handling, transport and disposal under strict phytosanitary precautions, with particular attention to limiting the escape of sawdust and wood fragments. Nearby plane trees should remain under surveillance because infection through root connections may occur before external symptoms become apparent. Where epidemiologically justified, measures aimed at interrupting root connections between diseased and neighbouring trees can form part of containment strategies. At a broader scale, urban forestry planning can reduce future vulnerability by avoiding extensive monocultural planting of Platanus and increasing taxonomic and functional diversity among street and park trees. Such diversification will not prevent *C. platani* infection in individual plane trees, but it can interrupt continuous host availability and reduce the landscape-level consequences of an outbreak. Similar principles are relevant to natural *P. orientalis* populations, particularly in riparian systems where contaminated water and injured roots can contribute to pathogen movement. The prominence of canker stain in cities (Erbay and Özden, 2018) is therefore best understood as the outcome of a strong interaction between pathogen biology, concentrated host availability and human disturbance. Effective control consequently requires coordinated prevention of

wounds, rigorous sanitation, rapid diagnosis, safe management of infected material, surveillance of neighbouring trees and long-term diversification of urban tree populations.

6. Conclusion and Future Perspectives

Ceratocystis platani remains a persistent threat to *Platanus* populations, as its capacity for aggressive vascular colonization is compounded by numerous transmission routes, many tied directly to human activity. Its spread from North America to Europe and, more recently, to Türkiye illustrates how the transport of infected material, intensive urban tree management, and repeated mechanical injury can turn a once-localized pathogen into a significant phytosanitary challenge. Managing the disease effectively therefore requires moving past simple removal of symptomatic trees toward a comprehensive prevention framework: reducing pruning and root damage, disinfecting tools rigorously, safely disposing of infected material, monitoring trees near confirmed cases, confirming suspected infections quickly through laboratory testing, and diversifying species in new plantings. This is especially urgent in Türkiye, where detections in both İstanbul and Denizli suggest the pathogen has already spread beyond a single point of introduction, and where native *P. orientalis* populations raise concerns about potential spread into riparian ecosystems. Moving forward, research priorities should include mapping the pathogen's current distribution nationwide, using population genetics to trace how it was introduced and how it has spread, evaluating root- and water-borne transmission risks in wild *P. orientalis*, and developing molecular diagnostics capable of detecting infection before visible crown symptoms emerge. Equally important is experimental work examining whether rising temperatures, drought, and urban heat stress interact with infection to influence disease progression, xylem damage, host defense responses, and mortality research that would help separate the effects of climatic stress from those driven by the pathogen itself or by human-assisted spread. Ultimately, safeguarding Platanus populations, whether in cities or natural landscapes, will require replacing reactive removal of dying trees with early detection, prevention grounded in disease ecology, and sustained long-term monitoring as climate conditions continue to shift.

References

Bakshi, B. K. (1950). Fungi associated with ambrosia beetles in Great Britain. Transactions of the British Mycological Society, 33(1-2), 111-IN11.

Beram, R. C., & Akyol, S. (2024). Türkiye'de Çınar Kanser Lekesi Etmeni Ceratocystis platani İçin Yeni Bir Lokalite Kaydı. Düzce Üniversitesi Orman Fakültesi Ormancılık Dergisi, 20(2), 103-118.

Boyd, I. L., Freer-Smith, P. H., Gilligan, C. A., & Godfray, H. C. J. (2013). The consequence of tree pests and diseases for ecosystem services. Science, 342(6160), 1235773.

Bréda, N., Huc, R., Granier, A., & Dreyer, E. (2006). Temperate forest trees and stands under severe drought: a review of ecophysiological responses, adaptation processes and long-term consequences. Annals of forest science, 6 Rennenberg, H., Loreto, F., Polle, A., Brilli, F., Fares, S., Beniwal, R. S., & Gessler, A. J. P. B. (2006). Physiological responses of forest trees to heat and drought. Plant biology, 8(05), 556-571.3(6), 625-644.

Czaja, M., Kołton, A., & Muras, P. (2020). The complex issue of urban trees-Stress factor accumulation and ecological service possibilities. Forests, 11(9), 932.

Çakar, S. (2012). Kent ağaçlarında iyileştirme çalışmalarının değerlendirilmesi: İstanbul örneği.

EFSA Panel on Plant Health (PLH), Jeger, M., Bragard, C., Chatzivassiliou, E., Dehnen-Schmutz, K., Gilioli, G., ... & Rossi, V. (2016). Risk assessment and reduction options for Ceratocystis platani in the EU. EFSA Journal, 14(12), e04640.

Engelbrecht, C. J. B. (2004). Host specialization, intersterility, and taxonomy of populations of Ceratocystis fimbriata from sweet potato, sycamore, and cacao. Iowa State University.

ERBAY, E. R., & Özden, M. (2018). Kentler Sürdürülebilir Kalkınma Hedeflerinin Gerçekleştirilmesine Nasıl Yardımcı Olabilirler?. Sosyal Bilimler Araştırma Dergisi, 7(4), 255-268.

Finch, D. M., Butler, J. L., Runyon, J. B., Fettig, C. J., Kilkenny, F. F., Jose, S., ... & Amelon, S. K. (2021). Effects of climate change on invasive species. In Invasive species in forests and rangelands of the United States: a comprehensive science synthesis for the United States forest sector (pp. 57-83). Cham: Springer International Publishing.

Garbelotto, M. (2008). Molecular analysis to study invasions by forest pathogens: examples from Mediterranean ecosystems. *Phytopathologia Mediterranea*, *47*(3), 183-203.

Hanson, P. J., & Weltzin, J. F. (2000). Drought disturbance from climate change: response of United States forests. Science of the total environment, 262(3), 205-220.

Harrington, T. C. (2013). Ceratocystis diseases. In Infectious forest diseases (pp. 230-255). Wallingford UK: CABI.

Hunt, J (1956). Taxonomy of the Genus Ceratocystis. Lloydia, 19:1-59.

Jackson, L. W. R., & Sleeth, B. (1935). A new disease affecting Platanus orientalis in the eastern United States.

Kamer Aksoy, Ö. (2022). Predicting the Potential Distribution Area of the Platanus orientalis L. in Turkey Today and in the Future. Sustainability, 14(18), 11706.

Lara, B., Rojo, J., Fernández-González, F., González-García-Saavedra, A., Serrano-Bravo, M. D., & Pérez-Badia, R. (2020). Impact of plane tree abundance on temporal and spatial variations in pollen concentration. Forests, 11(8), 817.

Lehtijärvi, A., Oskay, F., Doğmuş Lehtijärvi, H. T., Aday Kaya, A. G., Pecori, F., Santini, A., & Woodward, S. (2018). Ceratocystis platani is killing plane trees in Istanbul (Turkey). Forest Pathology, 48(1), e12375.

Luchi, N., Ghelardini, L., Belbahri, L., Quartier, M., & Santini, A. (2013). Rapid detection of Ceratocystis platani inoculum by quantitative real-time PCR assay. Applied and Environmental Microbiology, 79(17), 5394-5404.

May, C., & Palmer, J. G. (1959). Effect of selected fungicide-asphalt mixtures on the growth of Ceratocystis fimbriata f. platani in vitro.

McCracken, F. I., & Burkhardt, E. C. (1977). Destruction of sycamore by canker stain in the midsouth.

McDowell, N. G., Allen, C. D., Anderson-Teixeira, K., Aukema, B. H., Bond-Lamberty, B., Chini, L., ... & Xu, C. (2020). Pervasive shifts in forest dynamics in a changing world. Science, 368(6494), eaaz9463.

Moricca, S., Bracalini, M., Croci, F., Corsinovi, S., Tiberi, R., Ragazzi, A., & Panzavolta, T. (2018). Biotic factors affecting ecosystem services in urban and peri-urban forests in Italy: The role of introduced and impending pathogens and pests. Forests, 9(2), 65.

Ocasio-Morales, R. G., Tsopelas, P., & Harrington, T. C. (2007). Origin of Ceratocystis platani on native Platanus orientalis in Greece and its impact on natural forests. Plant Disease, 91(7), 901-904.

Özden, M. (2023). A qualitative research on the evaluation of corporate feedback practices in municipalities as a citizen participation practice. Journal of Management and Economics Research, 21(3), 95-112.

Özden, M. İ. R. A. Y., & Erbay, E. R. (2017). Demokrasi Ekonomik Kalkınma İçin Ön Koşul Mudur?. Sosyal Bilimler Araştırma Dergisi, 6(4), 347-358.

Özden, M., Kantar, G., & Çınar, S. (2021). Kentsel markalaşma sürecinde yerel yönetimlerin önemi. Yaşar Üniversitesi E-Dergisi, 16(62), 1005-1021.

Pakhira, R., Biswas, S., & Singh, H. (2024). Urbanization and climate change: impacts, adaption and mitigation strategies. In Urban forests, climate change and environmental pollution: Physio-biochemical and molecular perspectives to enhance urban resilience (pp. 47-72). Cham: Springer Nature Switzerland.ustainable Cities, 5, 1281430.

Panconesi A. (1981). Ceratocystis fimbriata of plane trees in Italy: biological aspects and control possibility. European Journal of Forest Pathology, 11(7):385-395

Panconesi, A. (1972). I nostri platani sono in pericolo. Informatore fitopatologico, 22(3), 10-13.

Panconesi, A. (1979). Il cancro del platano: aspetti biologici e possibilità di lotta. Atti Convegno "Produzione e Patologia delle Piante arboree forestali e ornamentali", Milano, 1979, 15-26.

Panconesi, A. (1999). Canker stain of plane trees: a serious danger to urban plantings in Europe. Journal of Plant Pathology, 3-15.

Pandey, B., & Ghosh, A. (2023). Urban ecosystem services and climate change: a dynamic interplay. Frontiers in S

Park, J. H., Juzwik, J., & Cavender-Bares, J. (2013). Multiple Ceratocystis smalleyi infections associated with reduced stem water transport in bitternut hickory. Phytopathology, 103(6), 565-574.

Perry, E., & McCain, A. H. (1988). Incidence and management of canker stain in London plane trees in Modesto, California. J Arboric, 14(1), 18-19.

Pilotti, M., Di Lernia, G., Modesti, V., Lumia, V., & Brunetti, A. (2016). Outcome of Ceratocystis platani inoculations in Platanus× acerifolia in relation to season and inoculum dose. IForest-Biogeosciences and Forestry, 9(4), 608.

Potter, C., & Urquhart, J. (2017). Tree disease and pest epidemics in the Anthropocene: A review of the drivers, impacts and policy responses in the UK. Forest Policy and Economics, 79, 61-68.

Priya, R. S., Yuvaraj, M., Sharmila, R., Jagathjothi, N., Saranya, M., Suganthi, N., ... & Sivaji, M. (2024). Effects of climate change on plant diseases. In Plant quarantine challenges under climate change anxiety (pp. 183-225). Cham: Springer Nature Switzerland.

Sanusi, R., & Livesley, S. J. (2020). London Plane trees (Platanus x acerifolia) before, during and after a heatwave: Losing leaves means less cooling benefit. Urban forestry & urban greening, 54, 126746.

Singh, H. (2024). Climate change and forests: Biological perspectives. In Forests and climate change: Biological perspectives on impact, adaptation, and mitigation strategies (pp. 1-17). Singapore: Springer Nature Singapore.

Sutherst, R. W., Constable, F., Finlay, K. J., Harrington, R., Luck, J., & Zalucki, M. P. (2011). Adapting to crop pest and pathogen risks under a changing climate. Wiley Interdisciplinary Reviews: Climate Change, 2(2), 220-237.

Trumbore, S., Brando, P., & Hartmann, H. (2015). Forest health and global change. Science, 349(6250), 814-818.

Tsopelas, P., & Angelopoulos, A. (2004). First report of canker stain disease of plane trees, caused by Ceratocystis fimbriata f. sp. platani in Greece. Plant Pathology, 53(4), 531.

Tsopelas, P., Santini, A., Wingfield, M. J., & Wilhelm de Beer, Z. (2017). Canker stain: a lethal disease destroying iconic plane trees. Plant Disease, 101(5), 645-658.

Tubby, K. V., & Pérez-Sierra, A. (2015). Pests and pathogen threats to plane (Platanus) in Britain. Arboricultural Journal, 37(2), 85-98.

URL-1 (2026). https://www.forestresearch.gov.uk/tools-and-resources/fthr/pest-and-disease-resources/canker-stain-of-plane-ceratocystis-platani/).

URL-2 (2026). https://www.internethaber.com/temadan-istanbulda-kesilen-cinar-agaclariyla-ilgili-aciklama-meger-kanser-olmuslar-2242631h.htm.

Walter, J.M. (1946) Canker stain of plane trees. Circular 742, US Department of Agriculture, Washington, DC.

Walter, J.M., Rex, E.G. and Schreiber, R. (1952) The rate of progress and destructiveness of canker stain ofplane-trees. Phytopathology 42, 236–239.

Yin, Y., Li, S., Xing, X., Zhou, X., Kang, Y., Hu, Q., & Li, Y. (2024). Cooling benefits of urban tree canopy: a systematic review. Sustainability, 16(12), 4955.

CHAPTER 5

Valorization of Agricultural Waste in Türkiye: A Circular Economy and Renewable Energy Perspective

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1. INTRODUCTION

1.1 Agricultural Waste as a Strategic Biomass Resource

Agriculture plays a fundamental role in ensuring food security, supporting rural development, and contributing to economic growth worldwide. However, increasing pressures on natural resources, climate change impacts, energy security concerns, and environmental degradation have created the need for more sustainable production systems. Within this context, agricultural sustainability requires not only improving production efficiency but also developing effective strategies for managing and valorizing the residues generated throughout agricultural activities (Bathaei & Štreimikienė, 2023; European Commission, 2018).

Agricultural wastes have traditionally been regarded as materials requiring disposal due to their potential environmental impacts. Nevertheless, recent approaches increasingly consider these residues as valuable renewable biomass resources that can be converted into energy, bio-based products, and other high-value applications. This transition from a disposal-oriented perspective toward a resource-oriented approach represents one of the key principles of sustainable waste management and circular economy practices (Ellen MacArthur Foundation, 2015; Carrillo-Rodríguez et al., 2025).

Agricultural wastes generally consist of plant-based residues, animal-based wastes, and agro-industrial by-products. Crop residues such as straw, stalks, pruning residues, and processing by-products, as well as animal manure and food-processing wastes, represent significant biomass resources. Türkiye has considerable potential for agricultural waste valorization due to its diverse agricultural production structure, extensive cultivated areas, and developed livestock sector. Existing studies indicate that crop and animal production activities generate substantial waste streams; however, their effective utilization remains limited due to technical, economic, and organizational constraints (Kayahan & Çarman, 2023; Özer, 2025).

The valorization of agricultural waste provides opportunities beyond waste management by supporting renewable energy production, bio-based material development, and sustainable rural development. Through appropriate conversion technologies, agricultural residues can contribute to reducing dependence on fossil resources, improving resource efficiency, and creating additional economic value within agricultural systems. In this context, biomass-based energy pathways and integrated valorization approaches have become important components of sustainable energy transitions (Scarlat et al., 2019; Spizzirri et al., 2026).

Türkiye has significant opportunities for agricultural waste valorization due to its diverse agricultural production patterns, livestock activities, and agro-

industrial infrastructure. Plant residues, animal wastes, and agro-industrial by-products can serve as feedstocks for biogas production, biomass energy generation, organic fertilizers, and bio-based products. Nevertheless, the effective implementation of these approaches requires improvements in collection systems, logistics infrastructure, technological capacity, and institutional coordination (Kayahan & Çarman, 2023; Özer, 2025; Echefu et al., 2026).

Therefore, agricultural waste should be considered not only as an environmental challenge but also as a strategic biomass resource supporting the transition toward circular and bio-based economies. The integration of agricultural waste valorization strategies into sustainable production systems can contribute to environmental protection, energy security, rural development, and the creation of new value chains (Carrillo-Rodríguez et al., 2025; European Commission, 2018).

1.2 Circular Economy and Bioeconomy Perspective

The conventional linear economic model, based on the extraction of natural resources, production, consumption, and disposal, has resulted in increasing pressure on ecosystems and limited resource availability. In response to these challenges, the circular economy concept has emerged as an alternative approach that aims to maintain resource value, minimize waste generation, and promote the continuous use of materials within production systems (Ellen MacArthur Foundation, 2015; Geissdoerfer et al., 2017).

Within agricultural systems, circular economy principles provide a framework for transforming residues and by-products into valuable resources rather than considering them as waste streams. Agricultural residues can be reintegrated into production cycles through various pathways, including renewable energy generation, nutrient recovery, compost production, and bio-based material development. This approach contributes to improved resource efficiency, reduced environmental impacts, and the creation of additional economic value within rural areas (Carrillo-Rodríguez et al., 2025; Bathaei & Štreimikienė, 2023).

The concept of bioeconomy complements circular economy approaches by focusing on the sustainable production and utilization of renewable biological resources. Through bio-based transformation processes, agricultural residues can serve as feedstocks for producing energy, chemicals, materials, and other value-added products. Therefore, the integration of circular economy and bioeconomy principles provides a comprehensive framework for developing sustainable agricultural systems and reducing dependence on fossil-based resources (European Commission, 2018; Bugge et al., 2016).

In this context, agricultural waste valorization represents an important pathway for establishing circular and bio-based value chains. Technologies such

as anaerobic digestion, biomass conversion, biorefineries, and the production of bio-based materials enable agricultural residues to be transformed into products with environmental and economic benefits. These approaches not only contribute to renewable energy generation but also support innovation, rural development, and sustainable industrial applications (Spizzirri et al., 2026; Sharma, 2024).

Therefore, circular economy and bioeconomy perspectives provide the conceptual foundation for evaluating agricultural waste as a strategic resource. Rather than focusing solely on waste disposal, these approaches emphasize resource recovery, value creation, and sustainable production models, which are essential components of agricultural transformation toward a more resilient and environmentally responsible future.

1.3 Agricultural Waste Valorization Pathways

Agricultural waste valorization encompasses a broad range of technological approaches that aim to transform residual biomass into renewable energy, bio-based materials, and value-added products. Unlike conventional waste management strategies based mainly on disposal, valorization approaches seek to recover the embedded energy and material potential of agricultural residues. In this context, agricultural waste streams have become important feedstocks for sustainable production systems and circular economy applications (Sharma, 2024; Spizzirri et al., 2026).

One of the most established valorization pathways is renewable energy production through anaerobic digestion and biomass conversion technologies. Animal manure and other organic agricultural residues can be converted into biogas through anaerobic digestion processes, providing renewable methane for electricity and heat generation while simultaneously reducing environmental impacts associated with uncontrolled waste disposal. Furthermore, the remaining digestate can be utilized as an organic fertilizer, enabling nutrient recovery and closing material cycles within agricultural systems (Özer, 2025; Islam et al., 2021).

Plant-based agricultural residues, including straw, stalks, pruning residues, and other lignocellulosic biomass resources, can also be utilized through various conversion pathways such as combustion, gasification, and biofuel production. Particularly, second-generation biofuel technologies have attracted increasing attention because they enable the utilization of non-food biomass resources while reducing competition with agricultural products used for food production (Bran et al., 2018; Spizzirri et al., 2026).

Beyond energy applications, recent research has increasingly focused on converting agricultural residues into high-value bio-based products. Agro-industrial wastes and lignocellulosic biomass can serve as raw materials for producing bioplastics, biopolymers, biocomposites, and sustainable material

alternatives. Lignocellulosic biomass has been recognized as a sustainable platform for producing bio-based chemicals and polymers due to its abundance, renewability, and potential for replacing fossil-derived materials (Isikgor & Becer, 2015). These applications expand the economic potential of agricultural waste by creating new value chains and supporting the development of bio-based industries (Carrillo-Rodríguez et al., 2025; Kumbasaroglu & Kumbasaroglu, 2025).

An integrated biorefinery approach represents an advanced pathway for maximizing the utilization of agricultural biomass by combining multiple conversion processes and generating several products from the same resource stream. The biorefinery concept aims to replace fossil-based production systems by utilizing biomass resources for the simultaneous generation of energy, chemicals, and value-added products (Cherubini, 2010). Such systems support resource efficiency, reduce waste generation, and contribute to the transition toward circular and bio-based economies. Waste biorefineries provide an integrated framework for recovering energy, nutrients, and valuable products from organic waste streams while supporting sustainable circular bioeconomy models (Venkata Mohan et al., 2016). Therefore, agricultural waste valorization should be considered as a multifunctional strategy that simultaneously addresses renewable energy needs, environmental challenges, and sustainable economic development (European Commission, 2018; Spizzirri et al., 2026).

1.4 Research Gap and Contribution of This Chapter

Although extensive research has been conducted on the utilization of agricultural wastes, existing studies often focus on specific waste streams, individual conversion technologies, or limited application areas. Previous investigations have provided valuable contributions regarding biomass energy production, biogas generation, and bio-based material development; however, integrated assessments combining technological, environmental, economic, and institutional perspectives remain relatively limited (Kirchherr et al., 2017; Rojas-Flores et al., 2024; Carrillo-Rodríguez et al., 2025).

In particular, the effective valorization of agricultural waste requires a comprehensive understanding of not only available biomass resources but also the interactions among waste generation patterns, conversion technologies, market opportunities, and implementation barriers. For Türkiye, where agricultural production is characterized by significant regional diversity and various crop and livestock activities, evaluating agricultural waste within a circular economy and bioeconomy framework is essential for developing sustainable management strategies. Existing challenges related to collection systems, logistics, investment mechanisms, and institutional coordination further highlight the need for a holistic assessment approach (Kayahan & Çarman, 2023; Özer, 2025; Echefu et al., 2026).

This chapter aims to provide a comprehensive assessment of agricultural waste valorization in Türkiye from circular economy and renewable energy perspectives. The chapter discusses agricultural waste potential, major valorization pathways, renewable energy applications, bio-based product opportunities, existing challenges, and future policy directions. By integrating technological, environmental, and socio-economic dimensions, this chapter provides a holistic framework for understanding how agricultural wastes can be transformed from environmental burdens into strategic resources supporting sustainable development, rural economies, and bio-based industries.

2. LITERATURE-BASED EVALUATION APPROACH

This chapter was developed as a literature-based review aiming to evaluate agricultural waste valorization in Türkiye from circular economy and renewable energy perspectives. Literature-based research approaches provide systematic frameworks for synthesizing existing knowledge, identifying research trends, comparing findings from different studies, and developing comprehensive interpretations of a specific research topic (Snyder, 2019; Xiao & Watson, 2019). Accordingly, this chapter follows a structured evaluation process to examine agricultural waste potential, valorization pathways, circular economy applications, existing challenges, and future policy perspectives.

The overall methodological workflow followed in this chapter is presented in Figure 1. The evaluation process consists of sequential stages, including definition of the research scope, literature search, study selection, thematic classification, comparative evaluation, Türkiye-focused assessment, and interpretation of findings.

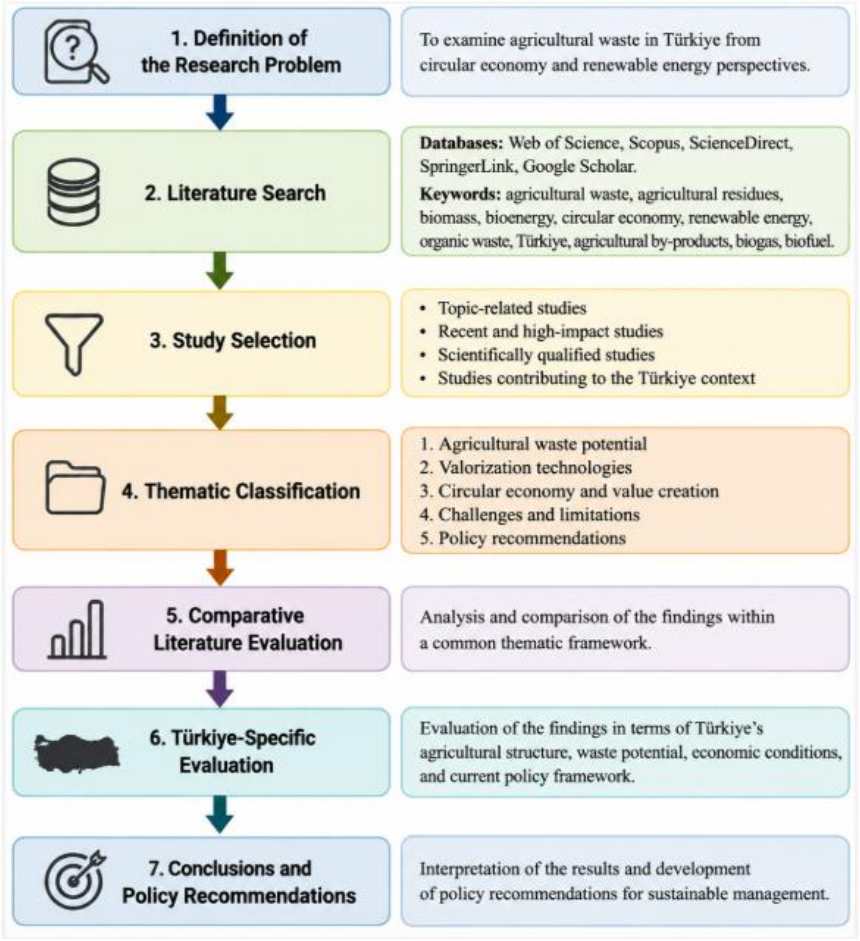


Figure 1. Methodological workflow of the literature-based evaluation process.

2.1 Literature Search Strategy

The literature search was conducted using internationally recognized academic databases, including Web of Science, Scopus, ScienceDirect, SpringerLink, and Google Scholar. The search process was performed using combinations of keywords related to agricultural waste valorization and sustainable resource management.

The main keywords included:

- "agricultural waste"
- "agricultural residues"
- "biomass"
- "circular economy"
- "renewable energy"
- "bioeconomy"

- “organic waste”

These keywords were used individually and in different combinations to identify relevant national and international studies. The selected publications were evaluated according to their relevance to agricultural waste management, scientific contribution, and applicability within the context of Türkiye.

2.2 Study Selection and Thematic Evaluation Framework

Following the literature search process, identified studies were screened based on their relevance, scientific quality, publication characteristics, and contribution to understanding agricultural waste valorization approaches. Studies outside the defined scope and duplicate records were excluded from further evaluation.

The selected studies were classified according to common research themes. As summarized in Table 1, the reviewed literature was evaluated under five main themes:

1. Agricultural waste potential,
2. Valorization technologies,
3. Circular economy applications and value creation,
4. Technical, economic, institutional, and social challenges,
5. Policy recommendations.

Table 1. Stages of literature review and thematic evaluation process.

Stage	Description
Definition of research problem	The scope and objectives of the chapter were established.
Literature search	National and international databases were searched using predefined keywords.
Study selection	Relevant, scientifically valuable, and Türkiye-related studies were selected.
Thematic classification	Selected studies were categorized according to common research themes.
Comparative evaluation	Findings were synthesized and compared to identify common trends.
Türkiye-focused assessment	Agricultural waste potential, challenges, and opportunities were evaluated within the Türkiye context.
Interpretation of findings	Results were interpreted to develop conclusions and policy recommendations.

2.3 Data Synthesis and Analytical Framework

The selected studies were analyzed through a thematic synthesis approach. Rather than focusing on individual studies separately, the findings were integrated according to common patterns and research trends.

The analysis framework was established around five major themes:

i. agricultural waste potential in Türkiye,
ii. agricultural waste valorization technologies,
iii. circular economy-based applications and value-added products,
iv. technical, economic, institutional, and social barriers, and
v. policy recommendations for sustainable implementation.

Through this comparative evaluation approach, the chapter aims to provide a holistic understanding of agricultural waste valorization opportunities and limitations in Türkiye. The methodology enables the integration of technological, environmental, and socio-economic perspectives, supporting the development of sustainable strategies for transforming agricultural residues into valuable resources.

3. AGRICULTURAL WASTE POTENTIAL IN TÜRKIYE

3.1 Overview of Agricultural Waste Generation in Türkiye

Türkiye has a diverse agricultural production structure characterized by extensive cultivated areas, a wide range of crop production activities, and a significant livestock sector. This agricultural diversity results in the generation of considerable amounts of plant-based residues, animal wastes, and agro-industrial by-products. Although these residues have traditionally been considered waste materials requiring disposal, current sustainability approaches increasingly recognize them as valuable biomass resources that can contribute to renewable energy generation, circular economy applications, and bio-based product development (Bathaei & Štreimikienė, 2023; Kayahan & Çarman, 2023).

Agricultural production activities generate various types of residues throughout cultivation, harvesting, processing, and livestock production processes. Plant-based residues such as straw, stalks, pruning wastes, and crop processing residues represent significant biomass resources, while animal manure and agro-industrial by-products constitute other important waste streams. The effective management and valorization of these resources can provide environmental benefits by reducing uncontrolled disposal practices and can create additional economic value through energy recovery and sustainable material production (Özer, 2025; Sharma, 2024).

The potential of agricultural wastes in Türkiye extends beyond their quantity and availability. The diversity of agricultural activities provides opportunities for developing multiple valorization pathways, including biogas production, biomass energy generation, organic fertilizer production, and bio-based material applications. However, despite this significant potential, a considerable portion of agricultural residues remains underutilized due to limitations related to

collection infrastructure, transportation systems, technological capacity, investment mechanisms, and institutional coordination (Kayahan & Çarman, 2023; Echefu et al., 2026).

Therefore, evaluating agricultural waste generation in Türkiye requires not only determining the amount and types of available residues but also considering their conversion potential within circular economy and bioeconomy frameworks. A comprehensive understanding of agricultural waste resources provides the foundation for identifying suitable valorization strategies and developing sustainable approaches for transforming agricultural residues into valuable resources.

3.2 Major Categories of Agricultural Waste Resources

Agricultural waste resources in Türkiye can broadly be classified into three major categories according to their origin and characteristics: plant-based agricultural residues, animal-based agricultural wastes, and agro-industrial by-products. Each category differs in terms of composition, availability, collection requirements, and suitability for valorization technologies. Consequently, identifying the characteristics of individual waste streams is essential for matching them with appropriate conversion pathways and maximizing their environmental and economic value (Kayahan & Çarman, 2023; Sharma, 2024; Spizzirri et al., 2026).

As summarized in Table 2, these agricultural waste categories provide diverse opportunities ranging from renewable energy and organic fertilizer production to bioplastics, biocomposites, and other value-added bio-based products. Their effective utilization can therefore contribute simultaneously to waste reduction, resource recovery, renewable energy generation, and the development of circular agricultural value chains (Carrillo-Rodríguez et al., 2025; Kumbasaroğlu & Kumbasaroğlu, 2025).

Table 2. Synthesis of Major Agricultural Waste Types and Valorization Potentials in Türkiye

Agricultural waste type	Major sources	Major valorization technologies	Potential value-added products/applications
Plant-based agricultural residues	Wheat and barley straw, corn stalks and cobs, rice husks, sunflower stalks, cotton residues, pruning wastes, fruit and vegetable residues	Biomass energy conversion, biofuel production, composting, biorefinery processes, biocomposite production	Electricity and heat, biofuels, organic fertilizers, bioplastics, insulation materials, composite panels, lightweight concrete and other bio-based construction materials
Animal-based agricultural wastes	Cattle manure, sheep and goat manure, poultry wastes,	Anaerobic digestion, biogas production, composting	Electricity and heat, biomethane/biogas, organic fertilizers and nutrient-rich soil amendments

Agricultural waste type	Major sources	Major valorization technologies	Potential value-added products/applications
	slaughterhouse-related organic wastes		
Agro-industrial by-products	Fruit and vegetable processing residues, sugar beet pulp, dairy-processing wastes, food-industry organic residues and other processing by-products	Biogas production, biorefinery processes, biochemical conversion, composting	Biogas, bioplastics, biochemicals, organic fertilizers, biocomposites and other value-added bio-based products

Source: Prepared by the authors based on the literature reviewed in this chapter, including Kumbasaroglu & Kumbasaroglu (2025); Kayahan & Çarman (2023); Sharma (2024); Özer (2025); Carrillo-Rodríguez et al. (2025); Bathaei & Štreimikienė (2023); Spizzirri et al. (2026); Islam et al. (2021); and Echefu et al. (2026).

3.2.1 Plant-Based Agricultural Residues

Plant-based residues constitute one of the most diverse agricultural biomass resource groups in Türkiye. Major residue streams include wheat and barley straw, corn stalks and cobs, rice husks, sunflower stalks, cotton residues, pruning wastes, and residues generated during fruit and vegetable production. Their availability is closely associated with crop type, production intensity, harvesting practices, and regional agricultural characteristics (Kayahan & Çarman, 2023; Bathaei & Štreimikienė, 2023).

These residues offer several valorization opportunities because of their biomass and lignocellulosic content. Depending on their physicochemical characteristics, they can be utilized for biomass energy generation, biofuel production, composting, biorefinery applications, and the manufacture of bio-based materials. Recent studies have also demonstrated increasing interest in utilizing agricultural residues in bioplastics, biocomposites, insulation products, composite panels, and construction-related applications, thereby extending valorization beyond conventional energy recovery (Carrillo-Rodríguez et al., 2025; Kumbasaroglu & Kumbasaroglu, 2025; Spizzirri et al., 2026).

This diversity is particularly important from a circular economy perspective because different plant residues can be directed toward different value chains rather than being treated through a single waste-management pathway. However, seasonal availability, geographically dispersed production, collection requirements, and transportation costs can limit the economic feasibility of large-scale utilization.

3.2.2 Animal-Based Agricultural Wastes

Animal-based agricultural wastes constitute another important biomass resource in Türkiye because of the country's substantial cattle, sheep, goat, and

poultry production activities. Manure generated by livestock operations represents the major waste stream, while other organic residues associated with animal production can also contribute to the overall biomass potential (Özer, 2025; Kayahan & Çarman, 2023).

Anaerobic digestion is among the most relevant valorization pathways for animal wastes because it enables organic residues to be converted into biogas while simultaneously supporting improved waste management. The resulting energy can be utilized for electricity and heat generation, while the remaining digestate can potentially be used as an organic fertilizer or soil amendment, thereby supporting nutrient recovery and circular resource use (Islam et al., 2021; Özer, 2025).

From a broader sustainability perspective, effective management of animal wastes can therefore provide multiple benefits, including renewable energy generation, nutrient recycling, and reduction of environmental pressures associated with uncontrolled manure management. Nevertheless, realizing this potential depends on appropriate collection systems, facility scale, investment capacity, and integration between livestock production and energy or fertilizer value chains.

3.2.3 Agro-Industrial By-Products

Agro-industrial activities generate heterogeneous organic by-products during the processing, transformation, and preparation of agricultural commodities. In Türkiye, relevant streams include fruit and vegetable processing residues, sugar beet pulp, dairy-processing wastes, food-industry organic residues, and other processing by-products. Unlike many primary agricultural residues, agro-industrial wastes are often generated at processing facilities, which may offer logistical advantages for their collection and subsequent valorization (Sharma, 2024; Carrillo-Rodríguez et al., 2025).

These by-products can be utilized through several technological pathways, including biogas production, biochemical conversion, composting, and integrated biorefinery processes. In addition to energy recovery, current valorization approaches increasingly emphasize the production of higher-value outputs such as bioplastics, biochemicals, biocomposites, organic fertilizers, and other bio-based products (Carrillo-Rodríguez et al., 2025; Sharma, 2024).

The potential of agro-industrial by-products is therefore particularly relevant to the development of circular bioeconomy models in which residual materials from one production process become feedstocks for another. Such integration can improve resource efficiency, reduce disposal requirements, and diversify the economic value generated from agricultural production systems.

3.3 Valorization Potential and Current Limitations in Türkiye

The existence of substantial agricultural residue streams alone does not guarantee their effective valorization. The actual value that can be derived from these resources depends on the compatibility between waste characteristics,

conversion technologies, local infrastructure, market conditions, and institutional arrangements. In Türkiye, the diversity of agricultural production provides opportunities for developing multiple valorization pathways; however, realizing this potential requires moving beyond assessments based solely on waste quantities toward integrated strategies that consider technological feasibility and economic value creation (Kayahan & Çarman, 2023; Özer, 2025; Spizzirri et al., 2026).

This distinction is particularly important from a circular economy perspective. Agricultural residues may generate greater environmental and economic benefits when appropriate waste streams are matched with locally suitable conversion pathways and incorporated into interconnected value chains. Therefore, valorization strategies should consider not only energy recovery but also nutrient recycling, bio-based material production, and higher-value applications where technically and economically feasible (Carrillo-Rodríguez et al., 2025; Sharma, 2024).

3.3.1 Valorization Opportunities

Agricultural waste valorization in Türkiye offers opportunities across several complementary application areas. Renewable energy production represents one of the most immediate pathways, particularly through anaerobic digestion of animal wastes and organic residues for biogas generation and through the utilization of plant-based biomass for energy production. These pathways can contribute to the diversification of renewable energy resources while simultaneously providing improved management options for agricultural residues (Özer, 2025; Islam et al., 2021; Spizzirri et al., 2026).

Nevertheless, the value of agricultural residues extends beyond energy recovery. Organic fractions and process residues can contribute to nutrient recovery and organic fertilizer production, while lignocellulosic and agro-industrial residues may serve as feedstocks for bioplastics, biocomposites, biomaterials, and other bio-based products. Such applications can increase the economic value retained within agricultural production systems and create new links between agriculture and bio-based industries (Carrillo-Rodríguez et al., 2025; Kumbasaroglu & Kumbasaroglu, 2025).

An important opportunity therefore lies in adopting a cascading approach to agricultural biomass utilization, in which waste streams are directed toward applications capable of generating appropriate environmental and economic value according to their characteristics. Integrated biorefinery and circular bioeconomy approaches can further strengthen this process by enabling multiple products, materials, and energy carriers to be obtained from biomass resources rather than relying on a single end-use pathway (Cherubini, 2010; Venkata Mohan et al., 2016). In the context of Türkiye, such diversification could support renewable energy generation, resource efficiency, rural value creation, and the development of new bio-based value chains.

3.3.2 Technical, Economic, and Institutional Limitations

Despite these opportunities, the effective valorization of agricultural waste in Türkiye is constrained by several interconnected technical and economic factors. Agricultural residues are frequently characterized by seasonal generation, dispersed geographical distribution, heterogeneous composition, and relatively low bulk density. These characteristics can increase the complexity and cost of collection, storage, transportation, and preprocessing, thereby reducing the economic feasibility of centralized valorization systems (Kayahan & Çarman, 2023; Sharma, 2024).

Economic constraints constitute another important barrier. Establishing biogas facilities, biomass conversion systems, biorefineries, or advanced bio-based production facilities may require considerable initial investment, while project feasibility can be influenced by feedstock continuity, transportation distances, energy and product markets, and access to financing. Consequently, the technical availability of agricultural residues does not necessarily translate directly into economically recoverable potential (Özer, 2025; Echefu et al., 2026).

Institutional and organizational conditions are equally important. Effective agricultural waste valorization requires coordination among farmers, producer organizations, municipalities, private enterprises, technology providers, research institutions, and public authorities. Fragmented supply structures, insufficient producer organization, limited awareness of valorization opportunities, and weaknesses in coordination mechanisms may restrict the establishment of stable biomass supply chains (Echefu et al., 2026). Strengthening producer cooperation, university–industry collaboration, technical capacity, and supportive financing mechanisms can therefore play an important role in overcoming these limitations.

Taken together, these challenges indicate that the principal issue is not simply whether Türkiye possesses agricultural waste resources, but whether these resources can be collected, processed, and integrated into economically viable and environmentally sustainable value chains. Future strategies should therefore combine regional resource assessments with appropriate technology selection, logistics planning, market development, financing mechanisms, and institutional coordination. Such an integrated approach would provide a stronger basis for converting Türkiye's agricultural waste potential into tangible circular economy and bioeconomy benefits.

4. CIRCULAR ECONOMY APPLICATIONS

4.1 Agricultural Waste Valorization within the Circular Economy

Agricultural waste valorization represents a fundamental component of circular economy approaches by transforming residual materials generated from agricultural activities into valuable resources, products, and energy carriers. Unlike conventional waste management strategies that primarily focus on disposal, circular approaches aim to maintain the value of biomass resources through recovery, reuse, and conversion processes. In this context, agricultural residues should be considered as secondary resources that can contribute to

renewable energy production, sustainable material development, and improved resource efficiency (Bathaei & Štreimikienė, 2023; Carrillo-Rodríguez et al., 2025).

The circular economy perspective emphasizes the transition from linear production systems toward regenerative systems in which materials remain within economic cycles for longer periods. Agricultural waste streams provide important opportunities for implementing these principles because they contain organic matter, nutrients, and biochemical components that can be recovered through appropriate technologies. Therefore, valorization strategies enable the simultaneous reduction of waste generation, conservation of natural resources, and creation of additional economic value within agricultural systems (Geissdoerfer et al., 2017; Kirchherr et al., 2017).

A significant advantage of agricultural waste valorization is that it extends beyond conventional energy recovery pathways. While biogas production and biomass energy remain important applications, emerging approaches increasingly focus on high-value products, including bioplastics, biopolymers, biocomposites, and other bio-based materials. Such applications enhance the economic potential of agricultural residues by establishing new connections between agricultural production, industrial processes, and sustainable material development (Kumbasaroglu & Kumbasaroglu, 2025; Spizzirri et al., 2026).

In Türkiye, the successful implementation of agricultural waste valorization requires an integrated approach that considers regional biomass characteristics, suitable conversion technologies, economic feasibility, and supply-chain organization. Although the country has considerable agricultural residue potential, effective utilization depends on establishing appropriate collection systems, improving technological capacity, and developing value chains that connect agricultural producers with energy and bio-based industries (Kayahan & Çarman, 2023; Özer, 2025).

Consequently, agricultural waste valorization within the circular economy should be regarded as a multifunctional strategy that simultaneously addresses environmental protection, renewable resource development, and economic sustainability. This perspective provides the foundation for evaluating specific valorization pathways, including renewable energy recovery, biorefinery applications, bio-based product development, and nutrient recycling strategies discussed in the following sections.

Different agricultural waste streams can be directed toward various valorization pathways depending on their physical and chemical characteristics, available technologies, and potential value creation opportunities. Table 3 summarizes the major agricultural waste valorization technologies, their corresponding feedstocks, main products, and economic and environmental contributions within circular economy frameworks.

Table 3. Agricultural Waste Valorization Technologies and Their Value-Added Applications within Circular Economy Frameworks.

Technology	Agricultural Waste Feedstocks	Main Products	Economic Contributions	Environmental Contributions
Biogas production	Animal wastes, organic residues	Electricity, heat, biomethane	Reduction in energy costs	Reduction of greenhouse gas emissions
Biomass energy	Plant-based agricultural residues	Electricity, heat	Diversification of energy resources	Reduction of fossil fuel consumption
Biorefinery applications	Agro-industrial residues	Biochemicals, bioplastics	Increased value creation	Improved resource efficiency
Biocomposite production	Lignocellulosic agricultural residues	High-value materials, composite panels	Development of new industrial markets	Increased material resource efficiency
Composting	Plant-based and animal-based residues	Organic fertilizers	Reduction in fertilizer costs	Improvement of soil quality

Source: Prepared by the authors based on the reviewed literature, including Sharma (2024), Kumbasaroglu & Kumbasaroglu (2025), Spizzirri et al. (2026), Carrillo-Rodríguez et al. (2025), Özer (2025), Sözer (2024), and Şirin & Erkuş (2026).

4.2 Renewable Energy Recovery

4.2.1 Biogas Production

Anaerobic digestion is one of the most widely applied technologies for converting organic agricultural wastes into renewable energy. Particularly, animal manure and other biodegradable agricultural residues provide suitable feedstocks for biogas production due to their high organic matter content. Through anaerobic digestion processes, these waste streams can be converted into biogas containing methane, which can be utilized for electricity and heat generation, while simultaneously reducing environmental impacts associated with uncontrolled waste disposal (Özer, 2025; Islam et al., 2021).

Beyond energy generation, anaerobic digestion contributes to circular resource management by producing digestate, a nutrient-rich by-product that can potentially be used as an organic fertilizer. This process enables the recovery of valuable nutrients and supports the integration of agricultural production and waste management systems. Therefore, biogas applications represent a multifunctional pathway by combining renewable energy generation, waste treatment, and nutrient recycling within circular economy frameworks (Islam et al., 2021; Özer, 2025).

In Türkiye, livestock production activities create substantial opportunities for biogas development, particularly through the utilization of cattle manure, poultry wastes, and other organic residues. However, the implementation of biogas systems depends on several factors, including feedstock availability, collection infrastructure, facility scale, investment capacity, and operational management. Consequently, regional planning and appropriate technology selection are essential for achieving economically feasible biogas applications (Kayahan & Çarman, 2023; Özer, 2025).

4.2.2 Biomass Energy and Biofuel Pathways

Plant-based agricultural residues represent important biomass resources that can be utilized for renewable energy generation and biofuel production. Residues such as straw, stalks, pruning wastes, and other lignocellulosic materials contain significant amounts of organic carbon and can be converted through various pathways, including direct combustion, thermochemical conversion, and biofuel production processes (Bran et al., 2018; Sharma, 2024).

The utilization of agricultural biomass for energy production provides several environmental benefits, including reduced dependence on fossil fuels, improved waste management, and lower greenhouse gas emissions. In particular, advanced conversion technologies enable the transformation of lignocellulosic residues into second-generation biofuels without directly competing with food production systems. These approaches are considered important components of sustainable bioenergy strategies (Bran et al., 2018; Spizzirri et al., 2026).

However, effective biomass energy utilization requires careful consideration of feedstock characteristics, transportation distances, seasonal availability, and conversion efficiency. Since agricultural residues are often distributed over large geographical areas, collection and logistics remain important factors affecting economic feasibility. Therefore, biomass energy systems should be designed according to regional resource availability and integrated with local agricultural production structures (Kayahan & Çarman, 2023; Sharma, 2024).

Within a circular economy perspective, biomass energy recovery should not be considered only as an alternative energy source but also as a strategy for maintaining resource value within agricultural systems. When combined with other valorization pathways, biomass conversion can contribute to diversified bio-based value chains and sustainable rural development (Spizzirri et al., 2026).

4.3 Biorefinery and High-Value Bio-Based Products

Beyond conventional energy recovery, agricultural residues can serve as renewable feedstocks for the production of chemicals, polymers, materials, and other value-added products. This broader valorization perspective is particularly important within the circular bioeconomy because it seeks to retain the material and economic value of biomass rather than limiting its utilization to a single end-use pathway. Biorefinery systems and bio-based material applications therefore provide complementary opportunities for diversifying agricultural waste value

chains and reducing dependence on fossil-derived resources (Cherubini, 2010; Venkata Mohan et al., 2016; Carrillo-Rodríguez et al., 2025).

4.3.1 Biorefinery Applications

Biorefineries represent integrated processing systems designed to convert biomass into a range of fuels, energy carriers, chemicals, materials, and other value-added products. Conceptually similar to petroleum refineries, biorefineries seek to maximize the utilization of renewable biomass by integrating different conversion processes and product streams. Agricultural residues and agro-industrial by-products are particularly relevant feedstocks because their utilization can simultaneously support waste reduction, resource recovery, and the development of bio-based production systems (Cherubini, 2010; Venkata Mohan et al., 2016).

The biorefinery approach differs from single-product valorization strategies by emphasizing the sequential or integrated recovery of multiple components from biomass. Depending on feedstock composition and the technologies employed, agricultural residues can provide carbohydrates, lignin, proteins, oils, and other fractions that may subsequently be converted into biofuels, biochemicals, polymers, and functional materials. Such integrated utilization can improve resource efficiency and potentially increase the economic value obtained from the same biomass stream (Cherubini, 2010; Isikgor & Becer, 2015).

Agro-industrial by-products offer particular opportunities for biorefinery applications because many are generated at processing facilities where relatively concentrated and continuous residue streams may be available. Their conversion into multiple products can facilitate industrial symbiosis, in which residues generated by one process become feedstocks for another production activity. From a circular economy perspective, this approach contributes to closing material loops and reducing dependence on virgin and fossil-based resources (Venkata Mohan et al., 2016; Carrillo-Rodríguez et al., 2025).

For Türkiye, the development of biorefinery-based value chains could provide an opportunity to move agricultural waste management beyond low-value disposal or single-purpose energy recovery. However, the suitability of such systems depends on regional feedstock availability, biomass composition, technological infrastructure, market demand, and economic feasibility. Therefore, biorefinery development should be based on locally appropriate combinations of biomass resources, conversion technologies, and potential end products.

4.3.2 Bioplastics, Biopolymers, and Biocomposites

The growing demand for sustainable alternatives to fossil-derived materials has increased interest in utilizing agricultural residues for the production of bioplastics, biopolymers, biocomposites, and other bio-based materials. In particular, lignocellulosic agricultural residues represent promising renewable feedstocks because their cellulose, hemicellulose, and lignin fractions can be

utilized in different material and chemical applications (Isikgor & Becer, 2015; Carrillo-Rodríguez et al., 2025).

Bioplastics and biopolymers provide opportunities for converting biomass-derived compounds into products with higher economic value than conventional waste-to-energy applications. Similarly, agricultural fibers and lignocellulosic residues can be incorporated into composite materials as reinforcements, fillers, or functional components. These approaches extend the useful life of agricultural biomass within economic systems and can reduce the consumption of virgin and fossil-based raw materials (Isikgor & Becer, 2015; Spizzirri et al., 2026).

The construction sector represents one potential application area for agricultural waste-based materials. Agro-waste resources have been investigated for use in composite panels, insulation materials, cementitious products, and other construction applications, demonstrating opportunities to combine waste valorization with material resource efficiency (Kumbasaroglu & Kumbasaroglu, 2025). Such applications are particularly relevant from a circular economy perspective because they create alternative value chains for residues that may otherwise remain underutilized or be directed toward lower-value uses.

Nevertheless, high-value material production should not be interpreted as universally preferable for every agricultural residue. Feedstock composition, preprocessing requirements, product performance, market demand, environmental impacts, and economic feasibility must be considered when selecting appropriate valorization pathways. Consequently, the most effective circular strategy is likely to involve matching individual agricultural waste streams with applications capable of providing suitable environmental, technical, and economic value rather than applying a single conversion route to all biomass resources (Carrillo-Rodríguez et al., 2025; Kumbasaroglu & Kumbasaroglu, 2025).

4.4 Composting, Organic Fertilizers, and Nutrient Recovery

Composting represents one of the most established biological valorization pathways for agricultural wastes, enabling the conversion of organic residues into stabilized materials that can be returned to agricultural systems. Unlike disposal-oriented approaches, composting supports circular resource management by maintaining organic matter and nutrients within agricultural production cycles. Plant residues, animal manure, and agro-industrial organic wastes can be utilized as composting feedstocks depending on their composition and availability (Benito et al., 2005a; Sharma, 2024).

The transformation of agricultural residues into organic fertilizers provides multiple environmental and economic benefits. Compost application can improve soil organic matter content, enhance nutrient availability, and contribute to soil quality improvement while reducing dependence on externally supplied mineral fertilizers. In this way, composting functions not only as a waste treatment process but also as a nutrient recovery strategy that supports sustainable agricultural productivity (Benito et al., 2005b; Özer, 2025).

Pruning wastes and other lignocellulosic agricultural residues represent important resources for composting applications. Previous studies have demonstrated that compost derived from agricultural residues can provide suitable physical and chemical properties for use as soil amendments or components of growing media, depending on processing conditions and final product characteristics (Benito et al., 2005a; Benito et al., 2005b). These applications demonstrate the potential of agricultural waste streams to generate value through relatively low-cost and accessible technologies.

From a circular economy perspective, composting contributes to closing nutrient cycles by returning carbon and essential elements from agricultural residues back to soil systems. Particularly in regions where agricultural activities generate dispersed organic waste streams, composting can provide a practical solution for reducing uncontrolled disposal, improving soil health, and supporting sustainable production practices.

However, the successful implementation of composting systems requires appropriate management of feedstock composition, moisture content, processing conditions, contamination control, and logistics. Therefore, composting should be considered as part of an integrated valorization strategy in which different agricultural waste streams are directed toward the most suitable pathways according to their characteristics and potential value.

4.5 Integrated Value Creation and Circular Agricultural Systems

Agricultural waste valorization within circular economy frameworks should not be considered as a collection of isolated conversion processes but rather as an integrated system in which different recovery pathways complement each other. The combination of energy recovery, material production, and nutrient recycling enables agricultural residues to be transformed into multiple value streams while minimizing resource losses and environmental impacts (Geissdoerfer et al., 2017; Carrillo-Rodríguez et al., 2025).

An integrated circular agricultural system can connect agricultural production, waste management, renewable energy generation, and bio-based industries through interconnected value chains. For example, animal wastes can be utilized for biogas production, with the remaining digestate returned to agricultural fields as an organic fertilizer. Similarly, plant-based residues can be directed toward biomass energy, biorefinery applications, or bio-based material production depending on their characteristics and economic feasibility. Such cascading utilization approaches improve resource efficiency by maximizing the value obtained from agricultural biomass streams (Cherubini, 2010; Venkata Mohan et al., 2016).

The implementation of integrated systems also provides opportunities for strengthening rural economies by creating new activities associated with biomass collection, processing, energy generation, and bio-based product manufacturing. In this context, agricultural waste valorization can contribute not only to environmental sustainability but also to local economic development through the

establishment of new circular value chains (Kayahan & Çarman, 2023; Spizzirri et al., 2026).

However, the development of integrated circular agricultural systems requires coordinated planning among multiple stakeholders, including farmers, industrial actors, researchers, and public institutions. The effectiveness of these systems depends on appropriate technology selection, reliable biomass supply chains, investment mechanisms, market development, and institutional cooperation. Therefore, future approaches should focus on region-specific strategies that match available agricultural resources with technically and economically suitable valorization pathways (Echefu et al., 2026).

Overall, agricultural waste valorization represents an important opportunity for Türkiye to strengthen circular economy practices by converting underutilized biomass resources into renewable energy, sustainable materials, and agricultural inputs. An integrated approach that combines environmental, technological, and economic perspectives can provide a more sustainable pathway for managing agricultural residues and developing resilient bio-based production systems.

5. CHALLENGES, BARRIERS, AND FUTURE PERSPECTIVES

5.1 Technical Challenges in Agricultural Waste Valorization

Agricultural waste valorization faces several technical challenges related to the characteristics, availability, and spatial distribution of biomass resources. Although Türkiye has considerable agricultural residue potential, these resources are generally generated through dispersed agricultural activities and vary significantly depending on crop type, production region, seasonal conditions, and agricultural practices. Such variability makes the continuous supply of homogeneous feedstock difficult and creates challenges for the design and operation of large-scale valorization systems (Kayahan & Çarman, 2023; Sharma, 2024).

One of the major technical limitations is associated with collection, transportation, and storage processes. Agricultural residues are frequently produced in geographically distributed locations and may have relatively low bulk density, which increases logistical requirements and transportation costs. In addition, seasonal production patterns may result in irregular feedstock availability, requiring appropriate storage strategies and supply-chain planning to ensure the continuous operation of conversion facilities. These issues are particularly important for biomass-based energy systems and biorefinery applications where stable feedstock supply is essential for economic and technical performance (Sharma, 2024; Tokmakçı et al., 2025).

Another important challenge is the compatibility between agricultural waste characteristics and selected valorization technologies. Different waste streams may require specific preprocessing methods, conversion conditions, and operational strategies depending on their physical and chemical properties. Therefore, successful implementation of agricultural waste valorization requires appropriate technology selection, technical expertise, and region-specific

planning rather than applying identical solutions to all biomass resources. Improving technological capacity and developing integrated waste management approaches are essential for increasing the efficiency and reliability of valorization systems (Kayahan & Çarman, 2023; Tokmakçı et al., 2025).

5.2 Economic and Market-Related Barriers

The economic feasibility of agricultural waste valorization depends not only on the availability of biomass resources and suitable technologies but also on investment conditions, market development, and financial sustainability. Although agricultural residues represent valuable renewable resources, establishing valorization systems such as biogas plants, biomass conversion facilities, and biorefineries generally requires considerable initial capital investment. These financial requirements may limit the participation of small and medium-sized stakeholders and slow the transition from pilot-scale applications to large-scale implementation (Aygan, 2025; Korkmaz & Hacıhasanoğlu, 2024).

A major economic challenge is the uncertainty associated with investment returns and payback periods. Valorization projects often involve relatively long-term investments because profitability depends on multiple interacting factors, including feedstock availability, operational costs, energy or product prices, and market acceptance. Uncertainty regarding future revenues can reduce investor confidence and create difficulties in attracting private-sector investment, particularly for emerging bio-based industries (Echefu et al., 2026). Similar studies have highlighted that unclear return expectations, high initial investment requirements, and limited financing opportunities are among the important barriers affecting the commercialization of agricultural waste-derived products.

Market-related factors represent another important limitation. Bio-based products generated from agricultural residues, including biofuels, biochemicals, bioplastics, and bio-based materials, often compete with conventional fossil-derived alternatives that benefit from established production systems and mature markets. Therefore, achieving economic competitiveness requires improvements in production efficiency, product quality, supply-chain organization, and market development. The establishment of reliable demand for circular products is essential for creating sustainable value chains and encouraging further investment in agricultural waste valorization systems (Sharma, 2024; Spizzirri et al., 2026).

Addressing these economic barriers requires supportive financial and institutional mechanisms that reduce investment risks and improve market conditions. Incentives such as green financing opportunities, targeted subsidies, investment support programs, and collaborative models between public institutions and private stakeholders can contribute to improving the feasibility of agricultural waste valorization projects. Furthermore, integrating economic planning with regional biomass availability and appropriate technology selection is necessary to develop financially sustainable circular economy models (Kayahan & Çarman, 2023; Echefu et al., 2026).

5.3 Institutional, Organizational, and Social Challenges

5.3.1 Institutional and Organizational Challenges

Institutional coordination represents one of the key factors influencing the successful implementation of agricultural waste valorization systems. Although Türkiye has considerable agricultural biomass potential, transforming these resources into economically viable circular systems requires cooperation among farmers, producer organizations, public institutions, private companies, and research organizations. Fragmented responsibilities and insufficient coordination among stakeholders may limit the development of effective collection systems, technology transfer mechanisms, and integrated value chains (Echefu et al., 2026; García Pérez et al., 2026).

Another important institutional challenge is the limited availability of coordinated planning and reliable data infrastructure. Effective valorization strategies require accurate information regarding biomass availability, spatial distribution, seasonal variations, and suitable conversion technologies. The absence of comprehensive databases and systematic information-sharing mechanisms may reduce the efficiency of investment planning and hinder the establishment of region-specific circular economy models (Kayahan & Çarman, 2023; García Pérez et al., 2026).

Regulatory frameworks and support mechanisms also play an important role in determining the scalability of agricultural waste valorization applications. Clear policies, technical standards, investment incentives, and long-term strategic planning are necessary to encourage private-sector participation and reduce uncertainty for stakeholders. Therefore, institutional development should focus not only on individual projects but also on establishing supportive environments that enable continuous innovation and collaboration within agricultural circular economy systems (Echefu et al., 2026).

5.3.2 Social Awareness and Capacity Development

The social dimension of agricultural waste valorization is closely related to stakeholder awareness, knowledge level, and willingness to participate in circular practices. Farmers and local producers are key actors because they are the primary sources of agricultural residues; however, limited awareness regarding the economic and environmental benefits of waste valorization may restrict their active involvement in collection and utilization systems. Increasing awareness about agricultural residues as valuable resources rather than unwanted wastes is therefore essential for improving participation in circular economy applications (Kazakou et al., 2025; Güneş & Karakaş, 2022).

Capacity development and knowledge transfer mechanisms are also important for accelerating the adoption of valorization technologies. Training programs, extension services, technical guidance, and collaboration between universities and agricultural stakeholders can contribute to improving understanding of available technologies and their potential benefits. Such approaches can support

producers in making informed decisions and facilitate the practical implementation of circular agricultural systems (Güneş & Karakaş, 2022).

Furthermore, social acceptance is influenced by factors such as perceived economic benefits, technological trust, organizational capacity, and accessibility of support mechanisms. Therefore, future agricultural waste valorization strategies should incorporate awareness-building activities, stakeholder participation, and locally adapted solutions. Strengthening human capacity alongside technological and economic development is essential for achieving sustainable and long-term circular economy outcomes (Kazakou et al., 2025; Echefu et al., 2026).

The successful implementation of agricultural waste valorization requires a comprehensive approach that simultaneously addresses technical, economic, institutional, and social challenges. These interconnected barriers cannot be overcome through technological solutions alone; instead, coordinated intervention strategies involving infrastructure development, financial support mechanisms, institutional collaboration, and capacity building are required. Figure 2 summarizes the major challenges affecting agricultural waste valorization in Türkiye and presents the corresponding strategic components and support mechanisms required for the transition toward circular agricultural systems.

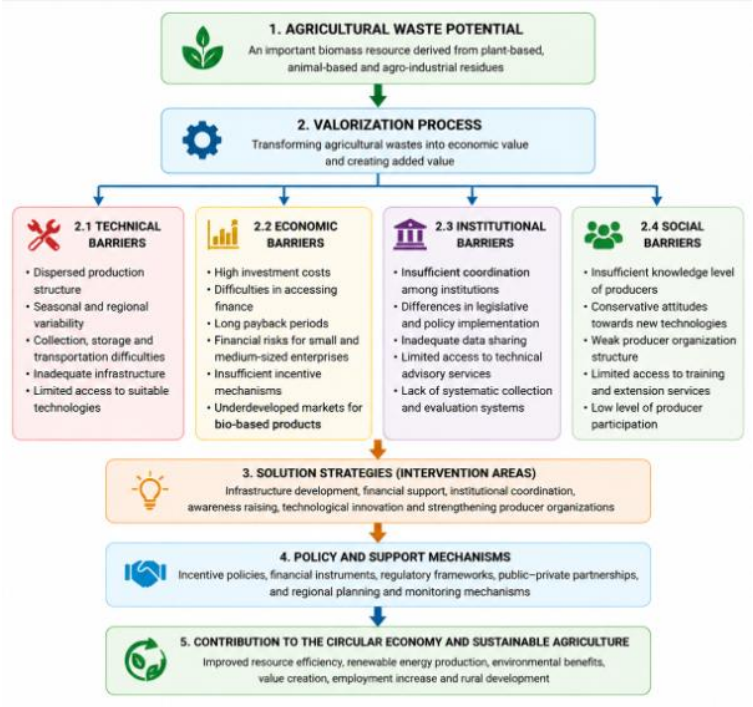


Figure 2. Challenges and strategic components for agricultural waste valorization in Türkiye.

Based on these challenges and strategic components, future agricultural waste valorization efforts should focus on integrated approaches that combine technological innovation, supportive policies, stakeholder collaboration, and circular economy principles.

5.4 Future Perspectives and Strategic Directions

5.4.1 Integrated Valorization Strategies for Sustainable Resource Management

Integrated valorization strategies provide a comprehensive framework for transforming agricultural residues into multiple value streams while improving resource efficiency within circular agricultural systems. Rather than relying on a single conversion pathway, integrated approaches combine different valorization options, including renewable energy production, biorefinery applications, bio-based material development, and nutrient recovery. Such strategies enable the cascading use of biomass resources and help maximize the economic and environmental benefits obtained from agricultural residues (Cherubini, 2010; Venkata Mohan et al., 2016).

The selection of appropriate valorization pathways should consider the specific characteristics of agricultural waste streams, including their composition, availability, geographic distribution, and seasonal variability. Therefore, future systems should be based on regional planning approaches that match local biomass resources with technically and economically suitable conversion technologies. For Türkiye, where agricultural production patterns vary considerably among regions, developing location-specific valorization models can improve feedstock management, reduce logistical constraints, and strengthen the feasibility of circular biomass systems (Cudecka-Purina et al., 2025; Kayahan & Çarman, 2023; Carrillo-Rodríguez et al., 2025).

An integrated approach also provides opportunities to establish interconnected value chains among agricultural producers, energy facilities, bio-based industries, and fertilizer systems. For example, organic residues can be converted into renewable energy, while remaining by-products can be returned to agricultural production through nutrient recovery pathways. Such circular linkages contribute to reducing resource losses, supporting rural development, and improving the sustainability of agricultural systems. Consequently, integrated valorization strategies represent an important pathway for strengthening the role of agricultural waste as a strategic resource within the circular bioeconomy (Carrillo-Rodríguez et al., 2025; Spizzirri et al., 2026).

5.4.2 Policy Support, Financing, and Multi-Stakeholder Collaboration

The successful implementation of agricultural waste valorization requires supportive policy frameworks that integrate environmental objectives, economic development goals, and agricultural management strategies. Although technological solutions provide important opportunities for resource recovery, their widespread adoption depends on regulatory support, long-term planning, and coordinated implementation mechanisms. Therefore, policy approaches

should move beyond waste management perspectives and recognize agricultural residues as strategic biomass resources contributing to circular economy and sustainable development objectives (Bathaei & Štreimikienė, 2023; Çetinkaya & Keskin, 2026).

The development of effective valorization systems also requires appropriate financial mechanisms to overcome investment barriers and improve economic feasibility. Many agricultural waste valorization technologies involve considerable initial investments, while the return period may depend on uncertain market conditions and developing bio-based product demand. In this context, green financing models, targeted incentive programs, investment supports, and mechanisms encouraging private-sector participation can contribute to reducing financial risks and accelerating the transition from pilot-scale applications toward larger-scale systems (Avgan, 2025; Korkmaz & Hacıhasanoğlu, 2024).

Multi-stakeholder collaboration represents another essential component of sustainable agricultural waste management. Farmers, producer organizations, cooperatives, private companies, universities, research institutions, and public authorities should participate in the development of integrated value chains. University–industry cooperation is particularly important for transferring scientific knowledge into practical applications, improving technological capacity, and supporting the development of high-value bio-based products from agricultural residues (Echefu et al., 2026; Kumbasaroglu & Kumbasaroglu, 2025).

In addition, effective governance structures should include reliable data systems, monitoring mechanisms, and region-specific implementation strategies. The establishment of coordinated platforms that connect biomass suppliers, technology providers, investors, and policy makers can improve decision-making processes and support the long-term sustainability of circular agricultural systems. Consequently, policy support and collaborative frameworks should be considered fundamental components for transforming agricultural waste from an underutilized residue into a valuable resource within the circular bioeconomy (García Pérez et al., 2026; Carrillo-Rodríguez et al., 2025).

5.4.3 Capacity Development and Future Role of Agricultural Waste in Circular Bioeconomy

The long-term success of agricultural waste valorization depends not only on technological advancement and financial support but also on the development of stakeholder capacity and awareness. Farmers, producers, and local organizations play a central role in the transformation of agricultural residues into valuable resources because they are directly involved in biomass generation, collection, and initial management processes. Therefore, strengthening education programs, extension services, and technical knowledge transfer mechanisms is essential for improving participation and accelerating the adoption of circular agricultural practices (Güneş & Karakaş, 2022; Kazakou et al., 2025).

Future agricultural waste management systems are also expected to benefit from digitalization and knowledge-based approaches. Digital monitoring tools, improved biomass databases, and data-supported decision-making mechanisms can contribute to better planning of collection processes, technology selection, and resource allocation. The integration of digital technologies with circular economy strategies may improve transparency, efficiency, and coordination among stakeholders involved in agricultural waste valorization systems (García Pérez et al., 2026).

From a broader perspective, agricultural waste has the potential to become a strategic component of the circular bioeconomy by supporting renewable energy production, bio-based material development, nutrient recycling, and sustainable rural development. Recognizing agricultural residues as valuable biomass resources rather than disposal problems can contribute to reducing resource losses and creating new economic opportunities within agricultural systems. In this context, Türkiye's agricultural waste potential represents an important opportunity for developing sustainable value chains that integrate environmental protection, economic development, and circular resource management principles (Spizzirri et al., 2026; Carrillo-Rodríguez et al., 2025; Kumbasaroglu & Kumbasaroglu, 2025).

6. CONCLUSIONS AND RECOMMENDATIONS

6.1 Key Findings and Contributions

The findings of this chapter demonstrate that agricultural waste in Türkiye should be considered not merely as a disposal problem but as a strategic biomass resource with significant potential for supporting circular economy and sustainable development objectives. By evaluating agricultural residues from technological, economic, institutional, and social perspectives, this chapter provides a comprehensive framework for understanding the opportunities and limitations associated with agricultural waste valorization.

The assessment presented in this chapter highlights that Türkiye possesses substantial agricultural biomass resources originating from plant-based residues, animal wastes, and agro-industrial by-products. These resources have the potential to be transformed into valuable products and services through various valorization pathways, including renewable energy generation, biogas production, biorefinery applications, bio-based materials, and nutrient recovery systems. Such approaches can contribute to improving resource efficiency, reducing environmental pressures, and creating additional economic opportunities within agricultural systems.

However, the analysis also demonstrates that the effective utilization of agricultural waste depends on more than technological availability. Technical limitations related to biomass collection and logistics, economic challenges associated with investment and market development, institutional coordination requirements, and social factors such as awareness and capacity development represent interconnected components that influence the success of circular

agricultural systems. Therefore, integrated strategies combining appropriate technologies, supportive financial mechanisms, stakeholder collaboration, and capacity-building activities are essential for achieving sustainable outcomes.

The main contribution of this chapter is the development of a holistic perspective that connects agricultural waste potential, circular economy applications, existing barriers, and future strategic directions within the context of Türkiye. This integrated evaluation provides a conceptual basis for researchers, practitioners, and policy makers seeking to develop sustainable agricultural waste management approaches and strengthen the transition toward a circular bioeconomy.

6.2 Implications for Sustainable Agricultural Waste Management

The findings of this chapter indicate that sustainable agricultural waste management requires a transition from conventional disposal-oriented approaches toward integrated resource management systems. Agricultural residues should be evaluated within the framework of circular economy principles, where waste streams are transformed into valuable inputs for energy production, bio-based materials, nutrient recovery, and sustainable agricultural practices. This perspective highlights the importance of considering agricultural waste management as a value creation process rather than only an environmental management issue.

For agricultural stakeholders, including farmers, producer organizations, and local agricultural enterprises, the effective utilization of residues requires increased awareness, improved organization, and participation in coordinated value chains. The development of regional collection systems, cooperation among producers, and access to technical information can support the transformation of dispersed biomass resources into economically valuable products. Therefore, strengthening stakeholder capacity and encouraging participation are important components of sustainable agricultural waste management.

For policy makers and institutional actors, the results emphasize the need for coordinated planning, supportive mechanisms, and integrated governance approaches. Effective management of agricultural residues requires cooperation among agricultural organizations, public authorities, research institutions, and private-sector stakeholders. The establishment of reliable data systems, appropriate incentive mechanisms, and long-term planning frameworks can contribute to improving the feasibility and continuity of agricultural waste valorization initiatives.

From a broader sustainability perspective, agricultural waste management has implications beyond residue utilization alone. The transformation of agricultural waste into renewable energy, bio-based products, and recycled nutrients can contribute simultaneously to environmental protection, resource efficiency, rural economic development, and sustainable agricultural production. Consequently, adopting integrated agricultural waste management strategies represents an

important step toward strengthening circular bioeconomy practices and achieving more resilient agricultural systems.

6.3 Recommendations for Future Research and Applications

Future research on agricultural waste valorization in Türkiye should focus on developing more detailed regional assessments of biomass resources and their potential applications. Although existing studies demonstrate significant agricultural waste potential, comprehensive analyses at provincial and regional scales are required to better identify resource availability, seasonal variations, collection possibilities, and suitable valorization pathways. Such studies can support the development of location-specific strategies and improve the planning of circular agricultural systems.

Further investigations should also integrate technological performance with economic and environmental assessments. Comparative analyses of different valorization technologies, including life-cycle assessments, techno-economic evaluations, and cost–benefit analyses, are needed to determine the most appropriate solutions under different agricultural and regional conditions. These approaches can provide more reliable guidance for investment decisions and support the transition from theoretical potential toward practical implementation.

Future studies should additionally consider the socio-economic dimensions of agricultural waste management. Understanding farmers' participation, organizational structures, knowledge levels, and economic expectations is essential for designing realistic and applicable valorization models. Research focusing on rural development impacts, income diversification opportunities, and stakeholder acceptance can contribute to developing more inclusive circular economy strategies.

Finally, future applications should move toward integrated and digitally supported circular bioeconomy systems. The combination of biomass monitoring technologies, data-driven planning tools, renewable energy systems, biorefineries, and bio-based product development can enhance resource efficiency and create new value chains. By strengthening cooperation among researchers, producers, industries, and policy institutions, future initiatives can contribute to establishing sustainable agricultural waste management models that support environmental protection, economic development, and circular resource utilization.

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REFERENCES

Avgan, S. (2025). Türkiye'nin yenilenebilir enerji potansiyeli ve sürdürülebilir pazarlama uygulamaları: Sektörel bir değerlendirme. Business, Economics and Management Research Journal, 8(3), 166–188. https://doi.org/10.58308/bemarej.1668836

Bathaei, A., & Štreimikienė, D. (2023). Renewable energy and sustainable agriculture: Review of indicators. Sustainability, 15(19), 14307. https://doi.org/10.3390/su151914307

Benito, M., Masaguer, A., Moliner, A., De Antonio, R. 2005a. Chemical and Physical Properties of Pruning Waste Compost and Their Seasonal Variability. Bioresource Technology. Article in Press.

Benito, M., Masaguer, A., De Antonio, R., Moliner, A. 2005b. Use of Pruning Waste Compost as a Component in Soilless Growing Media. Bioresource Technology 96, 597–603.

Bran, S. D., Chipurici, P., Bran, M., & Vlaicu, A. (2018). Renewable energy from agricultural waste. Revista de Chimie, 69(6), 1363–1366.

Bugge, M. M., Hansen, T., & Klitkou, A. (2016). What is the bioeconomy? A review of the literature. Sustainability, 8(7), 691. https://doi.org/10.3390/su8070691

Carrillo-Rodríguez, L. A., Cajigas Romero, M., & Galindo Larrahondo, J. A. (2025). The use of agro-industrial waste towards a sustainable circular economy: A systematic review. Detritus, 31, 45–61. https://doi.org/10.31025/2611-4135/2025.19491

Cherubini, F. (2010). The biorefinery concept: Using biomass instead of oil for producing energy and chemicals. Energy Conversion and Management, 51(7), 1412-1421. https://doi.org/10.1016/j.enconman.2010.01.015

Cudecka-Purina, N., Arina, D., Teibe, I., Bendere, R., Melnalksne, Z., Jakobsone, L., & Ruperta, Z. (2025). Food waste assessment and household biowaste management in Latvia: Towards a circular economy. Biomass, 5(4), 58. https://doi.org/10.3390/biomass5040058

Çetinkaya, Ö., & Keskin, A. (2026). Döngüsel ekonomi ve atık yönetimi performansı: AB–Türkiye karşılaştırması. Journal of Animal Science and Economics, 5(2), 82–95. https://doi.org/10.5281/zenodo.19453859

Echefu, S. U., Bappah, M., Ivanova, T. A., Madaki, M. Y., Ullah, A., Nkomoki, W., & Bavorova, M. (2026). Farmers' adoption of waste-to-energy valorisation as a circular economy pathway for sustainability transitions in Nigeria. Energy, Ecology and Environment. Advance online publication. https://doi.org/10.1007/s40974-026-00418-7

Ellen MacArthur Foundation. (2015). Towards a circular economy: Business rationale for an accelerated transition. Ellen MacArthur Foundation.

European Commission. (2018). A sustainable Bioeconomy for Europe: strengthening the connection between economy, society and the environment (Communication COM/2018/673 final). Brussels: European Commission.

García Pérez, M. A., Gavilánez Buñay, T. C., Casco Toapanta, M. G., & Rodríguez Céspedes, D. (2026). Circular economy and local development in La Maná: Agricultural, livestock and agroindustrial production. Cooperativismo y Desarrollo, 14(1), e753.

Geissdoerfer, M., Savaget, P., Bocken, N. M., & Hultink, E. J. (2017). The Circular Economy – A new sustainability paradigm?. Journal of Cleaner Production, 143, 757-768. https://doi.org/10.1016/j.jclepro.2016.12.048

Güneş, E., & Karakaş, T. (2022). Tarım ve gıda sistemlerinde sürdürülebilirlik yaklaşımları. Journal of Academic Value Studies, 8(3), 304–316. https://doi.org/10.29228/javs.63757

Isikgor, F. H., & Becer, C. R. (2015). Lignocellulosic biomass: a sustainable platform for the production of bio-based chemicals and polymers. Polymer Chemistry, 6(25), 4497-4559. https://doi.org/10.1039/C5PY00263J

Islam, K. N., Sarker, T., Taghizadeh-Hesary, F., Atri, A. C., & Alam, M. S. (2021). Renewable energy generation from livestock waste for a sustainable circular economy in Bangladesh. Renewable and Sustainable Energy Reviews, 139, 110695. https://doi.org/10.1016/j.rser.2020.110695

Kayahan, N., & Çarman, K. (2023). Determination of waste potential and emissions in crop and animal production in Konya Province. Turkish Journal of Agriculture – Food Science and Technology, 11(7), 1215–1221. https://doi.org/10.24925/turjaf.v11i7.1215-1221.6057

Kazkondu, İ. (2025). Tarımsal kalkınma kooperatifinde üretim sürecinde oluşan fonksiyonel gıda atıklarından döngüsel ekonomi kapsamında ürün geliştirme: Devrek kireni sorbesi ve Devrek kireni dondurması örneği. Üçüncü Sektör Sosyal Ekonomi Dergisi, 60(1), 631–656. https://doi.org/10.15659/3.sektor-sosyal-ekonomi.25.02.2583

Kirchherr, J., Reike, D., & Piscicelli, L. (2017). Conceptualizing the circular economy: An analysis of 114 definitions. Resources, Conservation and Recycling, 127, 221-232. https://doi.org/10.1016/j.resconrec.2017.09.005

Korkmaz, B., & Hacısalihoğlu, S. (2024). Fotovoltaik ve biyogaz enerji sistemlerinin enerji ve çevresel potansiyellerinin incelenmesi: Süt sığırı çiftliği örneği. Uludağ Üniversitesi Mühendislik Fakültesi Dergisi, 29(1), 245–262. https://doi.org/10.17482/uumfd.1434976

Kumbasaroglu, H., & Kumbasaroglu, A. (2025). Applicability of agro-waste materials in structural systems for building construction: A scoping review. Applied Sciences, 15(1), Article 71. https://doi.org/10.3390/app15010071

Özer, B. (2025). Türkiye, Kırklareli ilinde biyogaz bazlı döngüsel ekonomi için hayvan gübresi ve tarımsal artıkların değerlendirilmesi. Tekirdağ Ziraat Fakültesi Dergisi, 22(2), 513–530. https://doi.org/10.33462/jotaf.1570863

Rojas-Flores, S., De La Cruz-Noriega, M., Cabanillas-Chirinos, L., Otiniano, N. M., Soto-Deza, N., Terrones-Rodriguez, N., & De La Cruz-Cerquin, M. (2024). Bibliometric analysis: Use of agricultural waste in the generation of electrical energy. Processes, 12(6), 1178. https://doi.org/10.3390/pr12061178

Scarlat, N., Dallemand, J. F., Taylor, N., & Banja, M. (2019). Brief on biomass for energy in the European Union. Publications Office of the European Union. https://doi.org/10.2760/546943

Sharma, R. (2024). Agro-industrial waste to energy: Sustainable management. Sustainable Materials and Technologies, 41, e01117. https://doi.org/10.1016/j.susmat.2024.e01117

Snyder, H. (2019). Literature review as a research methodology: An overview and guidelines. Journal of Business Research, 104, 333–339. https://doi.org/10.1016/j.jbusres.2019.07.039

Sözer, S. (2024). Türkiye'deki Kesimhane Atıklarından ve Çiftlik Hayvanları Gübrelerinden Elde Edilebilecek Biyogaz Potansiyelinin Tespiti Üzerine Bir Araştırma. Black Sea Journal of Engineering and Science, 7(4), 627-634. https://doi.org/10.34248/bsengineering.1463671

Spizzirri, E., Maraldi, M., & Valenti, F. (2026). Valorising agricultural waste and by-products for renewable energy: Sustainable technologies and pathways. Energy Reports, 15, 109000. https://doi.org/10.1016/j.egyr.2025.109000

Şirin, Ü., Erkuş, F. Ş., & Tuncay, K. (2026). Sürdürülebilir hayvansal atık yönetimi: Doğu Anadolu Bölgesi biyogaz potansiyelinin çevresel ve ekonomik boyutları. ICONTECH International Journal, 8(5), 358–372.

Tokmakçı, M., Özdil, N. F. (Tümen), & Bilgili, M. (2025). Municipal solid waste to biomass energy in Türkiye: A life cycle assessment approach for circular economy integration. Biomass and Bioenergy, 200, 107982. https://doi.org/10.1016/j.biombioe.2025.107982

Xiao, Y., & Watson, M. (2019). Guidance on conducting a systematic literature review. Journal of Planning Education and Research, 39(1), 93–112. https://doi.org/10.1177/0739456X17723971

Venkata Mohan, S., Nikhil, G. N., Chiranjeevi, P., Reddy, C. N., Rohit, M. V., Kumar, A. N., & Sarkar, O. (2016). Waste biorefinery models towards sustainable circular bioeconomy: Critical review and future perspectives. Bioresource Technology, 215, 2-12. https://doi.org/10.1016/j.biortech.2016.03.130

CHAPTER 6

From Waste Biomass to Functional Rhizosphere Platforms: Integration of PGPR Supported Hazelnut Shell Biochar into Smart Agriculture

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1. Introduction

For decades, agriculture was largely defined through the pursuit of higher production outputs. Within the historical conditions of its time, such an approach was understandable. Rapid population growth, accelerating urbanization, and concerns surrounding food security gradually pushed yield maximization to the center of agricultural policy in many countries. Highyielding cultivars, expanded mineral fertilizer use, mechanization, and irrigation investments undeniably generated substantial gains. Yet the narrative of success carried a less visible balance sheet of its own. Declining soil organic matter, structural degradation, salinity, groundwater depletion, and increasing dependence on external inputs made it increasingly evident that agricultural performance could no longer be interpreted solely through tonnagebased productivity metrics (Lal 2015).

Agricultural systems are now evaluated through a considerably broader framework. Production quantity still matters, although the way that production is achieved under which resource conditions and at what ecological or economic costhas become equally significant. Indicators such as wateruse efficiency, fertilizeruse efficiency, energy demand, greenhouse gas pressure, and soil health have moved into the core of performance assessment. In response, the Food and Agriculture Organization has emphasized frameworks that simultaneously address productivity and resilience capacity (FAO 2014). At first glance, this may appear to represent a technical adjustment in management philosophy. In practice, however, it reflects a much deeper transformation in the way agricultural systems are conceptualized. Climate change has intensified these pressures even further. Irregular precipitation patterns, prolonged drought periods, heat waves, and increasingly abrupt climatic extremes have weakened the reliability of conventional production calendars. Practices once considered stable no longer produce consistent outcomes across seasons. (Ortiz Bobea et al. 2021) reported that anthropogenic climate change has already slowed the global rate of agricultural productivity growth. This observation carries implications beyond harsher weather conditions alone; it suggests that the adaptive and developmental capacity of production systems themselves is beginning to erode.

Against this backdrop, smart agriculture has become increasingly prominent. Sensorbased monitoring systems, remote sensing technologies, variablerate applications, decisionsupport software, and automation tools are no longer viewed merely as examples of technological modernization. They are increasingly interpreted as mechanisms that allow agricultural production to be managed with greater precision and responsiveness. Realtime monitoring of soil moisture, more accurate irrigation scheduling, early detection of plant stress, and sitespecific management practices tailored to withinfield variability all illustrate this transition. (Liakos et al. 2018) emphasized that datadriven systems may improve decision accuracy while accelerating management processes. Even so,

an important limitation should not be overlooked. No matter how advanced a digital infrastructure becomes, its effectiveness may remain constrained under biologically weakened production environments. This has directed growing attention toward models capable of integrating physical, biological, and digital components within the same production framework.

Biochar has emerged as one of the more visible materials within this context. Produced through the thermochemical conversion of organic biomass, biochar can exert multidimensional effects within soil systems because of its porous structure, high surface area, and relatively stable carbon composition. It may improve soil water retention, reduce nutrient losses, and provide favorable microhabitats for microbial communities (Lehmann & Joseph 2015). (Jeffery et al. 2017) reported that biochar applications can improve plant performance under certain environmental conditions. Yet these effects are far from universal. Feedstock characteristics, application rate, and environmental context remain among the principal variables shaping the outcome.

A comparable trajectory has occurred in research on plant growthpromoting rhizobacteria (PGPR). These microorganisms may support root development, enhance phosphorus solubilization, contribute to nitrogen cycling, and influence plant physiology through phytohormonerelated mechanisms. (Vessey 2003) initially approached PGPR largely from a biofertilizer perspective, whereas subsequent studies revealed a considerably broader functional spectrum. Under drought and salinity stress, PGPR have been reported to improve physiological resilience in plants through mechanisms involving ACC deaminase activity, osmoprotectant synthesis, and antioxidant defense pathways (Backer et al. 2018; Olanrewaju et al. 2017).

Perhaps the more compelling research direction lies in the combined evaluation of biochar and PGPR systems. The porous architecture of biochar may provide protected colonization sites for beneficial microorganisms, potentially supporting microbial persistence around the rhizosphere and contributing to more stable plant–microbe interactions. (Sashidhar et al. 2020) described biochar as a promising platform for the delivery and controlled release of agricultural inputs. Even so, much of the current literature continues to examine these two components independently. This fragmentation suggests that integrative approaches remain in a relatively early stage of development.

Within this framework, hazelnut shells deserve particular attention. Considering Türkiye's dominant role in global hazelnut production, shell residues generated during processing represent a substantial biomass resource (FAOSTAT 2023). Their lignocellulosic composition and carbonrich structure make them particularly suitable for biochar production (Demirbas, 2004). Existing studies have concentrated predominantly on energy potential, combustion

characteristics, or basic material characterization. By contrast, studies examining hazelnut shellderived biochar together with PGPR systems and smart irrigation technologies remain limited (Gwenzi et al. 2015). This gap in the literature is difficult to ignore.

Smart irrigation systems appear especially strategic in this regard. Water management remains one of the principal determinants of productivity across many agricultural systems. Soil moisture sensors and datadriven irrigation scheduling may reduce unnecessary water consumption while maintaining a more stable moisture regime around the root zone (Jones, 2004). Once soils are amended with biochar, water retention dynamics and moisture movement patterns may shift considerably (Edeh et al. 2020). PGPRmediated improvements in root functionality may further reinforce this process (Vessey 2003). Under such conditions, irrigation technologies may perform more effectively when combined with biologically strengthened rhizosphere environments rather than functioning as isolated technical tools.

The present study aims to evaluate, in light of current literature, how hazelnut shellderived biochar can be transformed into functional rhizosphere platforms through its integration with PGPR systems and smart irrigation technologies. Particular attention is given to the physicochemical properties of biochar, its microbial interaction capacity, contributions to water management, implications for plant stress physiology, and its broader integration potential within smart agriculture systems. The future role of agricultural residues can no longer be reduced to disposal concerns alone; increasingly, they are being reconsidered as strategic inputs within nextgeneration agricultural design frameworks.

1.1. Multidimensional Effects of Biochar on Soil–Plant–Microbial Systems

Biochar is commonly described through its carbonrich composition and its influence on soil microbiota. While this definition is technically accurate, it remains incomplete on its own because the agricultural effects of biochar cannot be reduced to a single mechanism. Alterations in soil physical structure, shifts in chemical equilibrium, restructuring of microbial communities, and biologically mediated responses developing around the root zone often emerge simultaneously and interactively (Lehmann & Joseph 2015).

From the perspective of soil physical structure, porosity remains one of the most widely discussed attributes. Porous materials may contribute to aggregate stability and, under certain conditions, reduce bulk density. This becomes particularly important in compactionprone soils where improved pore architecture may create a more favorable environment for root development. (BlancoCanqui 2017) reported that numerous studies observed improvements in structural parameters such as infiltration and aggregation following biochar application. Since soils do not respond uniformly, it is hardly surprising that biochar has attracted particular attention in relation to soil–water interactions.

Any approach capable of increasing plantavailable water within the root zone inevitably gains strategic relevance under conditions where water availability increasingly constrains production systems. Owing to its porous structure, biochar may enhance available waterholding capacity under specific conditions (Jeffery et al. 2011). The overall picture, however, remains far from uniform. Some studies reported only limited effects on water retention, whereas others observed declines associated with excessive application rates.

The chemical dimension presents an equally complex landscape. The pH, ash content, and surface characteristics of the applied material may directly influence soil reactions. In acidic soils, increases in pH can improve the availability of certain nutrients (Chan et al. 2007). Shifts in cation exchange capacity may also contribute to stronger retention of nutrient ions within the soil matrix (Glaser et al. 2002).

The microbiological dimension of biochar has become one of the most dynamic areas of contemporary research. Microorganisms actively participate in nutrient cycling, organic matter decomposition, and the regulation of plant stress responses (Van der Heijden et al. 2008). Biocharderived pore networks may provide protected microhabitats for these organisms. (Thies et al. 2015) reported that biochar can stimulate microbial activity under particular environmental conditions. Yet the response is not universally positive. Certain materials may exhibit transient toxicity and temporarily suppress microbial balance within the soil system (Spokas et al. 2012). Such observations suggest that the influence of biochar often becomes more pronounced at the rhizosphere scale. The rhizosphere itself represents a highly dynamic interface shaped by root exudates and intense microbial interactions (Philippot et al. 2013). Within this environment, biochar may exert indirect effects through simultaneous influences on root growth and microbial functionality.

The establishment of stable field colonization by beneficial rhizobacteria is rarely straightforward. Environmental stress and microbial competition may substantially complicate this process (Compant et al. 2010). The large surface area and microscale niches associated with biochar may offer more favorable habitats for these microorganisms. In this respect, the interaction between biochar and PGPR appears to rest on a functional ecological basis rather than a merely additive relationship Figure 1.

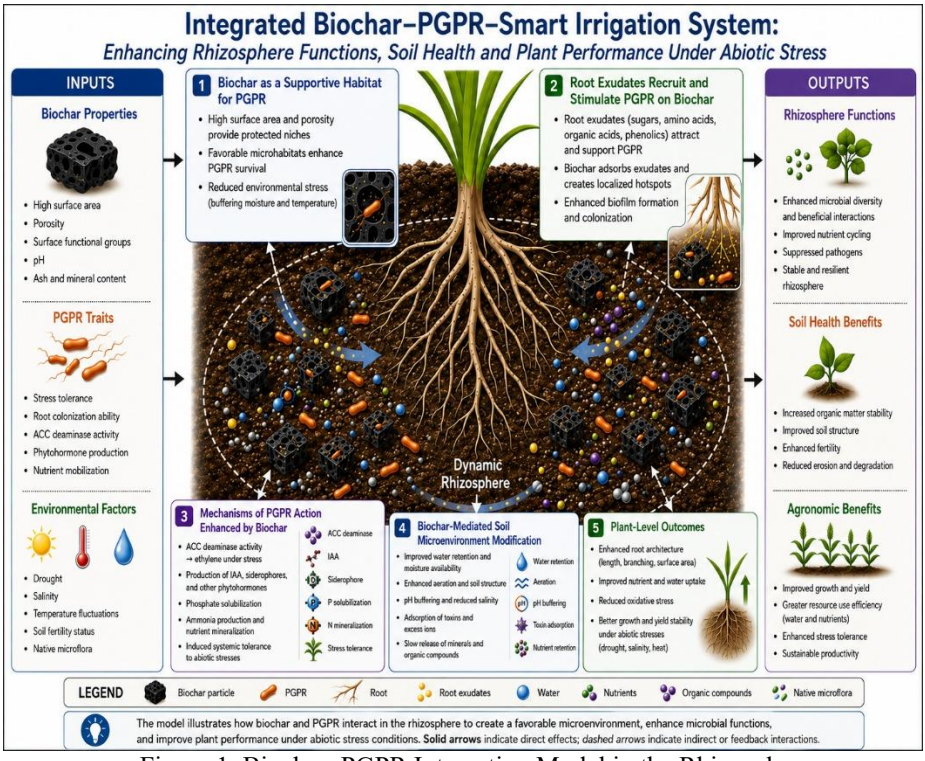


Figure 1. Biochar–PGPR Interaction Model in the Rhizosphere

When biochar is evaluated together with smart irrigation systems, the discussion moves beyond conventional soil amendment strategies and enters the domain of water management itself. Sensorbased irrigation models attempt to interpret moisture dynamics within the root zone, yet the reliability of these measurements is inherently linked to how soil retains, transmits, and supplies water to plants. (Edeh et al. 2020) demonstrated that the effects of biochar on soil hydraulic properties vary substantially depending on texture, application rate, and soil structure. Similarly, (Acharya et al. 2024) emphasized that the influence of biochar on water dynamics may become more pronounced in coarsetextured soils, although responses do not follow a uniform pattern across all soil types. If biochar alters infiltration behavior, water retention capacity, or the proportion of plantavailable moisture, then irrigation decision algorithms must inevitably be reconsidered within this newly modified physical environment.

Put more directly, digital systems interpret data, whereas biochar may alter the very environment from which those data emerge. This relationship becomes particularly important in terms of sensor calibration. Identical moisture readings may represent different levels of plantavailable water depending on whether biochar has been incorporated into the soil. (GómezAstorga et al. 2024) demonstrated that lowcost moisture sensors may require separate calibration procedures in biocharamended soils. Such findings suggest that biochar should

not be treated merely as an auxiliary soil material within smart irrigation systems; it also functions as a variable capable of influencing measurement accuracy and irrigation decisionmaking processes Figure 1. The relationship between biochar and sensor performance is therefore not a minor technical detail. It directly shapes the reliability of irrigation management itself.

A substantial proportion of current findings still originates from shortterm pot experiments or controlledenvironment studies. These studies are valuable for mechanistic interpretation, yet field conditions remain considerably more complex. Soil heterogeneity, climatic fluctuations, and management variability rarely follow the controlled logic of experimental designs. (Vijay et al. 2021) reported that crop responses observed in largescale biochar field trials remain highly variable and are closely associated with soil conditions, climate, application rates, and management practices. Variability in biochar quality further complicates interpretation of the results. (Freitas et al. 2020) demonstrated that differences in feedstock materials are directly reflected in biochar composition, creating substantial implications for agricultural applications. At this stage, the primary challenge is not necessarily the absence of information. Rather, the difficulty lies in the lack of a sufficiently unified evaluation framework resulting from the use of different materials, methodologies, and soil systems across studies.

For this reason, biochar should not be viewed as a passive carbon material simply incorporated into soil systems. Under suitable conditions, it may improve soil physical structure, alter water behavior within the root zone, provide chemical buffering capacity, and influence microbial processes simultaneously. (Bolan et al. 2024) demonstrated that the biological effects of biochar are closely associated with pore architecture, nutrient retention, microenvironment formation, and microbial community interactions. These multilayered rhizospherelevel effects position biochar as a far more strategic component within smart agriculture systems. The central question is no longer whether biochar functions effectively. Increasingly, the critical issue concerns which type of biochar, under which soil conditions, irrigation regime, and management framework, can generate the greatest agronomic value.

1.2. Biochar Systems Enriched with PGPR

One of the most persistent challenges in PGPR research remains the difficulty of reproducing controlledenvironment results under field conditions. In many studies, this inconsistency is primarily attributed to the biological capacity of the bacterial strains themselves. Field reality, however, is considerably more complex. Drought periods, sudden temperature fluctuations, elevated UV exposure, and competition with indigenous microbial communities in the rhizosphere directly constrain the persistence of introduced bacterial populations. Physical and chemical shifts occurring around the root zone further increase the

fragility of this process. Under such circumstances, the weakening of responses previously observed in controlled environments is hardly unexpected. (Backer et al. 2018) clearly identified this inconsistency in field performance as one of the principal obstacles limiting the broader adoption of PGPR applications.

Even so, much of the available literature still relies on shortterm and relatively smallscale experiments, whereas longterm fieldbased evidence remains limited. Results obtained under different ecological conditions also fail to converge consistently. The issue, therefore, extends beyond selecting an appropriate bacterial strain. The more critical challenge lies in establishing a suitable microenvironment capable of sustaining microbial persistence under field conditions.

This discussion inevitably draws attention toward the role of carrier materials, and biochar has gained increasing prominence within this context. Its high porosity and large surface area may provide a physical settlement matrix for microorganisms, while microscale cavities can support more stable colonization dynamics. Certain biochar types may also contribute to a more balanced moisture regime within the rhizosphere through enhanced water retention, thereby supporting the continuity of microbial activity. Despite this promising framework, major gaps remain within the literature. Comparative evaluations of different biochar types on microbial performance are still insufficient, and longterm field studies remain remarkably scarce.

The economic dimension is frequently overlooked as well, weakening assessments regarding practical sustainability and largescale applicability. (Sashidhar et al. 2020) emphasized that biochar possesses substantial potential as a controlled delivery platform for agricultural inputs, while simultaneously acknowledging that evidence concerning its performance across different production systems remains limited.

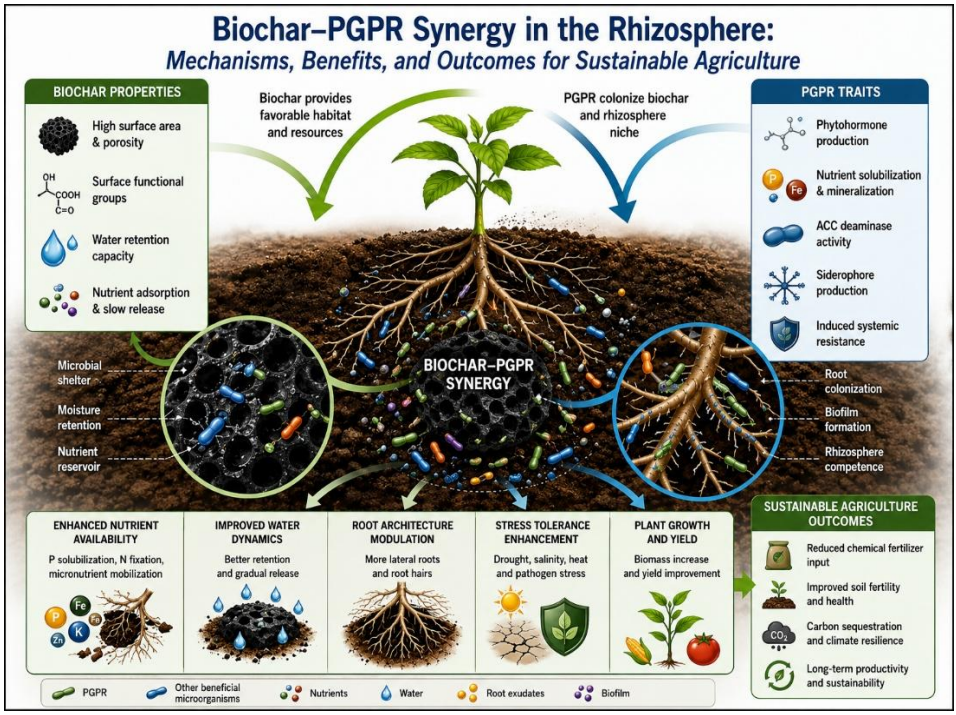


Figure 2. Conceptual framework illustrating the mechanistic pathways through which biochar enhances PGPR survival, colonization, and functional activity in the rhizosphere, ultimately improving plant growth and stress tolerance under variable environmental conditions.

Because bacteria attached to biochar surfaces may establish themselves closer to the root zone and maintain greater stability within the rhizosphere, the relationship between biochar and PGPR extends beyond a simple carrier function. Under these conditions, nutrient solubilization, root signaling, and microbial communication processes may proceed more effectively around the rhizosphere environment. (Egamberdieva et al. 2017) reported that combined applications of biochar and beneficial microorganisms produced stronger growth responses than individual treatments alone. This finding is particularly important because it suggests that the concept of synergy in these systems is supported by experimental observation rather than remaining a purely theoretical assumption Figure 2. The PGPR–biochar interaction also becomes highly relevant from the perspective of nutrient management. Numerous PGPR strains can convert insoluble phosphate forms into plantavailable forms, influence iron acquisition through siderophore production, and contribute to nitrogen cycling processes. (Olanrewaju et al. 2017) indicated that these mechanisms may directly translate into measurable agricultural outcomes Figure 2. Once supported by biochar systems, nutrient leaching losses may decline while a more stable nutrient reservoir develops around the root zone. Such effects may become particularly visible in marginal soils where nutrient retention capacity is inherently limited.

Table 1. Potential Functional Roles of PGPR–Biochar Integration

Component	Primary Effect	Potential Reflection on Plant Performance
PGPR	Root stimulation	Improved water and nutrient uptake
PGPR	Phytohormone regulation	Enhanced growth balance
Biochar	Moisture retention	Reduced drought pressure
Biochar	Surface carrier function	Stronger microbial colonization
Combined application	Synergistic interaction	More stable plant development

The significance of PGPR–biochar integration becomes even more pronounced under drought conditions because the resulting effects emerge through interconnected rather than isolated mechanisms. Certain PGPR groups may alleviate ethylenerelated stress through ACC deaminase activity while simultaneously stimulating proline accumulation and antioxidant defense pathways. Biochar, by retaining water within the root zone, may support the continuity of these biological responses Table 1. Although the positive findings reported by (Nadeem et al. 2019) support this interaction framework, the limited availability of longterm field data across different climatic regions still leaves a substantial gap in the literature.

A similar pattern can be observed under salinity stress. Elevated salt concentrations restrict plant growth through osmotic pressure and ion toxicity, whereas certain PGPR strains may help preserve root development and ionic balance (Yang et al. 2009; Etesami & Beattie 2018). Biochar applications may further contribute by improving rhizosphere conditions and supporting microbial activity (Laird et al. 2010; Kolton et al. 2011). Yet responses do not proceed uniformly under all conditions. Salt type, soil characteristics, and application rate remain among the main variables shaping the outcome (FarhangiAbriz & Torabian 2017). For this reason, contextdependent evaluations appear considerably more reliable than broad generalizations.

The integration of this biological infrastructure with smart irrigation systems introduces an additional operational threshold. Sensorbased irrigation approaches may optimize water management through continuous moisture monitoring, whereas a rhizosphere structured by biochar and strengthened through PGPR activity may amplify the effectiveness of those decisions (Adeyemi et al. 2017; Kourgialas et al. 2019). More balanced moisture conditions, more active root systems, and functionally enriched microbial communities may begin to operate as interconnected components of the same adaptive system Table 1. The literature, however, cannot yet be considered fully mature. Most available studies still rely on shortterm experimental designs, while questions surrounding field performance, economic feasibility, and microbial compatibility remain

unresolved (Gao et al. 2020). Even so, the broader picture is becoming increasingly clear: PGPRenriched biochar systems possess substantial potential. The central issue is no longer whether these systems can function effectively, but rather which combinations perform best under specific environmental and management conditions.

1.3. Integrated System Dynamics and Operational Framework

1.3.1. Conceptual Model

Within the scope of this study, the integrated structure formed by biochar, PGPR, and smart irrigation components is evaluated through a multilayered systems perspective. This framework encompasses not only the processes extending from inputs to outputs, but also the interactions and feedback mechanisms operating between these processes.

Agricultural production systems are too complex to be explained through the linear effects of isolated inputs alone. Once biochar, PGPR, and smart irrigation approaches are evaluated together, a multidimensional interaction network emerges that extends beyond conventional cause effect relationships. For this reason, these components should not be interpreted merely through their individual contributions, but rather through the functions they assume and the relationships they establish within the broader system structure.

This framework can be understood through four interconnected layers that follow one another without being separated by rigid boundaries. The first layer corresponds to the input stage, where the initial conditions of the system are defined. The feedstock source and production conditions of biochar, the environmental adaptability of microbial strains, and the data sensitivity of the irrigation system collectively establish the operational boundaries shaping system behavior from the outset (Joseph et al. 2021). Decisions made at this stage determine many of the parameters guiding subsequent processes.

The second layer represents the process stage, where the responses of the soil–plant system become increasingly visible. At this stage, biochar modifies soil pore architecture and alters the movement and distribution dynamics of water within the soil environment. PGPR simultaneously regulate biochemical processes around the root zone, reshaping nutrient acquisition and stressresponse mechanisms. Irrigation functions as a regulatory component controlling the timing and intensity of these interactions. The resulting structure evolves into a dynamic equilibrium zone where physical transformations and biological responses become tightly interconnected (O'Connor et al. 2018).

At the intersection of these processes, the interaction layer becomes more pronounced and begins to shape overall system behavior more directly. The microhabitats created by biochar reorganize microbial settlement patterns, while microbial activity itself may alter the physiological responses of plants to water

availability. Irrigation decisions may sometimes strengthen these interactions and, under other circumstances, impose limitations upon them. The system therefore cannot be reduced to a single behavioral pattern; its responses remain highly conditional and contextdependent (Lehmann et al. 2021).

This dynamic structure ultimately manifests within the output layer. Yield increase alone no longer represents a sufficient evaluation criterion. Indicators such as wateruse efficiency, production stability, and changes in inputuse patterns provide a considerably more informative assessment framework (Schmidt et al. 2021). Figure 3 Productivity, in this sense, must be interpreted alongside resourceuse efficiency and risk management capacity rather than through quantity alone.

One of the defining characteristics of this system emerges through its feedback capacity. Irrigation decisions shaped by sensorderived data may be continuously updated according to soil and plant responses. In this way, the system moves away from a static management model and gradually acquires a dynamic structure capable of adapting to changing environmental conditions. Such an approach reflects an increasingly visible management philosophy in contemporary agricultural production systems (Wolfert et al. 2017) Figure 3. This framework not only clarifies the effects of individual inputs, but also reveals how those effects are reorganized and reshaped over time.

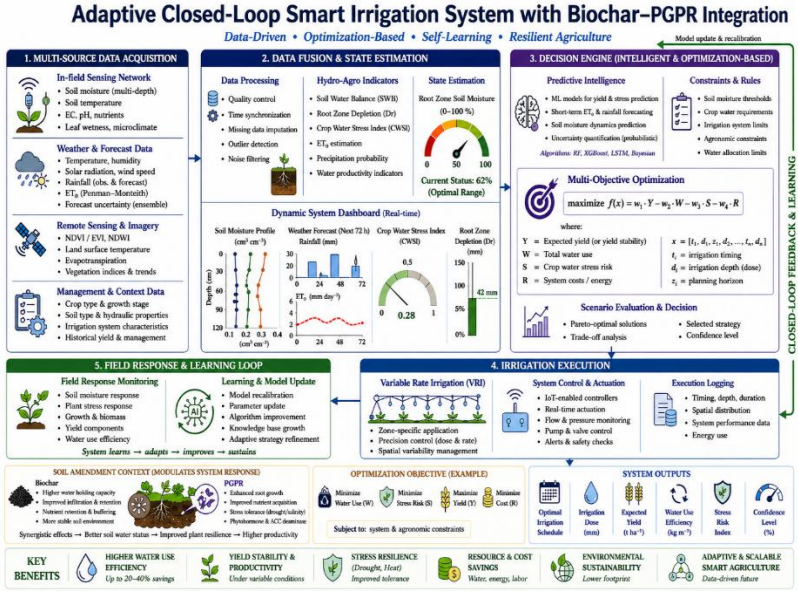


Figure 3. Closedloop irrigation system integrating biocharamended soil and PGPRmediated rhizosphere processes. Multisource data (soil moisture, plant and environmental signals) dynamically regulate irrigation timing and dosage. Feedback from rootzone hydraulic changes and plant responses enables adaptive, systemresponsive water management.

This section continues the conceptual framework introduced earlier and further clarifies how the system components operate as an interconnected interaction network rather than as isolated technological inputs Figure 3. At this stage, biochar emerges as one of the principal components reshaping the physical foundation of the system itself. Its porous structure and extensive surface area may substantially alter water retention and redistribution dynamics, particularly in lighttextured soils or soils characterized by low organic matter content (BlancoCanqui 2017). The effect extends beyond the amount of retained water alone. Infiltration behavior, surface runoff, and the redistribution of moisture within the root zone may also shift considerably. Yet the response does not proceed uniformly under all conditions. Feedstock type, pyrolysis temperature, application rate, and particle size may each redirect system behavior in different ways. Such variability weakens the reliability of fixed threshold values commonly used in irrigation management. The same moisture sensor reading may carry very different biophysical implications in soils amended with biochar compared with untreated soils. Under these conditions, the relationship between measurement and irrigation decisionmaking in datadriven systems requires reconsideration rather than simple calibration adjustments.

PGPR applications represent a third critical component within this watermanagement framework. Certain PGPR strains may stimulate root development, increase fineroot formation, and strengthen the plant's ability to access water. Others may alleviate drought pressure through phytohormonal regulation, osmoprotectant production, or activation of antioxidant defense systems. (Nadeem et al. 2014) reported that beneficial microorganisms can improve plant performance under stress conditions. Figure 3 These responses become especially valuable in environments characterized by irregular irrigation patterns or limited water availability.

When biochar and PGPR are evaluated together, a more integrated biological structure begins to emerge (Warnock et al. 2007). Biochar may support PGPR persistence by creating a more stable moisture environment around the root zone (Major et al. 2012; Karhu et al. 2011). PGPR, in turn, may enhance the translation of the physical advantages provided by biochar into measurable plant responses through their effects on root functionality and nutrient acquisition (Glick 2012). The interaction is not unidirectional. Instead, a reciprocal reinforcement dynamic becomes increasingly visible, particularly under environmental stress conditions where synergistic effects appear more pronounced (Ngumbi & Kloepper 2016). Smart irrigation systems may elevate this structure even further. While moisture sensor data guide irrigation timing and application intensity, biochar simultaneously regulates water retention behavior within the rhizosphere (Jones, 2009; Hedley & Yule 2009).

At the same time, PGPR applications may strengthen physiological responses by improving plant wateruse efficiency (Sandhya et al. 2010). Once these three components begin functioning collectively, the integrated structure gradually evolves into a more advanced and productivityoriented system. Decisionsupport mechanisms, soilconditioning processes, and biological reinforcement thus converge within the same management framework. The objective is no longer to apply greater volumes of water (Figure 3). Rather, the system seeks to achieve higher physiological efficiency and more stable production outcomes using the same water input. In this context, hazelnut shellderived biochar gains particular strategic importance. In countries such as Türkiye, where hazelnut production is concentrated, the integration of locally available biomass resources with irrigation technologies may reduce dependence on external inputs while simultaneously supporting regional and circular economic models (Ahmad et al. 2014; FAO 2024).

For example, sensorbased drip irrigation systems may be combined with soils amended using hazelnut shell biochar and rhizosphere environments supported through PGPR applications. Such an approach appears especially promising in semiarid regions experiencing water limitations (Rockström et al. 2010).

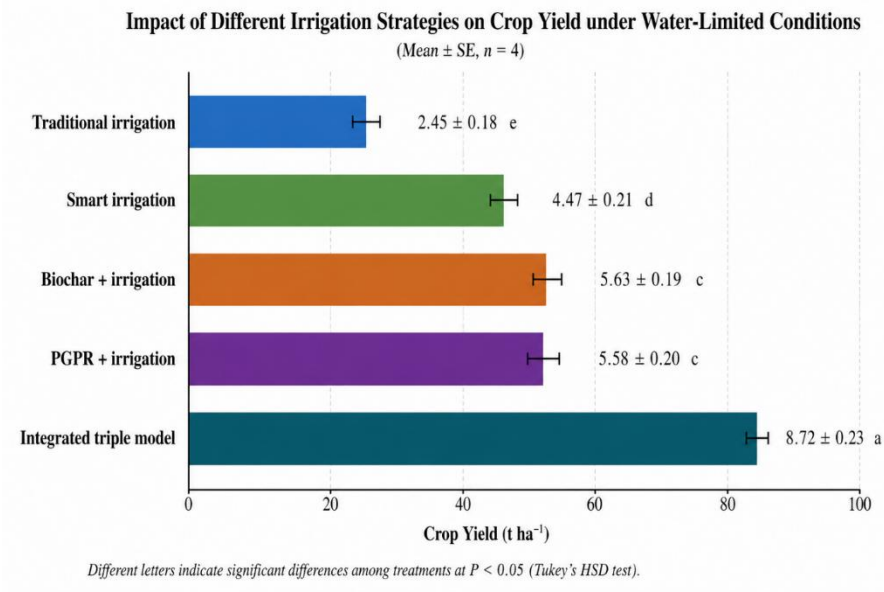


Figure 4. Effects of different irrigation strategies on crop yield under waterlimited conditions. The integrated triple model (smart irrigation + biochar + PGPR) produced the highest yield, clearly demonstrating a synergistic effect among components. Individual applications (biochar or PGPR combined with irrigation) resulted in moderate yield improvements, while smart irrigation alone outperformed traditional irrigation. Values represent mean ± SE (n = 4). Different letters indicate statistically significant differences among treatments at P < 0.05 (Tukey's HSD test).

In countries where agricultural production is intensive, such as Türkiye, the combined utilization of local biomass resources and irrigation technologies may contribute to more circular production systems by reducing dependency on external agricultural inputs (Agegnehu et al. 2017; Woolf et al. 2010). Within this framework, the simultaneous evaluation of biocharamended soils and PGPRsupported rhizosphere systems under sensorbased drip irrigation appears particularly meaningful Figure 4. When the waterretention and soilstructuring effects of biochar (BlancoCanqui 2017) are considered alongside the regulatory role of PGPR in root development and stress tolerance (Backer et al. 2018), an integrated systems perspective naturally emerges.

This approach appears to hold substantial research potential, particularly in semiarid environments where water scarcity increasingly constrains agricultural productivity (Omondi et al. 2016). Even so, the current literature reveals several major gaps. Standardized protocols for the combined use of biochar, PGPR, and smart irrigation systems across varying environmental conditions remain poorly established. Interactions between different biochar types and microbial strains are still insufficiently understood, while holistic optimization models integrating all system components remain limited (Palansooriya et al. 2019). Questions surrounding economic feasibility, sensor calibration, performance variability across soil types, and farmscale applicability also remain unresolved (Adeyemi et al. 2017; Kour et al. 2020). From a technological standpoint, many components of the system are already available. The more difficult challenge lies in determining how these components can be managed simultaneously under real field conditions in a balanced, economically sustainable, and operationally coherent manner. Future studies, therefore, should extend beyond technical performance alone and increasingly focus on system integration and fieldscale applicability (Gebbers & Adamchuk 2010).

Within scientific literature, many innovations initially appear highly promising. Agricultural success, however, rarely emerges from a single technology operating in isolation. More commonly, it depends on the coordinated interaction of complementary systems (Pretty et al. 2018). For this reason, biochar, PGPR, and smart irrigation should not be treated as separate technological categories, but rather as interconnected components of a shared production architecture (Lehmann & Joseph 2015; Vessey 2003). Decisionsupport systems occupy a central position within this transition. If soil moisture sensor data, weather forecasts, and plant developmental stages can be integrated within the same operational platform, irrigation management may shift away from fixed calendarbased scheduling toward a genuinely dynamic decision process (Liakos et al. 2018). Yet an important misconception frequently appears within this discussion: the assumption that sophisticated algorithms can compensate for weak field conditions. In reality, if soils remain physically and

biologically degraded, even the most advanced software systems may generate only limited benefits (Lal 2020).

A considerable portion of existing research continues to optimize individual system components separately. In actual agricultural environments, however, many problems arise not from the isolated performance of these components but from the incompatibilities emerging when they operate simultaneously under field conditions. Within this context, the relationship between biochar and PGPR cannot be adequately explained through a simple complementary interaction. Instead, it reflects the simultaneous operation of multiple processes functioning across different ecological layers within the same rhizosphere environment. How these interactions ultimately influence irrigation decisionmaking remains insufficiently clarified. This uncertainty becomes even more visible in production systems characterized by variable soil structure and unstable climatic conditions (Poorter et al. 2016).

At this stage, the challenge extends beyond understanding biological or physical processes individually. The more critical issue concerns whether these processes can be transformed into a manageable operational structure. Once sensorderived data, the heterogeneous structure of biochar, and the temporal variability of microbial activity are evaluated together, the system ceases to behave deterministically and instead acquires a contextsensitive character. This may also explain why standardized management protocols often fail to generate consistent results under field conditions (Jeffery et al. 2015).

At the same time, many technically successful approaches remain limited in practice because the primary constraints are often economic rather than biophysical. For producers, the decisive factor is rarely yield increase alone; what matters is the balance established between productivity gains and associated costs. The adoption of these systems therefore depends less on theoretical performance potential than on how predictable their economic returns appear under real production conditions (Pretty et al. 2018). Under such uncertainty, decisionsupport systems can no longer function merely as tools for displaying data. In particular, digital twin approaches may transform decisionmaking into a predictive process by evaluating multiple system components within the same operational model. Irrigation management, in this sense, becomes more than a reaction to current conditions; it evolves into a process capable of managing future scenarios before they emerge (Jones et al. 2017).

Ultimately, the major gap within the current literature is not the absence of new technological components. What remains insufficient is an operational framework capable of explaining how existing components can function together coherently within the same agricultural system. Developing such a framework may help shift agricultural production away from fragmented interventions and

toward integrated systems capable of managing interactions rather than isolated inputs alone.

2. Dıscussion

2.1. Integrated Evaluation and Future Perspectives in Integrated Agricultural Systems

Research focusing on biochar, PGPR, and smart irrigation systems has expanded considerably in recent years. At first glance, these areas may appear disconnected from one another. One primarily addresses soil structure, another centers on microbial processes, while the third emphasizes digital decisionmaking mechanisms. A closer examination, however, reveals that these approaches represent different yet simultaneously operating layers within the same production system. Agricultural losses should rarely be attributed to a single factor alone. Drought, nutrient imbalance, declining organic matter, and climatic variability may all exert influence within the same production cycle (Lal 2015). Such multidimensional pressure inevitably requires intervention strategies capable of moving beyond fragmented approaches toward more integrated frameworks that explicitly account for system interactions.

The responses obtained from biochar applications do not follow a fixed or universally predictable pattern. Feedstock origin, pyrolysis conditions, and soil characteristics directly shape both the magnitude and direction of the observed outcomes. For this reason, the variability reported throughout the literature should not necessarily be interpreted as inconsistency, but rather as a reflection of the contextsensitive nature of the system itself (Jeffery et al. 2017; Lehmann & Joseph 2015). A similar pattern emerges in PGPR applications. Certain strains capable of producing highly positive responses under controlled conditions may fail to maintain the same level of effectiveness under fluctuating environmental conditions. In many cases, this discrepancy appears to arise less from microbial incapacity than from competitive pressures and environmental instability occurring around the rhizosphere environment (Backer et al. 2018).

When these two components are evaluated together, the resulting structure cannot be explained merely through the accumulation of individual effects. As discussed in previous sections, the physical environment established by biochar and the biological processes regulated by PGPR evolve simultaneously within the same rhizosphere system. Reports suggest that these interactions become more visible under environmental stress conditions (Sashidhar et al. 2020). Even so, many critical thresholds governing this interaction remain poorly defined. The conditions under which these interactions intensify, weaken, or shift direction have yet to be clearly established. The temporal dimension of these processes, dose–response relationships, and the restructuring of microbial communities at the rhizosphere level all remain insufficiently clarified in relation to overall system performance.

Within this framework, the role of local biomass resources is becoming increasingly significant. Materials such as hazelnut shells were long regarded as lowvalue agricultural waste; however, once subjected to appropriate processing, they can be reintegrated into production systems as functional inputs (Lehmann & Joseph 2015). This perspective extends well beyond a purely technical improvement. The incorporation of local resources into agricultural production reshapes the origin of inputs themselves and may support more balanced regional production systems. What ultimately becomes decisive is not merely the material being used, but how its function is defined within the broader operational system.

Smart agriculture systems constitute the management dimension of this integrated structure. Sensorderived data are known to support more precise decisions regarding irrigation timing and application rates. Yet it has become increasingly evident that the effectiveness of these systems is directly associated with the physical and biological properties of the soils in which they operate (Liakos et al. 2018). This observation suggests that digital technologies alone are insufficient; their value becomes considerably greater when combined with biological and physical improvements within the production environment. Another issue frequently emphasized throughout the literature concerns the lack of standardization. The use of different biochar types, distinct PGPR strains, and varying irrigation strategies complicates direct comparisons among studies. As a result, the integration and interpretation of findings across experiments remain limited. (Jones et al. 2017), for example, highlighted the critical importance of data integration and model standardization within agricultural systems research.

From an applicationoriented perspective, the strongest approaches appear to emerge through integrated systems rather than isolated interventions. Studies combining locally derived biochar, regionally adapted PGPR strains, and datadriven irrigation systems have reported improvements in wateruse efficiency alongside greater production stability under stress conditions (Nadeem et al. 2014). Despite these promising findings, scalability remains unresolved. One of the major unanswered questions concerns how models that perform successfully at small experimental scales can be transferred reliably into large production environments. At this point, the direction of scientific inquiry becomes increasingly clear. Developing entirely new tools may be less urgent than generating robust and reliable fieldbased evidence regarding the realworld performance of existing systems. Multilocation trials, longterm field observations, and economically grounded analyses are likely to become central components of this process. The actual value of an agricultural approach is ultimately determined less by controlledenvironment outcomes than by its consistency under practical production conditions.

For this reason, the discussion is gradually moving away from the question of which tool is individually more effective. The more important issue concerns how

these tools can operate together under field conditions. The future of agricultural production appears increasingly dependent not on expanding input intensity, but on managing existing inputs more intelligently within interconnected production systems.

3. Conclusion And Recommendations

The present study demonstrates that the performance of integrated production systems depends less on the isolated effects of individual components than on how the interactions among those components are managed. Within this context, the primary challenge is no longer whether the system functions at all, but rather under which conditions it can function consistently and predictably.

A substantial proportion of current research assumes that outcomes obtained at the component level can be generalized across production systems. Fieldscale variability, however, indicates that such assumptions remain limited. This suggests that, before attempting direct optimization of integrated systems, greater emphasis must first be placed on identifying the threshold conditions governing overall system behavior.

In this regard, future research should focus on three central questions:

(i) Under which environmental and management conditions can the system maintain predictable performance?

(ii) How should the relationship between biophysical processes and sensorbased decision mechanisms be calibrated?

(iii) At what production scale do the economic returns of these systems become practically meaningful?

The answers to these questions will likely determine whether integrated approaches can move successfully from experimental frameworks into largescale agricultural implementation. Otherwise, even technically successful system components may remain limited in their capacity to generate sustainable outcomes under real production conditions.

Ultimately, progress in agricultural production appears increasingly linked not to the addition of new inputs, but to the more precise management of relationships among existing ones. Such an approach preserves the objective of improving productivity while simultaneously offering a framework capable of reducing uncertainty and making decisionmaking processes more predictable.

4. References

Acharya, B. S. Dodla, S. Gaston, L. A. Darapuneni, M. Wang, J. J. Sepat, S. & Bohara, H. (2024). Biochar impacts on soil water dynamics. *Plant and Soil*.

Adeyemi, O. Grove, I. Peets, S. Domun, Y. & Norton, T. (2017). Dynamic modelling of soil moisture content for precision irrigation. *Computers and Electronics in Agriculture, 143*, 260–274. https://doi.org/10.1016/j.compag.2017.10.028

Agegnehu, G. Bass, A. M. Nelson, P. N. Muirhead, B. Wright, G. & Bird, M. I. (2017). Biochar and biocharcompost as soil amendments: Effects on peanut yield, soil properties and greenhouse gas emissions in tropical soils. *Science of the Total Environment, 583*, 268–277. https://doi.org/10.1016/j.scitotenv.2017.01.054

Ahmad, M. Rajapaksha, A. U. Lim, J. E. Zhang, M. Bolan, N. Mohan, D. Vithanage, M. Lee, S. S. & Ok, Y. S. (2014). Biochar as a sorbent for contaminant management in soil and water: A review. *Chemosphere, 99*, 19–33. https://doi.org/10.1016/j.chemosphere.2013.10.071

Backer, R. Rokem, J. S. Ilangumaran, G. Lamont, J. Praslickova, D. Ricci, E. & Smith, D. L. (2018). Plant growthpromoting rhizobacteria: Context, mechanisms of action, and roadmap to commercialization of biostimulants for sustainable agriculture. *Frontiers in Plant Science, 9*, 1473. https://doi.org/10.3389/fpls.2018.01473

BlancoCanqui, H. (2017). Biochar and soil physical properties. *Soil Science Society of America Journal, 81*(4), 687–711. https://doi.org/10.2136/sssaj2017.01.0017

Bolan, S. Hou, D. Wang, L. Hale, L. Egamberdieva, D. Tammeorg, P. Li, R. Wang, B. Xu, J. Wang, T. & Bolan, N. (2024). Biochar modulating soil biological health: A review. *Science of the Total Environment, 914*, 169585. https://doi.org/10.1016/j.scitotenv.2023.169585

Chan, K. Y. Van Zwieten, L. Meszaros, I. Downie, A. & Joseph, S. (2007). Agronomic values of greenwaste biochar as a soil amendment. *Australian Journal of Soil Research, 45*(8), 629–634. https://doi.org/10.1071/SR07109

Compant, S. Clément, C. & Sessitsch, A. (2010). Plant growthpromoting bacteria in the rhizo and endosphere of plants. *Soil Biology and Biochemistry, 42*(5), 669–678. https://doi.org/10.1016/j.soilbio.2009.11.024

Demirbaş, A. (2004). Effects of temperature and particle size on biochar yield from pyrolysis of agricultural residues. *Journal of Analytical and Applied Pyrolysis, 72*(2), 243–248. https://doi.org/10.1016/j.jaap.2004.07.003

Edeh, I. G. Mašek, O. & Buss, W. (2020). A metaanalysis on biochar's effects on soil water properties. *Science of the Total Environment, 714*, 136857. https://doi.org/10.1016/j.scitotenv.2020.136857

Egamberdieva, D. Wirth, S. Behrendt, U. Abd_Allah, E. F. & Berg, G. (2017). Biochar treatment resulted in a combined effect on soybean growth promotion and a shift in plant growth promoting rhizobacteria. *Frontiers in Microbiology, 8*, 209. https://doi.org/10.3389/fmicb.2017.00209

Etesami, H. & Beattie, G. A. (2018). Mining halophytes for plant growthpromoting halotolerant bacteria to enhance plant growth under salinity stress. *Frontiers in Microbiology, 9*, 148. https://doi.org/10.3389/fmicb.2018.00148

FAO. (2023). *FAOSTAT: Food and agriculture data*. https://www.fao.org/faostat

FAO. (2024). *Crops and livestock products database (FAOSTAT)*. https://www.fao.org/faostat/en/#data/QCL

FarhangiAbriz, S. & Torabian, S. (2017). Biochar improved nodulation and nitrogen metabolism of soybean under salt stress. *Symbiosis, 72*(2), 215–223. https://doi.org/10.1007/s1319901704865

Food and Agriculture Organization of the United Nations (FAO). (2014). *Building a common vision for sustainable food and agriculture: Principles and approaches*. Rome: FAO. https://www.fao.org/3/i3940e/i3940e.pdf

Freitas, A. M. Jaynes, D. B. & van Kessel, C. (2020). Biochar as influenced by feedstock variability: Implications for carbon storage and nutrient management. *Frontiers in Sustainable Food Systems, 4*, 510982. https://doi.org/10.3389/fsufs.2020.510982

Gao, S. DeLuca, T. H. & Cleveland, C. C. (2020). Biochar additions alter phosphorus and nitrogen availability in agricultural ecosystems: A metaanalysis. *Science of the Total Environment, 654*, 463–472. https://doi.org/10.1016/j.scitotenv.2018.11.124

Gebbers, R. & Adamchuk, V. I. (2010). Precision agriculture and food security. *Science, 327*(5967), 828–831. https://doi.org/10.1126/science.1183899

Glaser, B. Lehmann, J. & Zech, W. (2002). Ameliorating physical and chemical properties of highly weathered soils using charcoal. *Biology and Fertility of Soils, 35*(4), 219–230. https://doi.org/10.1007/s0037400204664

Glick, B. R. (2012). Plant growthpromoting bacteria: Mechanisms and applications. *Scientifica, 2012*, 963401. https://doi.org/10.6064/2012/963401

GómezAstorga, M. J. et al. (2024). Calibration of lowcost moisture sensors in a biocharamended soil. *Sensors, 24*(18), 5978. https://doi.org/10.3390/s24185978

Gwenzi, W. Chaukura, N. Mukome, F. N. D. Machado, S. & Nyamasoka, B. (2015). Biochar production and applications in soil fertility and environmental management. *Journal of EnvironmentalManagement,150*,250261https://doi.org/10.1016/j.jenvman.2014.11.027

Hedley, C. B. & Yule, I. J. (2009). Soil water status mapping and irrigation scheduling. *Precision Agriculture, 10*(4), 342–355. https://doi.org/10.1007/s111190089097y

Jeffery, S. Abalos, D. Prodana, M. Bastos, A. C. van Groenigen, J. W. Hungate, B. A. & Verheijen, F. (2017). Biochar boosts tropical but not temperate crop yields. *Environmental Research Letters, 12*(5), 053001. https://doi.org/10.1088/17489326/aa67bd

Jeffery, S. Verheijen, F. G. A. Van der Velde, M. & Bastos, A. C. (2011). A quantitative review of the effects of biochar application to soils on crop productivity. *Agriculture, Ecosystems & Environment, 144*(1), 175–187. https://doi.org/10.1016/j.agee.2011.08.015

Jeffery, S. Verheijen, F. G. A. van der Velde, M. & Bastos, A. C. (2015). A quantitative review of the effects of biochar application to soils on crop productivity using metaanalysis. *Agriculture, Ecosystems & Environment, 144*(1), 175–187. https://doi.org/10.1016/j.agee.2011.08.015

Jones, H. G. (2004). Irrigation scheduling: Advantages and pitfalls of plantbased methods. *Journal of Experimental Botany, 55*(407), 2427–2436. https://doi.org/10.1093/jxb/erh213

Jones, H. G. Serraj, R. Loveys, B. R. Xiong, L. Wheaton, A. & Price, A. H. (2009). Thermal infrared imaging of crop canopies for the remote diagnosis and quantification of plant responses to water stress. *Journal of Experimental Botany, 60*(3), 1–13. https://doi.org/10.1093/jxb/ern232

Jones, J. W. Antle, J. M. Basso, B. Boote, K. J. Conant, R. T. Foster, I. & Wheeler, T. R. (2017). Toward a new generation of agricultural system data, models, and knowledge products. *Agricultural Systems, 155*, 269–288. https://doi.org/10.1016/j.agsy.2016.09.021

Joseph, S. Cowie, A. L. Van Zwieten, L. Bolan, N. Budai, A. Buss, W. … Lehmann, J. (2021). How biochar works, and when it doesn't: A review of mechanisms controlling soil and plant responses. *GCB Bioenergy, 13*(11), 1731–1764. https://doi.org/10.1111/gcbb.12885

Karhu, K. Mattila, T. Bergström, I. & Regina, K. (2011). Biochar addition to agricultural soil increased CH_4 uptake. *Agriculture, Ecosystems & Environment, 140*(1–2), 309–313. https://doi.org/10.1016/j.agee.2011.01.005

Kolton, M. Harel, Y. M. Pasternak, Z. Graber, E. R. Elad, Y. & Cytryn, E. (2011). Impact of biochar application to soil on the rootassociated bacterial community structure of fully developed greenhouse pepper plants. *Applied and Environmental Microbiology, 77*(14), 4924–4930. https://doi.org/10.1128/AEM.0014811

Kour, D. Rana, K. L. Yadav, N. Yadav, A. N. Kumar, M. Kumar, V. … Saxena, A. K. (2020). Microbial biofertilizers: Bioresources and ecofriendly technologies for agricultural and environmental sustainability. *Biocatalysis and Agricultural Biotechnology, 23*, 101487. https://doi.org/10.1016/j.bcab.2019.101487

Kourgialas, N. N. Dokou, Z. & Karatzas, G. P. (2019). Statistical analysis and ANN modeling for predicting soil moisture in precision irrigation systems. *Agricultural Water Management, 224*, 105748. https://doi.org/10.1016/j.agwat.2019.105748

Laird, D. A. Fleming, P. Wang, B. Horton, R. & Karlen, D. L. (2010). Biochar impact on nutrient leaching from a Midwestern agricultural soil. *Geoderma, 158*(3–4), 436–442. https://doi.org/10.1016/j.geoderma.2010.05.012

Lal, R. (2015). Restoring soil quality to mitigate soil degradation. *Sustainability, 7*(5), 5875–5895. https://doi.org/10.3390/su7055875

Lal, R. (2020). Soil health and carbon management. *Food and Energy Security, 9*(1), e183. https://doi.org/10.1002/fes3.183

Lehmann, J. & Joseph, S. (2015). *Biochar for environmental management: Science, technology and implementation* (2nd ed.). Routledge.

Lehmann, J. Kern, D. C. German, L. A. McCann, J. Martins, G. C. & Moreira, A. (2021). Soil fertility and production potential. *Nature Reviews Earth & Environment, 2*, 371–388. https://doi.org/10.1038/s43017021001620

Liakos, K. G. Busato, P. Moshou, D. et al. (2018). Machine learning in agriculture: A review. *Sensors, 18*(8), 2674. https://doi.org/10.3390/s18082674

Major, J. Rondon, M. Molina, D. Riha, S. J. & Lehmann, J. (2012). Nutrient leaching in a Colombian savanna Oxisol amended with biochar. *Soil Use and Management, 28*(4), 468–478. https://doi.org/10.1111/j.14752743.2012.00435.x

Nadeem, S. M. Ahmad, M. Zahir, Z. A. Javaid, A. & Ashraf, M. (2014). The role of mycorrhizae and plant growth promoting rhizobacteria (PGPR) in improving crop productivity under stressful environments. *Biotechnology Advances, 32*(2), 429–448. https://doi.org/10.1016/j.biotechadv.2013.12.005

Nadeem, S. M. Imran, M. Naveed, M. Khan, M. Y. Ahmad, M. Zahir, Z. A. & Crowley, D. E. (2019). Synergistic use of biochar, compost and plant growthpromoting rhizobacteria for enhancing cucumber growth under water deficit conditions. *Journal of the Science of Food and Agriculture, 99*(6), 2945–2954. https://doi.org/10.1002/jsfa.9505

Ngumbi, E. & Kloepper, J. (2016). Bacterialmediated drought tolerance: Current and future prospects. *Applied Soil Ecology, 105*, 109–125. https://doi.org/10.1016/j.apsoil.2016.04.009

O'Connor, D. Peng, T. Zhang, J. Tsang, D. C. W. Alessi, D. S. Shen, Z. … Hou, D. (2018). Biochar application for the remediation of heavy metal polluted land: A review of in situ field trials. *Science of the Total Environment, 619–620*, 815–826. https://doi.org/10.1016/j.scitotenv.2017.11.132

Olanrewaju, O. S. Glick, B. R. & Babalola, O. O. (2017). Mechanisms of action of plant growth promoting bacteria. *World Journal of Microbiology and Biotechnology, 33*, 197. https://doi.org/10.1007/s1127401723649

Omondi, M. O. Xia, X. Nahayo, A. Liu, X. Korai, P. K. & Pan, G. (2016). Quantification of biochar effects on soil hydrological properties using metaanalysis of literature data. *Geoderma, 274*, 28–34. https://doi.org/10.1016/j.geoderma.2016.03.029

OrtizBobea, A. Ault, T. R. Carrillo, C. M. Chambers, R. G. & Lobell, D. B. (2021). Anthropogenic climate change has slowed global agricultural productivity growth. *Nature Climate Change, 11*, 306–312. https://doi.org/10.1038/s41558021010001

Palansooriya, K. N. Wong, J. T. F. Hashimoto, Y. Huang, L. Rinklebe, J. Chang, S. X. … Ok, Y. S. (2019). Response of microbial communities to biocharamended soils: A critical review. *Biochar, 1*, 3–22. https://doi.org/10.1007/s42773019000092

Philippot, L. Raaijmakers, J. M. Lemanceau, P. & Van der Putten, W. H. (2013). Going back to the roots: The microbial ecology of the rhizosphere. *Nature Reviews Microbiology, 11*(11), 789–799. https://doi.org/10.1038/nrmicro3109

Poorter, H. Bühler, J. van Dusschoten, D. Climent, J. & Postma, J. A. (2016). Pot size matters: A metaanalysis of the effects of rooting volume on plant growth. *Functional Plant Biology, 39*(11), 839–850. https://doi.org/10.1071/FP12049

Pretty, J. Benton, T. G. Bharucha, Z. P. Dicks, L. V. Flora, C. B. Godfray, H. C. J. … Wratten, S. (2018). Global assessment of agricultural system redesign for sustainable intensification. *Nature Sustainability, 1*, 441–446. https://doi.org/10.1038/s4189301801140

Rockström, J. Karlberg, L. Wani, S. P. Barron, J. Hatibu, N. Oweis, T. Bruggeman, A. Farahani, J. & Qiang, Z. (2010). Managing water in rainfed agriculture. *Agricultural Water Management, 97*(4), 543–550. https://doi.org/10.1016/j.agwat.2009.11.010

Sandhya, V. Ali, S. Z. Grover, M. Reddy, G. & Venkateswarlu, B. (2010). Effect of plant growth promoting bacteria on drought tolerance. *Plant Growth Regulation, 62*(1), 21–30. https://doi.org/10.1007/s1072501094736

Sashidhar, P. Kochar, M. Singh, B. Gupta, M. Cahill, D. Adholeya, A. & Dubey, M. (2020). Biochar for delivery of agriinputs: Current status and future

perspectives. *Science of the Total Environment, 703*, 134892. https://doi.org/10.1016/j.scitotenv.2019.134892

Schmidt, H. P. Pandit, B. H. Martinsen, V. Cornelissen, G. Conte, P. & Kammann, C. I. (2021). Fourfold increase in pumpkin yield in response to lowdosage root zone application of biochar. *Agronomy, 11*(1), 1–18. https://doi.org/10.3390/agronomy11010021

Spokas, K. A. Cantrell, K. B. Novak, J. M. Archer, D. W. Ippolito, J. A. Collins, H. P. Boateng, A. A. Lima, I. M. Lamb, M. C. McAloon, A. J. Lentz, R. D. & Nichols, K. A. (2012). Biochar: A synthesis of its agronomic impact beyond carbon sequestration. *Plant and Soil, 350*(1–2), 117–132. https://doi.org/10.1007/s1110401109349

Thies, J. E. Rillig, M. C. & Graber, E. R. (2015). Biochar effects on the abundance, activity and diversity of the soil biota. In J. Lehmann & S. Joseph (Eds.), *Biochar for environmental management: Science, technology and implementation* (2nd ed. pp. 327–389). Routledge.

Van der Heijden, M. G. A. Bardgett, R. D. & Van Straalen, N. M. (2008). The unseen majority: Soil microbes as drivers of plant diversity and productivity in terrestrial ecosystems. *Ecology Letters, 11*(3), 296–310. https://doi.org/10.1111/j.14610248.2007.01139.x

Vessey, J. K. (2003). Plant growth promoting rhizobacteria as biofertilizers. *Plant and Soil, 255*, 571–586. https://doi.org/10.1023/A:1026037216893

Vijay, V. Shreedhar, S. Adlak, K. Payyanad, S. Sreedharan, V. Gopi, G. van der Voort, T. S. Malarvizhi, P. Yi, S. Gebert, J. & Aravind, P. V. (2021). Review of largescale biochar fieldtrials for soil amendment and the observed influences on crop yield variations. *Frontiers in Energy Research, 9*, 710766. https://doi.org/10.3389/fenrg.2021.710766

Warnock, D. D. Lehmann, J. Kuyper, T. W. & Rillig, M. C. (2007). Mycorrhizal responses to biochar in soil. *Plant and Soil, 300*(1–2), 9–20. https://doi.org/10.1007/s1110400793915

Wolfert, S. Ge, L. Verdouw, C. & Bogaardt, M. J. (2017). Big data in smart farming – A review. *Agricultural Systems, 153*, 69–80. https://doi.org/10.1016/j.agsy.2017.01.023

Woolf, D. Amonette, J. E. StreetPerrott, F. A. Lehmann, J. & Joseph, S. (2010). Sustainable biochar to mitigate global climate change. *Nature Communications, 1*, 56. https://doi.org/10.1038/ncomms1053

Yang, J. Kloepper, J. W. & Ryu, C. M. (2009). Rhizosphere bacteria help plants tolerate abiotic stress. *Trends in Plant Science, 14*(1), 1–4. https://doi.org/10.1016/j.tplants.2008.10.004

CHAPTER 7

Cereals And Functional Nutrition: Sustainable Health

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Introduction

Sustainable living means choosing not to produce products using processes besides methods which do not supporting the sustainability concept, or reducing the harm we clearly cause to the nature whereby change of way we realize the business. In late years, it is fair that there is a quite growing interest for the effects of nutrition and also physical activities over human health. Therefore, it is well known that climate based changes undoubtedly has today, and also may continue to have in the future, direct and indirect effects on food security and safety. Consumers are becoming increasingly aware and demanding diversified foods with positive effects on health. For the aim of fully realize the potential of supporting health sustainability in food, there is a need for the production of standardized products, increased interdisciplinary studies, and research into the interactive effects of nutritional composition.

From the perspective of the main components of the sustainability theme, increasing population, biodiversity loss, the intensification of climate based changes, and demolition over natural based resources stance serious risks to human life in the future and therefore necessitate a shift towards sustainable approaches in the field of nutrition (Tompa et al., 2020). Today, the main related with proteins obtained from other plant sources is remarkably increasing welded to their abundance in nature, low cost, consumption preferences, and high nutritional and functional values (Vahed et al., 2023; Kodaz et al., 2025; Dalda Sekerci et al., 2026). Global climate change is defined as long-term climatic differences caused by the influence of human activities as well as natural processes (Chandio et al., 2021). According to nutrition experts, the food industry is expected to need to produce 30% - 70% quantity more in 2050 year comparing with current levels of food production (Ahmed, 2022). In total, they examined the environmental and health impacts of 85 different Food-Based Dietary Guidelines (FBDG) and found that most of these guidelines exceeded the food-related greenhouse gas emission (GHGE) limits in same line by Paris Agreement targets (Springmann et al., 2020).

Functional based foods are described as the food substances or its components of bioactive compounds that, beyond meeting the basic nutritional requirements of individuals, aim to provide health benefits such as disease prevention and improvement of overall health (Crowe and Francis, 2013). The increasing interest in healthy eating focuses on improving quality of life as well as increasing life expectancy, and this has prompted manufacturers to incorporate new healthy foods into human nutrition (Abellán et al., 2019). While there are different definitions for the term functional food, the “United States Academy of Nutrition and Dietetics” describes about functional foods aspect as it “fortified, enriched or enhanced foods, as well as whole food types, which are holder potentially

beneficial based effect over health statues in case of regularly consumption in effective amounts as part of a varied diet" as well (Crowe and Francis, 2013).

By the recent pandemics, the main demands for the functional based foods to strengthen the immune system has increased (Le et al., 2020). Plant-based foods that have significantly smaller carbon footprints over environment compared with animal-based foods. Insomuch that the least sustainable vegetables besides grains cause to lesser environmental damage compared with dairy products and meat, which have the lowest impact (Poore and Nemecek, 2018; Coban and Özer, 2025). Phytochemicals are defined by chemical components which are produced by the plants owing to primary and also secondary metabolism and possess to several biological activities (Konstantinidi and Koutelidakis, 2019; Banwo et al., 2021). Activation of phenolic metabolism increases the totally phenolic besides flavonoid content. These kind of mentioned compounds known as exhibit quite strong antioxidant and anti-inflammatory properties and anti-carcinogenic type of properties. This increase has been particularly evident in red lentils, broccoli, and buckwheat sprouts (Miyahira et al., 2021). Various studies have evaluated the reductions in environmental based impact based indicators likewise GHGE, land usage, and also for freshwater consumption achieved by switching to mainly plant-based typed diets (Springmann et al., 2018; Fresán and Sabaté, 2019).

Bioactive components have preventive and curative effects against degenerative and chronic diseases associated by oxidative stress types, diabetes type-2, hypertension, cardiovascular disease, inflammation, cancer, obesity and aging (Amagloh et al., 2023). Studies show that sprouting alone reduces antinutrients and increases the bioavailability of micronutrients in legumes (Anaemene & Fadupin, 2022). Findings reveal that age, gender, education level, living environment, and motivation act a quite decisive role over consumption of vegetarian and vegan alternative products (BMEL, 2021). Cereal grains are rich in several minerals, mainly for the zinc besides iron, along with containing macronutrients (Temba et al., 2016).

Sustainable nutrition is not merely an individual choice, it is a universal responsibility to use natural resources efficiently, reduce environmental impacts, and leave a livable world for the future. Therefore, it is crucial for individuals to develop environmental awareness and for this awareness to be disseminated through media and policy support (Dernini et al., 2017). This review aims to bring together findings from studies in scientifically accepted online databases that investigate the effects of cereals, a type of functional food, on sustainable health. The studies examined particularly focused on their impact on sustainability.

Sustainable Health and Cereals

Conceptually, term sustainable nutrition is defined as "optimizing human and natural resources, respecting - protecting biodiversity and surely ecosystems, being cultural based acceptable, being accessible, economic based feasible and

also affordable, nutrition based adequate, reliable and especially being healthy" as well (Dernini et al., 2017; FAO, 2019). To meet this demand from consumers based on sustainability, in recent years' foods with the potential to have an impact on health based on their nutritional content and bioactive composition have been examined and characterized. Japan, a leader for regulation of the functional foods, and the country is the first to allowing of health claims due to functional foods and use scientific evidence with its FOSHU program. The FOSHU approval is used on the labels of products approved as FOSHU (Shimizu and Hachimura, 2011). Epidemiological based data presenting a positive sided relation between the main consumption of the foods that are rich by phenolic based compounds (flavonoids, tannins, lignans, carotenoids etc.) and human well-being (Banwo et al., 2021).

Grains, consumed as a staple food for approximately 10,000 years, now provide over 50% of global calories (Mallikarjuna et al., 2022; Ahmar et al., 2023; Vishnoi and Goel, 2024). Historically, plant-based diets were widely considered healthier and morally superior to meat consumption (Mason and Mullins, 2016). The recently proposed definition for "functional food" is the novel foods formulated for contain several substances with health-improving or the disease-preventing properties, or live microorganisms, that are both safely and present in quiet sufficient - high concentrations to achieve conceived advantage (Temple, 2022). Studies using various methods show that the cost of transitioning from current dietary habits to plant-based diets is generally more affordable in the highly-income countries; however, this transition might be more expensive for low- and also the middle-income qualified countries (Giskes et al., 2010; Darmon and Drewnowski, 2015). Additionally, food systems accounted as one-third (between 25% and 42% percent) over totally human-caused greenhouse based gas emissions types that cause to acceleration of global scaled warming facts (Crippa et al., 2021).

Functional foods may be divided under four base categories related to the following describe: modified foods, traditional foods, foods that are designed for specific dietary needs, besides medicinal foods (Abdul Hâkim, 2023). Numerous studies highlight the importance of bioavailability, bioavailability, and bioactivity, which will allow for the validation usage of new functional characterized ingredients and the foods which designed by the near future (Gan et al., 2017). Recently, functional bakery products have been among the most discussed topics (Rahaie et al., 2014).

Demand-side based measures of climate change mitigation, similar as dietary changes, have promising potential, especially in the high rated and also the middle rated -income figured countries, when compared to supply-side interventions (Costa et al., 2022). The food which human eat affects by the ways of mental health, physical condition and well-being statues. In USA as alone, the

cost of nutrition-welded diseases (likewise hypertension, cardiovascular diseases, cancer and diabetes), obesity problems and also the food insecurity is estimated at $1.1 trillion (Defraeye et al., 2025). In the recent past, edible sprouts have gained popularity and an important place in the human diet (Świeca & Dziki, 2015). Product development methods such as sprouting and especially fermentation contribute to gut health by increasing the nutritional value of legume powders while facilitating digestibility; this makes their use in functional foods such as vegan and gluten-free soups valuable (Kumari et al., 2023). One study indicated as the increased alfalfa sprouts consumption is due to the higher saponin content besides other beneficial bioactive compounds found inside of the sprouted seeds (Shi et al., 2014).

Since the bread is produced and consuming for pretty much every single region over world scale, enriching it with various elements is considered as most effective ways to combat nutritional deficiencies (Callejo et al., 2016; Kairam et al., 2021). It has also been revealed that adding legumes, in the form of flour, to cereal-based complementary foods improves their nutritional value (Anaemene & Fadupin, 2022). Tannins, naturally occurring in legumes and cereals, are high molecular weight, water-soluble, polyphenolic compounds that exhibit antioxidant properties and possess various pharmacological effects, including antimicrobial and anticancer properties (Smeriglio et al., 2017). Fermentation in bread production positively contributes to its nutritional value by reducing the quantity of the phytic acid and arising the main bio-availability in several mineral types (Zahra et al., 2022).

Functional foods offer significant opportunities not only for individual health but also in the field of gastronomy, increasing menu variety, creating sustainable recipes, and developing creative applications for specific nutritional needs (Alzuhairi and Doğan, 2021). Cereal seeds, similar to legumes, are quite widely used in the human nutrition, principally in various developing countries, due to rich protein ratio, providing approximately 33% of the protein primarily, nitrogen need, starch need, dietary fiber need, and minerals in human nutrition (Farag et al., 2021). Compared to many other foods, bread, being quite economical, easily accessible, and widely consumed, can offer a significant opportunity for adequate and balanced nutrition for a large portion of the population if enriched with various nutritional components and elements (Cavalcante et al., 2016). The fiber and protein content of functional foods can be effective factors in reducing appetite, thus offering an advantage in weight control (Esmaeili et al., 2022). It observed that sprouting of significantly increases the amounts of reduced based sugars, free type amino acids, phenolic compounds, and also for several organic acids as well (Gan et al., 2017). Researchers have shown that the main nutritional value and physical features of the gluten-free typed bread can be improved by adding chia flour and chia seeds (da Costa Borges et al., 2021).

Numerous studies highlight the need for equitable transition from unhealthy diets to healthy and environmentally sustainable diets for everyone (Rockström et al., 2023). In Europe, studies on functional foods are guided by FUFOSE (European Functional Food Science) and the International Food Information Council (Yiğit et al., 2018). Studies have shown that a diet by rich of vegetables besides fruits, whole grains, pulses, and also the n-3 including fatty acids can act as disease-preventing agents (Willett, 2006). It is reported that even a 35-gram daily increase in red meat consumption can raise the risk welded by diabetes type 2 by 6% ratio (Willett et al., 2019). Phytochemicals are procurable in foods as example fruits, nuts, vegetables, legumes, seeds, complete grains (whole), olive oil, seafood, herbs, fermented foods and the spices (ginger etc.), coffee, green and black tea (Konstantinidi and Koutelidakis, 2019; Banwo et al., 2021). Current studies show that various functional applications are used to improve the protein quality, enhance nutrient absorption, and impart probiotic properties to gluten-free products (Casciano et al., 2021).

Germination stands out as a natural and sustainable bioprocessing technique that improves the bioactive component content, antioxidant capacity, functional properties, and sensory qualities of cereals. Products obtained as a result of this biological transformation process generally have higher functionality and nutritional quality (Gan et al., 2017, Singh and Sharma, 2017). Sprouted type buckwheat is also well known owing to its anti-hypocholesterolemic, antioxidant and also the neuroprotective functions (Giménez-Bastida & Zieliński, 2015). Barley is cereal rich in soluble (3-20%) and insoluble (8-14%) fiber and is one of the leading resources that can be used for this purpose (Huang et al., 2020). In one study (Liu et al., 2017), it was reported that after fermentation of defatted wheat with *Bacillus subtilis*, the quantity of free phenolic based compounds increased and quantity of bound phenolic based compounds decreased. The use of health claims for β-glucans has been approved based on scientifically accepted cholesterol-lowering effects and their potential to balance the glycemic response. Therefore, barley and oats stand out among cereals for their high β-glucan content (Lante et al., 2023). Sprouting can cause changes in the nutritional composition of legumes through enzymatic hydrolysis of existing compounds and resynthesize of new compounds (Kathuria et al., 2024). The Food and Drug Administration (FDA) supports functional foods with a high level of evidence. For example, foods which made by oat bran (containing beta-glucan and also other types of healthy and bioactive substances) may contribute to decrease in the heart welded diseases in case of combined by low-fat typed diet (Tondt and Bays, 2022).

A study examining the physical, sensory, and nutritional properties of bread enriched with corn, sorghum, and rice bran (30%) presented; bran addition gave rise to increase in phytate content (Pauline et al., 2020), on the other hand, mixture is also effective in improving quality (Çopur Doğrusöz et al., 2024).

During the recent years' period, there is a rise for the prevalence of individuals choosing gluten-free diets based on their own preferences (Güçlü, 2023). It has been reported that functional bread prepared with a mixture of wheats, malted type of millets, flour of okara contain more protein content besides more calcium, phosphorus, magnesium and sodium compered with control bread, furthermore having 11.25% higher fiber content, 54.69% higher phenol content, and 104.86% higher flavonoid content (Ibidapo et al., 2020). Literature indicates that sprouting is generally carried out under dark conditions and at temperatures between 10–20°C, respectively (Aloo et al., 2021).

Functional based food types not only cause to provide several essential based nutrient compounds but can also modulate immune responses through bioactive components, increase resistance to infections, and regulate inflammation, thus providing protection against various chronic diseases (Ashaolu, 2020; Banwo et al., 2021). Shifting from the prevalent animal-based Western diets to plant-based diets not only supports environmental sustainability but may also decrease the risk over development of health problems likewise diabetes, obesity, cancer and heart disease (Hemler and Hu, 2019). In recent years, factors such as health concerns, sensitivity to animal rights, and environmental sustainability have made veganism a more widely adopted dietary choice worldwide (Hargreaves et al., 2023). For countries, the treatment of chronic diseases places a significant economic accountability on healthcare systems, this liability is further exacerbated by increased life expectancy and the growing elderly population (WHO, 2021). In summary, all foods that provide the energy and nutrients necessary for the continuation of life can be defined as functional foods and so is extremely closely related with sustainability of life.

Conclusions

Functional foods offer significant support in the body's fight against oxidative stress thanks to their rich antioxidant components. Functional foods are expected to constitute a valuable bioactive source that will contribute by delaying the starting of many chronic diseases and reducing their frequency/severity. Awareness campaigns regarding plant-based diets should be supported by practical and delicious recipes, and educational programs, especially for primary and secondary school children (Flynn et al., 2019; Folkvord et al., 2020).

Innovations and sustainable solutions in the agricultural sector can significantly improve quality of life. Sustainability-focused studies will contribute to supporting healthy living by revealing the potential benefits of functional foods more comprehensively. Well-planned and balanced nutritional models provide significant benefits in terms of both individual health and environmental sustainability. Consequently, adequate and balanced intake of functional components is considered important for maintaining overall health and therefore for the concept of sustainability. More clinical research and for long-

term period studies are also needed for understanding better about full oriented effects of functional foods and their optimal consumption amounts.

References

Abdul Hakim, B. N., Xuan, N. J., & Oslan, S. N. H. (2023). A comprehensive review of bioactive compounds from lactic acid bacteria: potential functions as functional food in dietetics and the food industry. *Foods, 12*(15), 2850.https://doi.org/10.3390/ foods12152850

Abellán, A., Domínguez-Perles, R., Moreno, D. A., & García-Viguera, C. (2019). Sorting out the value of cruciferous sprouts as sources of bioactive compounds for nutrition and health. *Nutrients, 11*(2), 429. https://doi.org/10.3390/NU11020429

Ahmar, S., Gill, R. A., Jung, K. H., Faheem, A., Qasim, M. U., Mubeen, M., & Zhou, W. (2023). A decade of omics approaches in cereals: Advanced strategies for crop improvement under changing climate. *Frontiers in Plant Science, 14*, 1134567.

Ahmed, M. H., Vasas, D., Hassan, A., & Molnár, J. (2022). The impact of functional food in prevention of malnutrition. *PharmaNutrition, 19*, 100288. https://doi.org/10.1016/j.phanu.2022.100288

Aloo, S. O., Ofosu, F. K., Kilonzi, S. M., Shabbir, U., & Oh, D. H. (2021). Edible plant sprouts: health benefits, trends, and opportunities for novel exploration. *Nutrients, 13*(8), 2882. https://doi.org/10.3390/NU13082882

Alzuhairi, S., & Doğan, M. (2021). The Importance of functional foods in gastronomy. *ART/icle: Sanat ve Tasarım Dergisi, 1*(2), 249-267.

Amagloh, F. C., Tumuhimbise, G. A., Yada, B., Katungisa, A., Amagloh, F. K., & Kaaya, A. N. (2023). Cooking sweetpotato roots increases the in vitro bioaccessibility of phytochemicals and antioxidant activities, but not vitamin C. *Journal of Functional Foods, 102*, 105453.

Anaemene, D., & Fadupin, G. (2022). Anti-nutrient reduction and nutrient retention capacity of fermentation, germination and combined germination-fermentation in legume processing. *Applied Food Research, 2*(1), 100059. https://doi.org/10.1016/J.AFRES.2022.100059

Ashaolu, T. J. (2020). Immune boosting functional foods and their mechanisms: A critical evaluation of probiotics and prebiotics. *Biomed Pharmacother, 130*, 110625.

Banwo, K., Olojede, A. O., Adesulu-Dahunsi, A. T., Verma, D. K., Thakur, M., Tripathy, S., ... & Utama, G. L. (2021). Functional importance of bioactive compounds of foods with potential health benefits: a review on recent trends. *Food Bioscience, 43*, 101320.https://doi.org/10.1016/j.fbio.2021.101320

BMEL (Bundesministerium für Ernährung und Landwirtschaft) (2021) Forsa-Ernährungsreport. (2021). *Tabellenband. BMEL*.

https://www.bmel.de/SharedDocs/Downloads/DE/_Ernaehrung/forsa-ernaehrungsreport-2021-tabellen.pdf

Callejo, M. J., Benavente, E., Ezpeleta, J. I., Laguna M. J., Carrillo J. M., & Rodríguez-Quijano, M., (2016). Influence of teff variety and wheat flour strength on breadmaking properties of healthier teffbased breads. *J. of Cereal Sci., 68*, 38-45.

Casciano, F., Nissen, L., & Gianotti, A. (2021). Effect of formulations and fermentation processes on volatile organic compounds and prebiotic potential of gluten-free bread fortified by spirulina (Arthrospira platensis). *Food & Function, 12*(20), 10226-10238.

Cavalcante, R. B. M., Morgano, M. A., Silva, K. J. D. E., Rocha, M. D. M., Araújo, M. A. D. M., & Moreira-Araújo, R. S. D. R. (2016). Cheese bread enriched with biofortified cowpea flour. *Ciência e Agrotecnologia, 40*(1), 97-103.

Chandio, A. A., Jiang, Y., Rehman, A., & Twumasi, M. A. (2021). Climate change and cereal production: Evidence from Pakistan. *Environmental Science and Pollution Research, 28*(19), 23826–23838.

Coban, F., & Özer, H. (2025). Agronomic performance of fenugreek genotypes grown under various sowing and nitrogen rates in a highland environment. *Turkish Journal of Agriculture and Forestry, 49*(1), 51-62. https://doi.org/10.55730/1300-011X.3248

Çopur Doğrusöz, M., Başaran, U., Gülümser, E., & Mut, H. (2024). The forage yield and silage quality of maize-sorghum-sainfoin mixtures. *Anadolu Journal of Agricultural Sciences, 39*(3), 469-483.

da Costa Borges, V., Fernandes, S. S., Rosa Zavareze, E., Haros, C. M., Hernandez, C. P., Dias, A. R. G., & las Mercedes Salas-Mellado, M. (2021). Production of gluten free bread with flour and chia seeds (Salvia hispânica L). *Food Bioscience, 43*, 101294.

Dalda Sekerci, A., Unlu, E., Avci, M., & Yetisir, H. (2026). Evaluation of the impact of IAA gene-expressing PGPR strains on rooting efficiency, seedling vigor, and protein profile in chrysanthemum cuttings. *Biologia, 81*(2), 47.

Costa, Jr., C., Wollenberg, E., Benitez, M., Newman, R., Gardner, N., & Bellone, F. (2022). Roadmap for achieving net-zero emissions in global food systems by 2050. *Scientific Reports, 12*(1), 15064.

Crippa, M., Solazzo, E., Guizzardi, D., Monforti- Ferrario, F., Tubiello, F. N., & Leip, A. J. N. F. (2021). Food systems are responsible for a third of global anthropogenic GHG emissions. *Nature Food, 2*(3), 198-209.

Crowe, K. M., Francis, C., (2013). Position of the academy of nutrition and dietetics: functional foods. *J. Acad Nutr Diet, 113*(8), 1096-103.

Darmon, N., & Drewnowski, A. (2015). Contribution of food prices and diet cost to socioeconomic disparities in diet quality and health: A systematic review and analysis. *Nutrition Reviews, 73*, 643–660. https://doi.org/10.1093/nutrit/nuv019

Defraeye, T., Bahrami, F., Kowatsch, T., Annaheim, S., Bragt, M. C., Rossi, R. M., & Greger, M. (2025). Advances in Food-as-Medicine interventions and their impact on future food production, processing, and supply chains. *Advances in Nutrition*, 100421. https://doi.org/10.1016/j.advnut.2025.100421

Dernini, S., Berry, E. M., Serra-Majem, L., La Vecchia, C., Capone, R., Medina, F. X., ... & Trichopoulou, A. (2017). Med Diet 4.0: the Mediterranean diet with four sustainable benefits. *Public Health Nutrition, 20*(7), 1322-1330. https://doi.org/10.1017/ S1368980017000196

Esmaeili, M., Ajami, M., Barati, M., Javanmardi, F., Houshiarrad, A., & Mousavi Khaneghah, A. (2022). The significance and potential of functional food ingredients for control appetite and food intake. *Food Science & Nutrition, 10*(5), 1602-1612. https://doi.org/10.1002/fsn3.2783

FAO, W. (2019). Sustainable healthy diets–Guiding principles. Rome: *Food and Agricultural Organization of the United Nations*, World Health Organization.

Farag, M. A., Sharaf El-Din, M. G., Selim, M. A., Owis, A. I., Abouzid, S. F., Porzel, A., Wessjohann, L. A., & Otify, A. (2021). Nuclear magnetic resonance metabolomics approach for the analysis of major legume sprouts coupled to chemometrics. *Molecules 26*(3), 761. https://doi.org/10.3390/MOLECULES26030761

Flynn, M. M., George, P., & Schiffman, F. J. (2019). Food is medicine: Using a 4-week cooking program of plant-based, olive oil recipes to improve diet and nutrition knowledge in medical students. *Medical Science Educator, 29*, 61–66. https:// doi.org/10.1007/s40670-019-00785-1

Folkvord, F., Anschütz, D., & Geurts, M. (2020). Watching TV cooking programs: Effects on actual food intake among children. *Journal of Nutrition Education and Behavior, 52*, 3–9. https://doi.org/10.1016/j.jneb.2019.09.004

Fresán, U., & Sabaté, J. (2019). Vegetarian diets: Planetary health and its alignment with human health. *Advances in Nutrition, 10*(4), 380–388. https://doi.org/10.1093/advances/nmz039

Gan, R. Y., Lui, W. Y., Wu, K., Chan, C. L., Dai, S. H., Sui, Z. Q., & Corke, H. (2017). Bioactive compounds and bioactivities of germinated edible seeds and sprouts: An updated review. *Trends in Food Science & Technology, 59*, 1–14. https://doi.org/10.1016/J.TIFS.2016.11.010

Giménez-Bastida, J. A., & Zieliński, H. (2015). Buckwheat as a functional food and its effects on health. *Journal of Agricultural and Food Chemistry, 63*(36), 7896–7913. https://doi.org/10.1021/ACS.JAFC.5B02498

Giskes, K., Avendaño, M., Brug, J., & Kunst, A. E. (2010). A systematic review of studies on socioeconomic inequalities in dietary intakes associated with weight gain and overweight/obesity conducted among European adults. *Obesity Reviews, 11*, 413–429. https://doi.org/10.1111/j.1467-789X.2009.00673.x

Güçlü, Z. (2023). An investigation into the factors influencing preferences for gluten-free diets: an example of participant dictionaries. Kırklareli Üniversitesi Sosyal Bilimler Meslek Yüksekokulu Dergisi, 4(2), 58-71. https://doi.org/10.51969/klusbmyo.1374430

Hargreaves, S. M., Rosenfeld, D. L., Moreira, A. V. B., & Zandonadi, R. P. (2023). Plant-based and vegetarian diets: an overview and definition of these dietary patterns. European *Journal Of Nutrition, 62*(3), 1109–1121. https://doi.org/10.1007/s00394-023-03086-z

Hemler, E. C., & Hu, F. B. (2019). Plant-based diets for personal, population, and planetary health. *Advances in Nutrition, 10*(4), 275–283.

Huang, H., Gao, X., Li, Y., Tian, P., Nima, Y., Laba, Z., ... & Liao, W. (2020). Content analysis of vitamins, dietary fibers and amino acids in a wide collection of barley (Hordeum vulgare L.) from Tibet, China. *Bioinformation, 16*(4), 314.

Ibidapo, OP., Henshaw, FO., Shittu, TA., & Afolabi, WA. (2020). Quality evaluation of functional bread developed from wheat, malted millet (Pennisetum Glaucum) and 'Okara' flour blends. *Scientific African, 10*, e00622.

Kairam, N., Kandi, S., & Sharma, M. (2021). Development of functional bread with flaxseed oil and garlic oil hybrid microcapsules. *Lebensmittel-Wissenschaft+Technologie, 136*(1), 110300.

Kathuria, D., Hamid, Chavan, P., Jaiswal, A. K., Thakur, A., & Dhiman, A. K. (2024). A comprehensive review on sprouted seeds bioactives, the impact of novel processing techniques and health benefits. *Food Reviews International, 40*(1), 370–398. https://doi.org/10.1080/87559129.2023.2169453

Kodaz, S., Haliloğlu, K., & Öztürk, A. (2025). Trait-based characterization of barley genotypes under simulated early drought stress conditions. *Turkish Journal Of Field Crops, 30*(1), 206-222. https://doi.org/10.17557/tjfc.1664378

Konstantinidi, M., & Koutelidakis, A. E. (2019). Functional foods and bioactive compounds: A review of its possible role on weight management and obesity's metabolic consequences. *Medicines, 6*(3), 94.https://doi.org/10.31665/JFB.2020.11235

Kumari, K., Kashyap, P., & Chakrabarti, P. (2023). Germination and probiotic fermentation: a way to enhance nutritional and biochemical properties of cereals and millets. *Food Science Biotechnology, 33*(3), 505–518.

Lante, A., Canazza, E., & Tessari, P. (2023). Beta-Glucans of Cereals: Functional and Technological Properties. *Nutrients, 15*(9), 2124. https://doi.org/10.3390/nu15092124

Le, T. N., Chiu, C. H., & Hsieh, P. C. (2020). Bioactive Compounds and Bioactivities of Brassica oleracea L. var. Italica Sprouts and Microgreens: An Updated Overview from a Nutraceutical Perspective. *Plants 9*(8), 946. https://doi.org/10.3390/PLANTS9080946

Liu, F. Chen, Z., Shao, J., Wang, C., & Zhan, C. (2017). Effect of fermentation on the peptide content, phenolics and antioxidant activity of defatted wheat germ. *Food Bioscience, 20*, 141-148.

Mallikarjuna, B. P., Sreevathsa, R., & Varshney, R. K. (2022). Genomics-assisted breeding for climate-resilient crops: Progress and prospects. *Theoretical and Applied Genetics, 135*(3), 751–776.

Mason, D. M., & Mullins, J. T. (2016). Vegetarian 101: History, health and tips. University of Kentucky, College of Agriculture, Food and Environment, Cooperative Extension Service. *FN-AP.041*. https://fcs-hes.ca.uky.edu/sites/fcs-hes.ca.uky.edu/files/ fn-ap-041.pdf

Miyahira, R. F., Lopes, J. de O., & Antunes, A. E. C. (2021). The use of sprouts to improve the nutritional value of food products: a brief review. *Plant Foods for Human Nutrition, 76*(2), 143–152.

Pauline, M., Roger, P., Nina, NESN., Arielle, T., Eugene, EE., & Robert, N. (2020). Physico-chemical and nutritional characterization of cereals brans enriched breads. *Scientific African, 7*, e00251.

Poore, J., & Nemecek, T. (2018). Reducing food's environmental impacts through producers and consumers. *Science, 360*(6392), 987-992.

Rahaie, S., Gharibzahedi, S. Y. T. Razavi, S. H., & Jafari, S. M., (2014). Recent developments on new formulations based on nutrient-dense ingredients for the production of healthy-functional bread: a review. *J. Food Sci Tech., 51*(11), 2896-2906.

Rockström, J., Thilsted, S., Willett, W., Gordon, L., Herrero, M., Agustina, R., ... & DeClerck, F. (2023). EAT– Lancet Commission 2.0: securing a just transition to healthy, environmentally sustainable diets for all. *The Lancet, 402*, 352-354.

Shi, Y. H., Wang, J., Guo, R., Wang, C. Z., Yan, X. B., Xu, B., & Zhang, D. Q. (2014). Effects of alfalfa saponin extract on growth performance and some antioxidant indices of weaned piglets. *Livestock Science, 167*(1), 257–262.

Shimizu, M., & Hachimura, S. (2011). Gut as a target for functional food. *Trends in Food Science & Technology, 22*(12), 646-650.

Singh, A., & Sharma, S. (2017). Bioactive components and functional properties of biologically activated cereal grains: A bibliographic review. *Critical Reviews in Food Science and Nutrition, 57*(14), 3051-3071.

Smeriglio, A., Barreca, D., Bellocco, E., & Trombetta, D. (2017). Proanthocyanidins and hydrolysable tannins: occurrence, dietary intake and pharmacological effects. *British journal of pharmacology, 174*(11), 1244-1262.

Springmann, M., Clark, M., Mason-D'Croz, D., Wiebe, K., Bodirsky, B. L., Lassaletta, L., De Vries, W., Vermeulen, S. J., Herrero, M., Carlson, K. M., et al. (2018). Options for keeping the food system within environmental limits. *Nature, 562,* 519–525. https://doi.org/10.1038/s41586-018-0594-0

Springmann, M., Spajic, L., Clark, M. A., Poore, J., Herforth, A., Webb, P., Rayner, M., & Scarborough, P. (2020). The healthiness and sustainability of national and global food-based dietary guidelines: Modelling study. *BMJ, 370*, m2322.

Świeca, M., & Dziki, D. (2015). Improvement in sprouted wheat flour functionality: effect of time, temperature and elicitation. *International Journal of Food Science and Technology, 50*(9), 2135–2142. https://doi.org/10.1111/IJFS.12881

Temba, M. C., Njobeh, P. B., Adebo, O. A., Olugbile, A. O., & Kayitesi, E. (2016). The role of compositing cereals with legumes to alleviate protein energy malnutrition in Africa. *International Journal of Food Science and Technology, 51*(3), 543–554. https://doi.org/10.1111/IJFS.13035

Temple, N. J. (2022). A rational definition for functional foods: A perspective. *Frontiers in Nutrition, 9*, p.957516.

Tompa, O., Lakner, Z., Oláh, J., Popp, J., & Kiss, A. (2020). Is the sustainable choice a healthy choice? Water footprint consequence of changing dietary patterns. *Nutrients, 12*(9), 2578. https://doi.org/10.3390/nu12092578

Tondt, J., & Bays, H. E. (2022). Concomitant medications, functional foods, and supplements: an obesity medicine association (OMA) clinical practice statement (CPS) 2022. *Obesity Pillars, 2*, 100017.

Vahed, S., Ahangar, H. A., Nourani, M., Dinani, S. T., & Nasr-Esfahani, M. (2023). Assessment of electrohydrodynamic (EHD) pretreatment effects on functional and structural properties of protein isolate from sprouted mung bean. *Journal of Food Process Engineering, 46*(4), e14284.

Vishnoi, R., & Goel, A. (2024). Climate-smart agriculture and the role of cereal crops in global food systems. *Agricultural Systems, 211*, 103767.

WHO, (2021). Noncommunicable diseases. *World Health Organization*, Available at: https://www.who.int/ news-room/fact-sheets/detail/noncommunicable-diseases.

Willett, W. C. (2006). The Mediterranean diet: science and practice. *Public Health Nutr, 9*(1a), 105-10.

Willett, W., Rockström, J., Loken, B., Springmann, M., Lang, T., Vermeulen, S., ... & Murray, C. J. (2019). Food in the Anthropocene: the EAT–Lancet Commission on healthy diets from sustainable food systems. *The Lancet, 393*(10170), 447-492.

Yiğit, G. G., Cerit, İ., & Demirkol, O. (2018). Functional cocoa and cocoa products. *The Journal of Food, 43*(4), 702-15. doi: 10.15237/gida.GD18045

Zahra, A., Farooq, U., Saeed, M. T., Quddoos, M. Y., Hameed, A., Iftikhar, M., ... & Chaudhry, F. (2022). Enhancement of sensory attributes and mineral content of Sourdough bread by means of microbial culture and yeast (Saccharomyces cerevisiae). *Food Chemistry Advances, 1*, 100094.

CHAPTER 8

Microplastic Pollution and Algae-Based Removal Techniques

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Introductıon

The term plastic entered the literature in the early 16th century, its use and commercialization became widespread in the 1950s, and today it is used in high numbers in the industry, textile, agriculture and automotive sectors. Durable and synthetic polymers materials are defined as 'plastic' (Surendran et al., 2023). Plastic waste released into the environment decomposes into smaller plastic pieces by physical, chemical and biological factors, especially temperature, precipitation and microbial activity (Liao and Chen, 2021). Plastic types are divided into different classes as macro, meso, micro and nanoplastics.

Microplastics are materials smaller than 5 mm in size through various degradation processes (Yu et al., 2021). It has been reported that the main sources of these materials, which have become a global concern, are sewage sludge, compost, plastic mulch and tire wear (Selonen et al., 2021). In addition, it has been stated in most studies that microplastics carry a wide variety of toxic pollutants such as heavy metals, polychlorinated biphenyls, polycyclic aromatic hydrocarbons, pesticides, and polybrominated diphenyl ethers (Fraser et al., 2020; Abbasi et al., 2022; Liu et al., 2022). This type of pollutant causes reproductive disorders, DNA damage, metabolic disorders and different toxic effects in humans and animals (Zahmatkesh Anbarani et al., 2024). Studies on microplastics and removal techniques are being carried out more widely, especially in aquatic environments such as seas, lakes and rivers. However, this situation has been studied less in the terrestrial system and there is a need to increase research on the subject (Zhang et al., 2016; Zhang et al., 2018).

Due to the danger posed by microplastic pollution in the ecosystem, this situation has been tried to be minimized with chemical, physical and biological removal techniques (Eskander and Saleh, 2017). Bioremediation applications, which are called removal techniques with living organisms, are the process of transforming pollutants into less toxic compounds by living organisms, especially algae, fungi and bacteria, through mechanisms such as biological degradation, accumulation and binding to the cell surface (Kılıç et al., 2026).

Algae-based removal techniques can be used as an alternative for the removal of pollutants such as heavy metals, antibiotics, pesticide residues and microplastics (Lotfigolsefidi et al., 2025). In general, the cell wall of algae consists of a structure rich in proteins and polysaccharides. High levels of protein and polysaccharides enable microplastics to bind to the cell wall. In addition, the extracellular secretions that algae produce during their development can limit the toxic effects of microplastics on living things. There are studies showing that algae do not produce toxic residues during their decomposition after completing their life cycle and that it can be a safe treatment (Barari et al., 2024).

Algae-based bioremediation techniques are important because they limit residue production and are environmentally friendly, more sustainable than

chemical removal techniques. In algae-based removal techniques, it is aimed to examine the basic mechanism in detail and evaluate it through studies conducted in water and soil environments.

1. Environmental Aspect of Microplastic Pollution

Plastic materials have become widespread in our daily lives due to their strength, flexibility, cost effectiveness and use in most production sectors. The annual plastic production rate is estimated to be around 367 million tons in 2021 (Geyer, 2020). In addition, it is assumed that this production level may be around 33 billion tons by 2050 (Saharma et al., 2020). Microplastics are formed when plastic wastes are broken down by environmental factors (biological degradation, the effect of sunlight, mechanical factors, etc.). Problems experienced in the recycling of plastic-derived wastes and inappropriate and unconscious waste disposal have become a serious source of concern for living things. It has been supported by many studies that microplastic particles are especially abundant in the atmosphere, water and terrestrial ecosystem (Cai et al., 2017; Corradini et al., 2019; Mintening et al., 2019).

The main sources of microplastics carried by oceans, lakes, seas and rivers are transportation by commercial drainage systems, water loss during waste collection in recycling centers, fishing equipment and fibrous synthetic products in nets (Duis and Coors, 2016). Microplastics are transported to long distances through currents in the aquatic ecosystem, increasing the risk potential (Eriksen et al., 2019). The transport of myroplastics into the aquatic ecosystem is shown in Figure 1.

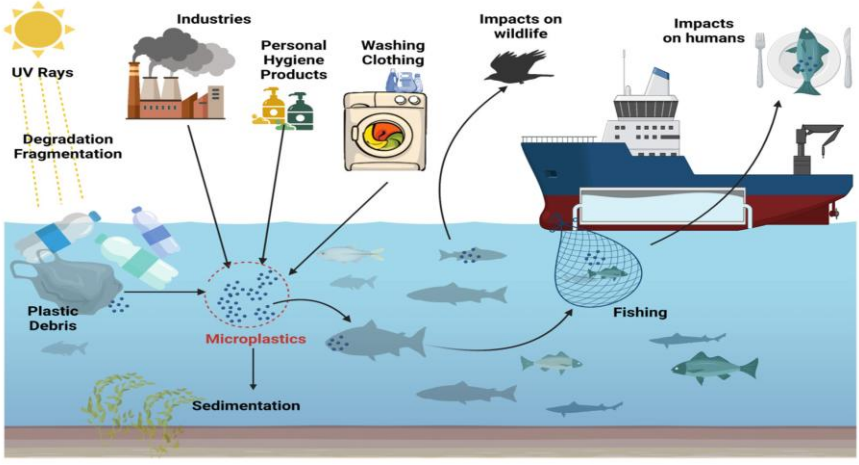


Figure 1. Transport of microplastics in the aquatic ecosystem (Ziani et al., 2023).

Compared to other environments, the toxic effects of microplastic accumulation in terrestrial ecosystems on living organisms have only recently begun to be elucidated through current studies (Yang et al., 2021). Primary

sources of microplastics in soil include tire wear, plastic waste from greenhouses, mulch materials, pesticide containers, and fertilizer materials (Sharma et al., 2025) (Figure 2).

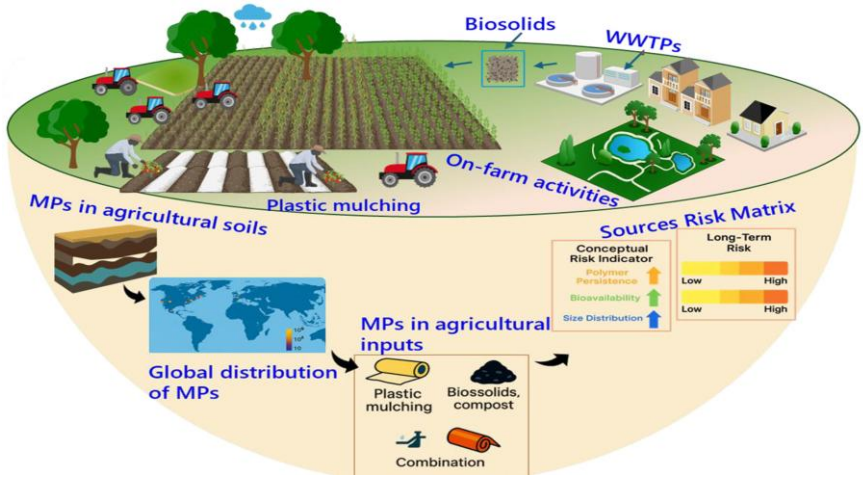


Figure 2. Sources and distribution of microplastics in terrestrial ecosystems (Roy et al., 2025).

Areas with high human population density in terrestrial ecosystems influence microplastic distribution through both direct and indirect pathways. In a study investigating microplastic distribution across various land-use types, soil samples were collected from residential areas, agricultural lands, parks, roadsides, and forest areas. Microplastics ranging in size from 20 to 500 µm were identified across the soil samples. Based on the density of microplastic accumulation, the order from highest to lowest was agricultural lands, roadsides, residential areas, parks, and forests (Yoon et al., 2024) (Figure 3).

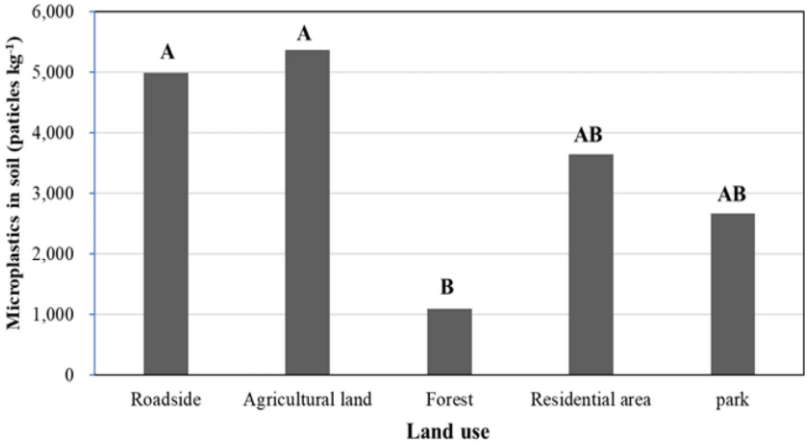


Figure 3. Distribution of microplastics according to land-use types.

Due to their low density and small size, microplastics can easily become airborne and be transported through the air (Allen et al., 2019). After a period of atmospheric transport, microplastic particles are deposited into aquatic and terrestrial ecosystems (Figure 4). Microplastic particles released into the atmosphere directly enter the bodies of living organisms through inhalation, causing adverse effects such as respiratory ailments and disorders of the digestive and metabolic systems (Yao et al., 2022).

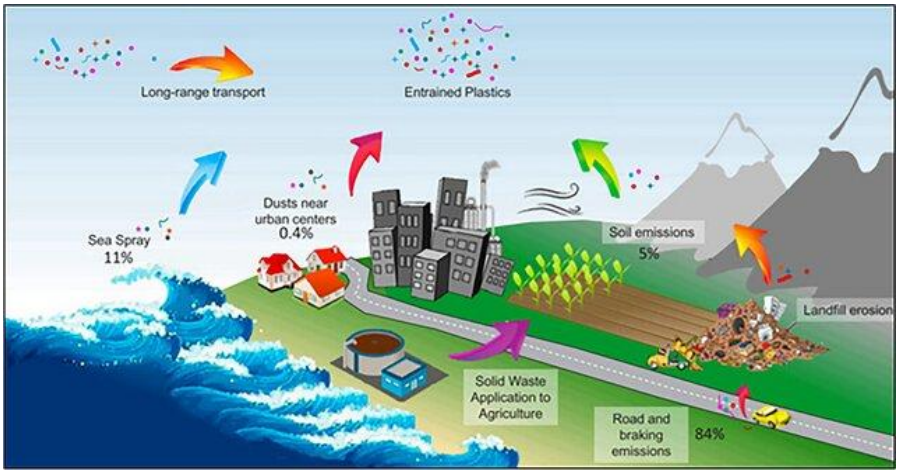


Figure 4. Atmospheric transport of microplastics (Kaydi et al., 2024).

2. Microplastic and Algae Interactions

Efforts are underway to remove microplastics using various techniques, such as mechanical methods (e.g., membrane filtration and sedimentation) and chemical separation methods. In addition, there are alternative removal applications based on biological methods involving bacteria, fungi, and macro/microalgae (Tyagi and Kumar, 2020; Raj et al., 2022; Touliabah et al., 2022; Das et al., 2023; Parial and Dey, 2024). Algae are organisms comprising photosynthetic eukaryotic and prokaryotic life forms consisting of over 200 000 species that can survive in almost every part of the Earth (Hallmann, 2007; Guiry, 2012; Calatrava et al., 2024). Thanks to their photosynthetic capabilities, algae can grow by utilizing solar radiation as an energy source. Together with cyanobacteria, they serve as a primary source of photosynthetic O_2 and a biological sink for atmospheric CO_2 (Ramaraj et al., 2015). Furthermore, they are organisms that facilitate the release of essential plant nutrients such as nitrogen, phosphorus, and potassium (Sasaki et al., 2020); support plant development by secreting substances like plant hormones, amino acids, and carotenoids (Silva et al., 2019); and can be used for soil remediation (Wu et al., 2022). Thanks to their biochemical compositions such as proteins, carbohydrates, and lipids they adapt

to the constantly changing environment and exhibit resistance to biotic and abiotic stress (Sharma and Rai, 2011) (Figure 5).

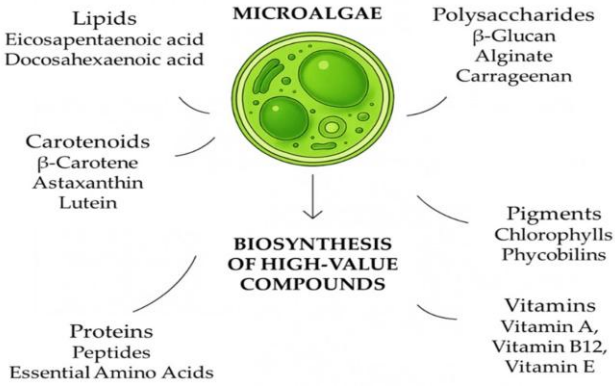


Figure 5. Biosynthesis of high-value compounds by microalgae (Arenas et al., 2018)

Algae exhibit high efficiency in microplastic removal due to their ecological compatibility and minimal secondary waste generation through processes such as aggregation, bioflocculation, and biodegradation. Algae possess natural flocculation capabilities attributed to their exopolysaccharides which enhance the adsorption of microplastics (Hadiyanto et al., 2025). Factors such as microplastic size, density, and exposure duration significantly influence the removal efficiency of algae (Oberbeckmann et al., 2015).

Algae possess a surface-to-volume ratio that is effective for pollution reduction, as functional groups such as carboxyl, hydroxyl, amino, and phosphate groups located on their cell walls interact with pollutants. Consequently, microalgae are employed in bioremediation due to their high tolerance for conditions such as high salinity, elevated temperatures, nutrient deficiency, and heavy metal concentrations (Ukaogo et al., 2020; Xu et al., 2022).

They mitigate the impact of pollutants through mechanisms such as biosorption, biodegradation, photodegradation, and bioaccumulation during the removal of microplastics and other contaminants (Ajibade et al., 2021; El-Sheekh et al., 2025). Biosorption refers to the adhesion of ions or molecules to a surface via physicochemical processes. Carboxyl, hydroxyl, phosphate, and amino groups present on algal cell walls determine the extent of biosorption (Parmar et al., 2025). In contrast to biosorption which is rapid and highly reversible bioaccumulation is a slow metabolic process occurring only in living algal cells, wherein metal ions are actively taken up and transported into the cell (Selatnia et al., 2004). While bioaccumulation is defined as a process in which the rate of a compound's uptake into cellular tissue exceeds the rate of its loss, leading to accumulation within the tissue over time (Wu and Zhao, 2023), photodegradation refers to the process by which a substance's chemical structure breaks down and decomposes as a result of excessive light exposure (He et al., 2025).

Biodegradation is defined as the process by which organic substances are broken down and converted into simpler compounds through the metabolic and enzymatic activities of organisms such as bacteria, fungi, and macro and microalgae (Shah et al., 2008). The mechanisms employed by algae for the removal or minimization of pollutants are illustrated in Figure 6.

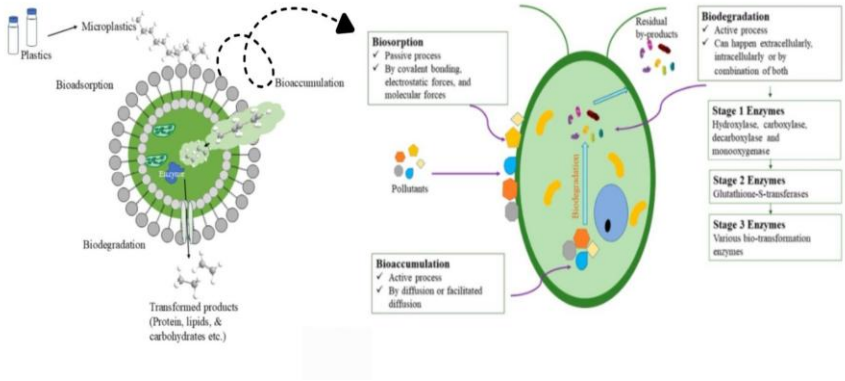


Figure 6. Schematic representation of the microalgal bioremediation process (Bai et al., 2025; Soni et al., 2026).

Algae can be effectively utilized in the degradation of microplastics by interacting with the microplastic surface through the enzymes they produce. Algal enzymes induce changes in the chemical structure by forming heterogeneous aggregates and colonizing the microplastic surface (Manzi et al., 2022). The algal biodegradation process primarily occurs through various mechanisms such as corrosion, hydrolysis, and penetration (China et al., 2020). Regarding studies in the literature, Sanniyasi et al. (2021) examined the surface degradation and fragmentation of polyethylene sheets by the alga *Uronema africanum* using scanning electron microscopy and reported that it enhanced the degradation of low-density polyethylene. Cunha et al. (2022) determined that the freshwater microalgae *Microcystis panniformis* and *Scenedesmus sp*. were capable of colonizing polystyrene (PS) and polymethyl methacrylate (PMMA) microplastics and inducing aggregate formation. In contrast, in a study investigating the degradation of high-density polyethylene (HDPE) by the microalga *Chlamydomonas reinhardtii*, Lagarde et al. (2016) did not observe aggregate formation resulting from algal colonization on the HDPE surface. They suggested that this outcome might be due to variations in extracellular polymeric substances, which can differ depending on the type of plastic. Sarmah and Rout (2018) determined that the microalgae *Oscillatoria subbrevis* and *Phormidium lucidum* were capable of colonizing low-density polyethylene surfaces and causing their degradation without the need for any pro-oxidative additives or pre-

treatment. Bisphenol A, an additive with biological activity in polymeric materials, is widely present, and studies have demonstrated that it undergoes degradation through the use of microalgae such as *Chlorella fusca* var. *vacuolate*, *Chlamydomonas mexicana*, *Stephanodiscus hantzschii*, and *Chlorella vulgaris* (Hirooka et al., 2005; Li et al., 2009; Ji et al., 2014; Kumar et al., 2017).



Figure 7. Polyethylene degradation percentage using various microalgae (Kumar et al., 2017)

Conclusion

Environmental pollution has increased directly in recent years due to industrial development and the intensity of industrial activities. Microplastics, which are among the primary pollutants, are encountered in every aspect of life and have entered the food chain of living organisms due to their small particle size. The intensity of their accumulation in living organisms raises concerns. Although physical, chemical, and biological techniques exist for microplastic removal, biological techniques are prioritized in terms of environmental sustainability. Numerous studies have demonstrated that algae can be utilized for the removal or stabilization of pollutants through components found in their cell walls and their extracellular secretions. The value and efficiency of algae-based approaches in microplastic removal are evident, even though they vary depending on the type of microplastic. Through mechanisms such as bioaccumulation and photodegradation, algae remove microplastics from the environment or minimize their presence by biologically degrading their chemical structure. This study addresses the sources and distribution of microplastics and the removal of this type of pollutant via algae-based mechanisms. While interactions between microplastics and algae have been extensively studied in aquatic ecosystems, research regarding terrestrial ecosystems is more limited. It is believed that evaluating microplastic types and structures alongside algal species and their mechanisms will contribute to future studies.

References

Abbasi, S., Moore, F., & Keshavarzi, B. (2021). PET-microplastics as a vector for polycyclic aromatic hydrocarbons in a simulated plant rhizosphere zone. *Environmental Technology & Innovation*, 21, 101370. doi: 10.1016/j.eti.2021.101370

Ajibade, F. O., Adelodun, B., Lasisi, K. H., Fadare, O. O., Ajibade, T. F., Nwogwu, N. A., ... & Wang, A. (2021). Environmental pollution and their socioeconomic impacts. *In Microbe mediated remediation of environmental contaminants* (pp. 321-354). Woodhead Publishing. doi: 10.1016/B978-0-12-821199-1.00025-0

Allen, S., Allen, D., Phoenix, V. R., Le Roux, G., Durántez Jiménez, P., Simonneau, A., ... & Galop, D. (2019). Atmospheric transport and deposition of microplastics in a remote mountain catchment. *Nature geoscience*, 12(5), 339-344. doi: 10.1038/s41561-019-0335-5

Arenas Colarte, C., Balic, I., Díaz, Ó., Moreno, A. A., Amenabar, M. J., Bruna Larenas, T., & Caro Fuentes, N. (2025). High-value bioactive molecules extracted from microalgae. *Microorganisms*, 13(9), 2018. doi: **/10.3390/microorganisms13092018**

Barari, F., Gabrabad, M. E., & Bonyadi, Z. (2024). Recent progress on the toxic effects of microplastics on Chlorella sp. in aquatic environments. *Heliyon*, 10(12). doi: 10.1016/j.heliyon.2024.e32881

Cai, L., Wang, J., Peng, J., Tan, Z., Zhan, Z., Tan, X., & Chen, Q. (2017). Characteristic of microplastics in the atmospheric fallout from Dongguan city, China: preliminary research and first evidence. *Environmental science and pollution research*, 24(32), 24928-24935. doi: 10.1007/s11356-017-0116-x

Calatrava, V., Gonzalez-Ballester, D., & Dubini, A. (2024). Microalgae for bioremediation: advances, challenges, and public perception on genetic engineering. *BMC Plant Biology*, 24(1), 1261. doi: 10.1186/s12870-024-05995-5

Chia, W. Y., Tang, D. Y. Y., Khoo, K. S., Lup, A. N. K., & Chew, K. W. (2020). Nature's fight against plastic pollution: Algae for plastic biodegradation and bioplastics production. *Environmental Science and Ecotechnology*, 4, 100065. doi: 10.1016/j.ese.2020.100065

Corradini, F., Meza, P., Eguiluz, R., Casado, F., Huerta-Lwanga, E., & Geissen, V. (2019). Evidence of microplastic accumulation in agricultural soils from sewage sludge disposal. *Science of the total environment*, *671*, 411-420. doi: 10.1016/j.scitotenv.2019.03.368

Cunha, C., Faria, M., Nogueira, N., Ferreira, A., & Cordeiro, N. (2019). Marine vs freshwater microalgae exopolymers as biosolutions to microplastics

pollution. *Environmental pollution*, 249, 372-380. doi: 10.1016/j.envpol.2019.03.046

Das, P., Halder, G., & Bal, M. (2023). A critical review on remediation of microplastics using microalgae from aqueous system. *Science of the Total Environment*, *898*, 166425. doi: 10.1016/j.scitotenv.2023.166425

Duis, K., & Coors, A. (2016). Microplastics in the aquatic and terrestrial environment: sources (with a specific focus on personal care products), fate and effects. *Environmental Sciences Europe*, 28(1), 2. doi: 10.1186/s12302-015-0069-y

El-Sheekh, M. M., El-Kassas, H. Y., & Ali, S. S. (2025). Microalgae-based bioremediation of refractory pollutants: an approach towards environmental sustainability. *Microbial Cell Factories*, 24(1), 19. doi: 10.1186/s12934-024-02638-0

Eriksen, M., Thiel, M., & Lebreton, L. (2017). Nature of plastic marine pollution in the subtropical gyres. In *Hazardous chemicals associated with plastics in the marine environment* (pp. 135-162). Cham: Springer International Publishing. doi: 10.1007/698-2016-123

Eskander, S., & Saleh, H. E. D. (2017). Biodegradation: process mechanism. *Environ. Sci. & Eng*, 8(8), 1-31.

Fraser, M. A., Chen, L., Ashar, M., Huang, W., Zeng, J., Zhang, C., & Zhang, D. (2020). Occurrence and distribution of microplastics and polychlorinated biphenyls in sediments from the Qiantang River and Hangzhou Bay, China. *Ecotoxicology and environmental safety*, 196, 110536. doi: 10.1016/j.ecoenv.2020.110536

Geyer, R. (2020). Production, use, and fate of synthetic polymers. In Plastic waste and recycling (pp. 13-32). *Academic Press*. doi: 10.1016/B978-0-12-817880-5.00002-5

Guiry, M. D. (2012). How many species of algae are there?. *Journal of phycology*, 48(5), 1057-1063. doi: 10.1111/j.1529-8817.2012.01222.x

Hadiyanto, H., Joelyna, F. A., Khoironi, A., Sudarno, S., Safaat, J. A., Pratama, W. D., & Nur, M. M. A. (2025). Harnessing Chlorella vulgaris-Aspergilus niger Interactions for effective microplastic removal in aquatic ecosystems. *Waste and Biomass Valorization*, *16*(11), 6257-6273. doi: 10.1007/s12649-025-03062-0

Hallmann, A. (2007). Algal transgenics and biotechnology. *Transgenic Plant J*, 1(1), 81-98.

He, X., Liu, D., Liao, Y., Wang, W., Wu, Q., Wang, H., ... & Zhu, L. (2025). Sequential treatment of UV254 photodegradation and microalgal bioremediation in aquaculture effluent: Florfenicol toxicity mitigation and

nutrient recovery. Journal of Hazardous Materials, 140393. doi: 10.1016/j.jhazmat.2025.140393

Hirooka, T., Nagase, H., Uchida, K., Hiroshige, Y., Ehara, Y., Nishikawa, J. I., ... & Hirata, Z. (2005). Biodegradation of bisphenol A and disappearance of its estrogenic activity by the green alga Chlorella fusca var. vacuolata. *Environmental toxicology and chemistry*, 24(8), 1896-1901. doi: 10.1897/04-259R.1

Ji, M. K., Kabra, A. N., Choi, J., Hwang, J. H., Kim, J. R., Abou-Shanab, R. A., ... & Jeon, B. H. (2014). Biodegradation of bisphenol A by the freshwater microalgae Chlamydomonas mexicana and Chlorella vulgaris. *Ecological engineering*, 73, 260-269. doi: 10.1016/j.ecoleng.2014.09.070

Kaydi, N., Jorfi, S., Takdastan, A., Jaafarzadeh Haghighifard, N., & Khafaie, M. A. (2024). Source identification and apportionment of ambient air microplastics: a systematic review. *Discover Applied Sciences*, *7*(1), 41. doi: 10.1007/s42452-024-06422-y

Kılıç, F. N., Sönmez, O., Ulaş, A., Aydın, S., & Noman, A. (2026). Harnessing microalgae–plant synergy for remediating metal contaminated soil: Festuca arundinacea and Haematococcus pluvialis in focus. *Functional Plant Biology*, 53(5), FP25407. doi: 10.1071/FP25407

Kumar, R. V., Elumalai, S. P., & Gopal, R. K. (2017). Biodegradation of polyethylene by green photosynthetic microalgae. *Journal of Bioremediation & Biodegradation*, 8(01). doi: 10.4172/2155-6199.1000381

Lagarde, F., Olivier, O., Zanella, M., Daniel, P., Hiard, S., & Caruso, A. (2016). Microplastic interactions with freshwater microalgae: hetero-aggregation and changes in plastic density appear strongly dependent on polymer type. *Environmental pollution*, 215, 331-339. doi: 10.1016/j.envpol.2016.05.006

Li, R., Chen, G. Z., Tam, N. F. Y., Luan, T. G., Shin, P. K., Cheung, S. G., & Liu, Y. (2009). Toxicity of bisphenol A and its bioaccumulation and removal by a marine microalga Stephanodiscus hantzschii. *Ecotoxicology and Environmental safety*, 72(2), 321-328. doi: 10.1016/j.ecoenv.2008.05.012

Liao, J., & Chen, Q. (2021). Biodegradable plastics in the air and soil environment: Low degradation rate and high microplastics formation. *Journal of hazardous materials*, 418, 126329. doi: 10.1016/j.jhazmat.2021.126329

Liu, S., Huang, J., Zhang, W., Shi, L., Yi, K., Yu, H., ... & Li, J. (2022). Microplastics as a vehicle of heavy metals in aquatic environments: A review of adsorption factors, mechanisms, and biological effects. *Journal of Environmental Management*, 302, 113995. doi: 10.1016/j.jenvman.2021.113995

Lotfigolsefidi, F., Davoudi, M., Sarkhosh, M., & Bonyadi, Z. (2025). Removal of microplastics by algal biomass from aqueous solutions: performance,

optimization, and modeling. *Scientific Reports*, 15(1), 501. doi: s41598-024-84114-8

Manzi, H. P., Abou-Shanab, R. A., Jeon, B. H., Wang, J., & Salama, E. S. (2022). Algae: a frontline photosynthetic organism in the microplastic catastrophe. *Trends in Plant Science*, 27(11), 1159-1172. doi: 10.1016/j.tplants.2022.06.005

Mintenig, S. M., Löder, M. G., Primpke, S., & Gerdts, G. (2019). Low numbers of microplastics detected in drinking water from ground water sources. *Science of the total environment*, 648, 631-635. doi: 10.1016/j.scitotenv.2018.08.178

Oberbeckmann, S., Löder, M. G., & Labrenz, M. (2015). Marine microplastic-associated biofilms–a review. *Environmental chemistry*, *12*(5), 551-562. doi: 10.1071/EN15069

Parial, D., & Dey, S. (2024). Potential Use of Algae and Bacteria for Bioremediation of Wastewater: A Critical Review. *Toxicity of Aquatic System and Remediation*, 219-236. doi: 10.1201/9781003297901-16

Parmar, K. S., & Patel, K. M. (2025). Biosorption and bioremediation of heavy metal ions from wastewater using algae: A comprehensive review. World Journal of Microbiology and Biotechnology, 41(7), 262. doi: 10.1007/s11274-025-04424-5

Raj, R., Manju, N. K., Fazil, T. S., Chatterji, N. S., Anandan, R., & Mathew, S. (2022). Seaweed and its role in bioremediation—a review. *Fish Technol*, 59, 147-153. doi: 10.56093/ft.v59i3.119215

Ramaraj, R., Tsai, D. D. W., & Chen, P. H. (2015). Biomass of algae growth on natural water medium. *Journal of Photochemistry and Photobiology B: Biology,* 142, 124-128. doi: 10.1016/j.jphotobiol.2014.12.007

Roy, T., Abinandan, S., Venkateswarlu, K., MacFarlane, G. R., & Megharaj, M. (2025). On-farm practices shape microplastics pathways and risks in agricultural soils: A review based on synthesis of global field data. *Environmental Chemistry and Ecotoxicology*. doi: 10.1016/j.enceco.2025.09.015

Sanniyasi, E., Gopal, R. K., Gunasekar, D. K., & Raj, P. P. (2021). Biodegradation of low-density polyethylene (LDPE) sheet by microalga, Uronema africanum Borge. *Scientific Reports*, 11(1), 17233. doi: 10.1038/s41598-021-96315-6

Sarmah, P., & Rout, J. (2018). Efficient biodegradation of low-density polyethylene by cyanobacteria isolated from submerged polyethylene surface in domestic sewage water. *Environmental Science and Pollution Research*, 25(33), 33508-33520. doi: 10.1007/s11356-018-3079-7

Sasaki, M., Takagi, A., Ota, S., Kawano, S., Sasaki, D., & Asayama, M. (2020). Coproduction of lipids and extracellular polysaccharides from the novel

green alga Parachlorella sp. BX1. 5 depending on cultivation conditions. *Biotechnology Reports*, 25, e00392. doi: 10.1016/j.btre.2019.e00392

Selatnia, A., Madani, A., Bakhti, M. Z., Kertous, L., Mansouri, Y., & Yous, R. (2004). Biosorption of Ni2+ from aqueous solution by a NaOH-treated bacterial dead Streptomyces rimosus biomass. Minerals Engineering, 17(7-8), 903-911. doi: 10.1016/j.mineng.2004.04.002

Selonen, S., Dolar, A., Kokalj, A. J., Sackey, L. N., Skalar, T., Fernandes, V. C., ... & Van Gestel, C. A. (2021). Exploring the impacts of microplastics and associated chemicals in the terrestrial environment–Exposure of soil invertebrates to tire particles. *Environmental Research*, 201, 111495. doi: 10.1016/j.envres.2021.111495

Shah, A. A., Hasan, F., Hameed, A., & Ahmed, S. (2008). Biological degradation of plastics: a comprehensive review. Biotechnology advances, 26(3), 246-265. doi: 10.1016/j.biotechadv.2007.12.005

Sharma, B., Kour, D., Bassi, A., Gusain, M., Sharma, A., Kaur, T., ... & Yadav, A. N. (2025). Microplastic pollution: challenges, ameliorating strategies and governance policies. *Water, Air, & Soil Pollution*, 236(9), 585. doi: 10.1007/s11270-025-08220-7

Sharma, M. D., Elanjickal, A. I., Mankar, J. S., & Krupadam, R. J. (2020). Assessment of cancer risk of microplastics enriched with polycyclic aromatic hydrocarbons. *Journal of Hazardous Materials*, 398, 122994. doi: 10.1016/j.jhazmat.2020.122994

Sharma, N. K., & Rai, A. K. (2011). Biodiversity and biogeography of microalgae: progress and pitfalls. *Environmental Reviews*, 19(NA), 1-15. doi: 10.1139/a10-020

Silva, G. H., Sueitt, A. P. E., Haimes, S., Tripidaki, A., Van Zwieten, R., & Fernandes, T. V. (2019). Feasibility of closing nutrient cycles from black water by microalgae-based technology. *Algal Research*, 44, 101715. doi: 10.1016/j.algal.2019.101715

Soni, K., Chaurasia, P., Singh, S., Singh, S., Singh, A. K., Chand, S. K., ... & Palaniappan, A. R. (2026). Microalgal Bioremediation of Microplastics: Current Advances, Challenges and Environmental Applications. *Microplastics*, 5(3), 149. doi: 10.3390/microplastics5030149

Surendran, U., Jayakumar, M., Raja, P., Gopinath, G., & Chellam, P. V. (2023). Microplastics in terrestrial ecosystem: Sources and migration in soil environment. *Chemosphere*, *318*, 137946. doi: 10.1016/j.chemosphere.2023.137946

Touliabah, H. E. S., El-Sheekh, M. M., Ismail, M. M., & El-Kassas, H. (2022). A review of microalgae-and cyanobacteria-based biodegradation of organic pollutants. *Molecules*, 27(3), 1141. doi: 10.3390/molecules27031141

Tyagi, B. and Kumar, N. (2020). Bioremediation: Principles and Applications in Environmental Management. INC

Ukaogo, P. O., Ewuzie, U., & Onwuka, C. V. (2020). Environmental pollution: causes, effects, and the remedies. In Microorganisms for sustainable environment and health (pp. 419-429). *Elsevier*. doi: 10.1016/B978-0-12-819001-2.00021-8

Wu, J., & Zhao, F. (2023). Machine learning: An effective technical method for future use in assessing the effectiveness of phosphorus-dissolving microbial agroremediation. Frontiers in Bioengineering and Biotechnology, 11, 1189166. doi: 10.3389/fbioe.2023.1189166

Wu, W., Ke, T., Zhou, X., Li, Q., Tao, Y., Zhang, Y., ... & Chen, L. (2022). Synergistic remediation of copper mine tailing sand by microalgae and fungi. *Applied Soil Ecology*, 175, 104453. doi: 10.1016/j.apsoil.2022.104453

Xu, H., Jia, Y., Sun, Z., Su, J., Liu, Q. S., Zhou, Q., & Jiang, G. (2022). Environmental pollution, a hidden culprit for health issues. *Eco-Environment & Health*, 1(1), 31-45. doi: 10.1016/j.eehl.2022.04.003

Yang, L., Zhang, Y., Kang, S., Wang, Z., & Wu, C. (2021). Microplastics in soil: A review on methods, occurrence, sources, and potential risk. *Science of the Total Environment*, 780, 146546. doi: 10.1016/j.scitotenv.2021.146546

Yao, X., Luo, X. S., Fan, J., Zhang, T., Li, H., & Wei, Y. (2022). Ecological and human health risks of atmospheric microplastics (MPs): a review. *Environmental Science: Atmospheres*, *2*(5), 921-942. doi: 10.1039/d2ea00041e

Yoon, J. H., Kim, B. H., & Kim, K. H. (2024). Distribution of microplastics in soil by types of land use in metropolitan area of Seoul. *Applied Biological Chemistry*, 67(1), 15. doi: 10.1186/s13765-024-00869-8

Yu, L., Zhang, J., Liu, Y., Chen, L., Tao, S., & Liu, W. (2021). Distribution characteristics of microplastics in agricultural soils from the largest vegetable production base in China. *Science of the Total Environment*, 756, 143860. doi: 10.1016/j.scitotenv.2020.143860

Zahmatkesh Anbarani, M., Esmaeili Nasrabadi, A., & Bonyadi, Z. (2024). Aging effect on the adsorption behavior of microfibers obtained from cigarette butts in aqueous solutions. *Applied Water Science*, 14(2), 30. doi: 10.1007/s13201-023-02092-0

Zhang, H., Zhou, Q., Xie, Z., Zhou, Y., Tu, C., Fu, C., ... & Luo, Y. (2018). Occurrences of organophosphorus esters and phthalates in the microplastics from the coastal beaches in north China. *Science of the total environment*, 616, 1505-1512. doi: 10.1016/j.scitotenv.2017.10.163

Zhang, K., Su, J., Xiong, X., Wu, X., Wu, C., & Liu, J. (2016). Microplastic pollution of lakeshore sediments from remote lakes in Tibet plateau, China. *Environmental pollution*, 219, 450-455. doi: 10.1016/j.envpol.2016.05.048

Ziani, K., Ioniță-Mîndrican, C. B., Mititelu, M., Neacșu, S. M., Negrei, C., Moroșan, E., ... & Preda, O. T. (2023). Microplastics: a real global threat for environment and food safety: a state of the art review. *Nutrients*, 15(3), 617. doi: 10.3390/nu15030617

CHAPTER 9

From Hive Defense to Human Aggression: The Evaluation of The Association of Conserved Genetic and Neurobiological Mechanisms

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1. Introduction

Aggression is widespread among animals, including humans. In animals, aggression is adaptive for many purposes, including territorial defense, parental protection, competition for resources, and responses to predators or social rivals (Mbiydzenyuy and Qulu, 2024; Miranda and Srikanth, 2026; Potegal and Elwood, 2026). Its expression is highly species-specific. A honey bee defending a colony by stinging an intruder (Breed et al., 2004) and a human responding aggressively to a social provocation are behaviorally and ecologically distinct phenomena. Nevertheless, both require sensory detection, central integration, changes in arousal, neuromodulatory control, and selection of an appropriate motor response.

This distinction provides the conceptual foundation for comparative behavioral genomics. The aim is not to claim that a honey bee possesses a miniature human aggression circuit. Instead, comparative analysis asks which molecular components involved in threat responsiveness and behavioral state are sufficiently ancient to be retained across large evolutionary distances. Such components may include receptors, neurotransmitter systems, transcription factors, intracellular signaling proteins, and regulatory networks. Human aggression is strongly influenced by heredity and non-genetic factors, but its genetic architecture is complex (Pavlov et al., 2011). A systematic review of genome-wide studies (GWAS) concluded that aggression has a substantial heritable component, while emphasizing that reported GWAS associations have not consistently replicated and that the molecular basis remains incompletely resolved. A later review incorporating epigenomic and other omics approaches similarly concluded that polygenic scores currently explain only a small fraction of individual variation and that larger, multi-omic studies are needed (Tielbeek et al., 2022; Van der Laan et al., 2023). This uncertainty creates an opportunity for comparative biology: rather than searching for a universal aggression gene, one can investigate conserved molecular systems that modulate neural responsiveness, arousal, inhibition, and plasticity.

The honey bee is particularly suitable because defensive behavior can be quantified while genetic, social, and environmental factors are manipulated or measured. Its eusocial organization also makes it possible to study an unusual phenomenon: the group genotype can influence an individual's phenotype through the social environment. This group-genetic architecture is a major reason why honey bee aggression is scientifically distinctive. The primary assertion of this chapter is that honey bee aggressiveness can provide a comparative perspective on conserved molecular frameworks pertinent to aggression-related biology in humans. The most persuasive evidence relates to the conservation of biological systems and orthologous genes, rather than the resemblance of behavioral traits. A honey bee does not exemplify human aggression in its social context; instead, it serves as a paradigm for conserved elements of brain threat response and behavioral control.

2. Conceptualizing Aggression Across Evolutionary Scales

Aggression must be operationally defined before conducting molecular comparisons. Investigations on honey bees often assess defensive behaviors via guarding, stinging, attack latency, recruiting, and reactions to standardized colony disturbances or alarm pheromones. Human research utilizes a markedly broader array of phenotypes, including reactive aggressiveness, physical aggression, antisocial behavior, conduct problems, and their corresponding quantitative traits. These phenotypic definitions are not interchangeable. For comparison, defensive aggression can be understood as a response to a salient threat that is influenced by one's state. The following sequence of events represents the sequence: environmental stimulus → sensory perception → brain processing → neurotransmitter secretion → physiological activation → behavioral choice → motor response → feedback and adaptability (Ippolitov et al., 2026).

The expected molecular conservation between insects and humans is most evident in this general scheme. This method indicates that care should be exercised in comparing neurotransmitters. Serotonin and dopamine are ancient neuromodulators but have taken different evolutionary paths in receptor localization and circuit function. Octopamine participates in insect stimulation and defense and is functionally analogous to the catecholaminergic arousal systems of vertebrates. However, it is not a chemical equivalent of norepinephrine. Similarly, GABAergic inhibition is preserved, yet the physical circuits in which it functions are fundamentally distinct. The suitable comparable unit is, hence, a biological mechanism or pathway rather than a behavioral designation (Kim and Jung, 2025).

3. Why Honey Bee Is a Powerful Sociogenomic Model

Honey bees combine a sequenced genome, extensive genetic resources, pronounced social organization, measurable behavioral variation, and experimentally accessible brain tissue. Workers can occupy different behavioral states, including nursing, foraging, guarding, and defensive guarding-like roles. Aggression is especially useful because researchers can measure the phenotype at both individual and colony levels. Studies on the relationship between colony- and individual-level responses have been mainly (perhaps exclusively) performed on the main actors, the female worker bees, in agreement with the literature. However, at the colony level, different techniques such as aggression, simulated attacks, behavioral ratings, and sting counts have shown that colony aggression is a strongly heritable trait in populations of honeybees, with an important effect of paternal inheritance (drone contribution) (Avalos et al., 2014). Since paternal inheritance is important for colony-level aggression, it is important to look for possible correlations between individual drone and worker bee behaviors and the colony phenotype as a whole (Guzman-Novoa et al., 2005). The classic literature established the organization and genetics of honey bee defense and identified guarding as a major component of colony-level stinging responses (Breed et al., 2004). Hunt et al. (2007) subsequently used QTL

mapping to connect variation in guarding and stinging with genomic regions and candidate genes. These studies demonstrated that behavioral variation can be genetically dissected in a eusocial insect.

Microarray research of honey bees, it demonstrates that aggression-associated genes exhibiting hereditary patterns of brain expression are also subject to environmental regulation. Expression variations in the brain were observed for numerous genes between the highly aggressive Africanised honey bee and the European honey bee (EHB) subspecies. Comparable outcomes were observed for EHB following exposure to alarm pheromone (which incites aggression) and when contrasting older and younger bees (aggressive inclinations escalate with age). The gene lists produced from these three microarray assays exhibited considerable overlap. Furthermore, there was a statistical abundance of various identical cis regulatory motifs in the promoters of genes across all three gene lists. Aggression exhibits a notably strong molecular imprint in the brain, irrespective of whether it arises from genetic, age-related, or environmental (social) influences. One factor in the development of varying levels of aggressive behaviour in honey bees seems to be alterations in the control of genes that govern the reaction to alarm pheromones (Alaux et al., 2009).

The most modern advantage is methodological. Honey bee aggression has now been studied using QTL mapping, GWAS, bulk RNA sequencing, single-cell RNA sequencing, gene-regulatory-network analysis, DNA methylation, and long-read direct RNA sequencing. This makes *Apis* one of the rare social-animal models in which multiple genomic layers can be connected to a clearly measurable behavioral phenotype (Bresnahan et al., 2023).

4. *Genetic Architecture: From QTLs to Colony-Level GWAS*

Preliminary QTL investigations identified three genetic loci associated with stinging and guarding behaviors. Genes of interest in these areas included substances involved in central nervous system function, neurodevelopment, serotonin pathways, sensory communication, and GABA-B receptor pathways (Hunt et al., 2007). Later studies suggested that these QTLs may also influence solitary guarding and stinging behaviors in different populations, showing the biological relevance of the identified regions. The next theoretical step was motivated by colony-level GWAS. Sequencing was performed on individuals from colonies with different levels of aggression. Avalos et al. (2020) found that individual aggression was not significantly correlated with individual alleles, but colony aggression was correlated with allele frequencies in those colonies. On linkage group 7 (chromosome), an ortholog of the *Drosophila* sensory gene dpr4 was significantly associated and showed evidence of selection and admixture associated with the evolution of tameness. This finding is important for the comparison of sociogenomics. In eusocial organisms, the behavior of an individual is influenced in part by the genetic composition of the individual and its nest mates. Some of this behavior is genetically conditioned by their nest mates. Thus, genetic architecture may refer to direct genetic effects or indirect genetic effects mediated through the social environment.

Hence, the aggressiveness of honey bees contradicts the classical assumption that the phenotype of the individual is determined only by its genotype. Therefore, a simple list of genes associated with honey bee aggression is not enough for human evaluation. It is critical to distinguish among direct neural effects, regulatory effects, and social-contextual effects. The honey bee provides a mechanistic illustration of how genetic information can indirectly affect behavior by molding the behavioral context encountered by individuals.

5. Brain Transcriptomics: Aggression as a Molecular State

Transcriptomics has revolutionized behavioral genetics, with evidence that behavior is correlated with variable gene expression. Genetic diversity, social contact, and age affect honey bee aggression and brain expression patterns. Alaux et al. (2009) found many similarities between aggressive Africanized bees, exposure to alarm pheromones, and older bees in gene-expression profiles and common cis-regulatory elements 7. The point is that genetics does not simply determine a static trait of aggressiveness. Genetic diversity can alter the sensitivity of regulatory systems, and environmental factors can switch on intersecting molecular pathways. This creates a gene-environment interaction in the brain. Further evidence is provided by social challenge experiments. Exposure to an invader increases the probability and intensity of aggressive responses to future threats in honey bees. In mushroom bodies, social challenges elicited temporally discrete waves of gene expression related to cytoskeletal reorganization, hormonal activity, stress responses, and transcription factors. The regulatory network analysis identified a limited number of transcription factors responsible for governing a broader transcriptional response.

Social interactions may change gene expression and lead to long-lasting changes in behavior, or they may simply tag brain circuits involved in behavior. Honey bee aggression and brain gene expression are strongly determined by social signals. Previous work suggests that expression changes only occur when social signals produce consistent, long-term changes in behavior. A research removed the olfactory cues that elicit aggression by using smoke exposure, a traditional beekeeping method for reducing aggression and determined whether behavioral changes occur without changes in the expression of four aggression-related biomarker genes (drat, cyp6g1/2, GB53860, inos). It also examines two markers of cerebral hypoxia response (hif1α, hsf) to see if there are smoke-induced molecular changes. Smoke-exposed bees, with impaired sensory perceptions, showed a pronounced and transient reduction in antagonism compared to bees able to receive social cues. The inhibition of sensory perception caused a hypoxic chemical reaction in the brain, but it had no effect on aggression gene expression. The findings show that certain genes distinguish social signal-induced aggressiveness changes from long-term changes (Harrison et al., 2019).

This idea has a direct conceptual correlation in the biology of human behavior. Social pressures, ongoing dangers, and ecological challenges can all change brain states and genetic expression. This makes the honey bee an easy model for

studying how experience becomes encoded at the molecular scale, not that the same genes will produce similar behavioral effects in people.

6. Single-Cell Genomics and Gene-Regulatory Networks

Recent research, therefore, represents a major methodological departure. Using single-cell transcriptomics and gene-regulatory-network analysis, researchers explored the effect of colony-level genetic diversity in aggression on the molecular architecture of individual brains. They compared soldiers and foragers from colonies differing in their levels of hostility. The striking finding was that variation in gene regulation was more strongly affected by the environment of the colony than variation in gene expression. Flexibility of regulatory networks Colony aggression had an important effect on adaptability of regulatory networks. Colony aggression was characterized by more variations of regulatory dynamics between soldiers and foragers in more aggressive colonies. Subnetworks including genes linked to colony aggression exhibited synchronized regulatory activity across several cell types and brain regions, especially in regions connected with olfaction, vision, and multimodal sensory integration (Traniello et al., 2023).

This finding shifts the question from which genes are activated during aggression? What regulatory architectures allow a brain to enter into and maintain an aggressive state? This distinction is especially relevant for human aggression where complex phenotypes are more likely to be derived from coordinated regulation of many genes, rather than from individual transcriptional changes.

Single cell approaches also allow isolation of processes specific to neurons, glia and regions. A prospective comparative atlas should consequently refrain from regarding the brain as a uniform tissue. If conserved human orthologs are present in cell types or pathways linked to defensive mechanisms in bees, their comparative significance may surpass that of genes identified just by whole-brain averages.

7. Serotonergic Signaling

Serotonin is one of the most famous historical contenders in the biology of aggression. In humans, serotonergic activity has been associated with impulse control, emotional regulation and reactive aggression. Genes like *SLC6A4, HTR1B* and *HTR2A* and members of the tryptophan hydroxylase (*TPH*) family have been widely studied (Popova, 2006; Fernàndez-Castillo & Cormand, 2016). Extensive research on animals has produced compelling neurochemical and physiological data indicating shared pathways preserved across species, including serotonergic and dopaminergic neurotransmission as well as hormonal signaling. This information has facilitated the identification of candidate genes for human research concentrating on serotonergic and dopaminergic genes (*5HTT, HTR1B, HTR2A, DAT, DRD2, and DRD4*) as well as hormone-associated genes (*AR, ESR1, AVP, and OXTR*) (Zhang-James et al., 2019). In the latest research on the neurobiological mechanisms of aggression in humans and the role of serotonin and dopamine as biomarkers, it has been reported that among

serotonin and other markers associated with the dopaminergic system, monoamine oxidase A (variable number of sequential repeat polymorphisms), serotonin transporter (*5-HTTLPR*), serotonin receptor *HTR1A* (*rs6295*), and catechol-O-methyltransferase (*rs4680*) polymorphisms may be associated with aggressive behaviors (Ippolitov et al., 2026).

In honey bee, serotonin and tyramine are involved in the complex interaction of neuromodulators that fine tune social hierarchy, aggression, motor functions and muscle specific activities. One of the defensive-behavior QTLs is *Am5HT7*, a gene associated with a serotonin receptor, indicating that serotonergic signaling is part of the genetic architecture of aggressive behaviors (Hunt et al., 2007; Raza, & Li, 2025).

Conservation of serotonin signaling between insects and vertebrates supports monoaminergic modulation of behavioral states as a fundamental element of ancient threat-response systems (Vleugels et al., 2015; Swallow et al., 2016). The comparison must still be confined to the pathway level. Receptor subtype, neuronal localization, and circuit connections dictate behavioral outcomes. A conserved receptor does not necessarily indicate a conserved behavioral response. The most compelling inference is that serotonergic systems are evolutionarily primordial controllers of brain reactivity and behavioral restraint, with their influence on aggression being subject to alteration by environment and circuit configuration.

8. Dopaminergic and Octopaminergic Signaling

Dopamine is implicated in motivation, salience, learning, reward, and behavioral activation. Studies on aggression-related traits have been conducted in humans and on genes such as *DRD2, DRD4, SLC6A3*, etc. However, candidate-gene studies have not produced consistent results to support simple causal claims (Waltes et al., 2016).

Dopamine is involved in learning and in the regulation of behavioral states in honey bees and thus modulates motivation and arousal to influence defensive reactions. Octopamine is of great importance in insects (Figure 1). It controls arousal, movement, sensitivity to sensory stimuli, and energy mobilization. Alarm signals in colony defense increase the alertness of workers, thereby increasing the behavioral salience of sensory cues. Octopaminergic signaling is hence an element of the insect's arsenal for responding to threats (Mezheritskiy et al., 2024).

Comparative analysis should utilize functional analogy rather than direct equivalence. The molecular framework of monoaminergic neuromodulation is highly preserved, although the particular transmitters, receptors, and circuit functions have evolved differently. This differentiation exemplifies evolutionary conservation by alteration: evolution retains beneficial signaling principles while altering their execution.

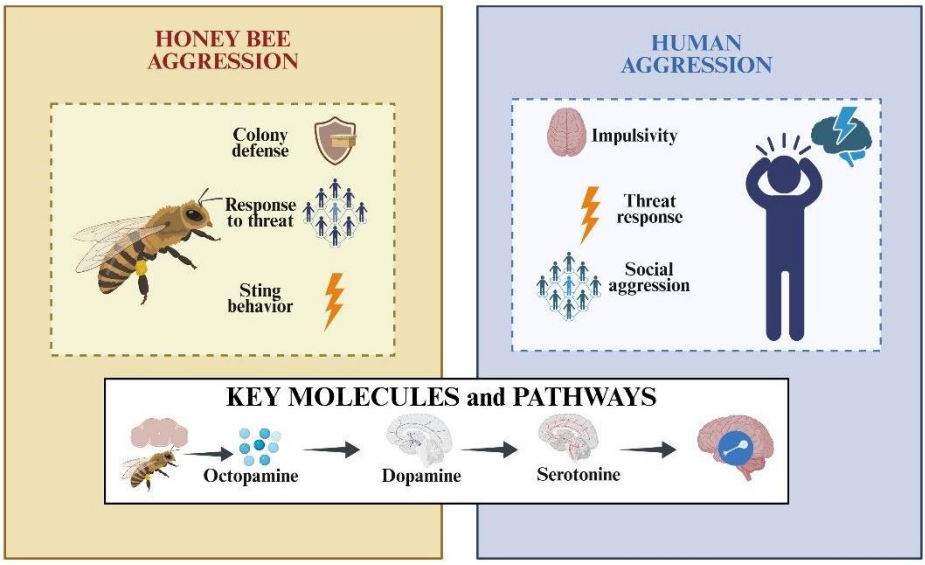


Figure 1. Common key molecules and signaling pathways

9. GABAergic Inhibition and Behavioral Thresholds

Arousal and inhibition are both needed for aggressive behavior. The nervous system must decide whether a stimulus is above a behavioral threshold and whether a triggered reaction must be continued or stopped. GABAergic transmission is a major inhibitory system for regulating neuronal excitability. Gamma-aminobutyric acid (GABA) is an inhibitory neurotransmitter, and is present in high concentrations in vertebrates and invertebrates. GABA is widely distributed in the central nervous system of insects. GABAergic neurons are found in the antennal lobes, optic lobes, mushroom bodies, central complex and hypoesophageal ganglia throughout the honeybee brain (Mustard et al., 2020). Quantitative trait loci analysis of honey bee defensive behavior identifies *GABA-B-R1* as a candidate gene (Hunt, 2007; Hunt et al., 2007). The significance of this finding is that it links genetic differences related to aggression to inhibitory brain control, not merely to excitatory or arousal mechanisms.

In humans, modified inhibitory control is pertinent to impulsivity and emotional instability, both of which may lead to reactive aggressiveness. The comparison does not suggest that bees' and humans' GABA circuits are structurally similar. It suggests that conserved molecular mechanisms throughout evolution have addressed a core computational challenge—reconciling excitation and inhibition —through evolution.

10. G-Protein Coupled Receptors (GPCRs) Signaling, Sensory Processing and Threat Detection

Aggression is driven by the external environment. Honey bee defensive choices are influenced by olfactory, optical, and tactile stimuli, but alarm pheromones are a particularly potent social signal. Metabolomic studies have

shown that glycolysis is up-regulated and oxidative phosphorylation down-regulated in the brains of aggressive worker bees. Physiological evidence also supports the idea that alarm pheromones serve as precursors to facilitate the release of neuropeptides in the brains of aggressive worker bees (Barros et al., 2015; Chandrasekaran et al., 2015). Recently, the neuropeptides *AmAST A* (59–76) and *AmTRP* (254–262) have been demonstrated to modulate aggressive behavior in worker honey bees. Previously, it has been shown that the simple presence of allatostatin and tachykinin-related peptides in the bee brain can induce aggressive behavior, and the present study elucidated metabolic pathways that are either activated or suppressed to promote complex defensive behaviors, such as aggression. In addition, it gave considerable insight into the molecular basis of individual and nest defense in honey bees (Paula et al., 2024).

A defense-behavior QTL harboring the GPCR-regulating arrestin *AmArr4* emphasizes the importance of receptor modulation and sensory signaling (Hunt, 2007; Hunt et al., 2007). Arrestins regulate receptor desensitization, trafficking, and downstream signaling. Such mechanisms regulate the strength of the neuronal response to a constant or repetitive stimulus. This rule is about behavioral sensitization: repeated threats alter the likelihood and severity of future defensive responses.

The single-cell study localized the aggression-related regulatory mechanisms to brain regions involved in olfaction, vision, and multimodal sensory integration. Collectively, these results indicate that aggression originates prior to motor execution, namely in the manner in which prominent social and environmental signals are perceived and prioritized (Traniello et al., 2023).

In humans, threat identification engages widespread sensory and limbic systems. The comparative analysis indicates that receptor modulation and sensory amplification serve as conserved molecular control mechanisms for adaptive responses to significant stimuli (Gonzalez-Hernandez et al., 2024).

11. Stress, Neuroendocrine Signaling and Behavioral State

Defensive aggression is inherently associated with physiological arousal. Alarm pheromone is a key component of the social organization and defensive behavior of honey bees. This is the chemical that worker bees release in the presence of a hazard to warn fellow members of the colony that danger is present. Isopentyl acetate is the major component of this pheromone and is released from special glands on either side of the worker's sting. Other chemicals like octyl acetate can also increase the efficacy of the alarm pheromone besides isopentyl acetate. The pheromone is detected by particular sensors on the antennae of the bees, allowing them to react rapidly and in unison to the threat (Prđun, 2026). Honey bee alarm pheromone can stimulate respiration and prepare workers for defensive behavior. The reaction is simultaneous, not limited to one neurotransmitter.

Human aggression also influences stress mechanisms, including the hypothalamic-pituitary-adrenal axis, glucocorticoid signaling, sympathetic

activation, and sex-steroid pathways. Vasopressin, oxytocin, and testosterone have all been studied in relation to social behavior and violence. However, their effects are extremely context-dependent (Mbiydzenyuy et al., 2024).

The relative significance of honey bees does not stem from their having a diminutive HPA axis. Instead, they offer a manageable illustration of how threats modify physiological conditions and how these conditions influence behavioral thresholds. Cellular stress responses, transcriptional regulators, and neuromodulators provide a connection between environmental challenges and behavioral outcomes (Even et al., 2022).

This approach elucidates the reason for the overlap between aggression-related genes and those involved with stress and immunological functions. Behavioral state and the health of an organism are not distinct molecular realms. The suggestion that behavioral and physiological states may be regulated by shared mechanisms is supported by a Tielbeek et al. (2019) transcriptome analysis of honey bees, in which expression patterns related to aggression were found to correlate with molecular responses to infection.

12. Epigenetics and Long-Term Behavioral Plasticity

This requires that the systems for behavioral adaptability be such that the ambient experiences can change subsequent reactions without changing the genetic code. The research on honey bees proves this regulation concretely. Exposure to intruders is linked to alterations in DNA methylation in the brain, such as differentially methylated regions related to genes involved in cognitive plasticity, chromatin remodeling and hormonal signaling. Social challenge experiments further illustrate persistence: an initial interaction can elevate both the likelihood and severity of a later hostile reaction. The molecular evidence indicates that transcriptional and epigenetic processes may play a role in the maintenance of modified behavioral states (Shpigler et al. 2017).

Research on human aggression is progressively including epigenome-wide association studies; however, establishing causal relationships continues to pose challenges. DNA methylation is tissue-specific, dynamic, and influenced by environmental factors. Thus, the epigenetic similarities among species ought to be seen as mechanistic indicators of adaptability instead of as confirmation of preserved causal methylation signatures (Dudko et al., 2025).

A particularly intriguing discovery about honey bees is the transcription bias linked to the parent of origin in relation to aggression. Long-read direct RNA sequencing revealed heightened transcription bias toward maternal and paternal alleles in aggressive bees relative to their non-aggressive counterparts, while RNA m6A modifications and alternative splicing did not seem to influence the identified intragenomic discord. This extends the comparative paradigm beyond traditional genotype and methylation to include allele-specific regulation (Bresnahan et al., 2023).

13. Honey Bee–Human Orthology: What Is Actually Conserved?

Research using the honey bee as a model for social interaction has revealed distinct patterns of gene expression in the brains of African and European honey bees . In a separate analysis of the evolutionary conservation of socially regulated genes in honey bees through orthology assessment across the Metazoa, genes identified as highly conserved were plentiful among gene sets with variable expression (associated with alarm pheromone responses, age-related variation and colony-wide effects on guard bees). Thus, variation in these traits might have shared chromosomal bases with many other metazoans. Conversely, the absence of broadly conserved genes in the differentially expressed gene clusters that distinguish African and European forager and guard bees suggests that the genetic basis for this particular social trait is unique to honey bees. Regarding the gene set associated with alarm pheromone responses, a notable degree of conservation was observed among mammals, despite alarm pheromone being a compound unique to bees. Gene Ontology analysis of the human orthologs of these strongly conserved honey bee genes related to alarm pheromones shows a predominance of terms related to protein metabolism, regulation of protein complex assembly, and protein folding. This may be related to the reorganization of critical neural circuits in response to alarm pheromones. The research suggests that this reorganization may be an adaptation, allowing social creatures to deftly interpret and respond to the complex dynamics of intraspecific communication essential to their social framework (Liu et al., 2016). An important feature of this research is the comparative study of conservation of genes associated with aggression-related behavioral traits in honey bees among mammals. They found that clusters of honey bee aggression-related transcriptional processes have conserved mammalian homologs. This finding should be interpreted cautiously. Orthology means that genes share a common evolutionary history but this does not mean that they share the same function. A conserved protein can be part of an essential biological function but incorporated in diverse brain pathways across species. However, orthology is very informative if multiple independent lines of evidence converge. A honey bee gene is notably intriguing when it is (i) linked to defensive behavior, (ii) variably expressed or regulated during aggressive states, (iii) preserved as a human ortholog, (iv) implicated in a pathway with evidence related to human aggression, and (v) strategically located within a pertinent interaction network (Alaux et al., 2009; Liu et al., 2016).

14. Human Aggression Genetics: From Candidate Genes to GWAS

Candidate-gene studies have a long history in the genetics of human aggression. The *MAOA*, *DRD4, COMT* and serotonergic genes have been extensively investigated. However, meta-analytic findings have failed to support the utility of singular candidate variations as reliable markers of danger or aggression. This is a major methodological insight for comparative studies. Aggression is expected to be polygenic and thus genome-wide approaches are more appropriate. Overall, the review found strong evidence for heritability but

only a small number of genome-wide associations were consistently replicated. Recent evaluations that include GWAS, EWAS, and other omics similarly determine that existing molecular predictors account for merely a limited fraction of phenotypic variation (Koyama et al., 2024).

15. Conserved Molecular Modules Rather Than Universal Aggression Genes

Aggression is a universal trait; it exists in all animals, including human beings and primates, and the inference is that the molecular substrates of aggression-related behaviors are conserved. The modules include regulation of sensory receptors, monoaminergic signaling pathways, inhibitory control mechanisms, stress response systems, transcriptional regulation processes, synaptic plasticity, and cellular adaptation. A molecular module may remain conserved despite variations in the significance of its constituent genes. Evolutionary conservation can manifest via the preservation of network structure, whereas species-specific adaptation alters receptor subtype expression, regulatory components, or circuit interconnections (Fritz et al., 2023).

This network viewpoint is especially suitable for honeybees, as the hostility of the colony represents an emergent phenotype. Individual behavior is a product of genetic heritage and social environment. A network model is more able to include indirect genetic influences and regulatory flexibility than a single gene model (Traniello et al., 2023). The proposed conceptual statement is that the basic chemical structure can be conserved, but the behavioral expression is species-specific. This distinction should be the main guiding principle for the interpretation of the research.

16. Conserved Versus Species-Specific Mechanisms

Species differences: as mentioned above, aggression in honeybees is a trait of colony defense, inherent to their eusocial structure. By contrast, human violence is rooted in more complex cognitive processes, linguistic capacity, social learning, and personal developmental experiences. Moreover, conserved mechanisms are also expected at more fundamental biological levels, such as receptor signal transduction, neurotransmitter metabolism, synaptic modulation, transcriptional responses, and cellular stress adaptation.

For example, a gene involved in threat detection by olfaction in honeybees may have an ortholog (matching gene) expressed in the human nervous system but not be very important in human-human aggression. Or, a gene associated with human aggression could be involved in a process not associated with defensive behaviors in bees. The main goal of such a comparison is not to find behavioral similarities, but to identify evolutionary toolkits.

17. A Multi-Omics Roadmap for Future Research

Genomics, transcriptomics, epigenomics, proteomics and metabolomics should be part of the next stage of comparative aggression biology. Single-cell and spatial transcriptomics can uncover cell-type and brain-region specialization

in honey bees. ATAC-seq and chromatin analysis might uncover regulatory elements that control genes involved in aggressiveness. Isoform and allele specific expression revealed by long read sequencing. Proteomics and metabolomics can evaluate whether transcriptional changes result in functional molecular aberrations (Bi & Weng, 2025). On the human side, large GWAS, meta-analyses, EWAS, and multi-ancestry datasets matter. Phenotype harmonization will be especially important, as 'aggressive' encompasses multiple traits (Tielbeek et al., 2022).

The most potent future design would entail a cross-species network-analysis framework in which genetic modules are independently delineated in bees and humans, thereafter analyzed for conservation. This circumvents circular reasoning and facilitates the identification of unforeseen conserved mechanisms.

A subsequent chance is empirical confirmation. Candidate genes identified from the comparative atlas may be examined in honey bees through applicable perturbation methods. The significance to humans ought to be assessed with independent human datasets instead of being only deduced from evolutionary conservation.

18. Conclusion

Aggression is a complex phenotype that is a consequence of the interaction of genetic diversity, brain conditions, hormonal control, social experiences, and environmental factors. Despite years of research into candidate genes, genome-wide associations, and epigenomics, the biological basis of aggression in humans is still poorly understood. Honey bees provide a unique chance to study aggression as an emergent behavioral trait from the perspectives of genetics, social context, transcriptome, and regulation. The honey bee offers a unique comparative framework, as defensive aggressiveness is quantifiable, socially structured, genetically diverse, and amenable to experimentation.

From first QTL investigations to colony-wide GWAS and single-cell gene-regulatory frameworks, honey bee studies have gradually unveiled that defensive behavior is influenced by the interplay of genetic and social mechanisms. These investigations on honey bees have pinpointed genetic areas harboring candidates associated with central nervous system function, neurogenesis, serotonin transmission, sensory processing, and GABAergic modulation. Subsequent transcriptome analyzes revealed strong molecular markers in the brain linked to inherited, age-related, and environmentally caused variations in aggression. Genome-wide association studies at the colony level have moved the focus from individual genotypes to collective genotypes, while single-cell transcriptomics and gene-regulatory-network analyzes have shown that colony aggression is correlated with the flexibility of regulatory structures across different brain cell types. The primary comparative observation is not that bees and humans possess a limited collection of 'aggressive genes. Both exhibits conserved molecular mechanisms that govern sensory significance, neuromodulation, inhibitory regulation, physiological activation, and behavioral adaptability. Studies of

human aggression suggest a polygenic model, with many small effects and a strong interaction with the environment.

In evaluating the biological substrates of aggression across hundreds of millions of years of evolutionary divergence, comparative sociogenomics reveals a fundamental principle: evolution repurposes an ancient, deeply conserved toolkit. The honey bee defending its hive with a fatal sting and a human reacting with aggression to an immediate social threat occupy vastly different behavioral, cognitive, and social landscapes. Yet beneath these divergent phenotypic surfaces lies a shared molecular syntax—governed by monoaminergic arousal, GABAergic gating, GPCR-mediated sensory sensitization, and dynamic epigenomic plasticity. The value of *Apis mellifera* is therefore not in serving as a behavioral mirror of humanity, but in functioning as a biological magnifying glass. By stripping away the confounding layers of language, complex culture, and individual biographical trauma that complicate human aggression genetics, the honey bee allows us to observe how genomes and social environments interact in real time to shift behavioral thresholds. Ultimately, studying the colony's aggression ury of the shows us that human aggression is not an isolated evolutionary anomaly, but an ancient, conserved biological script that evolution continues to edit across the tree of life.

References

Alaux, C., Sinha, S., Hasadsri, L., Hunt, G. J., Guzmán-Novoa, E., DeGrandi-Hoffman, G., ... & Robinson, G. E. (2009). Honey bee aggression supports a link between gene regulation and behavioral evolution. *Proceedings of the National Academy of Sciences*, *106*(36), 15400-15405. *DOI:10.1073/pnas.0907043106*

Avalos, A., Fang, M., Pan, H., Ramirez Lluch, A., Lipka, A. E., Zhao, S. D., ... & Hudson, M. E. (2020). Genomic regions influencing aggressive behavior in honey bees are defined by colony allele frequencies. *Proceedings of the National Academy of Sciences*, *117*(29), 17135-17141. *DOI:10.1073/pnas.1922927117*

Avalos, A., Rodríguez-Cruz, Y., & Giray, T. (2014). Individual responsiveness to shock and colony-level aggression in honey bees: evidence for a genetic component. *Behavioral Ecology and Sociobiology*, *68*(5), 761-771. *DOI:10.1007/s00265-014-1689-8*

Barros, L. F., Sierralta, J., & Weber, B. (2015). How doth the little busy bee: unexpected metabolism. *Trends in Neurosciences*, *38*(1), 1-2. *DOI:10.1016/j.tins.2014.11.005*

Bi, H., & Weng, X. (2025). Single-cell epigenomics and proteomics methods integrated in multiomics. *Fundamental Research*, *5*(5), 1988-2002. *DOI: 10.1016/j.fmre.2023.11.014*

Breed, M. D., Guzmán-Novoa, E., & Hunt, G. J. 3. (2004). Defensive behavior of honey bees: organization, genetics, and comparisons with other bees. *Annual Reviews in Entomology*, *49*(1), 271-298. *DOI: 10.1146/annurev.ento.49.061802.123155*

Bresnahan, S. T., Lee, E., Clark, L., Ma, R., Markey, M., Rangel, J., ... & Li-Byarlay, H. (2023). Examining parent-of-origin effects on transcription and RNA methylation in mediating aggressive behavior in honey bees (Apis mellifera). *BMC Genomics*, *24*(1), 315. *DOI:10.1186/s12864-023-09411-4*

Chandrasekaran, S., Rittschof, C. C., Djukovic, D., Gu, H., Raftery, D., Price, N. D., & Robinson, G. E. (2015). Aggression is associated with aerobic glycolysis in the honey bee brain1. *Genes, Brain and Behavior*, *14*(2), 158-166. *DOI:10.1111/gbb.12201*

Dudko, N. A., Nurieva, G. N., Kunizheva, S. S., & Kuznetsova, I. L. (2025). Epigenetics of Aggression: Recent Advances and Perspectives on Animal Models. *Russian Journal of Genetics*, *61*(10), 1177-1186. *DOI:10.1134/S1022795425700711*

Even, N., Devaud, J. M., & Barron, A. B. (2012). General stress responses in the honey bee. *Insects*, *3*(4), 1271-1298. *DOI:10.3390/insects3041271*

Fernàndez-Castillo, N., & Cormand, B. (2016). Aggressive behavior in humans: Genes and pathways identified through association studies. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, *171*(5), 676-696. *DOI:10.1002/ajmg.b.32419*

Fritz, M., Soravia, S. M., Dudeck, M., Malli, L., & Fakhoury, M. (2023). Neurobiology of aggression—Review of recent findings and relationship with alcohol and trauma. *Biology*, *12*(3), 469. *DOI:10.3390/biology12030469*

Gonzalez-Hernandez, A. J., Munguba, H., & Levitz, J. (2024). Emerging modes of regulation of neuromodulatory G protein-coupled receptors. Trends in neurosciences, 47(8), 635-650. *DOI:10.1016/j.tins.2024.05.008*

Guzman-Novoa, E., Hunt, G. J., Page Jr, R. E., Uribe-Rubio, J. L., Prieto-Merlos, D., & Becerra-Guzman, F. (2005). Paternal effects on the defensive behavior of honeybees. *Journal of Heredity*, *96*(4), 376-380. *DOI:10.1093/jhered/esi038*

Harrison, J. W., Palmer, J. H., & Rittschof, C. C. (2019). Altering social cue perception impacts honey bee aggression with minimal impacts on aggression-related brain gene expression. *Scientific Reports*, *9*(1), 14642. *DOI:10.1038/s41598-019-51223-8*

Hunt, G. J. (2007). Flight and fight: a comparative view of the neurophysiology and genetics of honey bee defensive behavior. *Journal of Insect Physiology*, *53*(5), 399-410. *DOI:10.1016/j.jinsphys.2007.01.010*

Hunt, G. J., Amdam, G. V., Schlipalius, D., Emore, C., Sardesai, N., Williams, C. E., ... & Page Jr, R. E. (2007). Behavioral genomics of honeybee foraging and nest defense. *Naturwissenschaften*, *94*(4), 247-267. *DOI:10.1007/s00114-006-0183-1*

Ippolitov, A. D., Pavlova, O. V., Peregud, D. I., Gadisov, T. G., Pavlov, K. A., & Shport, S. V. (2026). Neurobiological Mechanisms and Biomarkers of Aggression: The Role of Serotonin and Dopamine. *Neurochemical Journal*, *20*(2), 163-180. *DOI:10.1134/S1819712426700169*

Kim, B., & Jung, J. (2025). The Neuromodulatory Landscape of Honey Bee Cognition: Roles of Acetylcholine, Glutamate, GABA, and Biogenic Amines. *Journal of Apiculture*, *40*(2), 183-195. *DOI:10.17519/apiculture.2025.06.40.2.183*

Koyama, E., Kant, T., Takata, A., Kennedy, J. L., & Zai, C. C. (2024). Genetics of child aggression, a systematic review. *Translational Psychiatry*, *14*(1), 252. *DOI:*10.1038/s41398-024-02870-7

Liu, H., Robinson, G. E., & Jakobsson, E. (2016). Conservation in mammals of genes associated with aggression-related behavioral phenotypes in honey bees. *PLoS Computational Biology*, *12*(6), e1004921. *DOI: 10.1371/journal.pcbi.1004921*

Mbiydzenyuy, N. E., & Qulu, L. A. (2024). Stress, hypothalamic-pituitary-adrenal axis, hypothalamic-pituitary-gonadal axis, and aggression. *Metabolic Brain Disease*, *39*(8), 1613-1636. *DOI: 10.1007/s11011-024-01393-w*

Mezheritskiy, M. I., Vorontsov, D. D., Dyakonova, V. E., & Zakharov, I. S. (2024). Behavioral functions of octopamine in adult insects under stressful conditions. *Biology Bulletin Reviews*, *14*(5), 535-547. *DOI: 10.1134/S2079086424700014*

Miranda, C. D., & Srikanth, V. (2026). Social Dominance and Territoriality. In *Principles of Animal Behavior* (pp. 215-222). CRC Press.

Mustard, J. A., Jones, L., & Wright, G. A. (2020). GABA signaling affects motor function in the honey bee. Journal of Insect Physiology, 120, 103989. *DOI: 10.1016/j.jinsphys.2019.103989*

Paula, G. M., da Silva Menegasso, A. R., dos-Santos-Pinto, J. R. A., Malaspina, O., & Palma, M. S. (2024). Profiling the neuroproteomics of honeybee brain: A clue for understanding the role of neuropeptides in the modulation of aggressivity. *Journal of Proteomics*, *295*, 105089. *DOI:10.1016/j.jprot.2024.105089*

Pavlov, K. A., Chistiakov, D. A., & Chekhonin, V. P. (2012). Genetic determinants of aggression and impulsivity in humans. *Journal of Applied Genetics*, *53*(1), 61-82. *DOI:10.1007/s13353-011-0069-6*

Popova, N. K. (2006). From genes to aggressive behavior: the role of serotonergic system. *Bioessays*, *28*(5), 495-503. *DOI:10.1002/bies.20412*

Potegal, M., & Elwood, R. W. (2026). Integrating the behavioral ecology, social psychology, and neurobiology of aggression. *Frontiers in Ethology*, *5*, 1771240. *DOI:10.3389/fetho.2026.1771240*

Prđun, S. (2026). The role of alarm pheromone in honey bee (Apis mellifera L.) colonies. *Journal of Central European Agriculture*, *27*(1), 78-88. *DOI:10.5513/JCEA01/27.1.4529*

Raza, M. F., & Li, W. (2025). Biogenic amines in honey bee cognition: Neurochemical pathways and stress impacts. *Current Opinion in Insect Science*, *70*, 101376. *DOI:10.1016/j.cois.2025.101376*

Shpigler, H. Y., Saul, M. C., Murdoch, E. E., Cash-Ahmed, A. C., Seward, C. H., Sloofman, L., ... & Robinson, G. E. (2017). Behavioral, transcriptomic and epigenetic responses to social challenge in honey bees. *Genes, Brain and Behavior*, *16*(6), 579-591. *DOI:10.1111/gbb.12379*

Swallow, J. G., Bubak, A. N., Grace, J. L., & Guest Editors. (2016). The role of monoamines in modulating behavior. *Current Zoology*, *62*(3), 253-255. *DOI:10.1093/cz/zow046*

Tielbeek, J. J., Uffelmann, E., Williams, B. S., Colodro-Conde, L., Gagnon, É., Mallard, T. T., ... & Posthuma, D. (2022). Uncovering the genetic architecture of broad antisocial behavior through a genome-wide association study meta-analysis. *Molecular Psychiatry*, *27*(11), 4453-4463. *DOI:10.1038/s41380-022-01793-3*

Traniello, I. M., Bukhari, S. A., Dibaeinia, P., Serrano, G., Avalos, A., Ahmed, A. C., ... & Robinson, G. E. (2023). Single-cell dissection of aggression in honeybee colonies. Nature Ecology & Evolution, 7(8), 1232-1244. *DOI:10.1038/s41559-023-02090-0*

Van der Laan, C. M., van de Weijer, S. G., Pool, R., Hottenga, J. J., van Beijsterveldt, T. C., Willemsen, G., ... & Boomsma, D. I. (2023). Direct and indirect genetic effects on aggression. *Biological Psychiatry Global Open Science*, *3*(4), 958-968. *https://doi.org/ DOI:10.1016/j.bpsgos.2023.04.006*

Vleugels, R., Verlinden, H., & Vanden Broeck, J. (2015). Serotonin, serotonin receptors and their actions in insects. *Neurotransmitter*, *2*. *DOI: 10.14800/nt.314*

Waltes, R., Chiocchetti, A. G., & Freitag, C. M. (2016). The neurobiological basis of human aggression: a review on genetic and epigenetic mechanisms. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, *171*(5), 650-675. *DOI: 10.1002/ajmg.b.32388*

Zhang-James, Y., Fernàndez-Castillo, N., Hess, J. L., Malki, K., Glatt, S. J., Cormand, B., & Faraone, S. V. (2019). An integrated analysis of genes and functional pathways for aggression in human and rodent models. *Molecular Psychiatry*, *24*(11), 1655-1667. *DOI:10.1038/s41380-018-0068-7*

CHAPTER 10

From Sublethal Stress to Network Collapse: Pollination Resilience and Tipping Points in the Anthropocene

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1. INTRODUCTION: POLLINATION SYSTEMS IN THE ANTHROPOCENE

Pollination collapse arises through nonlinear degradation of interaction networks via sublethal impairment. Pollination is a keystone ecological process underlying biodiversity and food production globally. Foot-noted species of angiosperms 87.5% of plant species depend on animal-mediated pollination; such systems are critical for ecosystem sustainability and agricultural yields (Klein et al., 2007; Ollerton et al., 2011; Potts et al., 2016; IPBES, 2016). In addition to reproductive function, pollination networks regulate gene flow and evolutionary trajectories of interacting plants, preserving adaptive potential for species in a changing world (Bascompte & Jordano, 2007).

In the Anthropocene, pollination systems are subjected to multiple "cascading" interacting stressors of anthropogenic origin: habitat loss, agrochemical exposure, climate change, pathogens, and nutritional limitation. These might be acting simultaneously, in an additive or synergistic and nonlinear fashion across biological and spatial scales, to produce effects stronger than would have been predicted if assessed individually (Goulson et al., 2015; Dicks et al., 2021; Brook et al., 2008; Tylianakis and Morris, 2017; Lin et al., 2024). It follows that functional impairment of pollinators occurs long before declines in population size or species richness become overt, suggesting that we are often blind to (or underestimating) early stages of system degradation.

'Sublethal' stressors are key players in this process. By impairing behaviour, cognition, immunity and energetics, sublethal stressors cause lost opportunities without killing individuals. Foraging is less effective, navigation derailed, learning impaired, and the fidelity of plant–pollinator interaction dimmed (Gill et al., 2012; Siviter et al., 2021). These traits cascade from the biology of individuals through to that of colonies, and ultimately to interaction networks, progressively eroding the reliability and stability of ecological interaction; erosion of interaction quality, rather than species loss per se, is likely the first indication of the decline of a pollination system.

There has been much research into the decline in pollinators, however, the majority of studies have focused on either individual stressors or individual biological levels. While these studies have helped us to understand how to understand how mechanisms impact the demise of flowers, the reason that pollinators seem to have resiliency until they collapse are not well defined in most literature. There is now growing evidence that ecosystems approach critical thresholds where continued stress disrupts the stabilizing feedback mechanisms in that ecosystem. As a result, abrupt changes occur in the system, rather than gradual changes (Scheffer, et al., 2009; Dakos, et al., 2015). Therefore, the resiliency of the system will be determined by the structure of interaction networks (Bascompte & Jordano, 2007).

Pollination networks consist of a mixture of strong and weak interactions, such that weak links have a disproportionate role in promoting flexibility and buffering capacity (Memmott et al., 2004). Under compounded stress conditions, weak, context-dependent interactions are lost first, leading to continued loss of interactions, network simplification, and increasing dependence on a small number of highly connected species. This reorganization may sustain pollination function temporarily, even as it increases vulnerability by weakening alternative pathways for reassembly of interaction. This shift from redundancy-dependent to hub-dependent networks is a key component of the transition from resilient to fragile state.

This chapter adopts a systems perspective that connects Anthropocene stressors, sublethal impairment, network reconfiguration, and threshold dynamics across biological and spatial scales. Interacting pressures are treated not as isolated drivers but as forces that may converge through shared mechanistic pathways, progressively reducing buffering capacity and moving pollination systems toward critical thresholds. The framework also emphasizes early-warning indicators—including critical slowing down, increasing variability in interaction strength, and selective loss of weak links—and considers how threshold-sensitive management could help sustain pollination services under rapid global change.

The conceptual pathway developed throughout the chapter is summarized in Figure 1: interacting Anthropocene stressors progressively erode interaction diversity and functional redundancy, driving the transition from resilient plant–pollinator networks toward simplified, hub-dependent, and increasingly fragile network structures.

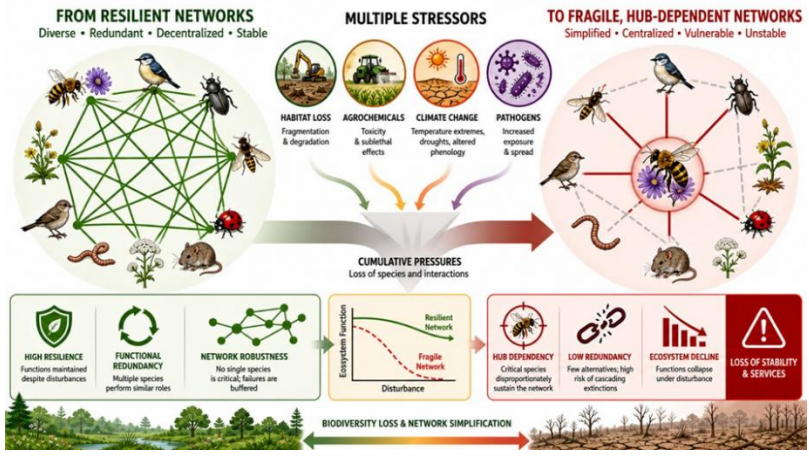


Figure 1. Conceptual Framework Illustrating the Transition from Resilient Plant–Pollinator Networks to Simplified, Hub-Dependent, and Increasingly Fragile Networks Under Interacting Anthropocene Stressors

2. ANTHROPOCENE STRESSORS DRIVING POLLINATION-SYSTEM DEGRADATION

Pollination systems in the Anthropocene are faced with multiple interacting stressors that operate across biological and spatial scales. While each stressor can operate on its own, the effects of multiple stressors are rarely straightforward and are often nonlinear and synergistic, if mediated through overlapping physiological and behavioural pathways. Rather than catastrophically collapsing, cumulative pressures debilitate system stability, ultimately leading to increased sensitivity over time.

The magnitude and direction of multiple stressor effects can be highly context dependent and vary with climate, landscape structure, and management practices (see Supplementary Text S2).

2.1 Habitat Loss, Fragmentation, and Land-Use Simplification

Habitat loss and landscape fragmentation constitute some of the most widespread drivers of pollination decline. The loss of semi natural habitat in favor of intensive agricultural or urban systems depletes availability of diverse floral resources, nesting sites, and movement corridors (Nicholls & Altieri, 2013; Blaauw & Isaacs, 2014; Kennedy et al., 2013; Senapathi et al., 2017). Fragmented landscapes undercut foraging ranges and elicit the loss of specialist and low-frequency interactions and, thus, overall reduce connectance, increasing modular isolation. These structural changes limit both buffering capacities and push the foraging around boundaries of energetics (Hannon & Sisk, 2009). Importantly, simplified landscapes also act to synchronize exposure to other stressors.

2.2 Agrochemical Exposure and Sublethal Disruption

Agrochemical exposure is a ubiquitous stressor that primarily affects pollinators through sublethal pathways. Insecticides, fungicides, and herbicides impair learning, navigation, and foraging efficiency at concentrations that do not cause immediate mortality (Gill et al., 2012; Siviter et al., 2018; Siviter et al., 2021). These impairments reduce interaction fidelity and increase temporal variability in visitation patterns, weakening network stability. Agrochemical effects are highly context-dependent, often interacting synergistically with nutritional stress and pathogen pressure to disrupt detoxification and immune pathways (Alaux et al., 2010; Doublet & Paxton, 2019; Carniel et al., 2024; Doublet et al., 2015; Brook et al., 2008).

2.3 Climate Change, Phenological Mismatch, and Extremes

Climate change acts as both direct driver and as a force multiplier for pollination decline. Rapid changes in temperature and precipitation regimes can disrupt synchrony between plant and pollinators leading to more inefficient interactions (Memmott et al., 2007; Kerr et al., 2015). Climatic stress further

increases energetic ontogeny and reduces tolerance for additional pressures potentiating effects of agrochemicals, nutritional limitation and pathogens (Tewksbury et al., 2002; Requier et al., 2024). Extreme events further exacerbate by disrupting synchronizing disturbances across scales.

2.4 Pathogens, Parasites, and Nutritional Stress

In organisms, pathogens and parasites impose a chronic cost to physiology that decreases life expectancy, foraging efficiency and colony performance at large (Genersch, 2010). These constraints are exacerbated when bundled with nutritional lack and exposure to chemicals, compromising immune and detoxifying systems (Di Pasquale et al., 2016; Nazzi & Pennacchio, 2014; Motta et al., 2024). Reduced dietary diversity in simplified landscapes limits resiliency still further, leading to vulnerability towards diseases and chemical exposures: at network level interaction diversity are decreased and so recovery impedance increases, along with vulnerability to the same chronic stressors noted above.

3. FROM INDIVIDUAL STRESS TO ECOSYSTEM-LEVEL DYSFUNCTION

Though acting independently environmental stressors can do this by accessing common mechanistic pathways that provide connective tissue between impaired levels of individual organisms to the biological processes of groups of individuals. This is leading to nonlinear cumulative responses by individuals to environmental disturbance through the simultaneous exposure of individuals to different environmental stressors and rapid approach to critical ecological thresholds. The physiological convergence of multiple stressors on neural, metabolic and immune systems illustrate how the exposure of individuals to discrete stressors will have cumulative effects on individual organisms. All of these physiological processes become impaired with exposure of individuals to multiple stressor types. (See Supplemental File S1).

3.1 Behavioural and Physiological Impairment

Transient effects of sublethal stressor exposure on cognition, navigation, and foraging behaviour compromises the reliability of interaction between individuals. When simultaneous exposure to agrochemical, thermal stress, nutritional limitations, and pathogens result in disruption of sensory processing and decision-making (Gill et al., 2012; Siviter et al., 2021; Kerr et al., 2015; Requier et al., 2024) individuals engage in less effective foraging behaviour and also experience a higher mean in their visitation pattern. While these transient sub-lethal stressor exposures are unlikely to lead to mortality, they thereby compromise the quality of interaction between individuals and lead to early stages of functional degradation.

3.2 Detoxification Overload and Impaired Immune Defences

The physiological pathways for detoxification and immune function are impaired through the convergence of multiple stressors. The detoxification of agrochemicals depends on common enzymatic systems which become overloaded with exposure to repeated and/or combined exposures to agrochemicals (Carniel et al., 2024) i.e. agrochemicals spatially compete for access. Nutritional limitations restrict access to the essential building blocks for detoxification and immune systems, while the competing presence of the pathogen system increases its energy demand (Di Pasquale et al., 2016; Genersch, 2010; Doublet et al., 2015; Nazzi & Pennacchio, 2014). All of these interactions give rise to synergistic effects that compound the effects of the individual stressors.

3.3 Declining Interaction Strength and Functional Redundancy

At the level of networks, sublethal impairment leading to impaired interaction strength and selective loss of weak links occurs with greater frequency. All of the inter-networks weak links are essential to both buffering capacity and flexibly permitting the reorganizing of the network following disturbance (Memmott et al., 2004; Bascompte & Jordano, 2007). Jointly with this functional capital to reorganize, the loss of those weak links will work to simplify the structure of the network leading to increased dependencies on smaller number of species that are highly connected (Albrecht et al., 2012; Kaiser-Bunbury et al., 2017).

4. POLLINATION NETWORKS UNDER COMPOUNDED STRESS

Rather than immediate collapse, pollination networks tend to reorganize structure in response to accumulating interacting stressors - these changes will alter interaction patterns, reduce redundancy, and make the entire system more vulnerable to further disruption (Memmott et al., 2004; Bascompte & Jordano, 2007).

4.1 Selective Loss of Weak Links

Increasing stress tends to preferentially lose weak and context dependent components of networks, species specific interactions which contribute less to immediate output but are critical for network flexibility and redundancy (Fenster et al., 2004; Memmott et al., 2004; Bascompte & Jordano, 2007). Their removal limits the capacity for adaptive rewiring and ecosystemic restoration (Albrecht et al., 2012; Kaiser-Bunbury et al., 2017).

4.2 Increasing Asymmetry and Hub Dependence

With species loss, networks become more asymmetric, dominated by species generalists, hub species, which may retain connectivity short-term, but rather functional dependency is more increased making the system riskier (Bascompte

& Jordano, 2007; Tylianakis et al., 2010). Failure of a single hub species can thus have cascading effects (Memmott et al., 2004).

4.3 Fragmentation, Modularity, and Declining Buffering Capacity

Compounded anthropogenic stress can alter network modularity by increasing fragmentation and decreasing connectance between modules. Moderate modularity tends to localize disturbance, but excessive fragmentation limits recolonization and recovery (Dunne et al., 2002; Olesen et al., 2007; Fortuna et al., 2010). Altered connectance between modules degrades buffering capacity and increases local risk of cascading failure pushing the system toward critical states (Kaiser-Bunbury et al., 2017; Scheffer et al., 2009; Dakos et al., 2015).

5. NONLINEAR DYNAMICS AND ECOLOGICAL TIPPING POINTS

Pollination systems exposed to interacting Anthropocene stressors will not exhibit linear decline, rather they will approach a critical threshold and then functional collapse (Scheffer et al., 2009, Dakos et al., 2015). These dynamics stem from progressive loss of buffer capacity than immediate species loss. These nonlinear dynamics are easily cast in the vernacular of transition between alternative states - of which we have varying degrees of proof across several systems. Gradual degradation leads to abrupt shifts across a threshold (Figure 2).

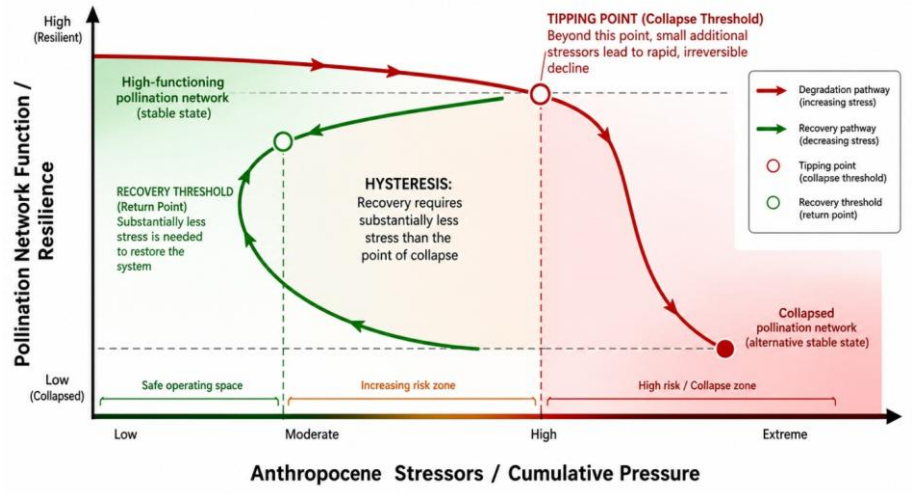


Figure 2. Conceptual Representation of Threshold Dynamics and Hysteresis in Pollination Systems Under Increasing Cumulative Anthropocene Pressure

Figure 2 illustrates a central implication of threshold dynamics: apparent stability can persist while underlying resilience is eroded. Once a tipping point is crossed, a comparatively small additional perturbation may produce disproportionate functional decline. The recovery trajectory may differ from the

degradation trajectory, illustrating hysteresis and the importance of preventing threshold crossings.

5.1 Gradual Degradation versus Abrupt Collapse

Systems may still appear to function under continued stress, although the quality of interactions have collapsed. Sublethal degradation reduces function without triggering an immediate collapse (so called hidden degradation). As the system loses its buffering capacity under an ever-increasing stress load, small perturbations to the system lead to disproportionately greater losses of function. The system suddenly collapses, after being in a state of stable apparent function (Scheffer et al., 2009; Dakos et al., 2015).

5.2 Critical Thresholds and Stability Landscapes

Critical thresholds appear when reductions in redundancy, connectedness or interaction diversity gradually constrain the flexibility of systems. The system (now with these properties) sits in an ever increasingly shallow 'basin' of state space (Bascompte & Jordano, 2007, loosely speaking) and degrades. Collapse (thus) occurs not due to the action of individual stressors, but as a consequence of changing structure of interaction networks through cumulative pressure being applied to the network.

5.3 Hysteresis and Limits of Recovery

Recovery from collapse does not follow the same route as degradation. Instead, a state of hysteresis can result in loss of a trajectory between biological states (Scheffer et al., 2009). Returning to pre-collapse environmental conditions may not restore network structure or function, as well-connected species may be lost; the species pool is reduced; key interactions lost; or connectivity lost. Following collapse recovery may be slower, more uncertain and/or more reliant on active restoration, rather than just removal restoration (Bascompte & Jordano, 2007).

6. EARLY-WARNING SIGNALS OF POLLINATION-SYSTEM COLLAPSE

As pollination systems near danger limits, warnings appear indicating that instability is decreasing—perhaps even before the cliff face comes into view. The cure interface lies here. New AI-supported monitoring systems or automated insect detection may improve our ability to catch warning signals in space before functional collapse becomes registerable (Ratnayake et al., 2021; Brandt et al., 2024).

6.1 Critical Slowing Down and Increased Variability

Critical slowing down (CSD) reflects waning resilience, manifesting typically as slower recovery post perturbation. CSD among pollination networks could

arise as delayed recovering visitation rates, increased variability of interaction strength, protracted instability following disturbance, etc. A self-evident increase in temporal variance and autocorrelation displays waning stabilizing feedbacks and a reducing buffering capacity (Dakos et al., 2015).

6.2 Structural Indicators of Instability

Changes in network structure also project early warnings, as changes in topology indicate declining redundancy and increasing vulnerability. Loss of connectivity, greater constancy of species roles (asymmetric networks), dependence on a larger number of hubs are attributes of more jeopardized networks (Bascompte & Jordano, 2007; Memmott et al., 2004; Olesen et al., 2007). Growing PCR (patch-coupling redundancy) ultimately precludes redistribution of interactions.

6.3 Loss of Weak Interactions as a Leading Indicator

Loss of weakness represents the growing tendency of ecological networks towards their constraints or bumps, and their terms for reorganizing without functional loss (Memmott et al., 2004; Bascompte & Jordano, 2007). The fact that even in the absence of extinction systems losing weak links are less able to recover has been documented (Albrecht et al., 2012; Kaiser-Bunbury et al., 2017).

7. Cross-Scale Coupling and Systemic Risk

Amplification of threshold dynamics in pollination systems occur through cross-scale interactions linking local disturbances to landscape- and regional-scale landscape instability (Levin, 1992; Peterson et al., 1998). These processes shortcut transitions throughout the system towards the critical thresholds.

7.1 From Impairment to Instability

Sublethal stress at the individual and colony level reduces foraging efficiency and reliability of interactions, diminishing workforce capacity (Dolezal & Toth, 2018; Nazzi & Pennacchio, 2014). If these impairments are spread among a multitude of colonies, this weakens network nodes and reduces opportunities for compensatory interaction, allowing a local disturbance to accrue through interaction networks (Newman, 2002).

7.2 Landscape Synchronization and Amplification

The spectral structure of the landscape determines whether local disturbances are attenuated or scaled up. Habitat fragmentation, simplification, and homogenization of land use and management synchronizes exposure to stressors, limiting natural spatial buffering (Blaauw & Isaacs, 2014; Kennedy et al., 2013; Senapathi et al., 2017). Climate extremes accentuate these effects by imposing simultaneous pressure on actors across regions, limiting recovery opportunities and hastening threshold dynamics (Dakos et al., 2015).

7.3 Migratory Beekeeping and Systemic Coupling

Migratory beekeeping knot together geographically distinctive systems exposing them to synchronized exposure to agrochemicals, pathogens, and climatic stress (Nazzi et al., 2012). Whilst directly advantageous to agricultural production, such coupling reduces spatial independence of pollination networks, facilitating their exposure to stressors through exposure to stressors in neighboring systems. Coupling between the wild and managed further accelerates these effects (Doublet et al., 2015; Motta et al., 2024).

8. RESILIENCE AS AN EMERGENT PROPERTY OF POLLINATION NETWORKS

Resilience of pollination systems does not derive from individual species persistence alone; it emerges as a property of the interaction network. Preserving pollination services in the Anthropocene requires maintaining redundancy, connectivity and adaptive capacity at multiple scales.

8.1 Functional Redundancy and Adaptive Capacity

"Functional redundancy", multiple species performing similar functional roles, allows networks to maintain a compensatory pollination function in response to disturbance (Bascompte & Jordano, 2007; Memmott et al., 2004). Weak, context-dependent action at any time between particles enhances this redundancy via alternative routes for reassigning interaction, reducing adaptive capacity and resilience (Olesen et al., 2007).

8.2 Connectivity and Redistribution of Pressures

Restoration of pollination can be accomplished by sufficient connectivity between species and landscape patches so as to redistribute or recruit pairs of interacting species across patches after disturbance. Maintaining habitat heterogeneity and movement corridors supports dispersal, and sufficient floral diversity promotes buffering diversity and capacity. High specialization reduces the acquisition of plants into the network (Fortuna et al., 2010).

9. THRESHOLD-AWARE MANAGEMENT OF POLLINATION SYSTEMS

Management strategies also need to move toward "Threshold Aware" management strategies away from single-stressor mitigation. Strategies should aim toward minimizing synchronized exposure to stressors, maintaining interaction diversity, avoiding loss of weak links. In agricultural scenarios, that means reducing unnecessary agrochemical exposure while improving nutritional resources and maintaining spatially distributed foraging opportunities.

9.1 Integrated Management across Scales

Threshold dynamics are amplified through cross-scale coupling, thus management at the colony level without addressing their coupling with landscape drivers may be insufficient to prevent collapse. A typological approach is needed for "networking" management based upon restoration and reconstruction of both ecological, agricultural and policy dimensions of these multiple feedback loops further threaten collaborative logistic support for pollination services among "a global attempt to bring the world together" (Cash et al., 2003; Cohen, 2020).

9.2 Tipping-Point Management for Pollination Resilience

Pollinator conservation has thus far been mainly focused on reducing individual stressors in isolation without consideration of their interaction. There is now growing evidence that pollination decline arises from interacting pressures for which the full set of pressures should be treated as a coupled system. Through nonlinear dynamics and threshold effects the interaction network itself undergoes structural degradation (Kéfi et al., 2016; Montoya et al., 2018; Dakos et al., 2019). Effective management, therefore, must be based on an integrated threshold-aware framework focusing on the fidelity of interaction networks rather than treating individual stressors.

9.3 Pollinator-Safe Pest Management and Reduction of Sublethal Risk

The sublethal impairment of pollinators with possible subsequent effects on behaviors, cognition and immune functions has been shown to be frequently associated with exposure to agrochemicals (Henry et al., 2012; Stanley et al., 2015; Sánchez-Bayo & Wyckhuys, 2019). Movement toward pollinator-safe pest management will require efforts to reduce sublethal exposure via refined pesticide application rates, adjusted timing and frequency, and other alternative forms such as biological control that will disrupt pollination interactions less and make them more resilient in the face of agricultural intensification (Rundlöf et al., 2015; Goulson et al., 2015).

9.4 Maintaining Interaction Diversity and Weak Links

Weak and context-dependent interactions enhance the stability of ecological networks through flexibility and buffering (McCann et al., 1998; Bascompte & Jordano, 2007). Management strategies that create heterogeneity among habitats, species' assemblages and timing of resources can maintain a high diversity of interactions associated with relationship networks between plants and pollinators (Garibaldi et al., 2013; Kennedy et al., 2013). Retaining these weak links permits capacity rebuilding after disturbances are realized and reducing the probability of catastrophic system closure (Kaiser-Bunbury et al., 2017).

9.5 Coordinated Landscape-Level Management and Spatial Buffering

Pollination systems play out at multiple spatial scales, therefore local actions in themselves are inadequate. Actions culminating at the landscape level, or at least better-coordinated activities - are required to prevent the synchronous exposure of components to stressors, and a compounding of risk throughout the system. (Senapathi et al., 2017; Tscharntke et al., 2012). A focus on maintaining semi-natural habitats, establishment of ecological corridors, and diversification of land use to increase spatial buffering capacity, enhances resilience of individual pollinator networks (Kennedy et al., 2013; Dainese et al., 2019).

9.6 Managing Cross-Scale Coupling and Migratory Practices

Cross-scale coupling, particularly migration by beekeepers in search for overall agricultural "efficiency" and ensuing synchronized exposures to stressors throughout such systems increases systemic vulnerability (Aizen et al., 2018; Alger et al., 2019). Migration retains high agricultural productivity but also envelopes the pollinators so moved with cumulative accumulations of stressors and a pathogenic ward. Migratory routes should be spatially planned, alongside more stringent regulations of hive, and applied together to stronger biosecurity protocols (Goulson et al., 2015; Vanbergen & Incect Polinators Initiative, 2013).

9.7 Toward a Network-Based Governance Framework

Moving towards an informed shift in ideal governance, rather than place-seeking disposition. Relying on therefore avoid forcing pollination systems into distasteful forms. Linking environmental processes with agricultural practice and policy to sustain networks with redundancy, connective assets, and adaptive capacity, rather than placing emphasis solely on species presence (Garibaldi et al., 2019; IPBES, 2016; Dicks et al., 2016). Managing network structure rather than attempting to conserve species (Tylianakis et al., 2010; Kéfi et al., 2016), to avoid threshold crossing and facilitate ecosystem service delivery.

10. RESEARCH GAPS AND FUTURE DIRECTIONS

The framework synthesized here highlights several priorities for future research. First, studies should connect sublethal physiological and behavioural responses more directly to measurable changes in interaction strength, visitation reliability, network topology, and pollination function. This would help bridge the current separation between organism-level stress biology and network-level ecological assessment.

Second, multiple-stressor experiments and monitoring programs should be designed across spatial and temporal scales. The effects of agrochemicals, climate variability, pathogens, nutritional limitation, and habitat simplification are strongly context dependent; consequently, results obtained at a single biological

level or in a single landscape may not capture the conditions under which cumulative pressures become nonlinear.

Third, early-warning indicators require stronger empirical evaluation in pollination systems. Critical slowing down, increased temporal variance, changing interaction strength, declining connectivity, increasing hub dependence, and selective loss of weak interactions are promising signals, but their reliability should be tested across taxa, regions, and management contexts. Automated insect detection and AI-supported monitoring may expand the temporal and spatial resolution at which such signals can be observed (Ratnayake et al., 2021; Brandt et al., 2024).

Finally, management research should evaluate whether interventions that preserve interaction diversity, habitat heterogeneity, connectivity, and spatial buffering can measurably increase the distance between pollination systems and critical thresholds. Such work would shift the emphasis from documenting decline after it becomes visible to identifying and maintaining the ecological conditions that sustain resilience before collapse occurs.

11. CONCLUSIONS

Pollination decline in the Anthropocene is better understood as an emergent outcome of interacting stressors than as the simple sum of isolated pressures. Across biological and spatial levels, stressors can converge through shared physiological pathways, impair behaviour and energetic or immune performance, and reduce the reliability of ecological interactions. Because these changes may precede conspicuous losses of species or abundance, functional degradation can remain partly hidden until the system approaches a critical threshold.

The synthesis developed in this chapter places interaction-network structure at the centre of pollination resilience. The progressive erosion of weak and context-dependent interactions can diminish buffering capacity and opportunities for adaptive rewiring, while increasing asymmetry and dependence on highly connected species. A network may therefore retain apparent short-term function while becoming structurally more fragile and more susceptible to cascading failure under additional stress.

Threshold dynamics also imply that prevention and recovery are not equivalent. Hysteresis means that returning environmental pressure to a previous level may be insufficient to restore the former network state once interaction diversity, connectivity, or key functional relationships have been lost. This asymmetry strengthens the case for identifying early-warning signals and acting before critical thresholds are crossed.

Finally, local processes cannot be separated from landscape and regional context. Habitat simplification, synchronized agrochemical exposure, climatic extremes, and migratory beekeeping can reduce spatial buffering and amplify risk

across scales. A threshold-aware approach to pollination resilience should therefore integrate pollinator-safe pest management, nutritional-resource enhancement, habitat heterogeneity, landscape connectivity, biosecurity, and coordinated governance. The central management objective is not merely to preserve individual species, but to maintain the diversity, redundancy, connectivity, and adaptive capacity of the interaction networks on which pollination services depend.

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REFERENCES

Aizen, M.A., Arbetman, M.P., Chacoff, N.P., Chalcoff, V.R., Feinsinger, P., Garibaldi, L.A., Harder, L.D., Morales, C.L., Sáez, A., & Vanbergen, A.J. (2020). Invasive bees and their impact on agriculture. Advances in Ecological Research. 63: 49–92. https://doi.org/10.1016/bs.aecr.2020.08.001.

Alaux, C., Brunet, J.L., Dussaubat, C., Mondet, F., Tchamitchian, S., Cousin, M., & Le Conte, Y. (2010). Interactions between Nosema microsporidia and a neonicotinoid weaken honeybees. Environmental Microbiology. 12(3): 774–782. https://doi.org/10.1111/j.1462-2920.2009.02123.x.

Albrecht, M., Schmid, B., Hautier, Y., & Müller, C.B. (2012). Diverse pollinator communities enhance plant reproductive success. Proceedings of the Royal Society B: Biological Sciences. 279(1748): 4845–4852. https://doi.org/10.1098/rspb.2012.1621.

Alger, S.A., Burnham, P.A., Boncristiani, H.F., & Brody, A.K. (2019). RNA virus spillover from managed honeybees to wild bumblebees: A network perspective. Ecology Letters. 22(3): 447–457. https://doi.org/10.1111/ele.13194.

Bascompte, J., & Jordano, P. (2007). Plant–animal mutualistic networks: The architecture of biodiversity. Annual Review of Ecology, Evolution, and Systematics. 38: 567–593. https://doi.org/10.1146/annurev.ecolsys.38.091206.095818.

Blaauw, B.R., & Isaacs, R. (2014). Larger patches of diverse floral resources increase insect pollinator density and diversity. Basic and Applied Ecology. 15(8): 701–711. https://doi.org/10.1016/j.baae.2014.10.001.

Brandt, A., Johnson, L., & Miller, R. (2024). Deep learning for automated insect monitoring in agricultural landscapes. Ecological Informatics. 82: 102323. https://doi.org/10.1016/j.ecoinf.2024.102323.

Brook, B.W., Sodhi, N.S., & Bradshaw, C.J.A. (2008). Synergies among extinction drivers under global change. Trends in Ecology & Evolution. 23(8): 453–460. https://doi.org/10.1016/j.tree.2008.03.011.

Carniel, Q., Silva, F., & Barros, A.T. (2024). Synergistic toxicity of fungicides and insecticides to pollinators. Environmental Pollution. 334: 122243. https://doi.org/10.1016/j.envpol.2024.122243.

Cash, D.W., Clark, W.C., Alcock, F., Dickson, N.M., Eckley, N., Guston, D.H., Jäger, J., & Mitchell, R.B. (2003). Knowledge systems for sustainable development. Proceedings of the National Academy of Sciences of the United States of America. 100(14): 8086–8091. https://doi.org/10.1073/pnas.1231332100.

Dainese, M., Martin, E.A., Aizen, M.A., Albrecht, M., Bartomeus, I., Bommarco, R., Carvalheiro, L.G., Chaplin-Kramer, R., Gagic, V., Garibaldi, L.A., Ghazoul, J., Grab, H., Jonsson, M., Karp, D.S., Kennedy, C.M., Kleijn, D., Kremen, C., Landis, D.A., Letourneau, D.K., & Steffan-Dewenter, I. (2019). A global synthesis reveals biodiversity-mediated benefits for crop production. Science Advances. 5(10): eaax0121. https://doi.org/10.1126/sciadv.aax0121.

Dakos, V., Carpenter, S.R., van Nes, E.H., & Scheffer, M. (2015). Resilience indicators: Prospects and limitations. Ecology Letters. 18(3): 269–282. https://doi.org/10.1098/rstb.2013.0263.

Dakos, V., Matthews, B., Hendry, A.P., Levine, J.M., Loeuille, N., Norberg, J., Nosil, P., Scheffer, M., & De Meester, L. (2019). Ecosystem tipping points in an evolving world. Nature Ecology & Evolution. 3(3): 355–362. https://doi.org/10.1038/s41559-019-0797-2.

Di Pasquale, G., Alaux, C., Le Conte, Y., & Odoux, J.F. (2016). Variations in pollen diversity and nutrition quality. Proceedings of the National Academy of Sciences of the United States of America. 113(28): 8206–8211. https://doi.org/10.1073/pnas.1603170113.

Dicks, L.V., Breeze, T.D., Ngo, H.T., Senapathi, D., An, J., Aizen, M.A., Basu, P., Buchori, D., Galetto, L., Garibaldi, L.A., Gemmill-Herren, B., Howlett, B.G., Imperatriz-Fonseca, V.L., Johnson, S.D., Kovács-Hostyánszki, A., Kwon, Y.J., Lattorff, H.M.G., Lungharwo, T., Seymour, C.L., Vanbergen, A.J., & Potts, S.G. (2021). A global-scale expert assessment of drivers and risks associated with pollinator decline. Nature Ecology & Evolution. 5(10): 1453–1461. https://doi.org/10.1038/s41559-021-01534-9.

Dolezal, A.G., & Toth, A.L. (2018). Feedbacks between nutrition and disease in honey bee health. Current Opinion in Insect Science. 26: 114–119. https://doi.org/10.1016/j.cois.2018.02.006.

Doublet, V., & Paxton, R.J. (2019). Interactions between pesticides and pathogens. Global Change Biology. 25(3): 1026–1035. https://doi.org/10.1111/gcb.14536.

Doublet, V., Labarussias, M., de Miranda, J.R., Moritz, R.F.A., & Paxton, R.J. (2015). Bees under stress. Proceedings of the National Academy of Sciences of the United States of America. 112(30): 9079–9084. https://doi.org/10.1073/pnas.1503530112.

Dunne, J.A., Williams, R.J., & Martinez, N.D. (2002). Network structure and biodiversity loss in food webs: Robustness increases with connectance. Ecology Letters. 5(4): 558–567. https://doi.org/10.1046/j.1461-0248.2002.00354.x.

Fenster, C.B., Armbruster, W.S., Wilson, P., Dudash, M.R., & Thomson, J.D. (2004). Pollination syndromes and floral specialization. Annual Review of Ecology,

Evolution, and Systematics. 35: 375–403. https://doi.org/10.1146/annurev.ecolsys.34.011802.132347.

Fortuna, M.A., Stouffer, D.B., Olesen, J.M., Jordano, P., Mouillot, D., Krasnov, B.R., & Poulin, R. (2010). Nestedness vs modularity in ecological networks. Journal of Animal Ecology. 79(4): 811–817. https://doi.org/10.1111/j.1365-2656.2010.01685.x.

Garibaldi, L.A., Pérez-Méndez, N., Garratt, M.P.D., Gemmill-Herren, B., Miguez, F.E., & Dicks, L.V. (2019). Policies for ecological intensification of crop production. Global Food Security. 22: 1–10. https://doi.org/10.1016/j.gfs.2019.06.003.

Garibaldi, L.A., Steffan-Dewenter, I., Winfree, R., Aizen, M.A., Bommarco, R., Cunningham, S.A., Kremen, C., Carvalheiro, L.G., Harder, L.D., Afik, O., Bartomeus, I., Benjamin, F., Boreux, V., Cariveau, D., Chacoff, N.P., Dudenhöffer, J.H., Freitas, B.M., Ghazoul, J., Greenleaf, S., & Klein, A.M. (2013). Wild pollinators enhance fruit set of crops regardless of honey bee abundance. Science. 339(6127): 1608–1611. https://doi.org/10.1126/science.1230200.

Genersch, E. (2010). Honeybee pathology: Current threats to honeybees and beekeeping. Veterinary Quarterly. 30(1): 1–14. https://doi.org/10.1080/01652176.2010.9694426.

Gill, R.J., Ramos-Rodriguez, O., & Raine, N.E. (2012). Combined pesticide exposure severely affects individual- and colony-level traits in bees. Nature. 491: 105–108. https://doi.org/10.1038/nature11585.

Goulson, D., Nicholls, E., Botías, C., & Rotheray, E.L. (2015). Bee declines driven by combined stress from parasites, pesticides, and lack of flowers. Science. 347(6229): 1255957. https://doi.org/10.1126/science.1255957.

Hannon, S.J., & Sisk, T.D. (2009). Hedgerows in an agricultural landscape. Landscape Ecology. 24(7): 843–858. https://doi.org/10.1007/s10980-009-9357-1.

Henry, M., Béguin, M., Requier, F., Rollin, O., Odoux, J.F., Aupinel, P., Aptel, J., Tchamitchian, S., & Decourtye, A. (2012). A common pesticide decreases foraging success and survival in honey bees. Science. 336(6079): 348–350. https://doi.org/10.1126/science.1215039.

Kaiser-Bunbury, C.N., Mougal, J., Whittington, A.E., Valentin, T., Gabriel, R., Olesen, J.M., Blüthgen, N., & Ghazoul, J. (2017). Ecosystem restoration strengthens pollination network resilience. Nature. 542: 223–227. https://doi.org/10.1038/nature21071.

Kéfi, S., Miele, V., Wieters, E.A., Navarrete, S.A., & Berlow, E.L. (2016). How structured is the entangled bank? The surprisingly simple organization of

multiplex ecological networks. Ecology Letters. 19(5): 584–593. https://doi.org/10.1111/ele.12598.

Kennedy, C.M., Lonsdorf, E., Neel, M.C., Williams, N.M., Ricketts, T.H., Winfree, R., Bommarco, R., Brittain, C., Burley, A.L., Cariveau, D., Carvalheiro, L.G., Chacoff, N.P., Cunningham, S.A., Danforth, B.N., Dudenhöffer, J.H., Elle, E., Gaines, H.R., Garibaldi, L.A., Gratton, C., & Kremen, C. (2013). A global quantitative synthesis of local and landscape effects on wild bee pollinators in agroecosystems. Ecology Letters. 16(5): 584–599. https://doi.org/10.1111/ele.12082.

Kerr, J.T., Pindar, A., Galpern, P., Packer, L., Potts, S.G., Roberts, S.M., Rasmont, P., Schweiger, O., Colla, S.R., Richardson, L.L., Wagner, D.L., Gall, L.F., Sikes, D.S., & Pantoja, A. (2015). Climate change impacts bumblebees converge across continents. Science. 349(6244): 177–180. https://doi.org/10.1126/science.aaa7031.

Klein, A.M., Vaissière, B.E., Cane, J.H., Steffan-Dewenter, I., Cunningham, S.A., Kremen, C., & Tscharntke, T. (2007). Importance of pollinators in changing landscapes for world crops. Proceedings of the Royal Society B: Biological Sciences. 274(1608): 303–313. https://doi.org/10.1098/rspb.2006.3721.

Levin, S.A. (1992). The problem of pattern and scale in ecology. Ecology. 73(6): 1943–1967. https://doi.org/10.2307/1941447.

Lin, Y., Wu, P., & Tsai, C. (2024). Climate-driven phenological mismatch reshapes plant–pollinator networks. Global Change Biology. 30(2): e16812. https://doi.org/10.1111/gcb.16812.

McCann, K.S., Hastings, A., & Huxel, G.R. (1998). Weak trophic interactions and the balance of nature. Nature. 395(6704): 794–798. https://doi.org/10.1038/27427.

Memmott, J., Craze, P.G., Waser, N.M., & Price, M.V. (2007). Global warming and the disruption of plant–pollinator interactions. Ecology. 88(6): 1569–1578. https://doi.org/10.1890/06-0847.

Memmott, J., Waser, N.M., & Price, M.V. (2004). Tolerance of pollination networks to species extinctions. Ecology Letters. 7(6): 512–521. https://doi.org/10.1111/j.1461-0248.2004.00611.x.

Montoya, J.M., Donohue, I., & Pimm, S.L. (2018). Planetary boundaries for biodiversity: Implausible science, pernicious policies. Trends in Ecology & Evolution. 33(2): 71–73. https://doi.org/10.1016/j.tree.2017.12.004.

Motta, E.V.S., Raymann, K., & Moran, N.A. (2024). Glyphosate perturbs the gut microbiota of honeybees. Environmental Health Perspectives. 132(1): 017004. https://doi.org/10.1073/pnas.1803880115.

Nazzi, F. & Pennacchio, F. (2014). Disentangling multiple interactions in the hive ecosystem. Trends in Parasitology. 30(12): 556–561. https://doi.org/10.1016/j.pt.2014.09.006.

Nazzi, F., Brown, S.P., Annoscia, D., Del Piccolo, F., Di Prisco, G., Varricchio, P., Della Vedova, G., Cattonaro, F., Caprio, E., & Pennacchio, F. (2012). Synergistic parasite–pathogen interactions mediated by host immunity can drive the collapse of honeybee colonies. PLoS Pathogens. 8(6): e1002735. https://doi.org/10.1371/journal.ppat.1002735.

Nicholls, C.I., & Altieri, M.A. (2013). Plant biodiversity enhances bees and other insect pollinators. Agriculture, Ecosystems & Environment. 166: 128–136. https://doi.org/10.1016/j.agee.2012.10.007.

Olesen, J.M., Bascompte, J., Dupont, Y.L., & Jordano, P. (2007). The modularity of pollination networks. Proceedings of the National Academy of Sciences of the United States of America. 104(50): 19891–19896. https://doi.org/10.1073/pnas.0706375104.

Ollerton, J., Winfree, R., & Tarrant, S. (2011). How many flowering plants are pollinated by animals? Annals of Botany. 108(3): 467–476. https://doi.org/10.1093/aob/mcr155.

Peterson, G.D., Allen, C.R., & Holling, C.S. (1998). Ecological resilience, biodiversity, and scale. Ecosystems. 1(1): 6–18. https://doi.org/10.1007/s100219900002.

Potts, S.G., Imperatriz-Fonseca, V.L., Ngo, H.T., Biesmeijer, J.C., Breeze, T.D., Dicks, L.V., Garibaldi, L.A., Hill, R., Settele, J., & Vanbergen, A.J. (2016). Safeguarding pollinators and their values to human well-being. Nature. 540(7632): 220–229. https://doi.org/10.1038/nature20588.

Ratnayake, A., Shimizu, K., & Saito, H. (2021). Automated insect detection using machine learning. Ecological Informatics. 61: 101209. https://doi.org/10.1016/j.ecoinf.2021.101209.

Requier, F., Deguines, N., Garibaldi, L.A., & Steffan-Dewenter, I. (2024). Extreme climate events disrupt pollination services. Nature Climate Change. 14(1): 45–52. https://doi.org/10.1038/s41558-023-01840-6.

Rundlöf, M., Andersson, G.K.S., Bommarco, R., Fries, I., Hederström, V., Herbertsson, L., Jonsson, O., Klatt, B.K., Pedersen, T.R., Yourstone, J., & Smith, H.G. (2015). Seed coating with a neonicotinoid insecticide negatively affects wild bees. Nature. 521(7550): 77–80. https://doi.org/10.1038/nature14420.

Sánchez-Bayo, F., & Wyckhuys, K.A.G. (2019). Worldwide decline of the entomofauna: A review of its drivers. Biological Conservation. 232: 8–27. https://doi.org/10.1016/j.biocon.2019.01.020.

Scheffer, M., Bascompte, J., Brock, W.A., Brovkin, V., Carpenter, S.R., Dakos, V., Held, H., van Nes, E.H., Rietkerk, M., & Sugihara, G. (2009). Early-warning signals for critical transitions. Nature. 461(7260): 53–59. https://doi.org/10.1038/nature08227.

Scheffer, M., Carpenter, S., Foley, J.A., Folke, C., & Walker, B. (2001). Catastrophic shifts in ecosystems. Nature. 413(6856): 591–596. https://doi.org/10.1038/35098000.

Senapathi, D., Goddard, M.A., Kunin, W.E., & Baldock, K.C.R. (2017). Landscape impacts on pollinator communities. Journal of Applied Ecology. 54(6): 1949–1958. https://doi.org/10.1111/1365-2664.12899.

Siviter, H., Bailes, E.J., Martin, C.D., Oliver, T.R., Koricheva, J., Leadbeater, E., & Brown, M.J.F. (2021). Agrochemicals interact synergistically to increase bee mortality. Science. 372(6538): 326–330. https://doi.org/10.1126/science.abd5601.

Siviter, H., Brown, M.J.F., & Leadbeater, E. (2018). Sulfoxaflor exposure reduces bumblebee reproductive success. Nature. 561(7721): 109–112. https://doi.org/10.1038/s41586-018-0430-6.

Stanley, D.A., Garratt, M.P.D., Wickens, J.B., Wickens, V.J., Potts, S.G., & Raine, N.E. (2015). Neonicotinoid pesticide exposure impairs crop pollination services provided by bumblebees. Nature. 528(7583): 548–550. https://doi.org/10.1038/nature16167.

Tewksbury, J.J., Huey, R.B., & Deutsch, C.A. (2002). Putting the heat on tropical animals. Science. 298(5595): 1013–1017. https://doi.org/10.1126/science.1075632.

Tscharntke, T., Tylianakis, J.M., Rand, T.A., Didham, R.K., Fahrig, L., Batáry, P., Bengtsson, J., Clough, Y., Crist, T.O., Dormann, C.F., Ewers, R.M., Fründ, J., Holt, R.D., Holzschuh, A., Klein, A.M., Kleijn, D., Kremen, C., Landis, D.A., Laurance, W., & Westphal, C. (2012). Landscape moderation of biodiversity patterns and processes—eight hypotheses. Biological Reviews. 87(3): 661–685. https://doi.org/10.1111/j.1469-185X.2011.00216.x.

Tylianakis, J.M., & Morris, R.J. (2017). Ecological networks across environmental gradients. Trends in Ecology & Evolution. 32(7): 488–499. https://doi.org/10.1016/j.tree.2017.03.012.

Tylianakis, J.M., Laliberté, E., Nielsen, A., & Bascompte, J. (2010). Conservation of species interaction networks. Biological Conservation. 143(10): 2270–2279. https://doi.org/10.1016/j.biocon.2009.12.004.

Vanbergen, A.J., & Insect Pollinators Initiative (2013). Threats to an ecosystem service: Pressures on pollinators. Frontiers in Ecology and the Environment. 11(5): 251–259. https://doi.org/10.1890/120126.

CHAPTER 11

Value Creation in Agricultural Production and Türkiye

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1. Introduction

Agriculture continues to play a fundamental role in food security, rural livelihoods, employment, and economic development. However, the economic contribution of agriculture is determined not only by the quantity of agricultural products produced but also by the value created throughout the process from production to final consumption. Changes in consumer preferences, increasing competition in domestic and international markets, technological developments, and growing concerns over sustainability have made the creation of added value increasingly important for the agricultural sector. In this context, processing, quality improvement, product differentiation, certification, technological innovation, and effective marketing provide opportunities to transform agricultural products into outputs with higher economic and market value.

Agricultural added value should therefore be considered within a broader framework that includes not only economic returns but also technological development, resource use efficiency, sustainability, and the position of producers within value chains. This chapter examines the concept and determinants of agricultural added value, the main methods used to create added value, and the approaches used to measure it. It then discusses recent global trends in agricultural value creation, with particular emphasis on digitalization, innovation, sustainability, and value chain integration, before evaluating Türkiye's current position, potential, and key areas for further development. In doing so, the chapter provides an integrated perspective on how agricultural production can be transformed into higher and more sustainable value.

2.1. The Concept of Agricultural Added Value

The concept of added value refers to the additional economic value that a product or service gains during the production and marketing process. In general terms, added value is defined as the difference between the total value of the inputs used in producing a product and the market value of the final product. Today, however, added value is no longer considered solely as an economic indicator. It is viewed as a multidimensional concept that also includes improving product quality, processing, differentiation, adapting products to consumer expectations, and creating a higher perception of value in the market. Therefore, added value can be created not only at the production stage but throughout the entire process, beginning before production and continuing through processing, storage, packaging, logistics, and marketing (Cucagna & Goldsmith, 2018; Lu & Dudensing, 2015).

In the agricultural sector, the concept of added value has a broader meaning than in many other sectors. This is mainly because most agricultural products are produced under natural conditions, are perishable, and are often marketed as raw products. While raw agricultural products are generally marketed at relatively low economic value, processing, grading, packaging, meeting quality standards,

or differentiating these products according to consumer demand can significantly increase their economic value. Agricultural added value therefore refers not only to an increase in product price but also to the increase in the economic, functional, and perceived value of a product resulting from activities carried out throughout the production process (Başer & Bozoğlu, 2018; Coltrain et al., 2000).

While traditional economic approaches generally explain added value in terms of the difference between production costs and sales value, contemporary value oriented approaches also consider the benefits perceived by consumers as one of the main components of added value. From this perspective, an agricultural product gains value not only through improvements in its physical characteristics but also through intangible attributes such as reliable production, traceability, environmental sustainability, food safety, certification, product story, and consumer trust. Particularly in markets serving higher income consumer groups, growing demand for information about product origin, production methods, and environmental impacts has increased the importance of the social and environmental dimensions of added value alongside its economic dimension (Cucagna & Goldsmith, 2018; FAO, 2014).

Agricultural added value not only enables producers to generate higher incomes but also makes important contributions to rural development, employment creation, and the competitiveness of the agricultural sector. The development of new industries through the processing of agricultural products, increased employment opportunities in rural areas, and the revitalization of local economies are among the major economic effects of added value creation. In addition, activities that create added value support sustainable agricultural development by reducing product losses, improving resource use efficiency, and encouraging the wider adoption of innovative technologies in production processes (Devaux et al., 2018; Adanacıoğlu et al., 2018).

The literature indicates that agricultural added value can be created in various ways. Physical processing of products, improvement of quality attributes, adoption of differentiation practices such as geographical indications or organic production, use of modern packaging techniques, improvement of storage conditions, and development of direct marketing channels are among the main activities that create added value. In addition, the use of digital technologies, data driven production management, and product development strategies tailored to consumer demand are increasingly regarded as important tools for enhancing added value (Lu & Dudensing, 2015; Başer & Bozoğlu, 2018).

The creation of added value is not limited to the efforts of individual producers. When producer organizations, agro industrial enterprises, logistics companies, retailers, research institutions, and public policies are considered together, it becomes clear that agricultural added value is generated through a multi stakeholder process. Therefore, the contemporary approach to added value

creation is viewed not simply as a set of activities aimed at increasing product prices, but as an integrated management approach that generates economic, social, and environmental benefits throughout the entire process from production to final consumption (Porter, 1985; Trienekens, 2011; FAO, 2014).

In conclusion, agricultural added value is a multidimensional concept that extends beyond increasing the economic value of a product through activities carried out during the production process and also encompasses quality, reliability, sustainability, and consumer satisfaction. In today's agricultural sector, competitive advantage depends not only on producing more but also on creating greater added value from the products produced. Identifying the factors that influence agricultural added value is therefore essential for developing effective value creation strategies. In this context, the following section examines the determinants of agricultural added value in detail.

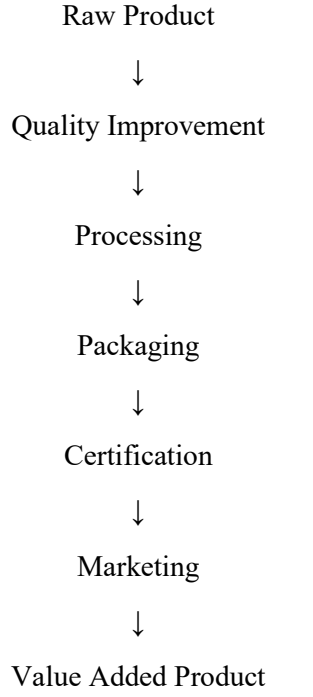


Figure 1. Transformation Process from a Raw Product to a Value Added Product

Source: Created by the authors.

These considerations show that agricultural added value does not arise solely from the physical characteristics of a product but results from the combined

influence of several factors, including quality, technology, organization, marketing, and consumer expectations. Therefore, increasing agricultural added value requires these factors to be addressed through an integrated approach. The following section examines in detail the main factors that determine agricultural added value.

2.2. Determinants of Agricultural Added Value

Agricultural added value is not determined by a single factor but results from the interaction of numerous complementary elements throughout the process from pre production activities to the final consumer. The factors determining the economic value of agricultural products in the market are not limited to production volume. Product quality, standardization, processing technologies, logistics infrastructure, certification systems, innovation capacity, and consumer expectations directly influence both the competitiveness and economic value of agricultural products. Therefore, strategies aimed at increasing agricultural added value should consider these factors not independently but as interconnected components of an integrated system (Lu & Dudensing, 2015; Cucagna & Goldsmith, 2018).

One of the main determinants of added value is product quality. The physical appearance, taste and aroma, nutritional value, shelf life, and food safety characteristics of agricultural products directly influence consumer purchasing decisions. Particularly in international markets, the growing importance of quality standards has made quality management necessary at every stage of the production process. High quality products can gain access to broader markets, command higher prices, and generate greater economic returns for producers. Quality is therefore regarded as one of the most fundamental determinants of agricultural added value (Başer & Bozoğlu, 2018).

Maintaining quality over time depends on the implementation of standardization and quality assurance systems. Classifying products according to specific quality criteria, standardizing postharvest practices, and ensuring compliance with national or international standards not only increase consumer confidence but also contribute to more effective marketing processes. Today, GLOBALG.A.P., organic farming certification, good agricultural practices, and various quality management systems have become important competitive tools, particularly in export oriented production. Standardized production systems also facilitate traceability practices and improve product reliability (Adanacıoğlu et al., 2018; FAO, 2014).

Another important determinant of added value is the level of processing and technological development. Marketing agricultural products in their raw form often generates relatively low economic returns, whereas processing expands their range of uses, extends shelf life, and enables the development of new products that respond to consumer demand. In addition, the use of modern

processing technologies helps reduce production losses, maintain product quality, and manage production costs more effectively. Particularly in the fruit, vegetable, dairy, and meat sectors, a well developed processing industry plays an important role in increasing agricultural added value (Al Hinai et al., 2022).

Technological developments are not limited to processing but also include the digitalization of production processes. Precision agriculture applications, sensor technologies, remote sensing systems, artificial intelligence based decision making tools, and data driven production management improve resource use efficiency while contributing to more sustainable management of production quality. The use of digital technologies also makes production processes more transparent, facilitates the implementation of quality standards, and enables producers to respond more rapidly to consumer demand. This demonstrates that added value is influenced not only by physical production activities but also by the effective use of information and technology (FAO, 2014; Trienekens, 2011).

Logistics and supply chain management are also important determinants of added value. Particularly for perishable products such as fresh fruits and vegetables, reducing postharvest losses, providing appropriate storage conditions, and developing effective cold chain practices make an important contribution to maintaining product quality. Delivering products to target markets at the right time and under appropriate conditions not only reduces economic losses but also increases consumer satisfaction and enhances the market value of the product (Gökkür & Çelik, 2016).

In recent years, changes in consumer behavior have also become increasingly influential in determining agricultural added value. Today, consumers are interested not only in affordable products but also in products that are safe, environmentally friendly, traceable, healthy, and produced using sustainable methods. This indicates that focusing solely on increasing production is no longer sufficient and that producers also need to develop production and marketing strategies that take consumer expectations into account. In particular, criteria such as environmental sustainability, animal welfare, carbon footprint, and ethical production have become important determinants of agricultural added value in developed markets (Cucagna & Goldsmith, 2018; FAO, 2014).

Institutional structure and organizational capacity are also among the key factors influencing the creation of added value. The effective functioning of producer organizations, stronger knowledge transfer between research institutions and producers, improved extension services, and public policies that support investments in value creation all make important contributions to increasing economic value in the agricultural sector. In value chains with strong institutional structures, information sharing is more effective, innovations are adopted more rapidly, and producers have greater bargaining power (Devaux et al., 2018).

In conclusion, agricultural added value is shaped by the combined influence of several factors, including quality, standardization, technology, processing capacity, logistics infrastructure, consumer expectations, and institutional structure. Although each of these factors is important in its own right, a sustainable increase in added value can only be achieved when they are managed as complementary components of an integrated system. Increasing added value in the agricultural sector therefore requires not only improvements in existing production processes but also the implementation of practices that enhance the economic value of agricultural products. In this context, the following section examines the main methods and practices used to create added value in the agricultural sector.

2.3. Methods of Creating Added Value in Agriculture

Increasing agricultural added value depends not only on increasing production but also on introducing innovative practices throughout the process from production to marketing. Today, agricultural enterprises that achieve competitive advantage are those that not only use natural resources more efficiently but also differentiate their products, improve quality standards, and adopt production models that respond to consumer expectations. Added value creation therefore refers to a wide range of activities that can be carried out at every stage of agricultural production. The literature indicates that the main methods of creating added value are centered around product processing, quality improvement, product differentiation, certification, digitalization, marketing strategies, and innovative production models (Lu & Dudensing, 2015; Cucagna & Goldsmith, 2018).

One of the most common ways of creating added value is the processing of agricultural products. Many agricultural products generate limited economic returns when marketed in their raw form, whereas processing expands their range of uses, extends their shelf life, and improves their marketability. Transforming fruits into juice or dried products, processing milk into products such as cheese and yogurt, or using olives to produce table olives and olive oil enables the same raw material to generate greater economic value. Processing activities not only increase the selling price of products but also contribute to the creation of new markets, the development of rural industries, and increased employment (Başer & Bozoğlu, 2018).

Product differentiation is another important strategy for increasing added value. Today, consumers seek not only products that meet their basic needs but also foods that can be distinguished from others by specific characteristics. Organic production, good agricultural practices, functional foods, local varieties, and products obtained through specialized production techniques are among the examples of such differentiation. Highlighting specific quality attributes strengthens consumers' perception of a product and can contribute to higher

market prices. Geographical indication products, in particular, can provide important economic benefits to both producers and regional economies through quality characteristics associated with a specific geographical area. However, a geographical indication alone is not sufficient to create added value. Its economic potential can be fully realized when it is supported by effective promotion, consistent quality, and appropriate marketing strategies.

Another important method is the effective implementation of quality management and certification systems. Production in compliance with food safety, traceability, and quality standards provides important competitive advantages, particularly for enterprises operating in international markets. GLOBALG.A.P., organic farming certification, good agricultural practices, and similar quality assurance systems increase consumer confidence and contribute to the marketing of products at higher economic value. Certification systems also enable production processes to be documented, helping to maintain consistent quality and improve export opportunities (FAO, 2014; Adanacıoğlu et al., 2018).

Technological developments have also become one of the main tools for creating added value. Precision agriculture applications, sensor technologies, remote sensing systems, artificial intelligence based decision making tools, and digital data management enable production processes to be managed more efficiently, reduce quality losses, and improve resource use efficiency. In addition, making production processes traceable through digital platforms contributes to greater consumer confidence and more effective marketing. Digital transformation in agriculture is therefore regarded not only as a technological investment that improves production efficiency but also as a strategic tool for increasing the added value of agricultural products in the market (Trienekens, 2011; FAO, 2014).

Marketing strategies and direct communication with consumers are also becoming increasingly important in creating added value. Alongside traditional marketing channels, e commerce platforms, direct producer to consumer sales models, digital marketing practices, and short supply chains increase producers' market visibility and reduce intermediary costs. Easier access to digital sales platforms, particularly for local producers, enables products to reach broader groups of consumers and can positively affect producer incomes. At the same time, effective packaging design, communicating the product story clearly, and building trust based relationships with consumers are among the factors that enhance the perceived value of a product.

Achieving a sustainable increase in added value requires strong cooperation among producer organizations, public institutions, research organizations, and the private sector. Improving producers' access to training, promoting the wider adoption of innovative technologies, expanding financing opportunities, and strengthening rural infrastructure contribute to the broader adoption of value

creating practices. In addition, stronger cooperation among universities, industry, and public institutions facilitates the transfer of research findings into practice and supports the wider adoption of innovative production models (Devaux et al., 2018).

In conclusion, creating added value in the agricultural sector is not limited to the physical processing of products. It is an integrated process that requires the combined implementation of complementary practices such as quality improvement, product differentiation, certification, digitalization, effective marketing, and institutional cooperation. Successful implementation of these practices makes an important contribution to increasing producer incomes, strengthening rural economies, and improving the competitiveness of the agricultural sector in national and international markets. However, the sustainable management of added value also requires these improvements to be assessed using measurable indicators. Therefore, the following section examines the main approaches and indicators used to measure agricultural added value.

2.4. Measurement of Agricultural Added Value

Developing effective strategies to increase agricultural added value first requires an accurate assessment of the existing level of added value. Therefore, measuring agricultural added value is considered important not only for evaluating enterprise performance but also for formulating agricultural policies, guiding investment decisions, and monitoring sectoral development. Today, added value indicators used by national and international organizations are among the main measures for assessing the contribution of the agricultural sector to economic growth (FAO, 2014; OECD, 2023).

From an economic perspective, added value refers to the economic value obtained by subtracting the value of intermediate inputs used in production from the total value of output generated during the production process. In other words, added value represents the new economic value created by an enterprise through its production activities. In the agricultural sector, this value includes not only revenue from product sales but also the economic contribution generated through quality enhancing practices, processing, storage, packaging, and marketing activities. In this respect, agricultural added value is considered an important indicator not only of production volume but also of the efficiency of the production process (Lu & Dudensing, 2015).

One of the most widely used indicators for assessing agricultural added value in the international literature is Gross Value Added (GVA). Gross value added is calculated by subtracting intermediate consumption costs from the total value of production generated within a given production process. This indicator is widely used to determine the contribution of the agricultural sector to the national economy and is also considered one of the main economic indicators used for comparisons across countries. Agricultural statistics published by the World

Bank, OECD, and FAO rely extensively on gross value added data when assessing sector performance.

In addition to gross value added, Net Value Added (NVA) also has an important place in economic analysis. Net value added is obtained by subtracting the consumption of fixed capital, or depreciation, from gross value added and provides a more detailed indication of the actual economic contribution generated by production activities. Particularly in long term investment analysis and the evaluation of enterprise performance, net value added can provide a more realistic assessment.

Economic indicators alone are no longer considered sufficient for evaluating added value. In recent years, criteria such as quality indicators, the degree of product differentiation, export performance, producer incomes, processing rates, postharvest losses, and marketing efficiency have also been taken into account. In particular, increases in the share of agricultural products that are processed, a greater proportion of high value added products in exports, and improvements in producer incomes are considered among the most important practical indicators of added value creation (Cucagna & Goldsmith, 2018; Başer & Bozoğlu, 2018).

With the development of digital technologies, the methods used to measure added value are also changing considerably. Big data analytics, digital record keeping systems, traceability applications, and decision support systems make it possible to monitor each stage of the production process in greater detail and to assess more accurately the economic contribution of activities that create added value. This contributes to the development of more informed agricultural policies not only at the enterprise level but also at regional and national levels.

In conclusion, the measurement of agricultural added value goes beyond determining the economic value created during the production process and provides an important analytical tool for assessing the competitiveness, sustainability, and economic efficiency of the agricultural sector. Evaluating economic, technical, and marketing indicators together, particularly gross and net value added, helps identify both the strengths of agricultural production systems and the areas that require further improvement. Regular measurement and monitoring of added value therefore have strategic importance for decision making at the enterprise level as well as for the formulation of national agricultural policies.

3. Global Trends and an Assessment from Türkiye's Perspective

3.1. Global Trends in Agricultural Added Value Creation

The global agricultural sector is gradually moving away from the traditional growth model based primarily on increasing production and toward a structure in which technology, knowledge, innovation, sustainability, and value chain integration play a more decisive role. Population growth, the increasing pressure

of climate change on agricultural production, limited natural resources, and changing consumer expectations make it necessary not only to improve productivity but also to generate greater economic, social, and environmental value per unit of production. This transformation means that agricultural added value creation is no longer confined to the production stage but has become an integrated process extending from production to processing, logistics, marketing, and final consumption (Sadovska et al., 2020).

One of the major global trends in agricultural added value creation is the movement of agricultural products beyond the primary production stage. Processing, grading, storage, packaging, and differentiation increase the economic value of agricultural products while also improving access to new markets. Differentiated production systems, such as organic production and good agricultural practices, also contribute to the development of products that respond to consumer expectations and can be marketed at higher values (Başer & Bozoğlu, 2018). Agricultural competitiveness today is therefore closely related not only to production volume but also to the extent to which production can be integrated with the subsequent stages of the value chain.

One of the most important developments accelerating this transformation in recent years has been the digitalization of the agricultural sector. Precision agriculture applications, sensor technologies, the Internet of Things, remote sensing, artificial intelligence, machine learning, and digital platforms are not only changing the technical structure of agricultural production but also reshaping how value is created and distributed along the value chain. Digitalization is bringing significant changes to production activities, information and product flows, value chain actors, and the governance structure of the chain. At the same time, how the economic value generated through digital transformation is shared among producers, technology providers, and other actors in the chain is becoming an increasingly important issue (Klingenberg et al., 2022).

Along with digital transformation, agricultural data have become an important source of added value creation. The collection and analysis of production, climate, soil, crop, market, and consumer data enable enterprises to make more informed decisions and manage production processes more effectively. The value creation potential of agricultural data emerges through mechanisms such as greater transparency, prediction and optimization, monitoring, learning, and the customization of products or services to specific needs. Data analytics offer important opportunities, particularly for reducing costs, predicting production and market risks, monitoring yields, and improving enterprise performance (Uyar et al., 2024).

The increasing use of data in agriculture also contributes to making production decisions more predictable. By combining historical and real time data, variables such as weather conditions, pest and disease risks, crop yields, and market

demand can be predicted more accurately, while the timing of activities such as planting, irrigation, and harvesting can be optimized. These applications contribute not only to reducing production costs but also to improving resource use efficiency and strengthening the resilience of agricultural enterprises to environmental and economic risks (Uyar et al., 2024). Technology and data use have therefore become strategic elements of agricultural added value creation, extending beyond increases in production volume to improvements in decision quality and resource use efficiency.

Another notable global change is the increasing consideration of added value from a sustainability perspective. While traditional approaches largely evaluated value creation in terms of economic returns and enterprise profitability, it is now widely recognized that environmental and social outcomes should also be considered alongside economic value. Sadovska et al. (2020) assess sustainable value creation in agriculture through nine main groups of factors: collaboration, communication, knowledge, production, diversification, entrepreneurship, financing, policies, and inclusiveness. This approach demonstrates that agricultural value creation cannot be limited to economic performance at the enterprise level and that different stakeholders and long term sustainability objectives also need to be incorporated into the process.

In this context, the Triple Bottom Line approach, which considers economic, environmental, and social dimensions together, is becoming increasingly important in the assessment of agricultural added value creation. Sustainable value creation requires not only economic performance but also the conservation of natural resources, reduction of environmental impacts, and consideration of the needs of different stakeholders. Knowledge and innovation, digital transformation, collaboration, circularity, and the bioeconomy are among the main areas that can strengthen the long term value creation capacity of agricultural enterprises (Sadovska et al., 2020). This development has led to agricultural added value being assessed not only in terms of "higher economic returns" but also in terms of the sustainability of the value created.

Another important issue in global agricultural added value creation is the integration of producers into global value chains and the position they hold within these chains. Particularly for developing countries, access to global markets offers important opportunities to increase production, reach new markets, and generate higher export revenues. However, participation in a value chain alone does not necessarily lead to higher added value. When producers remain primarily in the role of raw material suppliers, they may receive only a limited share of the total economic value created. It is therefore important to increase producers' participation in higher value activities such as processing, product development, quality management, logistics, and marketing (Trienekens, 2011; Devaux et al., 2018).

At the same time, technological transformation and the expansion of global value chains are creating new challenges regarding the distribution of added value among chain actors. The growing role of digital platforms, data providers, and technology companies in agricultural value chains may create new power asymmetries in terms of producers' bargaining power and their share of the value created. Future agricultural added value policies therefore need to focus not only on how much value is created but also on who creates that value and how it is distributed along the chain (Klingenberg et al., 2022).

Overall, global agricultural value creation is shifting from a production oriented model toward one increasingly driven by knowledge, technology, innovation, and sustainability. The integration of agricultural production with processing and marketing, the effective use of digital technologies and agricultural data, the development of sustainable production models, and the strengthening of producers' position within value chains are key elements of this transformation. In the future, the competitiveness of countries in agriculture will therefore be determined not only by how much agricultural output they produce but also by how much value they are able to create from that output and the extent to which they can make this value creation sustainable.

3.2. Assessment of Agricultural Added Value Creation in Türkiye

Türkiye has considerable potential for agricultural added value creation due to its diverse climatic regions, wide range of agricultural products, extensive experience in agricultural production, large domestic market, and well developed food industry. However, high production capacity alone does not necessarily translate into high added value. The extent to which agricultural products are processed, technology and innovation are integrated into production, producers are positioned within the value chain, and products reach national and international markets are among the main factors determining the level of added value created. Although Türkiye has a strong position in the agriculture and food sectors in terms of scale and diversity, there are still areas that need further development compared with similar countries, particularly in the widespread adoption of emerging technologies and innovative solutions and in the production of high value added products (Tümen & Özertan, 2020).

Studies examining Türkiye's international position in terms of agricultural added value indicate that the country has considerable production capacity, although patterns of development are not homogeneous across countries. Kaya (2020) examined Türkiye's convergence in agricultural added value with China, the United States, India, Brazil, and Indonesia and found convergence with China and the United States, while no convergence was identified with Brazil, India, or Indonesia. These findings indicate that Türkiye has significant capacity for agricultural added value creation while also highlighting the importance of

technology, innovation, and high value added production for maintaining its global competitiveness (Kaya, 2020).

One of the key issues for Türkiye is the stronger integration of primary agricultural production with the subsequent stages of the value chain. When agricultural raw materials are marketed directly or with only limited processing, a substantial share of the final product value may be created during post production stages. In contrast, integrating processing, grading, storage, packaging, logistics, and marketing activities with agricultural production makes it possible to generate greater economic value from the same agricultural raw material. Strengthening the relationship between agriculture and the food industry is therefore of strategic importance for increasing agricultural added value creation in Türkiye.

One notable example of this relationship in Türkiye is Gaziantep. Şahin Dereyurt and Varol (2026) reported that Gaziantep showed a more positive trend in agricultural added value creation than Türkiye as a whole during the 2004–2022 period and that the integration of industrial infrastructure with agricultural production played an important role in increasing added value, particularly after 2010. Gaziantep has not remained solely a producer of agricultural raw materials but has been able to transform these raw materials into higher value added final products through its strong food industry, demonstrating the importance of agriculture industry integration. This example shows that agricultural added value is shaped not only by improvements in farm level productivity but also by industrial infrastructure, processing capacity, logistics networks, trade, and marketing opportunities.

Technology, innovation, and digitalization are also important areas for further development in increasing added value in Türkiye. Digital technologies offer significant opportunities to reduce production costs, improve input use efficiency, monitor product quality, manage production and market risks more effectively, and strengthen information flows between producers and markets. However, technology adoption in Türkiye is influenced by structural factors such as farm size, investment costs, human resources, and producer organization. Particularly for small agricultural enterprises, the high cost of individual access to advanced technologies makes it necessary to develop shared use models and new forms of cooperation. In this context, Tümen and Özertan (2020) emphasize the importance of strengthening cooperation among producer organizations, technology companies, financial institutions, the private sector, and other value chain actors.

Making technological transformation sustainable requires more than simply importing technology or adopting new equipment. Strengthening research and development capacity, adapting agricultural innovations to local conditions, developing qualified human resources, and effectively transferring research

findings to producers are also important components of added value creation. Agricultural research and development, cooperation among universities, the private sector, and producers, and agricultural extension systems should therefore be considered together within added value policies. Tümen and Özertan (2020) particularly emphasize the importance of strengthening research and development capacity in Türkiye's agriculture and food sectors and encouraging qualified researchers to work in these fields.

Financing and public support also influence agricultural added value. The literature provides evidence from different countries showing that agricultural support, capital accumulation, labor, and institutional effectiveness are associated with agricultural added value. Akyol (2018), in a study of newly industrialized countries, found that agricultural incentives had a positive and significant effect on agricultural added value, while other studies have shown that factors such as agricultural labor, income, energy use, economic complexity, and government effectiveness are also associated with agricultural added value (Akyol, 2018; Soyyiğit & Yavuzaslan, 2019). Studies identifying long term relationships between agricultural credit and agricultural economic activity in Türkiye further support the importance of access to finance for agricultural development (Kaya, 2020).

However, from an added value perspective, attention should be given not only to how much value is created but also to how that value is distributed. An increase in the total economic value generated through agricultural production does not necessarily mean that producer incomes increase at the same rate. Differences in the shares of the final product value received by producers, processors, wholesalers, retailers, and other value chain actors make the distributional dimension of added value policies particularly important. Tümen and Özertan (2020) emphasize that one of the main objectives of product based added value analysis in Türkiye is to determine the shares of the total value created that are received by actors along the supply chain, particularly producers.

From this perspective, producer organization is important in Türkiye not only for creating added value but also for enabling producers to retain a greater share of that value. Collective action in input procurement, storage, processing, packaging, and marketing can enable producers to benefit from economies of scale and strengthen their bargaining power. In addition, producers can obtain a larger share of the final product value by moving beyond the role of raw material suppliers and participating in downstream stages of the value chain, such as processing and marketing. Developing support and organizational policies that increase the producer's share of total added value is therefore considered one of the key policy areas for Türkiye (Tümen & Özertan, 2020).

Regional differences also need to be considered when seeking to increase agricultural added value in Türkiye. Agricultural production structures, cropping

patterns, industrial infrastructure, logistics opportunities, and market access vary considerably among regions. Rather than adopting a uniform added value strategy across the country, it may therefore be more effective to develop differentiated models that reflect regional production characteristics and economic structures. As demonstrated by the Gaziantep example, the spatial integration of agricultural production with industry, trade, and logistics activities can accelerate regional added value creation (Şahin Dereyurt & Varol, 2026).

Türkiye's more effective participation in global value chains also represents an important area for future growth in added value. However, the primary objective should not simply be to export more agricultural products but to improve the quality of exports and increase their domestic value added content. Increasing the share of processed, differentiated, and technology intensive products in exports can help retain more economic value within the country compared with the export of primary products. This approach needs to be accompanied by policies that support domestic production capacity, agro industry, and relationships between producers and industry. In this regard, Tümen and Özertan (2020) highlight policy areas such as supporting supply side integration into global value chains, encouraging technology investments that increase productivity and added value, and strengthening agricultural statistical infrastructure.

Overall, Türkiye's main challenge in agricultural added value is not so much insufficient agricultural production capacity as the need to transform its existing production potential into higher and more sustainable economic value. Türkiye's product diversity, agricultural production experience, geographical location, and food industry provide important advantages. However, making more effective use of this potential depends on strengthening agriculture industry integration, increasing processing capacity, expanding the adoption of technology and innovation, improving producer organization, strengthening research and development and human capital, and increasing producers' participation in higher value activities within the value chain. Therefore, future assessments of Türkiye's agricultural performance should consider not only production volumes and export levels but also the added value generated per unit of output, the share of high value added products, and the producer's share of the total value created as key indicators.

References

Adanacıoğlu, H., Saner, G., & Ağır, H. B. (2018). Sürdürülebilir gıda değer zinciri yaklaşımı. *KSÜ Tarım ve Doğa Dergisi, 21*(Özel Sayı), 214–226. doi:10.18016/ksutarimdoga.vi.472847

Akyol, M. (2018). Tarımsal teşviklerle katma değer arasındaki ilişkinin incelenmesi: Yeni endüstrileşen ülkeler için panel eşanlı denklemler sistemi analizi. *The Journal of International Scientific Researches, 3*(3), 226–236.

Al Hinai, A., Jayasuriya, H., Al Shukaili, T., & Pathare, P. B. (2022). Value addition for agricultural produce and institutional capacity building to promote sustainable food security. *Open Agriculture, 7*, 207–216.

Başer, U., & Bozoğlu, M. (2018). Tarımsal değer zincirinde değer yaratan faaliyetlerin belirlenmesi. *Türk Tarım – Gıda Bilim ve Teknoloji Dergisi, 6*(8), 1002–1007. doi:10.24925/turjaf.v6i8.1002-1007.1835

Coltrain, D., Barton, D., & Boland, M. (2000). *Value added: Opportunities and strategies*. Manhattan, KS: Arthur Capper Cooperative Center, Department of Agricultural Economics, Kansas State University.

Cucagna, M. E., & Goldsmith, P. D. (2018). Value adding in the agri-food value chain. *International Food and Agribusiness Management Review, 21*(3), 293–316. doi:10.22434/IFAMR2017.0051

Devaux, A., Torero, M., Donovan, J., & Horton, D. (2018). Agricultural innovation and inclusive value-chain development: A review. *Journal of Agribusiness in Developing and Emerging Economies, 8*(1), 99–123. doi:10.1108/JADEE-06-2017-0065

Food and Agriculture Organization of the United Nations. (2014). *Developing sustainable food value chains: Guiding principles*. Rome, Italy: FAO.

Gökkür, S., & Çelik, Z. (2016). Meyve ve sebze ürünlerinde küresel değer zinciri. *VII. Bahçe Ürünlerinde Muhafaza ve Pazarlama Sempozyumu, 1*, 50–55.

Kaya, L. (2020). Türkiye ile seçilmiş ülkeler arasında tarımsal katma değer yakınsaması: Doğrusal ve doğrusal olmayan birim kök testleri. *Bingöl Üniversitesi İktisadi ve İdari Bilimler Fakültesi Dergisi, 4*(2), 41–60. doi:10.33399/biibfad.736598

Klingenberg, C. O., Valle Antunes Júnior, J. A., & Müller-Seitz, G. (2022). Impacts of digitalization on value creation and capture: Evidence from the agricultural value chain. *Agricultural Systems, 201*, 103468. doi:10.1016/j.agsy.2022.103468

Lu, R., & Dudensing, R. (2015). What do we mean by value-added agriculture? *Choices, 30*(4), 1–8.

Organisation for Economic Co-operation and Development. (2023). *Agricultural policy monitoring and evaluation 2023: Adapting agriculture to climate change*. Paris, France: OECD Publishing.

Porter, M. E. (1985). *Competitive advantage: Creating and sustaining superior performance*. New York, NY: Free Press.

Sadovska, V., Ekelund Axelson, L., & Mark-Herbert, C. (2020). Reviewing value creation in agriculture—A conceptual analysis and a new framework. *Sustainability, 12*(12), 5021. doi:10.3390/su12125021

Şahin Dereyurt, B., & Varol, Ç. (2026). Tarımsal üretimin katma değere dönüşüm sürecinde kırsal ve kentsel gelişimin izleri: Gaziantep örneği. *İDEALKENT, 51*, e1845377. doi:10.31198/idealkent.1845377

Soyyiğit, S., & Yavuzaslan, K. (2019). Tarımsal katma değeri etkileyen faktörler üzerine bir inceleme: E7 ülkeleri örneği. *Kafkas Üniversitesi İktisadi ve İdari Bilimler Fakültesi Dergisi, 10*(19), 403–429. doi:10.9775/kauiibfd.2019.017

Trienekens, J. H. (2011). Agricultural value chains in developing countries: A framework for analysis. *International Food and Agribusiness Management Review, 14*(2), 51–82.

Tümen, S., & Özertan, G. (2020). *Katma değerin artırılması, inovasyon ve dijital tarım* (Yayın No. TÜSİAD-T/2020-03/615). İstanbul, Türkiye: TÜSİAD.

Uyar, H., Karvelas, I., Rizou, S., & Fountas, S. (2024). Data value creation in agriculture: A review. *Computers and Electronics in Agriculture, 227*, 109602. doi:10.1016/j.compag.2024.109602

CHAPTER 12

Agricultural Value Chains: Conceptual Framework, Components, and Contemporary Approaches

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1. Introduction

The agricultural sector plays a strategic role not only in meeting the food needs of the world's population but also in economic development, rural employment, the sustainable management of natural resources, and international trade. However, global population growth, climate change, declining natural resources, changing consumer expectations, and increasing international competition have made it insufficient to evaluate agricultural production solely in terms of quantity. Today, the success of agricultural production depends on the effective management of the entire process, from pre production activities to harvesting, processing, storage, logistics, marketing, and final consumption. This has made the value chain approach increasingly important in the agricultural sector (Porter, 1985; Trienekens, 2011).

The value chain approach considers all activities carried out from the pre production stage until a product reaches the final consumer as an interconnected whole. This approach covers not only the flow of products but also the flow of information, finance, technology, and services, with the aim of improving coordination among all actors involved in the chain. In this way, it becomes possible to increase efficiency in production processes, improve quality standards, reduce product losses, and respond more effectively to consumer expectations. In recent years, in particular, advances in digital technologies, sustainable production practices, and global trade networks have made the value chain approach one of the key components of modern agricultural policies (Devaux et al., 2018; Neven, 2014).

Effective management of agricultural value chains not only improves the competitiveness of agricultural enterprises but also contributes to a range of economic, social, and environmental objectives, including increasing producer incomes, supporting rural development, ensuring food security, and promoting more efficient use of natural resources. For this reason, agricultural policies in many countries are increasingly shaped by integrated strategies that focus not only on increasing production but also on strengthening all stages of the value chain. In particular, integrating small scale producers into markets, strengthening producer organizations, improving postharvest processes, and promoting the wider use of digital technologies are among the main priorities of contemporary value chain approaches (Gereffi & Fernandez-Stark, 2016; Neven, 2014).

2. Agricultural Value Chains

2.1. The Concept of Agricultural Value Chains

Globalization, technological advances, changing consumer expectations, and the increasing complexity of international trade have made it insufficient to evaluate agricultural production systems solely from a production oriented perspective. Today, the economic success of agricultural products is determined

not only by the volume of production but also by the added value, quality, coordination, traceability, and marketing efficiency created throughout the process from pre production activities to the final consumer. This transformation has brought the value chain approach to the forefront in agriculture, shifting the focus from the physical movement of products to the analysis of the economic value created along the chain. Particularly over the past three decades, the increasing integration of agricultural production into global trade networks has made the value chain approach one of the key analytical tools in both academic research and international development policies (Devaux et al., 2018; Mac Clay & Feeney, 2019; Trienekens, 2011).

The concept of the value chain was first introduced by Porter (1985) to explain how firms achieve competitive advantage. According to Porter, a firm creates value through all the activities it performs in delivering a product or service to the customer, and competitive advantage depends on how effectively these activities are managed. Initially developed at the firm level, the approach was later expanded to include not only activities within a firm but also the relationships among producers, suppliers, processors, distributors, retailers, and consumers. As a result, the value chain came to be viewed as an integrated structure created collectively by all actors within an economic system rather than simply as a set of activities performed by a single firm (Kaplinsky & Morris, 2001; Gereffi & Fernandez-Stark, 2016; Trienekens, 2011).

In the agricultural sector, the value chain approach is more complex than in the industrial sector due to the biological characteristics of production, seasonality, the perishability of agricultural products, and the involvement of numerous stakeholders. An agricultural value chain encompasses all activities from input supply to production, harvesting, storage, processing, packaging, logistics, marketing, and final consumption, as well as the flows of goods, information, finance, and services among the actors involved in these activities. Therefore, an agricultural value chain is not simply a linear process describing the physical movement of a product, but rather a dynamic system characterized by continuous interaction among its actors (Neven, 2014; Neven, 2014; Trienekens, 2011).

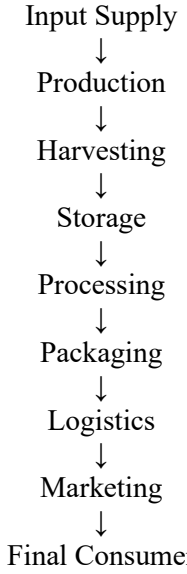


Figure 1. Main Components of the Agricultural Value Chain

Source: Created by the authors.

Although definitions of agricultural value chains vary across the literature, they share a common emphasis on linking all activities within the chain in a way that creates value for the consumer. Devaux et al. (2018) define the agricultural value chain as a set of activities that increase the economic value of a product throughout the process from producers to the market, while Mac Clay and Feeney (2019) emphasize that this structure is a multidimensional system that involves not only product flows but also governance, coordination, information sharing, and innovation processes. Similarly, FAO defines sustainable agricultural value chains as systems that are not only economically profitable but also socially inclusive and environmentally sustainable. Therefore, the value chain approach is now regarded as a holistic framework that aims not only to improve economic performance but also to enhance social well being, conserve natural resources, and support rural development.

An agricultural value chain is not a linear structure in which independent activities are carried out sequentially, but rather an integrated system in which all actors along the chain interact with one another. This system includes agricultural input suppliers, producers, producer organizations, processors, storage operators, logistics companies, wholesalers, retailers, and final consumers. In addition, supporting actors such as financial institutions, public agencies, research organizations, extension services, certification bodies, and information

technology providers play an important role in the effective functioning of the chain. The success of a value chain depends not only on the presence of these actors but also on the level of coordination among them, information sharing, mutual trust, and their capacity to act collectively. Agricultural value chains are therefore increasingly viewed as multi stakeholder systems that extend beyond production activities to include economic, social, and institutional relationships (Devaux et al., 2018; Kumari et al., 2021; Trienekens, 2011).

The main objective of the value chain approach is to increase the economic value of a product at each stage, from pre production activities until it reaches the final consumer, while generating higher returns for the stakeholders involved in the chain. In this context, quality improvements, processing activities, appropriate storage conditions, effective logistics management, product standardization, traceability systems, and marketing activities are among the main factors that increase the market value of agricultural products. At the same time, the value chain approach aims not only to improve the physical characteristics of products but also to enhance information flows, facilitate access to finance, promote risk sharing, and strengthen relationships between producers and markets. In this way, the economic value created along the chain can be distributed more equitably, while providing opportunities for small scale producers in particular to achieve higher incomes (Clark et al., 2021; Neven, 2014; Swamy & Dharani, 2016).

One of the concepts frequently confused in the literature is the distinction between value chains and supply chains. Although both approaches deal with the movement of products from producers to consumers, they differ considerably in terms of their objectives and areas of focus. The supply chain approach mainly focuses on planning the flow of products, raw materials, and information between firms, managing logistics processes, reducing costs, and improving operational efficiency. In contrast, the value chain approach examines how greater economic value can be created at each stage through which a product passes and how this value can be shared among the actors involved in the chain. Therefore, the value chain approach covers not only logistics and production processes but also product development, quality management, innovation, governance, marketing, consumer preferences, and competitive advantage. In this respect, the value chain approach provides a broader and more strategic perspective than supply chain management (Gereffi & Fernandez-Stark, 2016; Kaplinsky & Morris, 2001; Mac Clay & Feeney, 2019).

In recent years, the agricultural value chain approach has evolved beyond being merely an organizational model for bringing products to market and has increasingly been regarded as a strategic development tool for rural development, poverty reduction, food security, sustainable natural resource management, and improved international competitiveness. In particular, the expansion of global

trade networks has intensified competition among agricultural products in international markets, making quality standards, traceability, sustainable production practices, and digital technologies integral components of value chains. Therefore, a successful agricultural value chain is now considered a holistic system that not only increases production but also improves quality, enhances resource use efficiency, supports environmental sustainability, and increases the economic benefits that producers obtain from the market (Białowas & Budzyńska, 2022; Montalbano & Nenci, 2022).

From this perspective, an agricultural value chain can be defined as an integrated management approach that coordinates all activities from agricultural production to final consumption, aims to increase economic value, and promotes sustainable cooperation among all actors involved in the chain. In addition to improving productivity, product quality, and marketing performance, this approach also makes an important contribution to rural development and higher producer incomes and has become one of the key factors shaping the competitiveness of the agricultural sector. Understanding why agricultural value chains are important for the agricultural sector is therefore essential for a clearer understanding of the subject. The following section examines in detail the economic, social, and environmental contributions of agricultural value chains to the agricultural sector.

2.2. Importance of Agricultural Value Chains

Today, the agricultural value chain approach is regarded not only as an organizational model for managing the processes through which agricultural products move from production to consumption, but also as a strategic approach that improves the economic efficiency of the agricultural sector, supports rural development, and promotes sustainable agricultural production. The ability of the agricultural sector to remain competitive in increasingly globalized markets depends not only on increasing production volumes but also on managing production, processing, storage, logistics, and marketing processes in an integrated manner. For this reason, the value chain approach is considered an important tool not only for improving the efficiency of agricultural systems but also for enhancing product quality, facilitating market access, and increasing the economic value created along the chain (Devaux et al., 2018; Neven, 2014; Trienekens, 2011;).

One of the most important contributions of agricultural value chains is their ability to improve resource use efficiency by strengthening coordination among the actors involved in the production process. In traditional agricultural production systems, producers, processors, traders, and retailers often operate independently, which may lead to information gaps, high transaction costs, quality losses, and marketing problems. The value chain approach, in contrast, promotes information sharing, planning, and cooperation among actors along the

chain, thereby supporting more effective decision making throughout the entire process from production to marketing. This can help reduce production costs, prevent product losses, improve quality standards, and develop products that are better suited to market requirements (Mac Clay & Feeney, 2019; Swamy & Dharani, 2016).

The value chain approach also plays an important role in improving the competitiveness of agricultural enterprises. Today, consumers consider not only price but also factors such as quality, reliability, traceability, environmental sustainability, and food safety. This has made it necessary for agricultural production to become more market oriented rather than focusing solely on productivity. Through the value chain approach, producers can better understand consumer expectations, adjust production planning according to market demand, and shift toward products with higher added value. Managing the chain in an integrated manner also contributes to the ability of agricultural enterprises to gain competitive advantage in both domestic and international markets (Białowąs & Budzyńska, 2022; Greenville et al., 2017).

Another factor that increases the importance of agricultural value chains is their role in facilitating the integration of small scale producers into markets. Although a significant share of global agricultural production is carried out by small family farms, these farms often face considerable constraints in areas such as access to finance, technology use, marketing opportunities, and organization. Through producer organizations, cooperatives, and producer companies, the value chain approach can strengthen the bargaining power of small scale producers and enable them to act collectively in various activities ranging from input procurement to marketing. This allows producers to benefit from economies of scale, reduce transaction costs, and potentially achieve higher incomes. In particular, the effective integration of producer organizations into value chains is considered one of the key factors contributing to the success of rural development policies (Devaux et al., 2018; Kumari et al., 2021).

Another important contribution of the agricultural value chain approach is its role in food safety and quality management. Growing consumer demand for safe, high quality, and traceable food products has made the effective implementation of quality standards throughout the process from production to consumption increasingly necessary. The value chain approach strengthens coordination among actors along the chain, enabling the standardization of production processes, the development of quality control mechanisms, and improved product traceability. Record keeping systems, certification practices, and quality assurance mechanisms, which are particularly important for food safety, contribute to reducing risks at every stage of the chain. As a result, consumer confidence can be strengthened, product recall processes can be managed more

effectively, and compliance with international quality standards can be facilitated (Neven, 2014; Trienekens, 2011).

The value chain approach is also considered an important tool for achieving sustainable agricultural production goals. The efficient use of natural resources, reduction of environmental impacts, and development of production systems that are better adapted to climate change cannot be achieved solely through measures taken at the producer level, but require coordinated action across all stages of the chain. In this context, sustainable production practices, resource use efficiency, waste reduction, energy efficiency, and environmental responsibility have become integral components of agricultural value chains. Particularly for enterprises operating in international markets, environmental sustainability criteria and sustainable sourcing practices are among the key factors influencing competitiveness (Białowąs & Budzyńska, 2022; Devaux et al., 2018).

The benefits of agricultural value chains are not limited to the enterprise level but also have important implications for rural development. The effective development of value chains can create new employment opportunities by encouraging the expansion of processing, packaging, storage, logistics, and marketing activities in rural areas. In addition, stronger producer organizations, support for local entrepreneurship, and greater participation of women and young people in agricultural production processes are considered important factors contributing to socioeconomic development in rural areas. From this perspective, the agricultural value chain approach is regarded as a comprehensive development tool that contributes not only to economic growth but also to improved income distribution, poverty reduction, and a better quality of life in rural communities (Clark et al., 2021; Kumari et al., 2021).

The rapid expansion of global trade and increasing competition in agricultural markets have further strengthened the strategic importance of the value chain approach. Success in international markets today depends not only on high production volumes but also on product quality, compliance with standards, traceability, logistics performance, and the ability to respond quickly to changing market demands. Effective integration into global value chains can therefore provide countries with important opportunities to expand exports and strengthen their international competitiveness. Particularly in developing countries, strengthening agricultural value chains can facilitate producers' access to global markets, increase product diversification, and contribute to generating higher added value from agricultural exports (Greenville et al., 2017; Montalbano & Nenci, 2022).

Overall, the agricultural value chain approach represents a strategic management perspective that considers production, processing, storage, logistics, and marketing processes in an integrated manner and contributes to improving the economic, social, and environmental performance of the agricultural sector.

Its multidimensional contributions, including more efficient use of resources, stronger integration of producers into markets, improved food safety, support for rural development, and greater international competitiveness, have made the value chain approach an important component of contemporary agricultural policies. It is therefore necessary to examine not only the structural characteristics of agricultural value chains but also the actors involved and the relationships among them. In this context, the following section discusses the main components of agricultural value chains.

2.3. Main Components of Agricultural Value Chains

An agricultural value chain is an integrated system consisting of numerous actors who interact with one another throughout the process from pre production activities to the final consumer. The success of the chain depends not only on the performance of individual actors but also on the effectiveness of coordination, information sharing, and their capacity to act collectively. Therefore, the analysis of agricultural value chains should consider not only product flows but also the roles and responsibilities of the main components of the chain and the relationships among them. Although agricultural value chains are classified in different ways in the literature, a widely accepted approach defines the chain as a system of complementary components, including input suppliers, producers, producer organizations, processors, storage and logistics operators, marketing channels, consumers, and supporting institutions (Devaux et al., 2018; Neven, 2014; Trienekens, 2011).

Input suppliers, which form the first link in the value chain, provide producers with the goods and services required for agricultural production. The timely supply of seeds, seedlings, fertilizers, plant protection products, feed, irrigation equipment, agricultural machinery, and other production inputs at the required quality directly influences production performance. Today, the role of input suppliers is no longer limited to the provision of physical inputs but also includes technical advice, digital agriculture solutions, precision agriculture applications, and information support for production planning. This broader role places input suppliers in a strategic position at the beginning of the agricultural value chain (Mac Clay & Feeney, 2019; Swamy & Dharani, 2016).

The second and most fundamental component of the chain is agricultural producers. Producers are the key actors responsible for growing agricultural products by using natural resources and production inputs. Today, however, their role is no longer limited to production activities. Analyzing market demand, meeting quality standards, adopting principles of environmental sustainability, and developing production systems that respond to consumer expectations have also become part of their responsibilities. Therefore, in modern agricultural value chains, producers are increasingly regarded as entrepreneurs who maintain

continuous interaction with other actors in the chain and make market oriented decisions (Devaux et al., 2018; Trienekens, 2011).

Producer organizations, cooperatives, and producer companies are important institutional components that improve the effectiveness of value chains, particularly in agricultural systems dominated by small scale farms. These organizations provide producers with significant advantages in areas such as collective input procurement, production planning, product standardization, marketing, access to finance, and training services. They also play a critical role in strengthening producers' bargaining power, enabling them to benefit from economies of scale, and improving their access to markets. Recent studies have shown that value chains with effective producer organizations tend to have lower transaction costs, stronger information sharing, and an improved market position for producers (Devaux et al., 2018; Kumari et al., 2021).

Following agricultural production, processing, storage, and logistics operators form important links in the value chain. Processing activities play an important role not only in preserving the physical characteristics of agricultural products but also in meeting quality standards, extending shelf life, and preparing products in line with consumer demand. Storage and logistics activities directly influence the efficiency of the chain by reducing product losses, maintaining product quality, and ensuring that products reach the right market at the right time. Particularly for perishable products such as fresh fruits and vegetables, effective cold chain management makes an important contribution to both reducing economic losses and maintaining product quality (Al Hinai et al., 2022).

Wholesalers, retailers, and final consumers, located at the later stages of the chain, are important actors in bringing agricultural products to market and reflecting consumer demand back into the production system. In particular, the development of organized retailing, the growing use of e commerce platforms, and increasing consumer expectations regarding quality have made marketing activities a strategic component of the value chain. Consumer expectations regarding product quality, food safety, sustainable production, and traceability can directly influence decisions made at all stages of the chain. Consumers are therefore regarded not only as the final link in the chain but also as key stakeholders that influence production and marketing processes (Białowąs & Budzyńska, 2022).

Supporting institutions also play a critical role in the effective functioning of agricultural value chains. Public institutions, universities, research institutes, extension organizations, financial institutions, certification bodies, and civil society organizations contribute to knowledge generation, technology development, access to finance, quality assurance systems, and policy development, thereby supporting the sustainability of the chain. In particular, transferring innovative technologies to producers through research and extension

activities, improving investment opportunities through financial institutions, and establishing an appropriate regulatory framework through public policies are among the key factors determining the long term success of agricultural value chains (Devaux et al., 2018; Swamy & Dharani, 2016).

These considerations show that an agricultural value chain is not a linear structure consisting of a series of independent activities, but rather a multi stakeholder system in which different actors continuously interact with one another. Each component of the chain directly influences the overall performance of the system, and a disruption at any stage can reduce the efficiency of the entire chain. The success of an agricultural value chain therefore depends not only on individual actors performing their respective roles but also on the effective management of coordination and information flows among them. This dynamic structure makes it necessary to examine not only the individual components of the chain but also the relationships and processes that connect them. In this context, the following section examines the mechanisms through which agricultural value chains operate.

2.4. Functioning Mechanism of Agricultural Value Chains

The effectiveness of an agricultural value chain depends not only on the presence of the actors involved but also on how the relationships among these actors are managed. A value chain is a dynamic system in which flows of goods, information, finance, and services occur simultaneously throughout the process from pre production activities to the final consumer. Therefore, the success of the chain depends not only on each component performing its own function but also on effective coordination among all actors, efficient information sharing, and their ability to work toward common objectives. Today, agricultural value chains are increasingly viewed not as linear supply structures but as integrated systems characterized by continuous interaction and feedback mechanisms (Trienekens, 2011; Devaux et al., 2018; Neven, 2014).

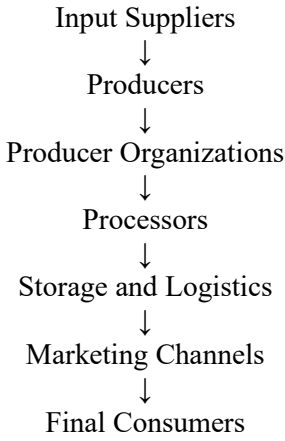


Figure 2. Functioning Mechanism of the Agricultural Value Chain
Source: Prepared by the authors based on the relevant literature.

Information flow: Takes place in both directions across all stages of the chain.

Financial flow: Continues among all actors, from producers to marketing channels.

Quality and traceability: Are maintained throughout the entire process.

Consumer feedback: Provides feedback from the market to the production stage.

The functioning of an agricultural value chain begins with the provision of inputs required for the production process. Seeds, seedlings, fertilizers, plant protection products, irrigation equipment, and other production materials supplied by input providers are used by producers in agricultural production. After harvesting, products pass through storage, grading, processing, packaging, and logistics processes before reaching marketing channels and, ultimately, the final consumer. However, this process involves much more than the physical movement of products. At each stage of the chain, information related to quality control, product standardization, traceability practices, and market demand is shared simultaneously among different actors. Production decisions are therefore shaped not only by producers themselves but also by information generated and exchanged throughout the entire chain (Mac Clay & Feeney, 2019; Al Hinai et al., 2022).

One of the key elements ensuring the effective functioning of a value chain is the flow of information. Information on production techniques, market demand, price movements, quality standards, climatic conditions, and consumer expectations is continuously shared among different actors along the chain. With

the development of digital agricultural technologies in particular, sensor systems, remote sensing technologies, big data analytics, and decision support systems have significantly improved the speed and efficiency of information flows. As a result, producers can plan their production based on current market data and technical information rather than relying solely on their own experience. The literature indicates that value chains with strong information sharing tend to achieve higher production efficiency, lower quality losses, and greater ability to respond to market demand (Swamy & Dharani, 2016; Trienekens, 2011).

Alongside information flows, financial flows are also critical to the sustainability of value chains. The financing of production inputs, management of working capital, investment decisions, and commercial relationships are shaped by financial transactions among different actors along the chain. Given the high level of risk associated with agricultural production, access to appropriate sources of finance, the ability to establish long term business relationships with other actors in the chain, and the sharing of financial risks are particularly important for producers. Contract farming models, collective marketing activities carried out through producer organizations, and credit facilities provided by financial institutions are therefore among the important mechanisms supporting the effective functioning of agricultural value chains (Devaux et al., 2018; Kumari et al., 2021).

Another important factor determining the success of agricultural value chains is their governance structure. Governance refers to how relationships among actors in the chain are organized, how decision making processes are carried out, and how quality standards are implemented. A strong governance structure helps establish trust among actors, clearly define roles and responsibilities, and resolve potential conflicts effectively. Particularly in value chains serving international markets, quality standards, certification systems, and contract based production models are commonly used as key governance mechanisms. These mechanisms help maintain consistent quality throughout the chain and support production in line with consumer expectations (Gereffi & Fernandez-Stark, 2016; Trienekens, 2011).

Feedback mechanisms are also among the key elements supporting the continuous development of modern agricultural value chains. Information on consumer expectations regarding quality, market trends, sales performance, and customer satisfaction is transmitted back through the different stages of the chain, from marketing channels to producers. This allows production planning, variety selection, quality criteria, and marketing strategies to be continuously updated. Such a dynamic structure enables value chains to respond more rapidly to changing market conditions and helps them maintain their competitiveness (Białowąs & Budzyńska, 2022; Montalbano & Nenci, 2022).

Overall, the functioning mechanism of an agricultural value chain is a multidimensional management system that involves not only product flows but also information, financial, and feedback processes. Strengthening coordination among actors, improving information sharing, establishing effective governance mechanisms, and applying quality standards throughout the entire process are among the key factors determining the success of the chain. Therefore, policies aimed at developing agricultural value chains today focus not only on increasing production but also on promoting effective cooperation and sustainable coordination across all stages of the chain. This integrated structure of agricultural value chains also contributes to a better understanding of the transformations taking place in global agricultural and food systems. In this context, the following section examines major trends shaping agricultural value chains worldwide, together with Türkiye's current situation and strategic approaches for the future.

3. Global Trends and an Assessment from Türkiye's Perspective

In recent years, economic, technological, and environmental transformations in global agricultural and food systems have significantly changed the structure and functioning of agricultural value chains. Agricultural systems, which were traditionally evaluated mainly in terms of production and trade, are now being reshaped around sustainability, digitalization, traceability, quality management, and consumer oriented production. The growth of global trade, the widespread adoption of international quality standards, and increasing consumer demand for safe and reliable food have made it necessary to evaluate value chains not only in terms of economic performance but also from social and environmental sustainability perspectives. As a result, the effective management of agricultural value chains has become a key component of agricultural policies in many countries (Devaux et al., 2018; Neven, 2014; Trienekens, 2011).

One of the most prominent trends at the global level is the rapid integration of digital technologies into agricultural value chains. Precision agriculture applications, the Internet of Things, artificial intelligence based decision support systems, remote sensing technologies, and big data analytics enable more effective production planning, improve resource use efficiency, and accelerate information sharing among different actors along the chain. In addition, blockchain based traceability systems and digital record keeping applications are increasingly being used as important tools for ensuring food safety and product reliability in international trade. These technologies allow consumers to access information about production processes more easily, while also helping producers implement quality standards more effectively.

Another important trend is the growing importance of sustainability as a core component of agricultural value chains. The European Green Deal, the United Nations Sustainable Development Goals, and international policies addressing

climate change have increased the need to reduce the environmental impacts of agricultural production. In this context, reducing carbon footprints, improving the efficiency of water and energy use, expanding circular economy practices, and reducing food losses are among the main priorities of contemporary agricultural value chains. Particularly in countries with export oriented agricultural sectors, environmental sustainability criteria have become an important source of competitiveness alongside product quality (Neven, 2014; OECD, 2023).

Another major development in global value chains is the increasing transparency and traceability of relationships between producers and consumers. The wider adoption of quality standards, the development of certification systems, and changing consumer expectations have made it necessary to assess production processes not only in terms of efficiency but also in their environmental, social, and ethical dimensions. As a result, agricultural enterprises seeking to compete in international markets are increasingly expected not only to produce high quality products but also to document their compliance with sustainable production practices.

Türkiye holds an important position in international markets for many agricultural products due to its diverse climatic conditions, wide range of agricultural products, and strong production potential. Its significant share in global trade in products such as fruits, vegetables, hazelnuts, raisins, apricots, figs, and olive oil provides important advantages for Türkiye's integration into global agricultural value chains. However, when assessed in terms of the effectiveness of agricultural value chains, several structural challenges remain. The predominance of small and fragmented farms, the limited effectiveness of producer organizations, postharvest losses, inadequate logistics infrastructure, and problems in marketing processes are among the main factors limiting the efficiency of agricultural value chains (Başer & Bozoğlu, 2018; Gökkür & Çelik, 2016).

In recent years, important steps have been taken to strengthen agricultural value chains in Türkiye. Policies aimed at strengthening producer organizations, the increasing number of products with geographical indications, the expansion of good agricultural practices and organic farming, support for digital agriculture applications, and the development of contract farming models are among the key components of this process. In addition, efforts to improve quality standards for export markets, expand cold chain investments, and strengthen the agro industry have contributed to the more effective functioning of agricultural value chains. Despite these developments, there is still considerable room for improvement in areas such as strengthening producer organizations, reducing postharvest losses, expanding the use of digital technologies, developing data driven decision making mechanisms, and enhancing cooperation among universities, public institutions, and the private sector (Adanacıoğlu et al., 2018).

In the coming years, the success of agricultural value chains will depend not only on increasing production but also on strengthening coordination across all stages of the chain, accelerating digital transformation, and expanding sustainable production practices. Challenges such as climate change, declining natural resources, and increasing global competition make it increasingly necessary to develop agricultural value chains that are more resilient, flexible, and innovative. For Türkiye to transform its agricultural production potential into greater economic value, all processes from production to marketing need to be addressed through an integrated approach, cooperation among actors along the chain needs to be strengthened, and activities that create added value need to be supported. Such efforts can contribute both to higher producer incomes and to the development of a more competitive agricultural sector in international markets.

References

Adanacıoğlu, H., Saner, G., & Ağır, H. B. (2018). Sürdürülebilir gıda değer zinciri yaklaşımı. *KSÜ Tarım ve Doğa Dergisi, 21*(Özel Sayı), 214–226. doi:10.18016/ksutarimdoga.vi.472847

Al Hinai, A., Jayasuriya, H., Pathare, P. B., & Al Shukaili, T. (2022). Present status and prospects of value addition industry for agricultural produce – A review. *Open Agriculture, 7*, 207–216. doi:10.1515/opag-2022-0084

Başer, U., & Bozoğlu, M. (2018). Tarımsal değer zincirinde değer yaratan faaliyetlerin belirlenmesi. *Türk Tarım – Gıda Bilim ve Teknoloji Dergisi, 6*(8), 1002–1007. doi:10.24925/turjaf.v6i8.1002-1007.1835

Białowąs, T., & Budzyńska, A. (2022). The importance of global value chains in developing countries' agricultural trade development. *Sustainability, 14*(3), 1389. doi:10.3390/su14031389

Clark, J. K., Jablonski, B. B. R., Inwood, S., Irish, A., & Freedgood, J. (2021). A contemporary concept of the value(s)-added food and agriculture sector and rural development. *Community Development, 52*(2), 186–204. doi:10.1080/15575330.2020.1854804

Devaux, A., Torero, M., Donovan, J., & Horton, D. (2018). Agricultural innovation and inclusive value-chain development: A review. *Journal of Agribusiness in Developing and Emerging Economies, 8*(1), 99–123. doi:10.1108/JADEE-06-2017-0065

Gereffi, G., & Fernandez-Stark, K. (2016). *Global value chain analysis: A primer* (2nd ed.). Durham, NC: Duke University.

Gökkür, S., & Çelik, Z. (2016). Meyve ve sebze ürünlerinde küresel değer zinciri. *Meyve Bilimi/Fruit Science, 1*(Özel Sayı), 50–55.

Greenville, J., Kawasaki, K., & Beaujeu, R. (2017). *A method for estimating global trade in value added within agriculture and food value chains* (OECD Food, Agriculture and Fisheries Papers No. 99). Paris, France: OECD Publishing. doi:10.1787/f3a84910-en

Kaplinsky, R., & Morris, M. (2001). *A handbook for value chain research*. Brighton, England: Institute of Development Studies.

Kumari, S., Bharti, N., & Tripathy, K. K. (2021). Strengthening agriculture value chain through collectives: Comparative case analysis. *International Journal of Rural Management, 17*(1S), 40S–68S. doi:10.1177/0973005221991438

Mac Clay, P., & Feeney, R. (2019). Analyzing agribusiness value chains: A literature review. *International Food and Agribusiness Management Review, 22*(1), 31–46. doi:10.22434/IFAMR2018.0089

Montalbano, P., & Nenci, S. (2022). Does global value chain participation and positioning in the agriculture and food sectors affect economic performance? A global assessment. *Food Policy, 108*, 102235. doi:10.1016/j.foodpol.2022.102235

Neven, D. (2014). *Developing sustainable food value chains: Guiding principles*. Rome, Italy: Food and Agriculture Organization of the United Nations.

OECD. (2023). *Agricultural policy monitoring and evaluation 2023*. Paris, France: OECD Publishing.

Porter, M. E. (1985). *Competitive advantage: Creating and sustaining superior performance*. New York, NY: Free Press.

Swamy, V., & Dharani, M. (2016). Analyzing the agricultural value chain financing: Approaches and tools in India. *Agricultural Finance Review, 76*(2), 211–232. doi:10.1108/AFR-11-2015-0051

Trienekens, J. H. (2011). Agricultural value chains in developing countries: A framework for analysis. *International Food and Agribusiness Management Review, 14*(2), 51–83.

CHAPTER 13

What Drives Apricot Production in Türkiye? Explainable Machine Learning Evidence from ERA5 Climate, Greenhouse Gas and Pesticide Data

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1. Introduction

Apricot (*Prunus armeniaca* L.) is a fruit species of strategic importance for the agricultural exports and rural economy of Türkiye. According to the Food and Agriculture Organization of the United Nations (FAO), Türkiye is the world's largest apricot producer, and the Malatya region in particular supplies a large share of the global dried apricot market (FAO, 2024). Nevertheless, apricot is highly sensitive to late spring frosts during flowering, to temperature fluctuations and to water stress, which leads to pronounced year-to-year variability in production.

Quantifying the effects of climate change on agricultural production is critical for sustainable production planning and policy design. In recent years, high-resolution reanalysis products and machine learning methods have been increasingly used in agricultural modelling because of their capacity to capture the non-linear structure of climate–production relationships. The aim of this chapter is to model national apricot production in Türkiye on the basis of climatic variables, greenhouse gas emissions and pesticide use with a comparative set of machine learning methods, to identify the most influential drivers of production by means of explainable artificial intelligence (XAI) techniques, and to generate short-term production projections.

2. Material and Methods

2.1. Study Area and Data Sources

An annual time series covering the 36 years between 1990 and 2025 was used. Climate data were obtained from the ECMWF ERA5 monthly reanalysis product and aggregated to annual means (Hersbach et al., 2020). The climatic variables comprise skin and soil temperatures, 2 m air temperature, wind components and wind speed, net solar and thermal radiation, total evaporation and precipitation, surface heat and moisture fluxes, and soil moisture. Apricot production data (harvested area, production quantity and yield) were taken from FAOSTAT and the Turkish Statistical Institute (FAO, 2024; TurkStat, 2024). Pesticide use data were obtained from the FAOSTAT Pesticides Use domain, and greenhouse gas emission data (total, CO_2, CH_4, N_2O and F-gases) from the environmental statistics of TurkStat. In total, 27 independent variables were included in the models.

2.2. Data Pre-processing

The analyses were carried out on 36 observations and 27 independent variables. The data set was split into a training set (n = 27) and a test set (n = 9). Variables were standardised by robust scaling based on the median and the interquartile range (IQR), missing values were completed by k-nearest neighbour (k-NN) imputation, and multicollinearity was assessed with the variance inflation factor (VIF) (Hair, Black, Babin, & Anderson, 2010).

2.3. Machine Learning Algorithms and Optimisation

Ten regression algorithms were evaluated comparatively. Ordinary least squares (OLS) regression served as the baseline model; Ridge (Hoerl & Kennard, 1970), LASSO (Tibshirani, 1996) and ElasticNet (Zou & Hastie, 2005) represented the regularisation-based methods; *k*-NN, support vector regression (SVR; Vapnik, 1995), the multilayer perceptron (MLP) and multivariate adaptive regression splines (MARS; Friedman, 1991; Milborrow, 2024) represented the non-linear methods; and XGBoost (Chen & Guestrin, 2016) and Random Forest (Breiman, 2001; Wright & Ziegler, 2017) represented the ensemble methods. Hyperparameters of all models were optimised with repeated *k*-fold cross-validation and grid search through the caret package in R (Kuhn, 2008).

2.4. Performance Criteria and Interpretability

Model performance was evaluated on the independent test set with the coefficient of determination (R^2), root mean square error (RMSE), mean absolute error (MAE), Nash–Sutcliffe efficiency (NSE; Nash & Sutcliffe, 1970), Kling–Gupta efficiency (KGE; Gupta, Kling, Yilmaz, & Martinez, 2009) and Willmott's index of agreement (Willmott, 1981), and the efficiency scores were interpreted in the light of widely used model evaluation guidelines (Moriasi et al., 2007). Model uncertainty was reported as 95% confidence intervals computed with a bootstrap of 1000 iterations (Efron & Tibshirani, 1993). The interpretability of the best model was examined with SHAP values (Lundberg & Lee, 2017), permutation importance (Breiman, 2001) and partial dependence plots (PDP; Friedman, 2001). All analyses were conducted in R 4.6.0 (R Core Team, 2024).

3. Results and Discussion

3.1. Production Trend

Over the study period, the apricot harvested area increased steadily from about 49,600 ha in 1990 to about 156,000 ha in 2025. Production, in contrast, showed marked inter-annual fluctuations and reached the highest value of the period, approximately 1.27 million t, in 2024 (Figure 1). The year-to-year volatility of yield reflects the sensitivity of apricot to climatic events, particularly frost and temperature variations.

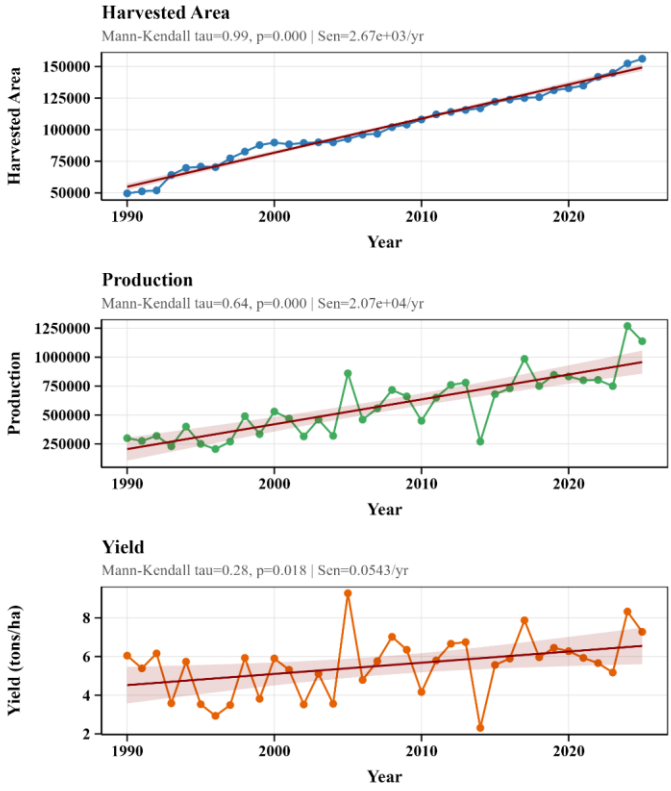


Figure 1. Trends in apricot harvested area (ha), production (t) and yield (t ha^{-1}) in Türkiye, 1990–2025.

3.2. Model Performance

The comparative performance of the ten algorithms is presented in Table 1. On the test set, the MARS model outperformed all other models with both the highest R^2 (0.50) and the lowest RMSE (155,838 t). Ensemble methods such as Random Forest and XGBoost performed below expectations on this data set because of the small sample size. The positive but limited NSE and KGE values indicate that the explanatory power of the model is moderate (Figures 2 and 3).

Table 1. Test-set performance of the models (in descending order of R^2).

Model	R^2	RMSE (t)	MAE (t)	NSE	KGE
MARS	0.502	155,838	113,448	0.193	0.298
LASSO	0.445	916,208	669,552	−26.893	−2.916
ElasticNet	0.414	623,727	401,273	−11.927	−1.465
OLS	0.324	1,488,533	1,236,928	−72.625	−5.668
Ridge	0.290	262,511	203,616	−1.290	−0.569
k-NN	0.246	320,115	249,206	−2.405	−0.686
SVR (RBF)	0.103	480,648	448,246	−6.677	−0.729
MLP	0.045	559,270	470,527	−9.393	−0.339
XGBoost	0.015	403,385	359,253	−4.407	−0.090
Random Forest	0.002	351,773	305,215	−3.112	−0.312

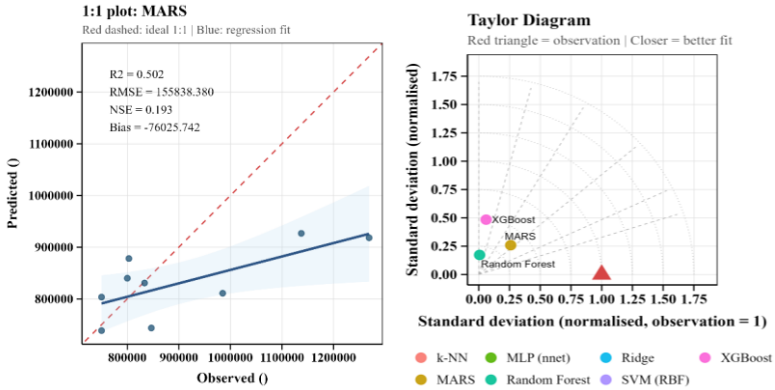


Figure 2. 1:1 plot of the MARS model (top) and Taylor diagram showing the agreement of the models with the observations in terms of correlation and standard deviation (bottom). OLS, LASSO and ElasticNet lie outside the plotted range of the Taylor diagram.

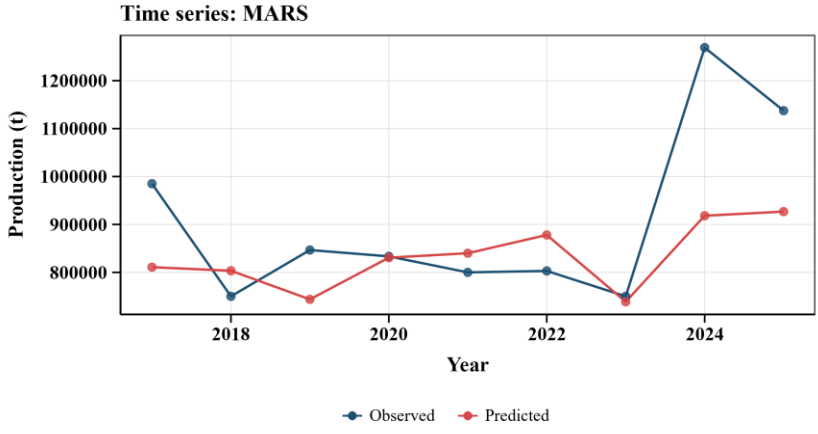


Figure 3. Observed and predicted production values of the MARS model for the test period.

3.3. Variable Importance and Interpretability

The permutation importance analysis (Table 2) revealed that the strongest determinants of apricot production are temperature-based climatic variables, namely soil temperature (7–28 cm and 0–7 cm layers), skin temperature and 2 m air temperature. Among the greenhouse gas components, CO_2 emissions made a clear contribution, whereas pesticide use per value of agricultural production and per unit of cropland were of moderate importance. The contributions of the CH_4, N_2O and F-gas components and of the soil type variable were negligible.

Table 2. The nine most influential variables according to permutation importance (ΔRMSE).

Variable	ΔRMSE (mean)	ΔRMSE (SD)
Soil temperature, 7–28 cm (K)	3,787,810	868,929
Soil temperature, 0–7 cm (K)	2,287,747	879,432
Skin temperature (K)	903,696	311,764
CO_2 emissions (Mt)	825,424	315,465
2 m air temperature (°C)	768,884	128,903
Total evaporation (m)	642,776	336,990
Instantaneous moisture flux (kg m^{-2} s^{-1})	512,259	364,298
Pesticide use per value of agricultural production (t)	325,833	175,925
Pesticide use per area of cropland (kg ha^{-1})	221,595	113,242

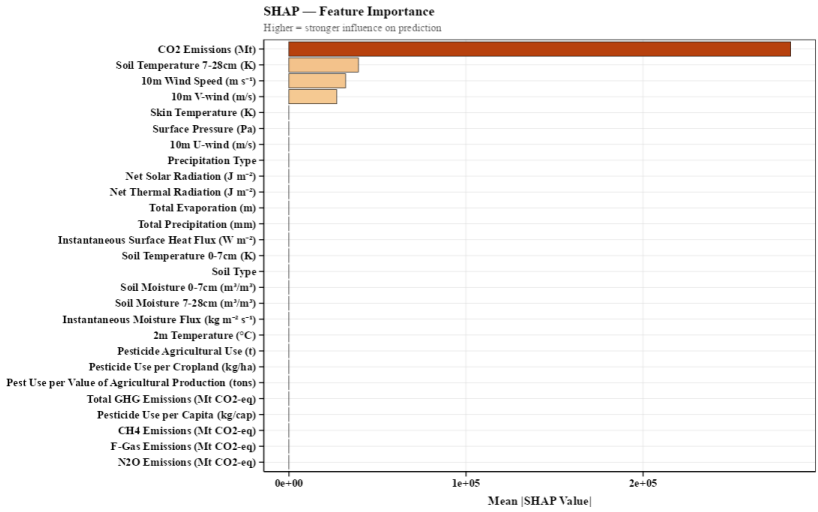


Figure 4. Ranking of mean variable importance based on SHAP values.

The SHAP analysis (Figure 4) ranks CO_2 emissions first, whereas permutation importance (Table 2) highlights the temperature-based variables. The common finding of the two methods is that production is shaped mainly along the axis of temperature and carbon emissions; the difference between the two rankings arises

from the fact that the methods measure the contribution of a variable in different ways, and both are therefore reported together in this chapter.

3.4. Future Projection

Based on the MARS model, a five-year projection for 2026–2030 was produced within the framework of the SSP scenarios of the Sixth Assessment Report (AR6) of the Intergovernmental Panel on Climate Change (IPCC, 2021). Production estimates under the optimistic (SSP1-2.6), reference (SSP2-4.5) and pessimistic (SSP3-7.0) scenarios remain close to each other (Table 3), and production in 2030 is projected at about 1.13–1.15 million t (Figure 5). The limited divergence between scenarios is related to the short five-year projection horizon and to the moderate explanatory power of the model. Forecast uncertainty is expressed by the test-set RMSE (±155,838 t).

Table 3. Production projection for 2030 under the SSP scenarios.

Scenario (2030)	Production (t)	Change (%)[a]
Optimistic (SSP1-2.6)	1,152,767	+1.35
Reference / BAU (SSP2-4.5)	1,145,185	+0.68
Pessimistic (SSP3-7.0)	1,128,915	−0.75

[a] Percentage change relative to the last historical value (2025).

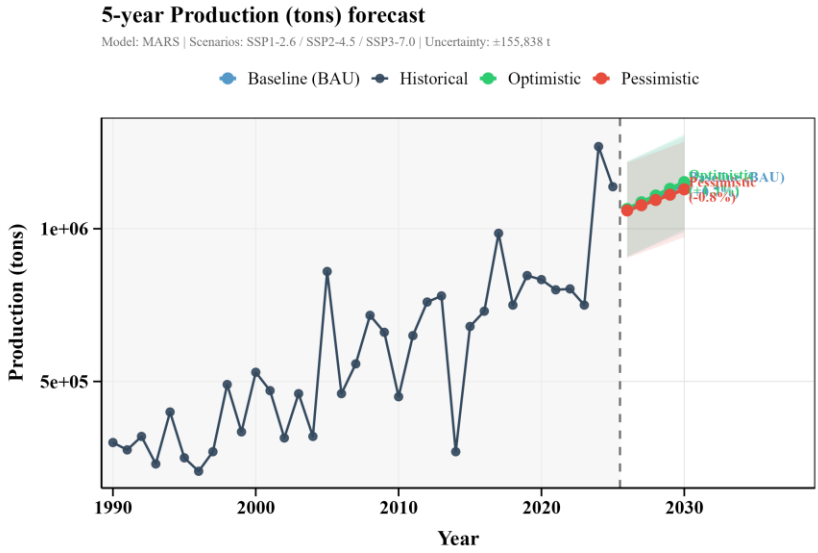


Figure 5. Historical production and five-year production projection under the SSP scenarios. The shaded band represents ±1 RMSE (model uncertainty); percentage changes compare the end of the forecast period with the last historical value.

3.5. Limitations of the Study

The main limitation of the study is the low ratio of the number of observations ($n = 36$) to the number of variables ($p = 27$) ($n/p \approx 1.3$). This increases the risk of overfitting in flexible models and contributes to the moderate level of the test-set performance metrics (especially NSE = 0.19). In addition, processing the ERA5 data as national averages masks regional differences, such as the microclimatic

conditions specific to the Malatya region. For future studies, the use of data disaggregated at province or basin scale, feature engineering (lagged variables and derived indicators such as the number of frost days) and longer time series are recommended to improve model performance.

4. Conclusion

This chapter modelled the apricot production of Türkiye comparatively with ten machine learning algorithms on the basis of climatic variables, greenhouse gas emissions and pesticide use. The MARS model showed the best performance; production was found to be determined mainly by soil and skin temperature and by CO_2 emissions, while pesticide use made a moderate contribution. The projections under the SSP scenarios indicate that production will follow a relatively stable course in the short term. The decisive role of temperature-based climatic pressure underlines the importance of climate-sensitive planning, cultivar breeding and frost protection measures in apricot production. Considering the limitations arising from the sample size, the findings need to be verified at regional scale and with extended data sets.

Acknowledgement

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References

Breiman, L. (2001). Random forests. *Machine Learning, 45*(1), 5–32.

Chen, T., & Guestrin, C. (2016). XGBoost: A scalable tree boosting system. In *Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining* (pp. 785–794). New York, NY: ACM.

Efron, B., & Tibshirani, R. J. (1993). *An introduction to the bootstrap*. New York, NY: Chapman & Hall.

FAO. (2024). *FAOSTAT statistical database*. Rome, Italy: Food and Agriculture Organization of the United Nations. Retrieved from https://www.fao.org/faostat

Friedman, J. H. (1991). Multivariate adaptive regression splines. *The Annals of Statistics, 19*(1), 1–67.

Friedman, J. H. (2001). Greedy function approximation: A gradient boosting machine. *The Annals of Statistics, 29*(5), 1189–1232.

Gupta, H. V., Kling, H., Yilmaz, K. K., & Martinez, G. F. (2009). Decomposition of the mean squared error and NSE performance criteria: Implications for improving hydrological modelling. *Journal of Hydrology, 377*(1–2), 80–91.

Hair, J. F., Black, W. C., Babin, B. J., & Anderson, R. E. (2010). *Multivariate data analysis* (7th ed.). Upper Saddle River, NJ: Pearson.

Hersbach, H., Bell, B., Berrisford, P., Hirahara, S., Horányi, A., Muñoz-Sabater, J., … Thépaut, J.-N. (2020). The ERA5 global reanalysis. *Quarterly Journal of the Royal Meteorological Society, 146*(730), 1999–2049.

Hoerl, A. E., & Kennard, R. W. (1970). Ridge regression: Biased estimation for nonorthogonal problems. *Technometrics, 12*(1), 55–67.

IPCC. (2021). *Climate change 2021: The physical science basis. Contribution of Working Group I to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change*. Cambridge, UK: Cambridge University Press.

Kuhn, M. (2008). Building predictive models in R using the caret package. *Journal of Statistical Software, 28*(5), 1–26.

Lundberg, S. M., & Lee, S.-I. (2017). A unified approach to interpreting model predictions. In *Advances in Neural Information Processing Systems 30* (pp. 4765–4774).

Milborrow, S. (2024). *earth: Multivariate adaptive regression splines* [R package]. Retrieved from https://CRAN.R-project.org/package=earth

Moriasi, D. N., Arnold, J. G., Van Liew, M. W., Bingner, R. L., Harmel, R. D., & Veith, T. L. (2007). Model evaluation guidelines for systematic

quantification of accuracy in watershed simulations. *Transactions of the ASABE, 50*(3), 885–900.

Nash, J. E., & Sutcliffe, J. V. (1970). River flow forecasting through conceptual models part I — A discussion of principles. *Journal of Hydrology, 10*(3), 282–290.

R Core Team. (2024). *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from https://www.R-project.org/

Tibshirani, R. (1996). Regression shrinkage and selection via the lasso. *Journal of the Royal Statistical Society: Series B (Methodological), 58*(1), 267–288.

TurkStat. (2024). *Crop production and environment statistics*. Ankara, Türkiye: Turkish Statistical Institute. Retrieved from https://www.tuik.gov.tr

Vapnik, V. N. (1995). *The nature of statistical learning theory*. New York, NY: Springer.

Willmott, C. J. (1981). On the validation of models. *Physical Geography, 2*(2), 184–194.

Wright, M. N., & Ziegler, A. (2017). ranger: A fast implementation of random forests for high dimensional data in C++ and R. *Journal of Statistical Software, 77*(1), 1–17.

Zou, H., & Hastie, T. (2005). Regularization and variable selection via the elastic net. *Journal of the Royal Statistical Society: Series B (Statistical Methodology), 67*(2), 301–320.

CHAPTER 14

Silkworm Excrement: From Waste to Valuable Bioresource

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Introduction

Silkworms contribute to biological diversity and serve as important model organisms in biological and biomedical research (Shao et al., 2024). Sericulture is a multifunctional agricultural activity that can generate economic value at different stages of the production chain, ranging from mulberry cultivation and the utilization of mulberry leaves and fruits to the production of insect-derived products such as pupae and silk. Beyond silk production itself, sericulture represents an ancient cultural heritage that has remained deeply embedded in the history and socioeconomic development of many societies. Its relatively small-scale production structure and potential for integration with other agricultural activities also make sericulture relevant to sustainable rural development. In this context, sericulture can contribute to more resource-efficient agricultural systems by enabling the utilization of different components and by-products generated throughout the production cycle. Altman and Farrell (2022) emphasized that the silk industry represents not only an important cultural heritage but also an opportunity to develop more environmentally conscious and value-added production systems. More recently, increasing attention has been directed toward the circular bioeconomy potential of sericulture, particularly through the valorization of production residues such as mulberry branches, silkworm excrement, low-grade cocoons, and sericin into fertilizers, animal feed, textiles, cosmetics, and other value-added products (Attri et al., 2024; Zhang et al., 2025). Such integrated approaches can increase resource-use efficiency and reduce waste generation across the silk value chain. Nevertheless, the sustainability of sericulture should not be considered independent of environmental constraints, as mulberry cultivation and silkworm rearing are sensitive to temperature, humidity, water availability, and other climatic factors. Recent studies have highlighted that climate change may negatively affect mulberry growth, silkworm development, cocoon production, and silk quality, emphasizing the need for climate-resilient production strategies (Manzoor & Qayoom, 2024). Therefore, the future sustainability of sericulture will depend not only on maintaining silk productivity but also on improving resource efficiency, reducing waste, valorizing by-products, and integrating environmentally responsible practices throughout the entire production chain.

Silkworm Excrement as a Sericultural By-product

Sericulture, recognized as an important global cultural heritage, generates substantial quantities of silkworm excrement (SE) annually, with production in China alone estimated to reach approximately 5 million tons (Liu et al., 2022; Zhang et al., 2025). Silkworm excrement is a granular material, generally dark green to grayish-black in color, with particles approximately 1-5 mm in diameter and a characteristic mild grassy odor. It is essentially a product derived from mulberry leaves after passage through the silkworm digestive system and therefore retains a considerable proportion of plant-derived chemical constituents and their metabolic derivatives (Tang et al., 2024). Approximately 60% of the mulberry leaf material consumed by silkworms may pass through the digestive tract without being fully digested, while the remaining fraction is subjected to enzymatic and microbial transformation within the digestive system, resulting in a chemically complex residue that differs from the original plant material (Tang et al., 2024).

The increasing adoption of artificial diets for silkworm rearing has further enabled year-round production and may consequently increase the continuous generation of SE. For example, a recent study reported that an industrial-scale facility using artificial diets generated approximately 20,000 tons of SE annually, illustrating the magnitude of the waste-management challenge associated with intensified sericulture (Shen et al., 2024). Despite its considerable production volume, a substantial proportion of SE remains underutilized or is discarded, potentially resulting in resource loss and environmental problems if its accumulation is not appropriately managed (Cai et al., 2021; Shen et al., 2024).

Nevertheless, SE should not be regarded simply as a waste material because it retains biologically active compounds originating from mulberry leaves and has a chemically diverse composition. Its dry matter contains substantial amounts of carbon, cellulose, crude protein, nitrogen-free extract, minerals, and other organic constituents, making it suitable for several valorization pathways (Łochyńska & Frankowski, 2018; Zhang et al., 2025). In particular, SE contains approximately 20% cellulose and exhibits a distinctive ordered, lamellar microstructure, which contributes to its suitability as a precursor for carbon-based functional materials (Zhang et al., 2025).

Recent studies have demonstrated that SE-derived porous carbon and carbon composites can be produced for applications such as adsorption, supercapacitors, and lithium–sulfur batteries (Jiang et al., 2024; Pimsawat et al., 2024). In addition, the biological and chemical constituents of SE have been investigated for potential health-related applications, including hepatoprotective activity

(Raghavendra et al., 2010), while SE-derived pigments and metabolites have also been explored for natural textile dyeing (Tang et al., 2024).

From an agricultural perspective, controlled processing of SE can produce organic fertilizers and compost with favorable nutrient characteristics and plant-growth-promoting microbial communities (Chen et al., 2011; Shen et al., 2024). Furthermore, emerging approaches involving microbial and insect-mediated bioconversion indicate that the cellulose-rich fraction of SE can be further converted into value-added products, thereby expanding its potential within a circular bioeconomy framework (Zhang et al., 2023; Zhang et al., 2025). Thus, the valorization of SE through feed, fertilizer, biomaterial, textile, pharmaceutical, energy, and biotechnological applications may provide an effective strategy for reducing waste while increasing the overall resource-use efficiency and economic value of the sericulture production chain (Figure 1).

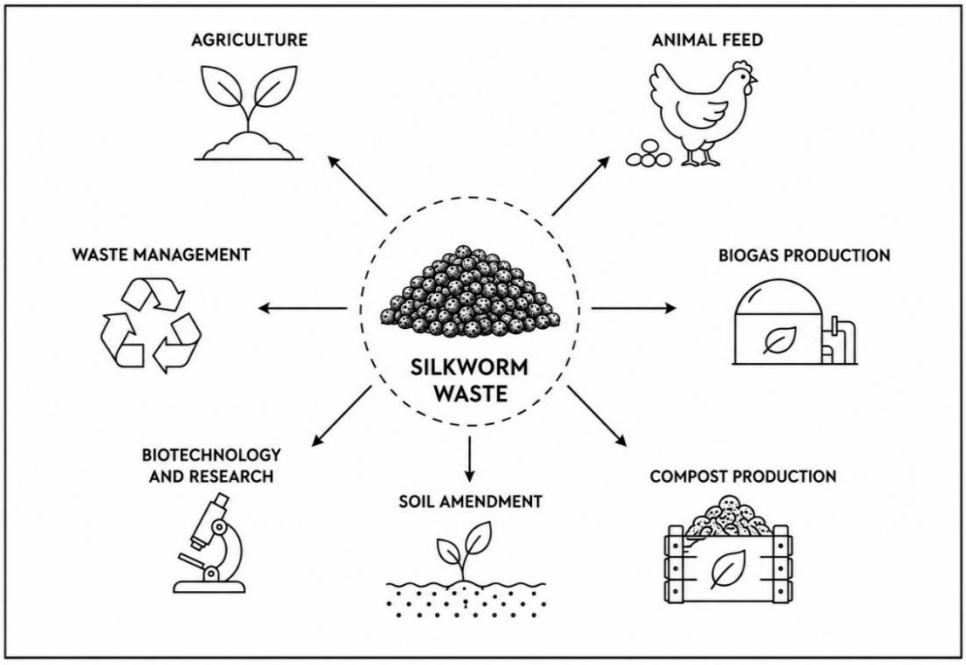


Figure 1. Applications of silkworm excrement

The economic potential of sericulture is determined not only by its primary product, silk filament, but also by the effective utilization and valorization of its various by-products, including silkworm pupae, excrement, and other rearing residues. Ensuring the long-term sustainability of sericulture and creating opportunities to increase the income of silkworm producers will therefore depend, at least in part, on the commercialization of these by-products and the development of new value-added applications (Hăbeanu et al., 2023).

Silkworm excrement (SE), which is commonly regarded as an agricultural waste, can be transformed into value-added products through appropriate processing, modification, fermentation, or extraction of its bioactive constituents. Such approaches can simultaneously reduce the environmental burden associated with SE disposal and contribute to circular-economy principles by returning organic resources and nutrients to productive systems. Recent studies have highlighted the potential of SE for a broad range of applications, including organic fertilizers and compost, animal and fish feed, vermicomposting, biogas production, natural dyes, bioactive compounds, activated carbon and other functional carbon materials, as well as microbial and biotechnological processes (Zhang et al., 2025). In this context, identifying and evaluating the diverse valorization pathways of SE is important not only for increasing the economic value of a previously underutilized sericultural by-product but also for reducing the environmental impacts associated with its accumulation and disposal. Moreover, the conversion of SE into higher-value products can enhance resource-use efficiency across the sericulture value chain and support the transition from a linear production model toward a more integrated circular bioeconomy. Therefore, this chapter critically reviews the structural and chemical composition of silkworm excrement and its current and emerging applications based on the recent scientific literature, with particular emphasis on its potential for value addition, waste reduction, and sustainable resource utilization.

Structural and Chemical Composition of Silkworm Excrement

Silkworm excrement is primarily composed of organic matter and ash, which have been reported to account for approximately 84-90% and 10-16% of its dry matter, respectively (Neelagund et al., 2007). Buhroo et al. (2018) reported that silkworm excrement contained 7.35% moisture, 13.88% crude protein, 1.44% crude fat, 15.41% crude cellulose, and 47.15% nitrogen-free extract. However, the reported values may vary considerably depending on the silkworm strain, larval developmental stage, mulberry cultivar, feeding conditions, and analytical methodology. For example, Łochyńska and Frankowski (2018) reported, on a dry-matter basis, 13.0% ash, 3.75% nitrogen, 42.31% carbon, 20.24% cellulose, 54.82% holocellulose, and 14.76% lignin in silkworm excrement, demonstrating its considerable carbonaceous and fibrous character.

The chemical composition of SE is closely related to the nature of the material passing through the silkworm digestive tract. Approximately 60% of the mulberry leaves consumed by silkworms may be excreted without complete digestion, whereas the remaining fraction undergoes enzymatic and microbial transformation in the digestive tract (Tang et al., 2024). Consequently, SE retains many of the chemical constituents of mulberry leaves while also containing metabolites and transformed compounds generated during digestion. Comparative metabolomic studies have provided evidence that silkworm metabolism can selectively retain, transform, and in some cases enrich specific bioactive compounds originally present in mulberry leaves. For example, Zhang et al. (2019) demonstrated dynamic transformation and enrichment of polyhydroxy alkaloids, including 1-deoxynojirimycin (DNJ), fagomine, and their derivatives, during silkworm feeding and excretion. Similarly, comprehensive chemical profiling has shown that fresh SE contains diverse flavonoid glycosides and Diels–Alder-type compounds, although some of these compounds may undergo degradation during storage, indicating that storage conditions can substantially affect the chemical profile and functional properties of SE (Zhang et al., 2020). These findings suggest that SE should not be regarded simply as undigested mulberry leaf residue; rather, it represents a chemically transformed biological material containing structural carbohydrates, proteins, minerals, and a range of secondary metabolites. Its relatively high carbon and cellulose contents, together with its ordered microstructure, also contribute to its suitability as a precursor for carbon-based functional materials and other biotechnological applications (Zhang et al., 2025). Therefore, the composition of SE should be evaluated in relation to both its nutritional characteristics and its bioactive and structural components, since these properties collectively determine its suitability for applications in animal nutrition, agriculture, biotechnology, biomaterial production, and other value-added processes.

Bioactive and Nutritional Components of Silkworm Excrement

The SE contains a variety of nutrients and organic compounds, including structural carbohydrates, lipids, proteins, and amino acids (Lu et al., 2018). In addition to these major components, SE contains several biologically active substances, including chlorophyll and its derivatives, flavonoids, and carotenoids (Li et al., 2021; Uzakova et al., 1987). The presence of these compounds is largely associated with the incomplete digestion and biotransformation of mulberry-derived constituents within the silkworm digestive tract. Uzakova et al. (1987) reported that the lipid fraction of SE was particularly rich in lipophilic compounds such as phytosterols, unsaturated fatty acids, phytol, carotenoids, and chlorophylls. Subsequent phytochemical investigations have identified several lipophilic bioactive compounds in silkworm excrement, including the phytosterols β-sitosterol and lupeol and the very-long-chain fatty alcohol 1-tritriacontanol, highlighting its potential as a source of bioactive lipid-related

compounds (Vimolmangkang et al., 2014). For example, phytochemical investigations of Bombyx mori droppings have led to the isolation of β-sitosterol, corchorifatty acid E methyl ester, and (8E)-10-hydroxydec-8-enoic acid methyl ester, highlighting the presence of structurally diverse lipid constituents in silkworm excrement (Sohn et al., 2009). Hashimoto et al. (2024) reported concentrations of protein, lipid, carbohydrate, sodium, potassium, iron, calcium, α-tocopherol, and β-carotene in SE of 18.6 g/kg, 3.7 g/kg, 55.2 g/kg, 3 mg, 3,503 mg, 20 mg, 2,875 mg, 8.4 mg, and 4.4 mg, respectively.

The chemical composition of SE is not constant and can be substantially affected by silkworm genotype, developmental stage, diet, mulberry cultivar, and rearing conditions. Diet appears to be particularly important because modern sericulture increasingly uses artificial diets to facilitate year-round production. Tagawa et al. (2023) demonstrated that the biological activities and functional constituents of SE from artificially fed silkworms could approach those observed in silkworms subsequently switched to a mulberry-leaf diet from the fifth larval instar, indicating that the chemical profiles of SE can change relatively rapidly in response to dietary conditions. Consistent with this observation, Qin et al. (2020) reported that, compared with silkworms fed mulberry leaves, artificially fed silkworms produced excrement with significantly lower levels of several amino acids, carbohydrates, and lipids, whereas metabolites such as urea and citric acid were markedly increased. These findings indicate that the nutritional and metabolic composition of SE is strongly diet-dependent and that changes in feed composition can rapidly modify the profiles of compounds excreted by silkworms. This dietary dependence is particularly relevant when SE is intended for specific applications, because its suitability as a feed ingredient, fertilizer, source of bioactive compounds, or raw material for biomaterial production may depend on the rearing system from which it originates.

Recent metabolomic and chemical studies further suggest that SE should be considered a metabolically transformed biological material rather than simply undigested mulberry-leaf residue (Li et al., 2021). Silkworm digestion can selectively retain, degrade, or transform plant-derived compounds, while the gut microbiota may contribute additional metabolic transformations (Zhang et al., 2020; Zhang et al., 2025). Consequently, characterization of the feed and rearing conditions is essential for standardizing the composition and functional properties of SE intended for value-added applications.

Applications of Silkworm Excrement

The SE, one of the major by-products of sericulture, represents a largely underutilized biomass resource with considerable potential for valorization. The amount generated can be substantial even at the small-farm level; for example, Łochyńska and Frankowski (2018) estimated that a small-scale silkworm-rearing

operation could generate approximately 250-300 kg of silkworm waste in a production period.

The diverse chemical composition of SE, including structural carbohydrates, proteins, lipids, minerals, chlorophylls, carotenoids, vitamins, and other bioactive compounds, provides a basis for its utilization in a wide range of applications. Historically, SE has been investigated as a source of chlorophyll and porphyrin-related compounds, intermediates for the production of vitamins E and K, and protein–mineral supplements for animal feeding (Uzakova et al., 1987). Importantly, the valorization potential of SE extends beyond direct use of the raw material. Following the extraction of bioactive and lipid-soluble compounds, the remaining solid fraction can also be further processed into useful products, thereby enabling a cascade approach to biomass utilization. Such compounds and derivatives have potential applications in pharmaceutical, nutraceutical, and cosmetic products, while pigment-related compounds present in silkworm excrement can also be exploited as natural dyes and functional materials for various industrial applications (Ju et al., 2014; Tang et al., 2024).

Recent research has considerably expanded the range of potential applications of silkworm excrement (SE), demonstrating its suitability for organic fertilizer and compost production, animal and aquatic feed, vermicomposting, anaerobic digestion and biogas production, microbial fermentation, natural pigment extraction, and the preparation of activated carbon and other functional carbon-based materials (Zhang et al., 2025; Xue et al., 2025). In particular, the high carbon content and cellulose-rich structure of SE make it a promising precursor for carbonaceous materials, while its residual nutrients and biologically active compounds support its use in agricultural and biotechnological applications. Therefore, rather than being considered a single-purpose agricultural waste, SE can be viewed as a multifunctional biomass resource that can be fractionated and converted into different value-added products. This cascade valorization strategy may improve resource-use efficiency, reduce waste-management costs and environmental impacts, and increase the economic value generated throughout the sericulture production chain.

Use of Silkworm Excrement in Animal Diets

The SE has attracted increasing attention as a potential alternative feed resource because of its relatively low cost and its content of protein, fiber, minerals, pigments, and other bioactive compounds. Feed costs constitute a major proportion of total livestock production costs, and corn is one of the most widely used energy ingredients in animal diets. According to Xue et al. (2025), corn was priced at approximately 2,920 RMB per ton, whereas fermented silkworm excrement was reported to have a market price of approximately 600 RMB per ton; when processed directly by sericulture farmers, the processing cost could be reduced to approximately 60 RMB per ton. Therefore, partial replacement of

conventional feed ingredients with appropriately processed SE may provide an economically attractive strategy for simultaneously managing sericultural waste, reducing environmental burdens, and lowering feed costs (Xue et al., 2025).

The nutritional characteristics of SE support its potential use as a feed ingredient. SE contains appreciable levels of crude protein, fiber, minerals, and other nutrients, although its composition can vary considerably depending on the mulberry diet, rearing conditions, and the proportion of residual leaf material. In addition to conventional nutrients, SE contains biologically active compounds, including chlorophyll-derived pigments, carotenoids, flavonoids, and phytosterols, which may provide additional functional value when SE or its extracts are incorporated into animal diets at appropriate levels. Recent feeding studies have also demonstrated that SE and SE-derived products can influence growth performance, antioxidant status, lipid metabolism, and immune responses, although these effects are strongly dependent on the inclusion level and form of the material used. Therefore, the nutritional and functional value of SE should be evaluated based on its complete nutrient and bioactive compound profile, together with processing conditions and dietary inclusion level, rather than on crude protein concentration alone (Qu et al., 2018; Jia et al., 2024; Xue et al., 2025; Yang et al., 2026).

Nevertheless, caution is required when considering SE as a feed ingredient. The material may contain residual mulberry leaf material and a complex mixture of compounds originating from silkworm metabolism and the rearing environment. In addition, the chemical composition of SF can change during storage, indicating that freshly collected and processed materials may differ in their nutritional and chemical profiles. Zhang et al. (2020) reported significant differences in the chemical composition of fresh and commercially stored silkworm excrement, suggesting that storage and processing conditions should be considered when evaluating its suitability as a feed ingredient. Therefore, SE intended for animal feeding should be obtained from well-managed silkworm production systems and should be appropriately dried, stored, or otherwise processed to minimize potential microbiological and chemical risks.

Fermentation has also been proposed as a strategy for improving the utilization of SE. A recent review reported that fermented silkworm excrement products may contain increased crude protein concentrations and improved natural-fiber degradation characteristics compared with untreated material, indicating that fermentation may enhance its potential as a feed resource (Yuan et al., 2025; Zhang et al., 2025). However, these potential benefits should be interpreted cautiously, as the effects of fermentation depend on the microorganisms, fermentation conditions, substrate characteristics, and processing duration. Further controlled feeding studies are therefore needed to

determine whether improvements in chemical composition and fiber degradation translate into greater nutrient availability and animal performance.

From a sustainability perspective, the utilization of SE in animal nutrition offers an opportunity to convert a readily available by-product of sericulture into a value-added feed resource. Large quantities of SE are generated during silkworm rearing, and its inappropriate disposal or uncontrolled accumulation may create environmental and biosecurity concerns. Incorporating SE into livestock diets may therefore contribute to circular bioeconomy approaches by recovering nutrients from the sericulture production chain, reducing the amount of biomass requiring disposal, and partially replacing conventional feed resources.

-Use of silkworm excrement in ruminant nutrition

The potential of SE as a feed ingredient for ruminants has been investigated particularly in goats and sheep. Bai et al. (2011) evaluated the ruminal degradation and digestion characteristics of SE in goats and reported effective degradation rates of 43.32%, 5.47%, and 36.05% for dry matter, crude protein, and crude fiber, respectively. In meat goats, apparent digestibility coefficients of crude fiber, neutral detergent fiber, and acid detergent fiber were reported as 73.93%, 70.86%, and 68.68%, respectively, indicating that a substantial proportion of the fiber fraction of SE can be utilized by ruminants. These findings suggest that, in addition to its protein and mineral contributions, the fibrous fraction of SE may have nutritional value for ruminants and could support its use as a complementary fibrous feed ingredient.

The feeding potential of SE has also been evaluated in sheep nutrition by Tian et al. (2008) who reported that sheep fed a diet containing 80% SE achieved a total body weight gain of 9.70 kg during the experimental period, which was 1.20 kg greater than that of sheep receiving a diet based on 100% concentrate. These findings suggest that SE can be utilized at relatively high dietary inclusion levels without adversely affecting growth performance and may have potential as a partial substitute for conventional concentrate feeds. However, the exceptionally high inclusion level evaluated in this study should be interpreted with caution and should not be directly extrapolated to practical feeding systems.

The relatively high fiber content and moderate crude protein concentration of SE indicate its potential as an alternative fibrous feed resource for ruminants. Qu et al. (2018) reported that SF contained approximately 14.75-17.08% crude protein and 30.69-35.92% neutral detergent fiber (NDF) on a dry matter basis, although considerable variation was observed among samples collected from different locations. The authors also reported differences in crude protein, fiber fractions, ash, calcium, and other nutritional characteristics among silkworm feces, mulberry leaves, and mulberry leaf stems, highlighting the influence of material origin and composition on its feeding value. Therefore, rather than

assuming a uniform nutritional profile the chemical composition and nutritive value of SE should be assessed on a batch-specific basis before its inclusion in experimental or commercial diets. Such characterization is particularly important when SE is considered as a partial replacement for conventional roughage sources, as variation in fiber concentration, protein content, and mineral composition may affect nutrient supply and animal performance.

Overall, the available evidence indicates that SE has potential as a low-cost alternative feed ingredient for ruminants, particularly as a source of fermentable fiber and supplementary nutrients. However, compared with conventional feedstuffs, the number of controlled feeding studies is still limited. More research is needed to establish optimum inclusion levels for cattle, sheep, and goats and to determine its effects on feed intake, nutrient digestibility, rumen fermentation, microbial protein synthesis, growth performance, carcass characteristics, and animal health. Importantly, future studies should use nutritionally balanced diets in which the inclusion of SE is evaluated at realistic levels rather than replacing large proportions of the diet without correcting for differences in protein, energy, mineral, and fiber concentrations.

Sun et al. (2015) investigated the effects of different dietary inclusion levels of SE on growth performance, slaughter performance, organ development, and serum biochemical parameters in sheep. In their experiment, 32 sheep were randomly assigned to four dietary treatments containing 0% (control), 20% (T20), 30% (T30), or 40% (T40) SE. Following a 15-day adaptation period, the animals were fed the experimental diets for 60 days. The average daily gain of sheep receiving 20% and 30% SE was numerically higher than that of the control group and significantly higher than that of the 40% SE group. These results suggest that moderate inclusion levels of SE, particularly 20–30% of the diet, may be more suitable for maintaining growth performance than a higher inclusion level of 40%. More broadly, the findings indicate that SE can be incorporated into sheep diets at substantial levels, although the optimal inclusion rate may depend on the composition of the basal diet and the characteristics of the SE used. Further research is warranted to establish optimal inclusion levels and to clarify the nutritional and physiological mechanisms underlying the responses to different dietary concentrations (Sun et al., 2015).

-Use of silkworm excrement in poultry nutrition

The SEhas potential as an alternative feed ingredient in poultry nutrition because of its relatively high protein and mineral contents and its continuous availability in silk-producing regions (Qu et al., 2018; Xue et al., 2025). The nutritional composition of SE is influenced by factors such as mulberry leaf quality, silkworm developmental stage, rearing conditions, and processing methods. In poultry diets, the use of SE may contribute to the valorization of a low-cost agricultural by-product while reducing dependence on conventional

feed ingredients. However, its relatively high ash and fiber contents should be considered when determining dietary inclusion levels, as excessive incorporation may dilute the concentrations of other nutrients and, due to its fiber fraction, potentially reduce nutrient digestion and feed utilization (Qu et al., 2018; Zhang et al., 2025; Xue et al., 2025). Therefore, SE should preferably be incorporated into nutritionally balanced diets at appropriate inclusion levels rather than being considered a direct substitute for conventional protein sources. Given the variability in its chemical composition and the potential effects of its relatively high fiber and ash contents on nutrient utilization, the inclusion level of SE should be carefully adjusted according to the nutrient profile of the basal diet (Qu et al., 2018; Xue et al., 2025). Further research is needed to establish the optimum dietary inclusion levels of SE in broilers and laying hens and to evaluate its effects on growth performance, feed efficiency, carcass characteristics, egg production, egg quality, nutrient digestibility, and intestinal health. In particular, controlled feeding trials using nutritionally balanced diets are needed to determine whether the inclusion of SE can provide measurable benefits without compromising nutrient utilization or animal performance (Xue et al., 2025).

The use of SE as an unconventional feed ingredient has also been investigated in poultry, although the available evidence remains relatively limited compared with that in ruminants and aquaculture species. Early studies in laying hens indicated that SE could serve as a dietary source of carotenoid pigments and thereby influence egg yolk pigmentation. Yamada and Saito (1957) reported that dietary inclusion of 5% SE approximately doubled the xanthophyll concentration of egg yolk, whereas further increases in the inclusion level resulted in a progressively smaller response. Based on these observations, relatively low inclusion levels of approximately 1-3% may be sufficient when SE is used primarily as a natural pigmentation source. However, higher inclusion levels were associated with adverse effects on egg production and digestive performance, indicating that the use of SE should be carefully controlled when incorporated into poultry diets. More recently, SE has also been investigated as a potential feed ingredient in broiler chickens and geese. In broiler chickens, dietary inclusion of SE was reported to improve body weight gain, while in geese, its supplementation influenced growth-related and meat-quality characteristics, indicating that the potential application of SE in poultry nutrition extends beyond its traditional use as a natural source of carotenoid pigments (Zheng et al., 2003; Yang et al., 2015; Zhang et al., 2025).

The dietary inclusion of SE was associated with approximately 3.8%, 4.8%, and 4.5% higher average body-weight gain in broilers during the early, late, and overall experimental periods, respectively, compared with the control group (Zheng et al., 2003; Zhang et al., 2025). These findings suggest that dietary SE may have the potential to support growth performance in broiler chickens; however, the magnitude and consistency of this response should be interpreted

cautiously given the limited number of available studies. In Yangzhou geese, Yang et al. (2015) evaluated different dietary inclusion levels of SE and reported significant effects on meat quality and muscle nutrient composition. SE supplementation was resulted in increased moisture content in both breast and leg muscles, whereas crude protein and crude fat concentrations were reduced. In addition, dietary SE affected breast-muscle color and leg-muscle shear force, suggesting that SE inclusion may influence not only growth performance but also certain physicochemical and quality characteristics of poultry meat (Yang et al., 2015; Zhang et al., 2025). Overall, these findings indicate that SE may have potential as an unconventional feed ingredient in poultry nutrition, although further controlled studies are required to establish appropriate inclusion levels and to determine its effects on nutrient utilization and productive performance.

In addition, previous studies indicated that the supplementation of SE in gosling diets at low inclusion levels (3% and 6%) caused any adverse effect on growth performance or carcass-related traits, whereas higher inclusion levels of 9-12% reduced the body weight and breast muscle percentage (Yang et al., 2015; Zhang et al., 2025). These findings suggest that the nutritional effects of SE may be dependent on the dietary inclusion level and may vary according to animal species and production purpose. Collectively, the available evidence indicates that SE has potential as an unconventional feed ingredient for poultry, particularly as a source of carotenoid pigments and supplementary nutrients. However, the limited number of controlled studies and the variation in responses among dietary inclusion levels highlight the need for further research. In particular, well-designed feeding trials using nutritionally balanced diets are required to establish appropriate inclusion levels of SE for broilers and laying hens and to evaluate its effects on growth performance, feed efficiency, egg production, egg quality, nutrient digestibility, and intestinal health. The main findings of different studies investigating the use of SE in poultry nutrition are presented in Table 1.

Table 1. Summary of studies investigating the use of SE in poultry nutrition

Poultry species	**SE level**	**Main findings**	**Reference**
Laying hens	1-3%	Recommended as an appropriate inclusion level for egg yolk pigmentation.	Yamada and Saito (1957)
	5%	An approximately twofold increase in the xanthophyll content of egg yolk.	
	>5%	A reduced pigmentation response as adverse effects reported at higher inclusion levels.	
Geese	3-6%	No marked adverse effects on growth performance or carcass characteristics.	Zhang (2015)

Poultry species	SE level	Main findings	Reference
	9-12%	Reductions in body weight and breast muscle percentage.	
Broilers	-	Average body-weight gain in the SE-supplemented groups approximately 3.8%, 4.8%, and 4.5% higher during the early, late, and overall periods, respectively.	Zheng and Li (2003)

-Use of silkworm excrement in aquaculture nutrition

The SE is rich in protein, essential minerals, and bioactive compounds such as flavonoids and chlorophyll. This unique composition also makes it a promising functional feed additive for aquaculture (Yang et al., 2026). In particular, it helps improve soil fertility, increase electrical conductivity, enhance physicochemical properties, immobilize heavy metals, and promote microbial activity (Zhang et al., 2025). Mastewal et al. (2018) found that SE is a good source of nutrients and promotes growth in fish, reporting that its inclusion in fish diets at levels of up to 15% had no adverse effects on fish growth or health. Hao et al. (2026) also reported that the inclusion of SE at 10-15% in fish diets significantly improved antioxidant activity, growth performance, intestinal function, and glucose and lipid utilization by reducing serum alanine aminotransferase and malondialdehyde levels and increasing serum catalase activity as well as hepatic acid and alkaline phosphatase activities. Yang et al. (2026) determined that two value-added products derived from SE including silkworm excrement concentrated extract (SCE) and sodium copper chlorophyll (SCC) were effective functional additives for common carp and that both significantly improved lipid metabolism. In conclusion, they reported that SCE provides broad-spectrum synergistic benefits suitable for holistic health management, whereas SCC provides specific biological activity, emphasizing the importance of selecting additives based on the desired functional outcomes in aquaculture.

Asfaw et al. (2018) investigated the potential of SE as an alternative feed ingredient (0, 5, 10, and 15% by replacing the basal diet) for Nile tilapia (*Oreochromis niloticus*) in an aquaculture system in Ziway, Southern Ethiopia. It has been indicated that the body weight gain, body length, fillet crude protein content, and Fulton's condition factor did not differ significantly among dietary treatments. Based on these findings, The SE could be included in Nile tilapia diets at levels of up to 15% without noticeable adverse effects on growth performance or fish health (Asfaw et al., 2018).

The SE, an abundant by-product of sericulture, has recently gained attention as a promising natural dye for sustainable textile applications. Its coloring properties are mainly associated with chlorophyll and its degradation products derived from mulberry leaves. In particular, chlorophyll-derived pyropheophytins are present in SE as a result of enzymatic and microbial processes occurring during digestion. These compounds exhibit high thermal and light stability, enhancing the durability of SE-derived coloration. Vila et al. (2018) demonstrated that aqueous SE extracts could successfully dye silk and polyamide 6.6 fabrics, producing mainly yellowish-brown shades, with silk showing higher dye uptake and good to excellent washing and rubbing fastness. More recently, Tang et al. (2024) reported that pyropheophytins in SE can interact with amino acid groups in protein fibers around their isoelectric point (approximately pH 4.8), producing deep green-brown shades with satisfactory washing and light fastness. SE-dyed fabrics also exhibited functional properties such as UV protection and antioxidant activity. Moreover, SE-based dyeing required lower amounts of water and chemicals, indicating its potential as a more environmentally friendly alternative to conventional dyeing methods. Overall, these findings highlight SE as a valuable bio-based colorant that can contribute to waste valorization and more sustainable textile production.

Use of Silkworm Excrement for the Production of Carbon Materials

The SE has recently emerged as a promising biomass precursor for carbon-based functional materials due to its abundant availability, carbon-rich organic fraction, naturally occurring heteroatoms and minerals, and unique layered structure. Carbon materials are widely used as adsorbents because of their environmental compatibility, structural stability, and large specific surface areas (Fu et al., 2026). In particular, the unique nanosheet structure and intrinsic carbon and heteroatom content of SE make it a suitable precursor for porous carbon and carbon-composite materials (Wu et al., 2023). Lei et al. (2018) reported that SE could be converted into N, P, S, and O-doped carbon electrodes with high surface areas and well-developed porosity, showing promising performance for supercapacitor applications. Similarly, Zhang et al. (2019) demonstrated the potential of SE-derived mesoporous carbons as cost-effective supercapacitor electrode materials.

SE-derived carbon materials have also shown considerable potential for environmental remediation. Wang et al. (2014) prepared activated carbons from SE using different chemical activators, obtaining well-developed microporous structures and high adsorption capacities for methylene blue and Cd^{2+}. More recently, Li et al. (2025) developed porous carbon from phosphoric-acid-modified SE for the efficient removal of radioactive iodine, while Fu et al. (2026) reported that SE-derived biochar could serve as an effective adsorbent for persistent tetracycline antibiotics. Microwave-assisted activation has further

enabled the production of highly porous activated carbon and carbon–silica composites with excellent adsorption and supercapacitor performance (Pimsawat et al., 2024; 2025). In addition, SE has been used as a precursor for fluorescent carbon dots with potential applications in chemical and metal-ion sensing (Huang et al., 2019; Zhang et al., 2025).

Overall, these studies demonstrate that SE can be valorized into a range of high-value carbon-based materials, including activated carbons, mesoporous carbons, carbon–silica composites, biochar, and carbon dots. Its abundance, low cost, renewable nature, and intrinsic carbon and heteroatom content make SE an attractive precursor for sustainable functional materials (Lu et al., 2018; Wu et al., 2023). Thus, SE valorization offers a promising circular-bioeconomy strategy that combines waste reduction with the production of functional materials for environmental remediation, sensing, and energy storage.

Health and Pharmaceutical Applications of Silkworm Excrement

The SE has a long history of use in traditional East Asian medicine and has recently attracted scientific interest as a valuable source of bioactive compounds. Its chemical composition includes flavonoids, phytosterols, fatty alcohols, carotenoid-related compounds, chlorophyll derivatives, and other plant-derived metabolites originating primarily from mulberry leaves and undergoing metabolic transformation during digestion (Wang et al., 2020). Historically, SE has been used for conditions such as rheumatic pain, headache, abdominal disorders, skin diseases, and other inflammatory conditions (Vimolmangkang et al., 2014; Singh & Jayasomu, 2002). Vimolmangkang et al. (2014) isolated 1-tritriacontanol, lupeol, and β-sitosterol from SE, while Uzakova et al. (1987) reported that its high sterol content, particularly β-sitosterol, makes SE a potential source of phytosterols with applications in cardiovascular health. SE extracts have also demonstrated antioxidant activity, with their biological effects depending on the extraction solvent and procedure (Ju et al., 2014).

Increasing evidence suggests that SE and its constituents possess diverse biological activities. Duan et al. (2021) demonstrated that SE extract inhibited α-glucosidase activity in vitro and suggested that the AMPK/PI3K/Akt signaling pathway may contribute to its hypoglycemic effects. SE has also shown potential in dermatological applications, as its methanolic extract exhibited depigmenting activity in a zebrafish model (Kim et al., 2018). Furthermore, SE extracts have been investigated for their potential role in iron metabolism and anemia. Huang et al. (2017) reported that SE supplementation not only provided iron but also modulated iron-regulatory pathways and suppressed hepcidin expression, thereby promoting the release of stored iron. Similarly, Li et al. (2021) found that SE extract improved hematological parameters in an animal model of renal anemia, suggesting potential effects on erythropoiesis and iron metabolism. Other recent studies have reported potential anti-inflammatory, antitumor, and neuroprotective

effects associated with SE-derived compounds, including polyphenols, flavonoids, chlorophyll, and phytol (Zheng et al., 2018; Song et al., 2023; Bao et al., 2025). In addition, SE-derived biochar has demonstrated free-radical-scavenging and antioxidant activity, highlighting its potential for biomedical applications (Liu et al., 2022).

Another important aspect of SE is its potential as a source of antimicrobial peptides (AMPs). Silkworms possess a diverse repertoire of AMPs, including attacins, cecropins, defensins, enbocins, gloverins, lebocins, and moricins, which contribute to innate defense against bacteria, fungi, and viruses (Makwana et al., 2023). The presence of antimicrobial and antiviral peptides in the feces of healthy silkworms suggests that SE may represent an economical and environmentally friendly source of biologically derived antimicrobial agents (Patnaik et al., 2012). In addition, SE may serve as a source of beneficial microorganisms. Suraporn et al. (2024) isolated five lactic acid bacterial strains from SE that exhibited bile salt hydrolase activity, epithelial adhesion capacity, and favorable antibiotic susceptibility profiles, suggesting their potential application as probiotics in animal feed. Such microorganisms may contribute to the prevention of viral and bacterial infections and improvement of host health.

SE also serves as a potential raw material for pharmaceutical and food-related products. Chlorophyll obtained from SE has traditionally been used for certain gastrointestinal and hepatic disorders, while its solanesol content makes it a potential source of precursors for pharmaceutical compounds (Singh & Jayasomu, 2002). Chlorophyll derived from SE has also been reported in traditional Chinese medicine for applications related to hepatitis, leukemia, and recovery from cancer treatments (Ding et al., 2021). Taken together, these findings demonstrate that SE contains a diverse range of bioactive compounds and may have antioxidant, antimicrobial, hypoglycemic, anti-inflammatory, dermatological, hematological, and other therapeutic potentials. However, most current evidence is based on in vitro studies or animal models; therefore, further pharmacokinetic, toxicological, clinical, and standardized-dose studies are required before SE-derived products can be established as therapeutic applications in humans.

Use of Silkworm Excrement as a Tea Beverage

The SE, also referred to as silkworm frass or silkworm feces, has traditionally been used in East Asian medicine and has recently attracted attention as a novel ingredient for tea and other beverage applications. In traditional Chinese medicine, dried SE (Can-Sha) has been used for various purposes, and its potential bioactive properties are associated with compounds originating from mulberry leaves and their metabolic derivatives (Duan et al., 2021). Since silkworms feed exclusively on mulberry leaves, the chemical composition of their excrement partially reflects that of the leaves, which may contribute to its

traditional use as a medicinal material (Li et al., 2021). Although insect-feces teas have traditionally been consumed in some regions, their consumption remains relatively limited outside China, partly because research has focused more on their traditional use and chemical composition than on their nutritional and sensory properties (Chou et al., 2018).

More recently, Rodríguez Valerón et al. (2024) investigated SE as a novel culinary tea ingredient by evaluating the effects of roasting conditions on its physicochemical properties, volatile compounds, flavor profile and consumer acceptance. Silkworm frass was roasted at 160 °C for 0, 30, 40, and 50 min before being prepared as a tea infusion. Roasting substantially affected moisture content, water activity, color, and pH, while volatile analysis identified 65 compounds, including alcohols, aldehydes, esters, ethers, ketones, phenols, pyrazines, and hydrocarbons. Sensory evaluation revealed characteristic earthy and roasted aromas, with additional notes such as roasted grain, brown herbal, tobacco-leaf, and cut-hay aromas depending on roasting duration. Importantly, roasting time did not significantly affect consumer acceptance of taste, flavor color, texture, or overall liking. These findings indicate that SE can be transformed into a novel tea-like beverage with favorable sensory characteristics and may represent a promising upcycled culinary product for the valorization of sericultural by-products (Rodríguez Valerón et al., 2024). However, further nutritional, toxicological, and clinical studies are required to establish its safety, health effects, and suitability for broader food and beverage applications.

Use of Silkworm Excrement as a Biological Substrate

The SE has considerable potential as a biological substrate for various bioconversion processes because it contains residual organic matter, cellulose, proteins, minerals, and other nutrients derived primarily from mulberry leaves (Łochyńska & Frankowski, 2018; Zhang et al., 2023). This nutrient-rich composition makes SE an attractive and sustainable alternative to conventional, often costly substrates used in biotechnological production. One of the earliest reported applications was its use in mushroom cultivation. Bisaria et al. (1989) demonstrated that silkworm litter could be utilized as a substrate for mushroom production while also serving as a nitrogen source, highlighting its potential for converting sericultural waste into value-added biological products.

More recently, SE has been investigated as a substrate for earthworm cultivation and vermicomposting. Qian et al. (2024) used composted SE as a substrate for *Eisenia foetida* and reported a 92.31% survival rate after 21 days, compared with 88.46% for earthworms maintained on cow manure. Although cow manure resulted in slightly greater weight gain and reproductive performance, the differences were not significant, indicating that SE can provide a suitable substrate for earthworm production and vermicompost generation. SE has also attracted attention as a nutrient-rich substrate for microbial fermentation

and enzyme production. Lu et al. (2023) demonstrated that SE could be used as the principal substrate for solid-state fermentation with *Aspergillus niger* to produce pectinase, while Lu et al. (2025) further confirmed its potential using optimized submerged fermentation. The latter study reported a maximum pectinase activity of 20.505 U/mL, demonstrating that SE can serve as a low-cost and sustainable substrate for industrial enzyme production. In addition, Wang et al. (2022) showed that SE could function as a carbon source in fermentation with Haloferax mediterranei for PHBV production, with a mixed carbon source containing SE extract and glucose increasing PHBV production by 26% compared with fermentation without SE.

Overall, these findings demonstrate that SE can function not only as a physical growth substrate but also as a valuable nutrient and carbon source for microorganisms and other biological organisms. Its application in mushroom cultivation, vermicomposting, enzyme production, and microbial bioconversion provides an effective approach for valorizing sericultural waste while reducing the cost of conventional substrates and supporting circular bioeconomy strategies.

Use of Silkworm Excrement as Compost

The SE represents a promising organic waste material for compost production and soil amendment because of its high organic matter and nutrient content. It contains substantial amounts of macronutrients such as nitrogen (N), phosphorus (P), and potassium (K), as well as secondary and micronutrients, making it a potentially valuable alternative to conventional organic fertilizers (Beesigamukama et al., 2022; Gowrisankar et al., 2025). Wang et al. (2016) reported that SE contained 2.97% N, 1.03% P, 3.52% K, and approximately 77.68–81.15% organic matter, while Łochynska and Frankowski (2018) demonstrated that its application could improve soil nutrient availability and microbial activity. However, fresh SE requires appropriate biological stabilization before direct agricultural application. Controlled composting can reduce the environmental risks associated with SE accumulation while converting it into a stable and nutrient-rich organic fertilizer.

Chen et al. (2011) demonstrated that controlled fermentation of SE increased total N, P, and K contents by 58.0%, 84.4%, and 29.7%, respectively, compared with the raw material. The resulting fertilizer showed a seed germination index above 80% and improved soil properties, plant nutrient content, and Chinese cabbage yield. Composting conditions can also be optimized through the addition of auxiliary materials. Chen et al. (2016) reported that SE supplemented with hydrated lime, effective microorganisms, or mulberry sawdust achieved satisfactory compost maturity, while mulberry sawdust reduced moisture content and effective microorganisms increased total phosphorus. More recently, Yang et al. (2025) showed that compost produced from SE and mulberry leaves under aerobic, high-temperature conditions improved soil pH, organic carbon, available

N and P, soil enzyme activities, and the abundance of beneficial bacterial groups, resulting in improved bamboo shoot yield.

Beyond its value as a fertilizer, SE can contribute to soil remediation. Shi et al. (2023) demonstrated that SE could immobilize As, Sb, Cd, Pb, and Cr in contaminated soils by increasing soil pH, reducing the availability of cationic metals, and binding metal(loid)s through functional groups such as carboxyl and hydroxyl groups. SE application may also promote the restoration of soil microbial communities and nutrient cycling. Shen et al. (2024) found that SE compost had high nutritional value, relatively low heavy-metal concentrations, and diverse beneficial microorganisms, including Klebsiella pneumoniae and Bacillus licheniformis, which were associated with plant growth promotion, biological control, and feed-related functions. Similarly, SE application has been shown to improve plant growth and yield while enhancing soil physical, chemical, and biological properties (Łochynska & Frankowski, 2019, 2022; Aboyo et al., 2025; Luan et al., 2025).

SE also shows potential in microbial soil remediation. Chen et al. (2026) reported that an immobilized Pseudomonas aeruginosa PS1 preparation using SE significantly enhanced the degradation of phthalate esters and reduced their accumulation in plant products by 81–90%, while selectively enriching key degrading bacterial groups such as Proteobacteria and Bacteroidetes. This approach illustrates how SE can serve as both a waste-derived carrier and a functional component of sustainable bioremediation systems.

Overall, these findings demonstrate that SE can be effectively valorized through composting and direct soil application to produce organic fertilizers, improve soil fertility and microbial activity, support plant growth, and contribute to the remediation of contaminated soils. Its abundant nutrient content, low cost, and renewable nature make SE a promising alternative to synthetic fertilizers and a valuable resource within a circular bioeconomy. Nevertheless, further research is needed to establish crop-specific application rates, optimize composting conditions, and assess the long-term environmental safety of SE-based soil amendments.

Use of Silkworm Excrement for Biogas Production

The SE is a promising substrate for anaerobic digestion and biogas production because it contains considerable amounts of biodegradable organic matter, including carbohydrates, proteins, and other organic compounds remaining after silkworm digestion of mulberry leaves. The potential of SE for methane production was systematically evaluated by Łochyńska and Frankowski (2018), who compared silkworm excrement with silkworm breeding waste under mesophilic anaerobic digestion conditions. Both substrates were efficiently degraded within 19 days, and approximately 80% of

the cumulative methane production was obtained during the first 10 days of fermentation. The SE produced 331.97 m³ of biogas and 167.32 m³ of methane per Mg of total solids (TS), with a methane concentration of approximately 50.4%. When expressed on a volatile total solids basis, methane production reached 211.59 m³/Mg VTS. The authors concluded that the methane yield of SE was comparable to that obtained from several conventional agricultural substrates and demonstrated that silkworm excrement could serve as a valuable feedstock for renewable energy production (Łochyńska & Frankowski, 2018). The relatively rapid degradation of SE was attributed to its content of readily biodegradable organic compounds. Interestingly, methane production from SE showed two distinct peaks, with the second peak associated with the degradation of more complex compounds, including lipids and fatty acids derived from larval metabolism (Łochyńska & Frankowski, 2018). In a previous study, silkworm larval litter was co-digested with cashew nut fruit waste and dairy manure under mesophilic conditions at approximately 35 °C. The results demonstrated that appropriate combinations of these substrates could increase biogas and methane production compared with individual substrates, highlighting the potential of co-digestion to balance nutrient composition and improve anaerobic digestion efficiency (Narendra et al., 2022). Beyond direct energy recovery, the anaerobic digestion of silkworm waste also provides an integrated waste-management pathway because the process generates both biogas and a nutrient-containing digestate that can potentially be further utilized as an organic fertilizer. Thus, anaerobic digestion may contribute to a circular bioeconomy in sericulture by converting silkworm excrement and other rearing residues into renewable energy and agricultural inputs. Nevertheless, further studies are required to optimize substrate preparation, loading rate, C/N ratio, hydraulic retention time, and co-digestion strategies at pilot and industrial scales.

Conclusion

Silkworm excrement should not be regarded merely as an agricultural waste but as a multifunctional and valuable bioresource. Its diverse chemical composition enables its utilization in a wide range of applications, including organic fertilizers, animal feed, compost, biogas production, natural dyes, carbon-based materials, and pharmaceutical and biotechnological products. Valorization of SE can contribute to waste reduction, nutrient recycling, resource-use efficiency, and the development of additional economic opportunities within the sericulture sector. However, its composition and functional properties may vary depending on the silkworm diet, genotype, developmental stage, and rearing conditions, highlighting the need for standardization and further research. Overall, the effective utilization of SE represents a promising approach for supporting circular economy principles and developing more sustainable and environmentally friendly sericulture systems.

CHAPTER 15

From Traditional Livestock Farming to Future Production Systems: Transformation in Animal Production

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1. Introduction

Throughout human history, livestock production has been not only an activity aimed at providing food but also an important component of rural economies, livelihoods, agricultural production systems, and the social structure of societies. Animal-source foods, particularly meat, milk, and eggs, contribute to the provision of high-quality proteins as well as a range of highly bioavailable micronutrients, while livestock production provides income, employment, capital accumulation, and food security under a wide variety of ecological and socioeconomic conditions worldwide. Animals can also convert pasture resources that cannot be directly utilized for crop production and various biological resources unsuitable for human consumption into food, provide organic fertilizer, and contribute to maintaining nutrient cycles in mixed farming systems. Therefore, the role of livestock within food systems is too multidimensional to be assessed solely in terms of the quantity of animal products produced. Indeed, livestock value chains are reported to be associated with the livelihoods of more than one billion people worldwide, with animals playing particularly critical roles in economic and social resilience among smallholder farmers and pastoral communities (FAO, 2023; Thornton et al., 2024a). This importance is even more pronounced in low- and middle-income countries; Adesogan et al. (2025) reported that the incomes and livelihoods of approximately 1.7 billion people in these countries are linked to livestock production. Although these estimates differ in scope and according to the definitions employed, they collectively demonstrate that livestock production is a strategic sector not only for the global food system but also for rural livelihoods and economic development.

Climate change is one of the most important factors making this transformation necessary. The relationship between livestock production and climate change is bidirectional. On the one hand, livestock production contributes to greenhouse gas emissions through processes such as enteric fermentation, manure management, feed production, energy use, and land use; on the other hand, rising temperatures, heat waves, drought, water scarcity, fluctuations in feed production, changes in the distribution of diseases and vectors, and extreme climatic events threaten the biological and economic sustainability of livestock production. Thornton et al. (2024b) emphasized that the livestock sector of the future will simultaneously need to meet future consumer demand, contribute to climate-neutrality targets, withstand increasing climate-related hazards, and deliver acceptable outcomes in terms of water resources, biodiversity, social resilience, and economic development. Achieving such diverse objectives simultaneously is not a challenge that can be addressed through a single technology or management practice. All components of the production system, ranging from animal genetics and nutrition to health management and housing,

and from energy use and manure management to farm economics, must therefore be considered together.

Within this framework, the circular bioeconomy represents one of the key conceptual frameworks for understanding the future of livestock production. Whereas linear production systems are fundamentally based on extracting resources, converting them into products, and removing unused fractions from the system as waste, circular systems aim to reintegrate by-products and residual materials into the production process to the greatest extent possible. Within such systems, animals can perform an important biological function by converting biomass that cannot be directly consumed by humans into animal-source products of high nutritional value. Examples of this approach include the use of by-products from the food and agricultural industries as feed, the recovery of organic materials through insect bioconversion, the use of manure as a nutrient source in crop production or its conversion into biogas, and the re-establishment of nutrient cycles among different production sectors. Pugliese et al. (2026) identified more efficient resource use, nutrient cycling, and the valorization of livestock and agricultural by-products as key components of circular livestock systems. However, it should be recognized that circularity does not inherently imply sustainability; health considerations, economic feasibility, pathogen control, and impacts occurring throughout the life cycle must also be evaluated (Pugliese et al., 2026).

Within this framework, the remainder of this chapter will first examine the historical transformation of livestock production and the global dynamics shaping modern production systems, followed by the transition from the productivity paradigm to multidimensional sustainability and the concept of innovation in livestock production. After discussing the implications of Agriculture 4.0 and Agriculture 5.0 for livestock production, the emerging animal-centered management paradigm, and the convergence of biological and digital technologies, the chapter will address circular bioeconomy, climate-smart livestock production, One Health, and One Welfare approaches. The distinctive transformation dynamics of different livestock sectors, the economic and sociotechnical factors constraining the adoption of innovations, and ethical, societal, and regulatory issues will also be considered as integral components of this transformation. Accordingly, this chapter aims to conceptualize the future of livestock production not through a single technology or production model, but as a multidimensional transformation process in which biology, technology, the environment, the economy, animals, and humans interact within the same system.

2. Historical Transformation of Livestock Production

The historical development of livestock production should be considered in conjunction with changes over time in the relationship between humans and animals and in the ways animals have been utilized. Following domestication,

animals became an integral part of human life and agricultural production not only as a source of food but also for a wide range of purposes, including labor, transportation, and the provision of fiber, hides, and manure. In these early production systems, the fundamental characteristics of animal husbandry were largely determined by the natural environment, available feed resources, the characteristics of local animal populations, and farmers' experience accumulated over generations. Animal feeding was primarily based on locally available resources, health and performance were assessed through direct observation, and husbandry decisions were shaped more by practical knowledge than by scientific measurement systems. The emergence of modern livestock production did not result from the disappearance of this traditional structure through a single technological breakthrough; rather, it occurred through the cumulative development of genetics, nutrition, animal health, housing, mechanization, automation, and, more recently, information technologies. The historical transformation of livestock production should therefore be regarded not as a sequence of sharply defined periods replacing one another, but as a process characterized by the gradual expansion of biological knowledge and technological capacity.

The development of animal nutrition science has been equally important in the emergence of modern production systems. Whereas animal feeding in traditional systems was largely determined by the quality and seasonal availability of existing feed resources, the experimental determination of energy, protein, amino acid, mineral, and vitamin requirements enabled nutrition to evolve into an increasingly precise scientific discipline. More accurate estimation of the chemical composition, digestibility, and nutritional value of feeds made it possible to formulate diets according to the requirements of animals at different ages and physiological stages. With this development, nutrition evolved from merely providing available feeds to sustain the animal into one of the principal tools used to realize genetic production potential, maintain health status, manage product quality, and improve economic efficiency. More conceptually, whereas animal feeding in traditional systems was largely adapted to the feed resources available, modern nutrition has increasingly involved adjusting feed resources to the calculated biological requirements of the animal.

This transformation has also created a new information challenge. While a limited number of performance records can be directly evaluated by the farmer, the continuous streams of image, sound, activity, physiological, feed intake, production, and environmental data generated from hundreds or thousands of animals cannot be evaluated in the same manner. Therefore, the next stage in the digital transformation of livestock production has involved not merely collecting data, but developing analytical methods capable of extracting meaningful information from large and heterogeneous data streams. Machine learning and artificial intelligence methods have begun to be applied across a wide range of

areas, including the classification of animal behavior, early detection of disease and welfare problems, prediction of body weight and production performance, identification of environmental stress, and support for management decisions (Mata, 2026). Akinyemi et al. (2026) demonstrated that scientific developments in precision livestock farming and animal welfare progressed from hardware and sensor validation studies during 2006–2015, to the assessment of welfare outcomes during 2016–2020, and subsequently toward a research framework characterized by increasing integration of artificial intelligence during 2021–2025. This progression is important because it demonstrates that the technological value of livestock production systems is increasingly shifting away from the sensor itself toward the capacity to transform sensor-generated data into biologically meaningful information.

At this point, the historical development of livestock production converges with the central argument of this chapter. Throughout the progression from traditional husbandry to science-based production, from mechanization to automation, and from automation to data-driven management, it is not only the tools being used that have changed; the nature of the information that can be obtained about animals, the timescale of management decisions, and the outcomes expected from production systems have also changed. In the past, the central question was largely how much product could be obtained from an animal. Today, this question has been expanded to include how much feed, water, and energy are required to produce that product, the environmental impacts associated with its production, the health and welfare conditions under which it is produced, its economic cost, and the resilience of the production system to changing conditions. Thus, the historical transformation of livestock production represents not merely a process of modernization extending from traditional systems to smart technologies, but also the history of a transition from a productivity-centered approach to livestock production toward a multidimensional, knowledge-based, and systems-oriented perspective. Understanding why this transformation is accelerating today requires the integrated consideration of the global dynamics reshaping modern livestock production, ranging from population growth and food demand to climate change, pressures on natural resources, labor challenges, and biosecurity concerns.

3. Global Dynamics Transforming Modern Livestock Production

The transformation observed in livestock production in recent years is not merely the result of the development of new technologies or advances in production techniques. More fundamental forces reshaping the structure of the sector arise largely from demographic, environmental, economic, and societal processes that develop beyond the direct control of producers. Population growth and urbanization, regional shifts in demand for animal-source foods, intensifying competition for natural resources, particularly land and water, climate change,

fluctuations in feed and energy costs, changes in the structure of the rural workforce, animal diseases and biosecurity risks, and changing consumer expectations regarding how food is produced are among the major drivers of this transformation. Although each of these factors affects livestock production through different mechanisms, the fundamental transformation arises from the simultaneous occurrence of these pressures and their potential to amplify one another. Consequently, it is becoming increasingly difficult to explain the future of modern livestock production in terms of a single technological development, production indicator, or environmental challenge.

Whereas the principal challenge facing livestock production in the past was often defined as increasing the quantity of production, production systems today are expected to fulfill a much broader set of functions. Livestock production must meet increasing or changing consumer demand while simultaneously adapting to climate change, contributing to reductions in greenhouse gas emissions, using land and water resources more efficiently, limiting pressure on biodiversity, safeguarding animal health and welfare, and maintaining economic viability. Thornton et al. (2024a) emphasized that future livestock systems must meet consumer demand while becoming aligned with low-emission development objectives, building resilience to increasing climate risks, and simultaneously delivering acceptable outcomes in terms of water resources, biodiversity, social resilience, and economic development. This is changing the concept of success in livestock production, shifting the focus from maximizing a single output toward the simultaneous management of multiple biological, economic, environmental, and societal objectives that may, at times, conflict with one another.

Feed resources lie at the center of this competition. The biological and economic performance of livestock production depends on the continuous availability of feed in sufficient quantities, of appropriate quality, and at predictable costs. However, the use of agricultural land for human food, animal feed, energy production, and industrial raw materials can intensify food–feed competition for certain feed resources. The effects of climate change on the yield and nutritional value of feed crops will also make the stability of feed supply increasingly important in the future. Particularly in low-income production systems, the challenge extends beyond feed prices; the physical availability of feed, its nutrient quality, storage opportunities, and producers' access to the knowledge and resources required to formulate balanced diets directly determine production capacity (Ludgate et al., 2026). These conditions are accelerating research not only into the more efficient use of conventional feed ingredients but also into alternative resources such as by-products from the agricultural and food industries, insects, algae, single-cell proteins, and fermentation products. Pressure on feed resources is therefore not merely an economic problem but also

an important driver of innovation that is strengthening the relationship between animal nutrition and the circular bioeconomy.

This relationship between labor and technology also indicates that the human capital required by future production systems will change. In addition to traditional husbandry knowledge, new competencies are becoming increasingly important, including the ability to interpret data generated by sensors, understand the operating principles of automated systems, assess errors and alarm conditions, and communicate with technology providers when necessary. This particularly demonstrates that technological transformation cannot be achieved through investment in hardware alone. The technical capacity of producers and the ability of farms to integrate new technologies into routine decision-making processes are becoming key factors determining the actual economic and biological value of automation.

These developments also necessitate a redefinition of the criteria used to evaluate success in livestock production. Conventional performance indicators such as production per animal, growth rate, milk or egg yield, and feed efficiency remain important; however, they can no longer, on their own, adequately characterize the success of a modern production system. Resource-use efficiency, environmental footprint, animal health and welfare, economic resilience, and the capacity of the system to adapt to external shocks require production performance to be evaluated within a broader framework. Thus, the question of "how much is produced," which long occupied a central position in the historical development of livestock production, is increasingly accompanied by questions of "with what resources, with what environmental and biological consequences, and within a system of what degree of resilience is it produced?" This shift provides the foundation for the transition of livestock production from a unidimensional concept of productivity toward an approach based on multidimensional sustainability and establishes the conceptual basis for the paradigm shift addressed in the following section.

4. Transition from the Productivity Paradigm to Multidimensional Sustainability

One of the historical objectives of scientific and technological progress in livestock production has been to increase the amount of product obtained per animal. Through genetic selection, balanced nutrition, disease control, reproductive technologies, and improvements in environmental conditions, substantial advances have been achieved in economically important traits such as milk yield, growth rate, egg production, carcass characteristics, and feed efficiency. These developments have played a decisive role in meeting the growing demand for animal products and in the emergence of modern production systems. Therefore, it would be inappropriate to regard improvements in productivity as an outdated objective or as inherently incompatible with

sustainability. What has fundamentally changed is not the importance of productivity, but whether productivity alone is sufficient to evaluate the success of a production system. Although achieving high levels of production remains important, the resources used to achieve this production, the environmental impacts generated, the extent to which production can be economically sustained, and its consequences for animal health and welfare have also become integral components of production performance.

Underlying this shift is the recognition that productivity and sustainability are not synonymous. An animal or farm exhibiting exceptionally high performance for a particular production trait may simultaneously depend heavily on external inputs, generate substantial environmental burdens, be vulnerable to economic fluctuations, or produce outcomes that are difficult to accept from the perspective of animal health and welfare. Conversely, a system with low environmental impacts may have limited long-term sustainability if it is not economically viable or fails to generate sufficient income to support the producer's livelihood. Sustainability therefore requires the simultaneous consideration of relationships among biological performance, resource use, environmental impacts, economic viability, and social outcomes rather than the maximization of a single trait. Dougherty et al. (2023) emphasized that treating the environmental, economic, and social dimensions of sustainability in livestock production independently may be insufficient to explain the actual performance of the system and that assessments should encompass different scales, including the animal, farm, food system, and human nutrition. This approach positions sustainability as a broader system-level property rather than merely the performance of a particular farm or a specific environmental indicator.

Life cycle assessment (LCA) has become one of the principal methods for addressing this requirement. Rather than limiting the assessment of the environmental impacts of livestock production to direct emissions occurring within the farm, LCA enables these impacts to be evaluated together with feed ingredient production, energy use, manure management, and, depending on the defined system boundaries, other stages of the production chain. This approach can make it more apparent whether a change that appears environmentally beneficial at the farm level shifts environmental burdens to another stage of the production chain. Nevertheless, LCA alone is not sufficient to capture sustainability in its entirety. Keohavong (2026) stated that integrating environmental assessments with economic and socioeconomic analyses can contribute to a more comprehensive evaluation of the relationships among production costs, resource-use efficiency, and environmental performance. Thus, the principal contribution of the life cycle approach is not to generate a single sustainability value, but rather to make visible the impacts of production decisions across system boundaries.

The transition toward a system-level perspective also makes it insufficient to evaluate the environmental role of livestock solely in terms of the burdens it generates. Under inappropriate management conditions, livestock production can contribute to land degradation, overgrazing, nutrient losses, water pollution, and pressures on biodiversity. Paul et al. (2023) noted that the conversion of natural ecosystems, particularly for grazing or feed production, can result in significant environmental consequences. Conversely, in appropriately designed mixed crop–livestock systems, animals can convert plant materials that are not directly consumable by humans and certain agricultural by-products into foods of high nutritional value, facilitate the return of nutrients to agricultural systems through manure, and contribute to food production from areas unsuitable for crop production. Dougherty et al. (2023) likewise emphasized that the capacity of animals to convert resources inedible to humans into products of value for human nutrition should be evaluated at the system level within the context of sustainable food systems.

Within this framework, the central challenge of modern livestock production is no longer simply to achieve the highest possible level of productivity. The fundamental scientific and managerial challenge is the extent to which the biological capacity of animals can be utilized while simultaneously reconciling the economic continuity of producers, conservation of natural resources, animal health and welfare, and society's food requirements within the same production system. This perspective also explains why innovation in livestock production does not merely mean developing a new technology or adding new equipment to an existing system. The actual value of an innovation is determined less by its degree of technological novelty than by which of these multidimensional production challenges it addresses, through which scientific mechanism it does so, and the extent to which it is applicable under real-world production conditions. The transition from productivity to multidimensional sustainability therefore also provides the fundamental conceptual framework for the concept of innovation in livestock production addressed in the following section.

5. The Concept of Innovation in Livestock Production

The transformation that has taken place in livestock production in recent years is often explained in terms of advanced technologies such as sensors, artificial intelligence, robotic systems, genomic technologies, and automation. Although these technologies play an important role in the transformation of modern livestock production, restricting the concept of innovation solely to technological advances is insufficient to explain either the historical development of livestock production or the nature of the challenges it currently faces. In a broader sense, innovation can be regarded as the process of translating scientific knowledge, technological capabilities, or new management approaches into solutions to real problems encountered within production systems, thereby creating measurable

value. From this perspective, innovation does not necessarily have to take the form of a new device, software application, or high-technology product. A better understanding of an existing biological process, the application of an established nutritional approach in a different manner, the reorganization of resources, or the redesign of relationships among components of the production system may also constitute significant innovation.

In contrast, some innovations may be sufficiently transformative to alter the way decisions are made within a production system. The continuous generation of data by sensors, integration of different data sources within the same platform, generation of predictions regarding the future status of an animal through artificial intelligence or other analytical methods, and translation of these predictions into automated or semi-automated interventions represent more than simply performing an existing task more rapidly. In such a system, the fundamental logic of management shifts from periodic observation and retrospective evaluation toward continuous measurement, early detection, prediction, and timely intervention. Therefore, the transformative nature of innovation often arises not from the complexity of a single technology, but from the integration of different technologies in ways that alter production decision-making. Mata (2026) emphasized that precision livestock farming should be considered along a continuum ranging from incremental optimization to system-level transformation and that deeper transformations emerge when sensors, automation, and analytics operate within an integrated framework. From this perspective, installing a camera, activity sensor, or automated feeding system on a farm does not, by itself, create a smart production system; genuine transformation occurs to the extent that the information generated by these tools changes the way decisions are made.

One of the most powerful examples of biological innovation in livestock production is genetic improvement. Genetic progress achieved through selection differs from many management interventions because its effects are transmitted to subsequent generations and accumulate over time. Genomic selection, high-throughput genotyping technologies, and increasingly advanced gene-editing methods represent contemporary extensions of this historical process. Van Eenennaam (2025) demonstrated that the integration of genomic information into animal breeding programs improves selection accuracy and, particularly, the estimation of genetic merit at an early age, while gene editing has the potential to enable more targeted genetic changes in specific traits. However, biological innovation in the future will not be limited to achieving genetic progress for higher production. The increasing importance of traits such as disease resistance, feed efficiency, heat tolerance, reduced environmental impact, longevity, and the ability to maintain performance under changing environmental conditions within breeding objectives is creating a more direct link between genetic innovation, sustainability, and climate adaptation.

This context-specific nature makes producer adoption an integral part of the innovation process. An application that produces successful results under research conditions is not guaranteed to become widely adopted on commercial farms. From the producer's perspective, factors such as investment cost, expected economic return, ease of use, reliability, maintenance requirements, technical support, compatibility with existing farm infrastructure, and perceived risk are as important as the scientific performance of the technology. In digital systems, internet connectivity, software subscriptions, data security, interoperability among different devices, and confidence in algorithm-generated recommendations must also be included in this assessment. Mihret et al. (2025) noted that the widespread adoption of Agriculture 4.0 technologies, particularly in developing countries, may be constrained by limited technical knowledge, inadequate infrastructure, high capital requirements, and the absence of appropriate policies and standards. Khwidzhilli and Ijatuyi (2026), in turn, emphasized that the technology development process should be supported through localized training, inclusive policies, infrastructure investment, and enhancement of producers' digital capabilities.

Within this broad framework of innovation in livestock production, digitalization occupies a distinct position. The importance of digital technologies does not arise from the mere presence of individual sensors, robots, or software applications, but from the ability to continuously collect data on animals, their environment, and production processes, to integrate information originating from different sources, and to translate this information into management decisions. Without completely replacing traditional decision-making processes based on observation and experience, this transformation is leading to the emergence of a new production architecture in livestock systems that supports these processes through continuous data streams and analytical capacity. Agriculture 4.0 and Livestock 4.0, which provide the conceptual foundation for this architecture, will be addressed in the following section.

6. Agriculture 4.0 and Livestock 4.0

Digital transformation in livestock production represents a more comprehensive change than simply the introduction of electronic devices, sensors, or automated systems on farms. Automated feeding and milking systems, electronic animal identification, environmental control equipment, and computer-assisted record-keeping systems had already been introduced into livestock production long before the concept of digital transformation became widespread. The fundamental feature distinguishing the Agriculture 4.0 approach from earlier technological eras is not merely the presence of these tools, but rather the integration of physical production processes with digital systems, the continuous acquisition of data from animals and their production environment, the integration of data originating from different sources, and the translation of the

resulting information into management decisions. Digitalization is thus evolving from the use of machines or computers to perform specific tasks into a new management architecture that connects the different components of the production system (Khwidzhilli & Ijatuyi, 2026; Losacco et al., 2025; Mihret et al., 2025).

However, from the perspective of Livestock 4.0, the key issue is not the increasing diversity of sensors, but the ability of these technologies to monitor the biological status of animals at a frequency and continuity that cannot be achieved through conventional observation. In traditional herd management, farmers or veterinarians observe animals at specific times, and many changes are detected only after they become visibly apparent. Continuous digital monitoring, by contrast, enables animal behavior and physiology to be evaluated as time-series data. Thus, conventional phenotypes recorded at specific intervals, such as body weight, milk yield, or egg production, are complemented by dynamic traits such as activity, rumination, social interaction, body temperature, and responses to environmental conditions. This change affects not only farm management but also animal breeding, welfare assessment, and biological research, because traits that were previously difficult or costly to measure can now be recorded in large populations.

This transformation should not be expected to follow the same technological pathway across all animal species. The economic value and lifespan of the animal, herd or flock size, housing conditions, and management practices directly determine the appropriate digital architecture. In dairy cattle, the long productive lifespan and high individual economic value of animals make systems that generate intensive individual-level data, such as activity sensors, rumen boluses, automated milking systems, and milk analysis technologies, more economically feasible. Neethirajan (2026) noted that digital models in dairy cattle focus on areas such as the early detection of mastitis, lameness, and metabolic disorders, improvement of feed efficiency, and monitoring of long-term physiological changes in individual animals. In poultry production, by contrast, the lower economic value of individual animals, substantially larger flock sizes, and, particularly in broilers, short production cycles bring contactless technologies that generate flock-level data, such as cameras, acoustic analysis, thermal imaging, and environmental sensors, to the forefront rather than individual wearable sensors. In extensive cattle, sheep, and goat production, GPS and activity sensors designed to determine location, movement, and pasture use may become more relevant (Mata, 2026; Neethirajan, 2026). Livestock 4.0 therefore does not involve applying a specific technology package across different species; rather, it involves developing a digital architecture appropriate to the biological and economic characteristics of the production system.

From an animal science perspective, the most important consequence of digital transformation is not the generation of more data, but the change it brings to the timing and reference points of management. In conventional herd management, a substantial proportion of decisions are based on observations made at specific times, herd averages, and visible clinical signs. Continuous digital monitoring, however, may enable the establishment of normal behavioral and performance patterns for an animal or herd and allow small deviations from these patterns to be detected at an earlier stage. Management can therefore shift from a reactive structure that responds after a problem has emerged toward a proactive approach that identifies risks earlier and, under certain conditions, attempts to predict future states (Losacco et al., 2025; Mata, 2026). For example, whereas disease may be detected in conventional systems only after clinical signs become apparent, the integrated evaluation of small changes in activity, feed intake, rumination, body temperature, and other measurements may enable earlier identification of disease risk. Similarly, measuring only the temperature of a poultry house or barn provides information about environmental conditions, whereas evaluating environmental measurements together with animals' behavioral and physiological responses may help determine the actual biological effects of those conditions on the animals. Thus, the focus of digitalization is shifting from how comprehensively the environment or the animal can be measured toward understanding the biological meaning of the changes being measured.

Nevertheless, the ultimate objective of Livestock 4.0 is not to remove the producer from the production system. The principal value of digital technologies lies in complementing observations that humans can make only at specific times with continuous measurements, making biological processes that cannot be directly observed more visible, and enabling producers to make earlier and better-informed decisions. However, as digital systems become increasingly complex, new questions arise concerning the producer's role, decision-making autonomy, dependence on technology, control over data, and the human–machine relationship. Therefore, the discussion following Agriculture 4.0 is not merely about the extent to which farms can be automated; the question of how technology can complement, rather than replace, human knowledge and experience while simultaneously enhancing sustainability and system resilience is becoming increasingly important. This discussion provides the starting point for Agriculture 5.0 and the human-centered smart livestock production approach.

7. Agriculture 5.0 and Human-Centered Smart Livestock Production

Agriculture 4.0 has enabled agricultural production to become increasingly measurable, connected, and automated through sensors, the Internet of Things (IoT), big data, cloud computing, robotic systems, and artificial intelligence. However, the advancement of digitalization has also brought about a more

fundamental debate concerning the future of agricultural production. Should the primary objective of technological development be to minimize human intervention in production processes as much as possible, or should technology be used as a tool to enhance human knowledge, experience, and decision-making capacity? The concept of Agriculture 5.0 has largely emerged from this second perspective. Rather than abandoning the technology-driven framework of Agriculture 4.0 centered on efficiency, connectivity, automation, and optimization, Agriculture 5.0 redefines the purposes for which this infrastructure is used and links technological development with the concepts of human-centeredness, sustainability, and resilience. Khwidzhilli and Ijatuyi (2026) therefore interpret the progression from Agriculture 3.0 to Agriculture 5.0 not merely as increasing technological complexity, but as a change in the objectives of production systems. Whereas Agriculture 3.0 primarily emphasized the more precise use of inputs, and Agriculture 4.0 focused on the development of connected and real-time production systems through IoT, artificial intelligence, robotics, and cloud computing, Agriculture 5.0 adds new dimensions to this technological infrastructure, including human–machine collaboration, ethical governance, inclusiveness, ecological sustainability, and system resilience. Thus, the mere presence of technology is no longer an indicator of progress in itself; for whom and for what purpose technology is used, and with what biological, economic, environmental, and societal consequences, become more central questions.

This approach requires the relationship between humans and machines to be based on complementarity rather than competition. Machines may have a greater capacity than humans for the continuous collection of large volumes of data, execution of repetitive tasks, identification of complex patterns, and simultaneous analysis of numerous variables. In contrast, farmers or farm managers possess contextual knowledge that is not embedded in algorithms, including knowledge of local conditions, the animals' history, the physical characteristics of the farm, equipment behavior, changes in feed, and unusual circumstances. Therefore, the most effective model for the smart livestock production system of the future is not one in which either humans or machines make decisions independently, but rather one in which these two capacities complement each other. Khwidzhilli and Ijatuyi (2026) conceptualized this relationship as a cognitive partnership in which human intuition and machine intelligence operate together. However, the same authors also noted that this partnership has not yet been fully established in current applications and that, in some digital systems, algorithmic outputs may take precedence over farmers' experience and autonomy. This makes it more appropriate to regard Agriculture 5.0 not as a completed new technological era with clearly defined boundaries, but as a paradigm defining the principles according to which digital agriculture should develop in the future.

Another factor increasing the importance of human–machine collaboration is the impact of robotization on labor in livestock production. At first glance, robotic technologies may be regarded as systems that reduce physical workload and labor requirements. However, the effects of farm robots on working life are more complex. In their review of the literature on farm robotization, Martin et al. (2022) demonstrated that although robots can reduce physical workload, they do not always reduce working time to the same extent and that, in some cases, physical workload may be replaced by new tasks such as monitoring, system supervision, and responding to technical problems. Particularly in automated milking systems, the farmer's role shifts away from directly performing physical tasks toward that of a manager who monitors the system and the data generated from animals. This transformation represents a change in the nature of work rather than the elimination of work itself. In future livestock farms, competencies such as data literacy, interpretation of biological data, supervision of technological systems, and evaluation of the reliability of algorithmic recommendations are expected to become increasingly important alongside physical skills.

However, the assumption that digital technologies are inherently sustainable should also be questioned. The production and operation of sensors, data centers, communication infrastructure, robots, and other electronic equipment require energy and materials. While digitalization may improve resource efficiency by enhancing feed utilization, health management, or environmental control, it also generates its own energy and material footprint. Neethirajan (2026) drew attention to the fact that the environmental burdens generated throughout the life cycle of data- and computation-intensive technologies, particularly digital twins, have not been sufficiently evaluated in the existing literature. Akinyemi et al. (2026) likewise stated that the environmental costs of precision livestock farming hardware should, in the future, be evaluated alongside the productivity and welfare gains they provide. Therefore, digitalization and sustainability cannot be assumed to be inherently equivalent. The actual sustainability value of a technology can be determined by evaluating the biological and managerial benefits it provides together with the energy, materials, and economic resources required for its installation, operation, and replacement.

Within this framework, the fundamental question of Livestock 5.0 extends beyond determining which tasks currently performed by humans can be transferred to machines. The central issue is how human contextual knowledge and responsibility can be combined with the capacity of machines for continuous measurement, high-speed computation, and pattern recognition in ways that generate better-informed decisions for animals, farmers, the environment, and the production system. Such an approach shifts technology from being an objective of the production system itself to being a tool used to achieve biological and societal goals. The smart farm of the future should therefore not be conceived as

a production facility from which humans have been removed, but rather as an integrated production system comprising biological, digital, and human components, in which information is continuously obtained from animals and their environment, machines process this information at high speed, analytical systems identify risks and potential options, while production objectives and critical decisions remain shaped by human knowledge, oversight, and responsibility.

8. The New Animal-Centered Production Paradigm

A substantial proportion of the productivity gains achieved in livestock production over the past century have resulted from standardized management strategies applied at the herd or group level. The selection of genetically higher-performing animals, development of balanced diets, control of housing conditions, implementation of vaccination and biosecurity programs, and mechanization of production processes have made it possible to efficiently manage large numbers of animals under similar conditions, particularly in intensive production systems. However, one of the fundamental assumptions underlying this approach is that the requirements of animals within the same herd and their responses to environmental conditions are similar to a certain extent. Diets are generally formulated for the herd or production group, the housing environment is managed uniformly for all animals, and health management is largely based on identifying animals that exhibit clinical signs. Nevertheless, it is well established that even animals of the same genotype, age, sex, or production level may exhibit substantial individual variation in feed intake, metabolic status, behavior, disease susceptibility, responses to thermal stress, and production potential. One of the most important consequences of digital technologies for livestock production is that they have made it possible to measure this biological variation at a level of detail and frequency that was previously unattainable. Consequently, the unit of management in livestock production is increasingly shifting from the herd average toward the individual animal, while management strategies are moving from standardized practices toward systems that can be adapted according to the animal's real-time biological status (Losacco et al., 2025; Mata, 2026).

Understanding the scientific basis of this transformation requires recognition that an animal is not a production machine with fixed characteristics, but a dynamic biological system that continuously interacts with its environment. In placing the animal's biological response at the center of the precision livestock farming approach, Losacco et al. (2025) described living organisms as complex, individually variable, temporally changing, and dynamic systems. This perspective is particularly important because it implies that the same environmental change or stressor will not elicit a response of the same magnitude or at the same time in all animals. For example, while a particular combination

of temperature and humidity may appear acceptable based on the herd average, a high-yielding dairy cow, an animal at a particular stage of pregnancy, or another individual experiencing a health problem may be more severely affected by the same environmental conditions. Papakonstantinou et al. (2024) likewise noted that susceptibility to heat stress varies according to factors such as species, breed, life stage, genetic background, nutritional status, body size, and previous environmental exposure. Therefore, measuring the environment alone is insufficient to understand the animal's condition; it is also necessary to monitor how different animals within the same environment respond to those conditions.

This approach also introduces an important change in the conventional concept of environmental management. Housing temperature, relative humidity, air velocity, and gas concentrations have traditionally been maintained within specified reference ranges. In animal-centered systems, however, the ultimate objective of environmental control is not to maintain the physical environment at a particular numerical value, but to keep the animal's biological response within acceptable limits. For example, if two cows exhibit different thermal stress responses at the same temperature–humidity index, a single cooling strategy based on the herd average may not be optimal for both animals. Similarly, even when the average temperature in a poultry house is within the recommended range, changes in indicators such as the spatial distribution of birds, wing spreading, panting, or water consumption may indicate that the environment is not as suitable for the animals as expected. Future environmental control systems are therefore expected to rely not only on physical sensors but also on biological feedback obtained directly from the animals themselves.

However, an important paradox exists within the animal-centered production paradigm. Obtaining more data about an animal does not automatically mean that management becomes more animal-centered. The same sensor data may be used to improve animal health and welfare or solely to maximize production performance. For example, early detection of changes in feed intake may help reduce disease risk; however, if the same technology is used exclusively to achieve higher production without considering the animal's biological limits, its being "precision" does not make it animal-centered. Mata (2026) drew attention to the ethical risks associated with automation, including the possibility that productivity may take precedence over animal welfare and that human–animal interaction may be reduced, despite the substantial opportunities automation offers for improving welfare. Therefore, measuring the animal and placing the animal at the center of management are not the same. Genuine animal-centeredness requires that the data obtained on animal health, welfare, and biological requirements have meaningful weight in the decision-making process.

Accordingly, the fundamental question in future livestock production will no longer be limited to "How much does the herd produce?" Increasing importance

will also be placed on how much each animal or biologically meaningful group consumes, how it behaves, how it responds to its environment, how its health and welfare status changes over time, and how it responds to the current management practices. In such a system, the animal ceases to be regarded as a static unit defined solely by its genetic potential and production records and is instead considered a dynamic biological system in which interactions among genotype, phenotype, behavior, physiology, and environment are continuously monitored. The next natural stage of this transformation is the integration of these biological data with genomic information, environmental sensors, artificial intelligence, precision feeding, and automation systems within the same management architecture. The animal-centered production paradigm therefore provides the foundation for the convergence of biological and digital technologies addressed in the following section.

9. Convergence of Biological and Digital Technologies

The technological transformation that has emerged in livestock production in recent years is often addressed through distinct areas of innovation, such as genomics, sensor technologies, artificial intelligence, precision feeding, automation, and robotics. Although this approach is useful for explaining the development of each individual technology, it is insufficient on its own to characterize the fundamental nature of future livestock production systems. This is because the most powerful aspect of the transformation lies not in the independent advancement of any single technology, but in the increasing convergence of biological sciences and digital technologies within the same decision-making system. Genomics provides information about the animal's inherited potential, while phenomics reveals how this potential is expressed under real-world conditions; sensors continuously measure phenotypic and environmental changes; artificial intelligence identifies relationships within high-volume data originating from different sources and generates predictions about future states; precision feeding and environmental control translate these predictions into animal- or group-specific management decisions; and automation and robotic systems enable these decisions to be implemented in a timely and consistent manner. Therefore, the fundamental framework defining the smart livestock production systems of the future is not simply "digitalization," but rather the biological–digital integration established among genomics + phenomics + sensors + artificial intelligence + precision management + automation (Van Eenennaam, 2025; Losacco et al., 2025; Mata, 2026).

To understand the importance of this integration, it is necessary to consider how information has historically been generated in livestock production. In traditional animal husbandry, information about the animal was largely based on observable phenotypes. With the widespread adoption of systematic recording, traits such as body weight, milk and egg production, growth, reproduction, and

health became quantifiable; with the development of quantitative genetic methods, these phenotypic records were combined with pedigree information to estimate the genetic merit of animals. Subsequently, molecular genetics and genomic technologies made it possible to directly incorporate DNA-level variation into selection programs. Van Eenennaam (2025) described progress in modern animal breeding as a cumulative process in which conventional selection has been integrated with genomic information, advanced reproductive technologies, and increasingly precise biotechnological tools. Genomic selection has represented an important stage in this transformation; particularly in economically important species, the use of large numbers of genetic markers distributed across the genome has enabled the genetic merit of breeding candidates to be estimated at an earlier age and with greater accuracy. More recent technologies, such as gene editing, are creating new opportunities to directly target the genetic basis of specific traits, including disease resistance, polledness, and heat tolerance (Van Eenennaam, 2025). Nevertheless, the value of genomic information remains dependent on the accurate measurement of the phenotype expressed by the animal under actual production conditions.

However, the availability of numerous data sources does not, by itself, constitute integration. When sensors, genomic platforms, feeding systems, production records, and environmental control systems operate independently of one another, a farm may generate large volumes of data without establishing functional relationships among them. The true value of biological–digital convergence arises from the ability to align different data streams for the same animal, at the same time, and within the same environmental context. If the genomic breeding value of a dairy cow is stored in one database, milk yield in the milking robot, activity data in a neck-mounted sensor, rumination records on another commercial platform, diet information in feeding software, and barn temperature in an environmental control system, an exceptionally rich data structure theoretically exists. However, in the absence of interoperability among these systems, the integrated value of this information is substantially reduced. Mata (2026) noted that the integration of different sensors and data sources enables more comprehensive assessments of animal health, performance, and environmental conditions than can be achieved using individual sensors alone. In the context of digital twins, Neethirajan (2026) further emphasized that interoperability among sensor systems from different manufacturers, variation in data quality, and the lack of long-term validation remain among the major challenges.

The approach to agricultural technological transformation proposed by Mukherji et al. (2023) similarly considers genetic progress, digital services, climate-smart livestock production, emission mitigation, and productivity improvement not as independent solutions, but as complementary pathways capable of driving the transformation of the agrifood system. From this

perspective, the strategic importance of biological–digital convergence extends beyond the marginal gains that can be achieved through any single technology. Raising a genetically more efficient animal under an inappropriate diet or environment may constrain the realization of its genetic potential; the inability to analyze data on a farm equipped with excellent sensors reduces the value of the sensor investment; a highly successful artificial intelligence model can do little more than generate alerts in the absence of an intervention mechanism; and advanced automation, when operated according to biologically inappropriate targets, may simply implement errors more rapidly and consistently. Thus, the true value of technological progress derives less from the performance of individual components than from their compatibility and integration within the overall system.

From this perspective, the principal innovation in future livestock production is not artificial intelligence, genomic selection, robotic feeding, or a new sensor in isolation. The fundamental innovation lies in establishing a continuous and bidirectional information loop between animal biology and the digital system. The animal is no longer merely a source of outputs measured at the end of the production process, but a biological actor at the center of the system, continuously generating information ranging from its genome and behavior to its metabolism and responses to the environment. Digital technologies, in turn, are not tools that replace this biology, but tools that enable us to observe, understand, and manage it at a higher resolution. Therefore, the fundamental paradigm that will shape the future of livestock production will not involve a choice between "biology or technology," but rather the extent to which biological knowledge can be meaningfully integrated with digital capacity. It is precisely this convergence that provides the common scientific backbone for precision livestock farming, artificial intelligence, next-generation nutrition, genomics, and sustainable production technologies, each of which will be addressed separately in subsequent chapters of this book.

10. Circular Bioeconomy and Livestock Production

For many years, the position of livestock production within sustainability debates has been evaluated largely in terms of the resources it consumes and the environmental burdens it generates. Land and water used for feed production, the use of feed ingredients suitable for human consumption in animal diets, enteric methane emissions, manure management, nitrogen and phosphorus losses, energy consumption, and organic residues generated during the processing of animal products have constituted major elements of this debate. However, when the role of livestock within the agrifood system is viewed solely as a linear production activity that consumes resources and generates waste, an important characteristic of the system is overlooked. Animals can convert biological materials that are not directly consumable by humans into foods of high nutritional value; utilize by-

products generated from crop production and food processing; return nutrients to the soil through manure; and, when appropriate technologies are employed, enable organic residues to be transformed into energy, fertilizers, or raw materials for new biological products. Therefore, when appropriately designed, livestock production has the potential not only to form part of the circular bioeconomy but also to become one of the key transformative sectors linking different biological resource flows (Dougherty et al., 2023; Paul et al., 2023; Pugliese et al., 2026).

This approach differs substantially from the conventional linear production model. The fundamental logic of the linear economy can be summarized as resources entering the production system, being transformed into products and consumed, with the residues generated at the end of the process subsequently discarded from the system. In other words, the system largely operates according to a "take–produce–consume–dispose" model. When applied to livestock production, this structure involves bringing inputs such as feed and energy into the farm from external sources, converting them into animal products, and removing a substantial proportion of manure, wastewater, processing residues, and other by-products from the production cycle. The circular economy, by contrast, seeks to disrupt this unidirectional flow by transforming residues or by-products generated at one stage of production into inputs for another production process. Pugliese et al. (2026) described the foundation of this approach as retaining the value of products and biological resources within the system for as long as possible through reduced resource use, reuse of materials, and recycling of residual materials. Thus, material generated at the end of a production chain ceases to be "waste" and becomes the initial input of a new economic and biological cycle.

The importance of alternative feed resources becomes even more apparent in this context. Circular livestock production encompasses not only the use of existing agricultural by-products but also the development of new biological resources that can reduce dependence on conventional feed production systems. Insect proteins, microalgae, yeasts, bacterial proteins, and other single-cell proteins are major examples of this group. Ludgate et al. (2026) noted that underutilized feed resources, such as locally available roots and tubers, their by-products, and insects, may provide alternatives particularly in production systems where feed scarcity and seasonal feed deficits are major constraints, while simultaneously supporting circular economy practices. From a poultry nutrition perspective, Keohavong (2026) emphasized that insect meals, single-cell proteins, and plant-derived by-products have considerable potential to partially replace conventional protein sources such as soybean meal and fishmeal; however, variability in nutrient composition, amino acid digestibility, production costs, and regulatory requirements remain critical determinants of their large-scale utilization.

The circular bioeconomy also demonstrates that the concept of waste is context dependent. Dougherty et al. (2023) noted that, in life cycle assessments, distinctions among co-products, by-products, residues, and waste have important implications for system boundaries and the allocation of environmental burdens. A material with no economic value today may become a valuable raw material following the development of a new processing technology. Similarly, a food-processing residue that previously incurred disposal costs may become an economically valuable product once demand for it emerges within the feed sector. Although this transformation is beneficial, it creates a new challenge for assessment: can a material whose economic value has increased still genuinely be regarded as "waste," and what proportion of the environmental burdens of the production process should be allocated to it? This question is particularly important when assessing the environmental performance of insect production, biofuel by-products, and alternative feed ingredients. Scientific analysis of circular systems should therefore consider not only physical material flows but also changes in the economic value of materials and their alternative uses.

The role of the livestock sector within the circular economy also differs among species. Ruminants perform an important upcycling function through their capacity to utilize cellulose-rich biomass that is inedible to humans, including pasture, forages, and crop residues. Pigs may offer advantages in utilizing certain by-products from food and agricultural processing, whereas the high nutrient requirements of poultry make the amino acid balance and digestibility of alternative feed ingredients more critical. Keohavong (2026) demonstrated that, despite the potential of insects, yeasts, algae, and other alternative protein sources in poultry, amino acid profile, digestibility, cost, and processing requirements remain major determinants of their commercial use. In aquaculture, insect and microbial proteins are becoming increasingly important, particularly as substitutes for fishmeal and other limited protein resources, while insect production represents a distinct trophic level capable of converting organic resources originating from other sectors into insect biomass. Therefore, the objective of the circular bioeconomy is not to direct all species toward the same production model, but rather to match the biological conversion capacity of each species with the most appropriate resource flow within the food system.

Accordingly, the fundamental question in future livestock production will no longer be limited to "How many resources were used to produce one kilogram of animal product?" Additional questions will need to be addressed, including "What proportion of the resources used could have been directly consumed by humans? How much of the carbon, nitrogen, phosphorus, biomass, and energy generated during production could be retained within the system? To what extent could the residual material from one sector be transformed into a valuable input for another sector?" This perspective moves livestock production beyond an isolated production activity and positions it within the resource cycles of the

broader agrifood system, demonstrating that sustainability can be achieved not only by consuming fewer resources but also by circulating resources more intelligently within the system. This approach also provides a strong foundation for climate-smart livestock production, which will be addressed in the following section, because closing resource cycles, reducing feed and energy inputs, recovering nutrients, and transforming waste into economic value are directly related to climate change mitigation and the development of production systems that are more resilient to changing environmental conditions.

11. Climate-Smart Livestock Production

The relationship between climate change and livestock production is bidirectional and multilayered. On the one hand, livestock production contributes to greenhouse gas emissions through methane from enteric fermentation, methane and nitrous oxide from manure management, feed production, energy use, and land-use change. On the other hand, the same sector is directly exposed to the impacts of climate change through rising temperatures, heat waves, drought, changing precipitation patterns, water scarcity, changes in pasture and feed resources, shifts in the geographical distribution of diseases and parasites, and extreme climatic events. Therefore, from a livestock production perspective, the climate challenge is not limited to reducing greenhouse gas emissions from the sector; it also raises the question of in which regions, with which species and genotypes, using which feed resources, and under which production systems livestock production can be sustained in the future. Climate-smart livestock production should therefore be considered as a holistic production paradigm that extends beyond emission mitigation and addresses productivity, adaptation, and mitigation within the same system (Thornton et al., 2024b; Adesogan et al., 2025).

Three fundamental objectives emerge in adapting the climate-smart agriculture approach to livestock production: sustainably increasing productivity and the contribution to food security, enhancing the adaptive capacity and resilience of production systems to climate change, and reducing greenhouse gas emissions where feasible. In livestock production, these three objectives are not independent of one another. Improving animal health, using higher-quality feeds, increasing reproductive efficiency, or reducing heat stress can increase production per animal; the same interventions may reduce resource use and greenhouse gas emission intensity per unit of production while simultaneously increasing the resilience of the production system to climate shocks. However, not every intervention can be expected to affect all three objectives in the same direction. Some practices may have a strong mitigation effect while contributing little to adaptation, whereas certain adaptation measures may increase the use of energy or other inputs and thereby create new trade-offs in terms of emissions. The distinguishing feature of climate-smart livestock production is therefore not

the use of a specific group of technologies, but the integrated management of productivity–adaptation–mitigation relationships at the system level (Adesogan et al., 2025; Thornton et al., 2024a).

Energy use is also becoming increasingly important, particularly in intensive dairy, pig, poultry, and other confined livestock production systems. Ventilation, cooling, heating, lighting, milking, feeding, manure removal, water pumping, and product cooling may require substantial amounts of energy. The use of energy-efficient equipment, improvements in building design, management of automation to minimize unnecessary energy use, and integration of solar energy, biogas, and other renewable energy sources into farm operations can reduce dependence on fossil energy. Thornton et al. (2024b) identified energy efficiency and renewable energy use, particularly in dairy production systems, as important components of low-emission livestock production. However, digitalization itself also consumes energy. Sensors, automated systems, data storage infrastructure, and the production and disposal of electronic equipment can generate additional environmental costs. Papakonstantinou et al. (2024) therefore emphasized that the potential of precision livestock farming technologies to optimize resource use should be evaluated together with their indirect impacts, including energy consumption and electronic waste. In other words, “smart” technology is not automatically “low-carbon” technology.

Another dimension of mitigation strategies involves carbon sequestration in soils and biomass. Improved pasture management, prevention of overgrazing, restoration of degraded pastures, appropriate grazing intensity, the use of legumes, and silvopastoral systems may contribute to maintaining or increasing soil carbon stocks under certain conditions. These practices are important not only for mitigation but also for the stability of feed supply, soil water-holding capacity, erosion control, biodiversity, and resilience to drought. Paul et al. (2023) demonstrated that livestock production can contribute to soil and landscape restoration, particularly within integrated crop–livestock systems and under appropriate pasture management. Thornton et al. (2024a) likewise identified pasture restoration, rotational grazing, and silvopastoral practices as important options within livestock climate strategies. However, it should be recognized that soil carbon sequestration potential depends on climate, soil characteristics, initial carbon stocks, grazing management, and timescale; therefore, carbon sequestration should not be regarded as an equally effective or unlimited offsetting mechanism across all production systems.

However, resource efficiency and low-carbon production should not be treated as equivalent concepts. Lower feed intake or improved feed efficiency can generally enhance environmental performance, but the total carbon footprint of a production system is influenced by numerous other variables, including the source of feed production, land-use change, the energy mix, manure management,

production duration, and product processing. Similarly, the use of locally sourced feed may reduce transport-related emissions, but if its low nutritional value substantially reduces production per animal, total emission intensity may increase. Low-carbon livestock production therefore involves not the optimization of a single biological efficiency indicator, but the integrated management of different emission sources throughout the production chain. Life cycle assessment, carbon footprinting, and other environmental assessment methods are therefore critical tools for evaluating the environmental performance of climate-smart livestock production and for identifying potential trade-offs across different stages of the production chain.

Within this framework, the fundamental question for the future of livestock production is not simply, "How can we reduce greenhouse gas emissions?" A more comprehensive question should be formulated as follows: "Under changing and increasingly uncertain climatic conditions, how can we produce sufficient animal products while using resources more efficiently, generating lower emissions, and maintaining the resilience of production systems to shocks?" The answer to this question will not be the same for all species, regions, and farm scales. Nevertheless, the fundamental direction of climate-smart livestock production is clear: a transition from production growth based on increasing inputs toward systems that integrate biological efficiency with resource efficiency, anticipate climate risks, reduce emissions at their source, adapt to local ecological and economic conditions, and maintain long-term production capacity. This approach also provides a conceptual foundation for carbon and water foot printing, life cycle assessment, emission mitigation strategies, and broader assessments of environmental sustainability in livestock production.

12. One Health and One Welfare Perspective

The transformation of livestock production cannot be evaluated solely in terms of higher productivity, lower environmental impacts, or the adoption of more advanced technologies. Livestock production systems are also biological and social systems in which animals, humans, and the ecosystems they inhabit continuously interact. A health problem arising in animals may not remain confined within the physical boundaries of the farm; it may have consequences for human and ecosystem health through the food chain, direct contact, water, soil, manure, wildlife, and other environmental pathways. Similarly, environmental degradation, climate change, biodiversity loss, or changes in water quality may affect animal health and welfare, while the health and welfare status of animals may, in turn, influence antimicrobial use, the risk of zoonotic diseases, food safety, and the resource-use efficiency of the production system. This interdependence among humans, animals, and the environment has made the One Health and closely related One Welfare approaches increasingly important in the

evaluation of modern livestock production (Emikpe et al., 2024; Elbehiry & Marzouk, 2025).

The One Health nature of antimicrobial resistance becomes more apparent when the transmission pathways of resistant bacteria and resistance genes are considered. Elbehiry and Marzouk (2025) noted that resistant bacteria selected following antimicrobial use in animals can reach humans not only through animal-source foods and direct contact, but also through environmental pathways involving soil, water, manure, and wildlife. Mobile genetic elements such as plasmids, integrons, and transposons facilitate the horizontal transfer of resistance genes among bacteria, making it difficult to confine the problem to a single bacterial species or animal population. Therefore, the impact of an antimicrobial used on a farm cannot be evaluated solely in terms of the clinical outcome in the treated animal; the selection of resistance and the potential movement of resistance genes among animals, manure, soil, water, food, and human populations must also be considered (Elbehiry & Marzouk, 2025).

While One Health places the health relationships among humans, animals, and the environment at its center, the One Welfare approach extends this integrated perspective to the relationships among animal welfare, human well-being, and the surrounding social and environmental conditions. From this perspective, animal welfare is not an ethical criterion added to sustainable production as an afterthought, but one of the fundamental components directly associated with the biological and social functioning of the production system. Inadequate housing conditions, excessive stocking density, poor ventilation, heat stress, inadequate hygiene, social stress, and inappropriate management directly compromise animal welfare, while the same conditions may increase disease risk and, in some cases, the need for treatment. Consequently, it is often impossible to draw a clear boundary between health and welfare. A production system in which welfare is severely compromised may also be more vulnerable from a health perspective, while a system with a high prevalence of disease cannot be considered to provide a high level of welfare solely on the basis of its production indicators (Emikpe et al., 2024; Papakonstantinou et al., 2024).

The relationships between animal health and welfare, production efficiency, and environmental sustainability should also be evaluated within this integrated framework. Feed efficiency, growth, milk or egg production, and reproductive performance may be adversely affected in animals experiencing disease or chronic stress. Producing the same quantity of product may therefore require greater amounts of feed, water, energy, housing capacity, or time, while premature culling and mortality due to disease may result in a proportion of the resources used throughout an animal's life being lost without being converted into food. Improving health and welfare may therefore provide benefits in terms of economic performance and resource-use efficiency in some production

systems. However, this relationship should not lead to animal welfare being justified solely on the basis of its contribution to production performance. Animal welfare has an ethical value independent of increased production and represents a dimension that should be considered in its own right when evaluating sustainable livestock production. Papakonstantinou et al. (2024) evaluated animal welfare together with climate and environmental sustainability, demonstrating that technological transformation should account for the relationships among these objectives.

This approach directly converges with the concept of multidimensional sustainability discussed previously. Dougherty et al. (2023) argued that evaluating the sustainability of livestock systems solely through individual indicators such as carbon footprint or production output is insufficient and that environmental, economic, and social indicators should be considered together across different scales, including the animal, farm, and food system. One Welfare more explicitly incorporates into this framework the relationships between the quality of life of animals and the well-being of farmers, workers, and communities. Thus, the evaluation of a production system considers not only how much product is obtained or how much environmental burden is generated, but also the conditions under which animals live, the conditions under which farmers and workers operate, and the consequences of the system for surrounding communities and ecosystems.

Within this framework, although the effect of a technology or management practice on production performance is an important criterion in evaluating future livestock production systems, it is not sufficient on its own. The consequences of the same intervention for animal health and welfare, antimicrobial use requirements, the likelihood of disease emergence and spread, food safety, environmental transmission pathways, and the conditions of farmers and workers must also be considered. The fundamental contribution of the One Health and One Welfare perspectives is to extend the boundaries of assessment beyond an individual animal or farm to a broader system. When animals, humans, and the environment are regarded not as independent categories of outcomes but as continuously interacting components of the same production system, the meaning of innovation in livestock production also broadens. Technological advancement can become genuine progress for the future of livestock production only when it is considered together with biological safety, animal welfare, environmental responsibility, and social sustainability.

13. Barriers to the Adoption of Innovations

The development of innovations in livestock production and their widespread and sustained use within production systems represent successive but distinct stages of the same process. The ability of a technology to operate with high accuracy under controlled research conditions, produce favorable results in

scientific studies, or demonstrate technical feasibility does not guarantee its adoption by commercial farms. Although research and development capacity is rapidly expanding across many areas, ranging from precision livestock farming technologies and artificial intelligence-based decision-support systems to alternative feed resources and climate-smart practices, commercial adoption has not progressed at the same pace, clearly illustrating this distinction. This situation is sometimes attributed to farmers' reluctance or resistance to innovation; however, such an explanation substantially oversimplifies the complexity of the adoption process. A farmer's decision to adopt a new technology is determined by numerous interacting factors, including the economic return on investment, farm scale, compatibility of the technology with the existing production system, the farmer's level of knowledge and digital competence, availability of technical support services, infrastructure conditions, data security, interoperability among different systems, and the reliability of the technology under actual production conditions. The systematic review conducted by Castellini et al. (2025) similarly demonstrated that economic and farm-related risks are particularly influential in farmers' evaluations of new technologies, whereas education, economic incentives, access to information, and social networks can facilitate adoption. Therefore, the diffusion of innovations should be evaluated not solely in terms of the technical characteristics of a technology, but within the framework of interactions among the technology, the farm, the farmer, the economic environment, and the institutional structure.

Research on technology acceptance also demonstrates that adoption cannot be explained solely by ease of use. Gouroubera et al. (2026) evaluated the findings of 33 studies involving 13,660 farmers across 17 countries using meta-analytic structural equation modeling and demonstrated that perceived usefulness is one of the strongest determinants of attitudes toward digital technologies. In contrast, the effect of perceived ease of use on behavioral intention was found to be more limited than expected, while facilitating conditions and social influence also played important roles in explaining the adoption process. More importantly, an intention–use gap was identified, indicating that positive attitudes toward a technology and intentions to use it do not always translate into actual use (Gouroubera et al., 2026). This finding demonstrates that believing a technology to be useful and actually integrating it into routine production practices are distinct processes.

Another less visible but equally important dimension of technological dependence is the farmer's decision-making autonomy. As artificial intelligence-based systems increasingly generate recommendations, there is a potential risk that farmers may place their own observations and experience in a secondary position or accept algorithmic outputs without critical evaluation. Khwidzhilli and Ijatuyi (2026) noted that excessive dependence on artificial intelligence systems may weaken farmer autonomy and traditional knowledge systems and

therefore emphasized that human-centered systems should be designed to be explainable, transparent, and participatory. The solution is not to restrict the use of digital technologies, but to position technology not as an independent authority that makes decisions on behalf of the farmer, but as a tool that expands the farmer's decision-making capacity. An algorithm indicating disease risk should not replace the clinical assessment of a veterinarian, just as a feeding algorithm should not replace expert knowledge of animal physiology. As the level of automation increases, it becomes increasingly important to clearly define which decisions can be safely automated, under which circumstances human evaluation is required, and how responsibility should be allocated when incorrect decisions occur.

When economic accessibility, digital competence, reliability, and technological dependence are considered together, the potential for digital transformation to widen existing structural disparities within the livestock sector becomes more apparent. Large farms may adopt new technologies earlier, generate greater volumes of data, and use these data to optimize management processes in greater detail. When the resulting economic gains further increase their capacity to invest in new technologies, a self-reinforcing advantage may emerge over time. If small farms remain outside this process, digitalization may widen rather than reduce productivity gaps. Akinyemi et al. (2026) emphasized the importance of socio-technical research and the development of low-cost solutions suitable for small farms in order to increase the real-world impact of precision livestock farming technologies. Adesogan et al. (2025) further noted that, in low- and middle-income countries, conditions such as affordability, simplicity, access to credit, low risk, limited additional labor requirements, availability of necessary inputs, and a clearly demonstrable return on investment are critical to the adoption of climate-smart livestock practices.

Therefore, digitalization, the convergence of biological and digital technologies, the circular bioeconomy, climate-smart production, and the other innovative approaches discussed throughout this chapter can transform production systems only to the extent that they can be used sustainably under actual farm conditions. A technology that demonstrates high accuracy under research conditions but is economically inaccessible, not trusted by farmers, difficult to maintain, unable to communicate with other systems, or poorly adapted to local production conditions cannot translate its theoretical potential into commercial production. The success of an innovation should therefore be evaluated not only by its technical performance, but also by the extent to which it can be permanently integrated into the production system and by the net biological, economic, environmental, and managerial value generated through that integration. Only at this point can the true transformative capacity of an innovation be discussed. Nevertheless, the existence of an innovation that is technically and economically feasible does not conclude the discussion, because

the fact that a technology can be used does not necessarily mean that it is ethically acceptable, socially accepted, or free from regulatory challenges. The next level of assessment in the transformation of livestock production therefore concerns the ethical, societal, and regulatory issues associated with innovation.

14. Ethical, Societal, and Regulatory Issues

Technological transformation in livestock production cannot be evaluated solely in terms of which technologies can be developed or the extent to which they improve production performance. The fact that an innovation is scientifically possible, technically feasible, and economically profitable does not necessarily mean that it is ethically and socially acceptable. Gene-editing technologies may contribute to making animals resistant to certain diseases; artificial intelligence may detect disease or welfare problems earlier than farmers; cameras and biosensors may continuously monitor animals throughout their lives; and robotic systems may automate many tasks traditionally performed by humans. However, these developments raise new questions concerning the status of animals within production systems, farmers' responsibilities and decision-making autonomy, ownership of agricultural data, accountability for algorithmic decisions, consumer trust in emerging technologies, and the criteria according to which public authorities should regulate innovation. While Papakonstantinou et al. (2024) noted that precision livestock farming technologies offer important opportunities in terms of production efficiency, environmental sustainability, animal health, and welfare, they particularly emphasized the need to consider ethical issues and existing legal frameworks in the implementation of these technologies. Similarly, within the Agriculture 5.0 approach, technology is no longer regarded solely as a tool for optimization, but as part of a socio-technical system that must be evaluated in relation to humans, animals, and the environment (Khwidzhilli & Ijatuyi, 2026). Therefore, the fundamental question for future livestock production should not simply be "Which technologies can we use?" but rather "For what purposes, within what boundaries, and for whose benefit should these technologies be used?"

However, the ethical evaluation of gene editing should not be reduced solely to the question, "Is it right to modify the genome?" The purpose of the intervention, its effects on the animal, the availability of alternative solutions, and whether the modification contributes to animal welfare should be considered together. For example, a genetic modification that provides resistance to a serious infectious disease and reduces the disease burden experienced by animals cannot be evaluated within the same ethical framework as a modification intended to make animals biologically more tolerant of a production environment that is problematic from a welfare perspective. In the latter case, there is a risk that genetic technology may be used to adapt the animal to a problematic system rather than to address the underlying welfare problem within the production

system. Therefore, the ethical evaluation of gene editing should address not only the question “Is the modification safe?” but also “Why is this modification being made, and which production problem is it intended to solve?”

In addition, the increasing complexity of artificial intelligence systems raises the issue of explainability. When a farmer or veterinarian cannot understand why an algorithm has made a particular decision, the extent to which that system should be trusted becomes debatable. Khwidzhilli and Ijatuyi (2026) stated that one of the defining characteristics of Agriculture 5.0 is ethical, explainable, and human-centered artificial intelligence, and that algorithms should be evaluated not only according to their optimization performance but also in terms of transparency, accountability, and alignment with socio-ecological values. High predictive accuracy alone will therefore not be a sufficient indicator of quality in the future. Particularly for decisions affecting biological outcomes such as animal health and welfare, it is important that users can understand the data on which a system bases its decisions, that the system can communicate its uncertainty, and that its decisions can be overridden by humans when necessary. The preservation of local control and manual intervention capacity proposed by Neethirajan (2026) for digital systems is therefore not merely a technical safety measure, but also an ethical principle concerning the preservation of the decision-making authority of farmers and veterinarians.

From this perspective, ethical principles should not be regarded as barriers to technological progress, but as design criteria that determine the direction in which innovation should develop. A system that can measure animal welfare but does not improve it, generates vast amounts of data but reduces farmers’ control over those data, achieves high predictive accuracy but cannot explain its decisions, or is biologically effective but not considered trustworthy by society may be technologically advanced; however, it does not constitute an innovative livestock production model in a holistic sense. This is also the natural conclusion of the approach developed throughout this chapter: the livestock production systems of the future must not only be more digital, more automated, or more powerful in terms of biotechnology, but also more transparent, accountable, animal-centered, human-centered, and socially responsible. This framework also requires that the future research areas addressed in the final part of this chapter be considered not only through the question “Which new technologies will be developed?” but also through the question “How can these technologies be made more trustworthy, equitable, explainable, and responsible?”

15. Future Research Areas

The future research agenda for livestock production requires a transformation that extends beyond the development of individual new technologies. Although precision livestock farming, artificial intelligence, genomics, next-generation feed resources, the circular bioeconomy, climate-smart production, One Health,

and One Welfare approaches discussed throughout this chapter may appear to represent independent fields of research, the most significant scientific advances in the future are expected to occur at the intersections of these areas. Accordingly, the research question is increasingly shifting away from "Which new technology can be developed?" toward "How can biological, digital, environmental, and socioeconomic systems be managed more effectively together?" Dougherty et al. (2023) emphasized that sustainable livestock production cannot be evaluated solely through indicators at the animal or farm level and that environmental, economic, and social dimensions need to be modeled together across different biological and spatial scales. Similarly, Thornton et al. (2024b) noted that future livestock systems will need to simultaneously respond to increasing food demand, adapt to the intensifying impacts of climate change, contribute to greenhouse gas mitigation targets, and manage interconnected outcomes related to water, biodiversity, economic development, and societal resilience. Within this framework, a defining characteristic of the future research agenda will be the transition from a technology-centered toward a system-centered perspective.

The convergence of genomics and digital phenotyping is also opening a new era of research in animal breeding. Although genomic selection has substantially accelerated the rate of genetic progress, the success of selection remains dependent on the availability of reliable phenotypes. Continuous sensor data may enable traits that were previously expensive or difficult to measure, including feed intake, behavior, disease resistance, heat tolerance, stress response, mobility, and welfare, to be phenotyped in large populations. Consequently, integrating genomic data with high-frequency digital phenotypes may enable selection not only for conventional production traits but also for more complex characteristics such as resilience, robustness, resource-use efficiency, longevity, and animal welfare. Van Eenennaam (2025) demonstrated that genomic selection and other reproductive technologies have accelerated genetic progress in animal breeding, while gene editing offers new opportunities for directly introducing targeted genetic variation. However, the primary objective of future genetic research should not be limited to maximizing production capacity; increasing emphasis should be placed on developing animals capable of maintaining performance across different environments and exhibiting greater resilience to changes in climate, disease pressure, or nutritional conditions.

This development creates new opportunities, particularly for investigating genotype × environment interactions dynamically. Traditional genotype × environment studies have generally been based on differences in performance among regions, farms, or production conditions, whereas continuous environmental and animal-based sensor data make it possible to monitor how the same animal responds to changing environmental conditions over time. For example, simultaneous monitoring of changes in temperature and humidity together with changes in feed intake, activity, body temperature, and production

performance may reveal not only which genotype performs better under high temperatures, but also which animals adapt more rapidly to environmental change and return more quickly to their normal state. In this way, “resilience” can move from being an abstract characteristic to a set of measurable phenotypes derived from time-series data. As the pressure of climate change on livestock production increases, such resilience phenotypes and their genetic basis will become increasingly important areas of research.

However, a substantial proportion of future research should focus not on developing new technologies, but on understanding why existing technologies are not adopted. Akinyemi et al. (2026) noted that the major factors limiting the real-world impact of precision livestock farming on animal welfare may increasingly relate not to the need for further technological advances, but to economic feasibility, adoption barriers, and socio-technical conditions. Mata (2026) similarly stated that future research should focus on low-cost and scalable technologies, standardized data frameworks, and supportive regulations applicable across different production systems. This directly brings the issue of scale discussed previously into the research agenda. A sensor system that is economically feasible on a large dairy farm may be impractical for a small family farm; conversely, a simple mobile phone-based decision-support system may provide greater marginal benefits for small-scale farms. Future innovation research should therefore aim to develop not merely the most advanced technology, but the most appropriate technology for specific conditions.

This is particularly important for low- and middle-income countries. Thornton et al. (2024a) noted that industrialized livestock production systems have a greater capacity than small-scale farms to invest in climate adaptation and mitigation technologies, whereas livestock may be substantially more critical to the food security and livelihoods of smallholders. Van Eenennaam (2025) also emphasized that implementing proven genetic technologies, such as genomic selection and artificial insemination, can be difficult in regions where the necessary infrastructure is lacking. One of the major questions for global livestock research will therefore be how to develop innovations appropriate to local production systems, climatic conditions, capital structures, and farmer needs, rather than directly transferring high-technology systems from developed countries to lower-income regions. This approach is also important for preventing the widening of technological inequalities.

Accordingly, the fundamental research question for the future of livestock production is shifting away from “How can we produce more?” A more meaningful question can be formulated as follows: “Under changing climatic conditions, limited resources, and increasing societal expectations, how can sufficient animal-source food be produced in systems that are more resilient, resource-efficient, environmentally sustainable, economically viable, and

socially acceptable while safeguarding the biological capacity and welfare of animals?" No single discipline, technology, or animal species can provide a complete answer to this question. Future livestock production will therefore increasingly become a transdisciplinary field of research in which biology, engineering, data science, environmental science, economics, and the social sciences converge around a shared production-system challenge rather than a race to develop individual technologies. This is where the scientific significance of the transformation described throughout this chapter fundamentally lies: innovative livestock production of the future will emerge not from the sum of individual technologies, but from their meaningful integration in pursuit of biological and societal objectives.

16. Conclusion

Livestock production is entering a period of transformation in which the conventional objective of maximizing production per animal is being incorporated into a much broader framework of biological efficiency, environmental sustainability, economic viability, animal health and welfare, and societal responsibility. This transformation does not imply that productivity has lost its importance. On the contrary, meeting the nutritional requirements of a growing and changing global population will continue to require efficient livestock production. What has changed is the context in which productivity is evaluated. The amount of product obtained can no longer be considered independently of the resources required to produce it, the environmental burdens generated throughout the production chain, the conditions under which animals are raised, the resilience of production systems to climatic and economic shocks, and the capacity of producers to maintain economically viable operations.

Technological development is one of the principal forces enabling this transition, but technology alone does not define the future of livestock production. Agriculture 4.0 has expanded the capacity to continuously measure animals, their environment, and production processes, while Agriculture 5.0 has broadened the discussion toward the purposes for which these technological capabilities should be used. Sensors, artificial intelligence, robotics, genomic technologies, digital phenotyping, and automated systems are therefore most valuable not when they simply replace human labor or increase the volume of data generated, but when they improve the capacity to understand biological processes and support more informed, timely, and responsible decisions. The emerging production paradigm is consequently neither entirely technology-centered nor entirely human-centered. It is based on the integration of biological information, digital capacity, human knowledge, and managerial responsibility within the same decision-making architecture.

At the center of this transformation is the animal itself. The increasing ability to continuously monitor behavior, physiology, feed intake, health, performance,

and responses to environmental conditions is gradually shifting livestock management from standardized herd-level practices toward systems that recognize biological variation among individuals or meaningful biological groups. At the same time, the convergence of these phenotypic data with genomics, environmental measurements, artificial intelligence, precision nutrition, and automated intervention creates opportunities to move from retrospective management toward prediction and proactive management. However, greater measurement precision does not automatically result in more animal-centered production. The biological information generated by these systems must meaningfully contribute to decisions concerning animal health, welfare, and biological requirements rather than being used exclusively to maximize production.

The same systems perspective applies to environmental sustainability. Circular bioeconomy approaches demonstrate that livestock should not be evaluated solely as a consumer of resources and a source of emissions, but also according to its capacity to convert biomass inedible to humans, utilize agricultural and food-processing by-products, recycle nutrients, and connect resource flows among different components of the agrifood system. Climate-smart livestock production similarly requires productivity, adaptation, and mitigation to be considered simultaneously rather than as independent objectives. Future production systems will therefore need not only to use fewer resources or generate lower emissions, but also to maintain their productive capacity under increasingly variable climatic conditions and to manage carbon, nutrients, water, energy, and biological resources more effectively across the entire production system.

The boundaries of livestock sustainability also extend beyond the farm. One Health and One Welfare perspectives demonstrate that animal health, human health, environmental integrity, animal welfare, and human well-being are interconnected outcomes of the same production system. Similarly, the success of technological innovation cannot be assessed solely by predictive accuracy, biological performance, or engineering sophistication. Economic accessibility, farmer adoption, interoperability, data governance, transparency, explainability, ethical acceptability, and regulatory compatibility ultimately determine whether technological potential can be translated into meaningful change under commercial production conditions. Innovation that cannot be sustainably adopted, trusted, maintained, or responsibly governed remains limited regardless of its technical performance.

The future of livestock production should therefore not be understood as a transition from traditional farming to a fully automated system in which biology and human knowledge are replaced by technology. Rather, it represents a transition toward production systems in which biological knowledge becomes

increasingly precise, digital technologies make previously invisible processes measurable, human expertise provides context and responsibility, and environmental and societal objectives become integral components of production decisions. The defining challenge will not be to determine whether genomics, artificial intelligence, automation, alternative feeds, or other emerging technologies will shape livestock production, but how these tools can be integrated into coherent systems that simultaneously support food production, animal health and welfare, environmental sustainability, economic viability, and societal expectations.

Ultimately, the livestock production systems of the future will not be defined by the number or sophistication of technologies they contain, but by how effectively those technologies are integrated with animal biology, human knowledge, and the ecological and socioeconomic context in which production occurs. The transition from traditional livestock farming to future production systems is therefore not simply a technological transition. It is a transformation in how livestock production itself is understood: from the management of animals primarily for production toward the management of complex biological, environmental, digital, economic, and social systems. Within this perspective, genuine innovation will arise not from producing more through technology alone, but from developing livestock production systems in which biological efficiency, technological capacity, environmental sustainability, animal welfare, human knowledge, and economic viability are meaningfully integrated.

References

Adesogan, A. T., Gebremikael, M. B., Varijakshapanicker, P., & Vyas, D. (2025). Climate-smart approaches for enhancing livestock productivity, human nutrition, and livelihoods in low- and middle-income countries. Animal Production Science, 65, AN24215. https://doi.org/10.1071/AN24215

Akinyemi, B. E., Akaichi, F., Turner, S. P., Johnson, A. K., & Siegford, J. M. (2026). Precision livestock farming and farm animal welfare: A scientometric analysis of research trends and technological innovations. Computers and Electronics in Agriculture, 255, 112341. https://doi.org/10.1016/j.compag.2026.112341

Castellini, G., Romanò, S., Merlino, V. M., Barbera, F., Costamagna, C., Brun, F., & Graffigna, G. (2025). Determinants of consumer and farmer acceptance of new production technologies: A systematic review. Frontiers in Sustainable Food Systems, 9, 1557974. https://doi.org/10.3389/fsufs.2025.1557974

Dougherty, J. C. H., Ridoutt, B., Jackson, M. K., Arsic, M., Juliano, P., & Oddy, V. H. (2023). A conceptual framework for modelling the role of livestock systems in sustainable diets and a sustainable planet. Animal Production Science, 63(18), 1866–1886. https://doi.org/10.1071/AN23300

Elbehiry, A., & Marzouk, E. (2025). From farm to fork: Antimicrobial-resistant bacterial pathogens in livestock production and the food chain. *Veterinary Sciences, 12(9), 862*. https://doi.org/10.3390/vetsci12090862

Emikpe, B. O., Tachie, H. F., Takyi, P. N., & Asare, D. A. (2024). One Health and sustainable agricultural system in the 21st century. PAMJ-One Health, 15(11). https://doi.org/10.11604/pamj-oh.2024.15.11.43594

Food and Agriculture Organization of the United Nations (FAO). (2023). *Contribution of terrestrial animal source food to healthy diets for improved nutrition and health outcomes: An evidence and policy overview on the state of knowledge and gaps*. Rome: FAO. ISBN 978-92-5-137536-5.

Gouroubera, M. W., Gouthon, M., Segnon, A. C., Dosso, F., Togbévi, Q. F., Moumouni-Moussa, I., & Zougmoré, R. B. (2026). Understanding farmers' acceptance of digital technologies: a meta-analytic structural equation modeling approach based on the technology acceptance model. *Frontiers in Sustainable Food Systems*, *10*, 1723715. https://doi.org/10.3389/fsufs.2026.1723715

Keohavong, B. (2026). Life cycle assessment of precision nutrition and feed innovations for sustainable poultry production. *Discover Agriculture, 4*, 239. https://doi.org/10.1007/s44279-026-00690-5

Khwidzhilli, R. H., & Ijatuyi, E. J. (2026). Leveraging digital tools for sustainable precision in Agriculture 3.0–5.0: A scoping review of trends, benefits, and

challenges. *Frontiers in Sustainable Food Systems, 10*, 1768902. https://doi.org/10.3389/fsufs.2026.1768902

Losacco, C., Pugliese, G., Forte, L., Tufarelli, V., Maggiolino, A., & De Palo, P. (2025). Digital transition as a driver for sustainable tailor-made farm management: An up-to-date overview on precision livestock farming. Agriculture, 15, 1383. https://doi.org/10.3390/agriculture15131383

Ludgate, N., Umutoni, C., Vyas, D., Serra, R., Adeoti, T. M., Bonna, A. S., & Adesogan, A. T. (2026). Transforming livestock systems with better feeds: A triple win for food and nutrition security, climate resilience, and women and youth empowerment in low- and lower-middle-income countries. Annual Review of Animal Biosciences, 14, 181–206. https://doi.org/10.1146/annurev-animal-111523-102141

Martin, T., Gasselin, P., Hostiou, N., Feron, G., Laurens, L., Purseigle, F., & Ollivier, G. (2022). Robots and transformations of work in farm: A systematic review of the literature and a research agenda. Agronomy for Sustainable Development, 42(4), 66. https://doi.org/10.1007/s13593-022-00796-2

Mata, F. (2026). The impact of precision livestock farming technologies on productivity, animal welfare, and environmental sustainability. *J, 9(2), 13*. https://doi.org/10.3390/j9020013

Mihret, Y. C., Takele, M. M., & Mintesinot, S. M. (2025). Advancements in agriculture 4.0 and the needs for introduction and adoption in Ethiopia: a review. *Advances in Agriculture*, *2025*(1), 8828400. https://doi.org/10.1155/aia/8828400

Mukherji, A., Arndt, C., Arango, J., Flintan, F., Derera, J., Francesconi, W., Jones, S., Loboguerrero, A. M., Merrey, D., Mockshell, J., Quintero, M., Mulat, D. G., Ringler, C., Ronchi, L., Sanchez, M. E. N., Sapkota, T., & Thilsted, S. (2023). Achieving agricultural breakthrough: A deep dive into seven technological areas. CGIAR. https://hdl.handle.net/10568/131852

Neethirajan, S. (2026). Digital twins for cows and chickens: From hype cycles to hard evidence in precision livestock farming. *Agriculture, 16(2), 166*. https://doi.org/10.3390/agriculture16020166

Papakonstantinou, G. I., Voulgarakis, N., Terzidou, G., Fotos, L., Giamouri, E., & Papatsiros, V. G. (2024). Precision livestock farming technology: Applications and challenges of animal welfare and climate change. Agriculture, 14, 620. https://doi.org/10.3390/agriculture14040620

Paul, B. K., Mutegi, J. K., Wironen, M. B., Wood, S. A., Peters, M., Nyawira, S. S., Misiko, M. T., Dutta, S. K., Zingore, S., Oberthür, T., Notenbaert, A. M. O., & Cook, S. (2023). Livestock solutions to regenerate soils and landscapes for sustainable agri-food systems transformation in Africa. Outlook on Agriculture, 52(2), 103–115. https://doi.org/10.1177/00307270231179747

Pugliese, G., Puvača, N., Passantino, L., Perillo, A., Laudadio, V., Tateo, A., Piemontese, L., Dimuccio, M. M., Lauriola, S., Tufarelli, V., & Losacco, C. (2026). Drawing a circle for the livestock and agrifood sector: Fundamentals to a sustainable supply chain. Frontiers in Animal Science, 7, 1765104. https://doi.org/10.3389/fanim.2026.1765104

Thornton, P., Herrero, M., Nelson, G., & Mayberry, D. (2024a). Resilient livelihoods in Africa's pastoral–agropastoral transition zones will increasingly depend on heat stress adaptation and systemic change. *Nature Food, 5(12), 976–981*. https://doi.org/10.1038/s43016-024-01079-7

Thornton, P., Wollenberg, E., & Cramer, L. (2024b). *Livestock and climate change: Outlook for a more sustainable and equitable future*. CGIAR Initiative on Livestock and Climate.

Van Eenennaam, A. L. (2025). Current and future uses of genetic improvement technologies in livestock breeding programs. *Animal Frontiers, 15(1), 80–90.* https://doi.org/10.1093/af/vfae042

CHAPTER 16

Precision Livestock Farming and Smart Farm Technologies

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1. Introduction

Effective management in livestock production depends fundamentally on obtaining accurate, timely, and reliable information about animals and their production environment. In conventional production systems, such information has largely been derived from direct farmer observation, periodic measurements of traits such as body weight or milk yield, clinical examinations, and routine production records. This approach has long been effective in farms where animal numbers are limited and farmers can maintain close contact with individual animals. However, increasing farm size, production intensity, and the number of animals requiring simultaneous supervision have progressively exposed the limitations of management based primarily on human observation. Subtle changes in activity, feed intake, rumination, body temperature, vocalization, or social behavior may precede clinically apparent deterioration in health or welfare, yet continuously detecting such changes through direct observation becomes increasingly difficult in populations containing hundreds or thousands of animals. A similar challenge occurs in extensive cattle, sheep, and goat systems, where large grazing areas and limited direct contact with individual animals restrict continuous monitoring. Recent assessments of extensive production systems indicate that conventional visual observation and periodic veterinary examination may therefore detect changes in animal health and behavior only after considerable delay or may fail to detect them altogether (Zhao et al., 2026).

Precision Livestock Farming (PLF) has emerged as a technological and management approach intended primarily to reduce this information gap. At its core, PLF involves the continuous or high-frequency monitoring of animals, their production environment, and production processes through sensors and other digital technologies, followed by the transformation of the resulting data into biologically meaningful indicators that can support management decisions. Precision livestock farming should therefore not be defined simply by the presence of sensors, cameras, or automated equipment on a farm. Its fundamental contribution is to transform observations that were traditionally obtained at discrete time points and from a limited number of variables into a more continuous, objective, and, where appropriate, animal-specific flow of information. Wearable technologies such as smart collars, electronic ear tags, accelerometers, GPS devices, and physiological sensors can continuously monitor activity, location, rumination, body temperature, and other biological indicators, creating opportunities to identify health or behavioral changes before their clinical or economic consequences become evident (Mokashi et al., 2026).

This transformation is also changing the nature of measurement in livestock science. Conventional recording systems commonly treat body weight, milk yield, feed intake, health status, and similar traits as separate observations collected at predefined intervals. PLF, in contrast, allows multiple data streams

originating from the same animal or biologically meaningful group of animals to be monitored simultaneously over time. The animal can consequently be characterized not only by its body weight on a particular day, daily milk yield, or the occurrence of a clinical disease event, but also by dynamic biological and behavioral patterns. Changes in activity, posture, feeding behavior, rumination, spatial distribution, vocalization, or other continuously measured characteristics may reveal deviations from an animal's normal state. One of the most important consequences of this capability is the transition from reactive management, in which events are recorded after they have occurred, toward predictive and increasingly proactive management based on the early detection of biologically meaningful deviations.

Nevertheless, the capacity to detect patterns does not by itself demonstrate that a technology is suitable for commercial decision-making. Systems showing high classification or prediction performance under experimental conditions cannot automatically be assumed to perform equally well across heterogeneous commercial populations. Acoustic monitoring of respiratory symptoms in pigs provides a useful example. Automated classification of coughing events demonstrates considerable potential for continuous surveillance and early identification of respiratory disorders, including during periods when direct human observation is absent. However, models developed from limited numbers of animals or respiratory events require broader external validation before their reported performance can be generalized to commercial populations (Zhang et al., 2026). This distinction between technological performance and biological or commercial validity is fundamental to the evaluation of PLF technologies.

PLF also facilitates a transition from management based predominantly on herd or flock averages toward management at higher biological resolution. Animals within the same population may differ substantially in genetic background, age, physiological status, health, social position, and responses to environmental stressors. The integration of electronic identification with wearable sensors, automated feeders, milking systems, weighing platforms, and other measurement technologies makes it increasingly possible to associate different measurements with the same individual and thereby support individualized management. However, precision does not necessarily require individual-animal monitoring in every production system. In commercial broiler production, where thousands of birds may occupy the same environment, flock activity, spatial distribution, feed and water consumption, or changes in flock vocalization may provide more practical and biologically meaningful management indicators than continuous identification of every bird. Current poultry technologies can generate behavioral and welfare indicators at both flock and individual levels, although fully integrated systems remain relatively uncommon under commercial conditions (Mekonnen, 2026). The appropriate unit of measurement in PLF should therefore be determined primarily by the

biological characteristics of the species, the structure of the production system, and the management problem being addressed rather than by the technological capacity to identify individual animals.

The scope of precision livestock farming also extends beyond sensors attached directly to animals. Biological responses cannot be interpreted independently of the conditions in which they occur. Continuous measurements of temperature, relative humidity, air movement, light, carbon dioxide, ammonia, particulate matter, and other environmental variables therefore constitute an important component of smart livestock systems. Combining environmental information with animal-based measurements can improve interpretation of observed biological changes. In enclosed production systems, environmental monitoring can also be linked to ventilation, cooling, heating, and other control systems, whereas in extensive systems information on microclimate, pasture use, and access to water or shade can be integrated with animal behavior and physiological responses (Zhao et al., 2026). PLF thus extends from monitoring the animal toward a broader smart-farm architecture in which animals, the physical environment, digital information, and management interventions are increasingly interconnected.

Automation represents another component of this architecture but should not be considered synonymous with precision livestock farming. Automation enables predefined tasks to be performed with reduced human intervention, whereas PLF seeks to establish a functional relationship among measurement, biological interpretation, decision-making, and intervention. Robotic systems increasingly bring these processes together by combining sensing, data collection, physical interaction, and automated action within the same platform. However, greater automation does not necessarily imply better livestock management. The scientific and practical value of a PLF system depends on whether the data it generates are biologically valid, technically reliable, and actionable for the farmer. Measurement accuracy, repeatability across animals and environments, false-positive and false-negative alarms, equipment durability, missing data, communication failures, and interoperability among different systems can all influence practical performance. Technologies that perform well under controlled experimental conditions may not maintain the same accuracy across commercial farms containing different genotypes, age groups, housing systems, environmental conditions, and management practices. Current assessments identify cost, data standardization, interoperability, and limited long-term external validation as major constraints on the widespread commercial implementation of PLF technologies (Giannico et al., 2026; Mekonnen, 2026).

For these reasons, precision livestock farming should not be regarded as a fully autonomous production model intended to eliminate human observation and expertise. Rather, it should be understood as a management approach that

expands the farmer's limited capacity for continuous observation by providing a higher-resolution and more persistent flow of biological and environmental information. Sensors and automated systems may generate thousands of measurements continuously, but determining which changes are biologically important, which alarms require intervention, and under which production conditions a technology provides meaningful economic and managerial value still requires livestock knowledge. The central challenge is therefore not simply to collect more data, but to convert data into reliable biological information and that information into better management decisions.

Accordingly, this chapter approaches precision livestock farming not as a catalogue of individual devices, but as an integrated system connecting measurement, biological interpretation, decision support, and intervention. Electronic identification, wearable and contactless sensors, location tracking, computer vision, thermal and acoustic monitoring, automated performance recording, environmental sensing, robotics, multisensor integration, and digital twins will be considered according to the biological information they generate and the management functions they support. Their contribution to health, reproduction, welfare, and production management will be evaluated together with their validation under real farm conditions and their economic, operational, and governance constraints. The central question throughout the chapter is therefore not how technologically sophisticated a sensor, algorithm, or robot may be, but whether the information it generates can be translated into earlier, more accurate, and more effective livestock management.

2. Conceptual Framework of Precision Livestock Farming and Smart Farm Architecture

Precision Livestock Farming (PLF) represents a more specific and functional concept than the general use of digital technologies in livestock production. Its defining principle is the continuous or high-frequency monitoring of animals and their production environment, the transformation of these measurements into biologically meaningful information, and the use of that information to support management decisions. Consequently, the presence of electronic recording systems, automated feeding equipment, environmental sensors, or other digital devices does not by itself constitute a PLF system. The essential requirement is the establishment of a functional connection between measurement and management. Qiao et al. (2021) described PLF as a management approach based on the integration and interpretation of information obtained from multiple sensors for continuous and real-time monitoring of animal health, behavior, production, reproduction, and environmental effects. This definition emphasizes that the fundamental characteristic of PLF lies not in the sophistication of individual devices, but in the capacity to measure biological change and convert that measurement into actionable information.

Within this conceptual framework, the information chain begins with biological responses arising from the continuous interaction between the animal and its environment. Movement, posture, feeding and drinking behavior, rumination, body temperature, respiratory characteristics, vocalization, milk yield, and changes in body weight are not independent phenomena; they represent different components of the phenotype emerging from the combined effects of genotype, physiological status, health, nutrition, management, and environmental conditions. Similarly, temperature, relative humidity, air velocity, gas concentrations, lighting, and spatial variation within the production environment provide the context required to interpret these responses. The scientific value of PLF therefore arises not merely from increasing measurement frequency, but from its capacity to characterize animal–environment interactions quantitatively over time.

The technologies used to obtain these measurements can be classified according to both their physical relationship with the animal and the source of information being measured. Animal-mounted systems include accelerometer-equipped ear tags and collars, pedometers, GPS devices, rumen boluses, and temperature sensors. Contactless technologies include RGB and depth cameras, computer vision systems, microphones, and infrared thermal imaging. Environmental sensors provide another information layer by measuring variables such as temperature, relative humidity, ventilation, ammonia, carbon dioxide, and other characteristics of the production environment, while measurements derived from biological materials such as milk, blood, or feces may provide information on metabolic status, health, and product characteristics (Fotos et al., 2026). These technologies should not necessarily be regarded as competing alternatives. Rather, they measure different dimensions of biological processes and may provide complementary information. An accelerometer, for example, may identify a reduction in activity but cannot necessarily determine whether that change results from disease, heat stress, reproductive status, or another biological process. Interpretation therefore becomes increasingly dependent on the biological and environmental context in which the measurement occurs.

The second major component of PLF architecture concerns data transmission and storage. Raw sensor output is rarely information that can be interpreted directly by a farmer. A three-axis accelerometer may generate multiple measurements every second, a camera may continuously produce images or video, and microphones may record hours of acoustic signals. Such systems can rapidly generate data volumes that exceed the capacity for direct human interpretation. Communication infrastructure is therefore required to connect measurement devices with analytical systems. Contemporary PLF architectures may include sensors, wireless communication technologies, gateways, local or edge-processing devices, cloud platforms, and centralized databases. Mokashi et al. (2026) described IoT-based cattle monitoring as an integrated architecture in

which data generated by sensors are transmitted through gateways and communication networks to platforms capable of storing, processing, visualizing, and integrating large volumes of information. In this way, biological processes occurring in the physical animal and its environment become continuous digital data streams.

Collecting and transmitting data, however, does not itself generate management value. The critical analytical step is the conversion of high-volume, frequently noisy raw data into indicators that represent biologically meaningful states or events. This process may involve data cleaning, signal processing, feature extraction, threshold-based rules, statistical modeling, and machine-learning methods. Raw accelerometer coordinates do not directly represent behaviors such as feeding, walking, resting, or rumination; the recorded signals must first be processed and associated with validated behavioral categories. Similarly, images must be transformed into estimates of body weight, posture, locomotion, or behavior; acoustic signals into indicators such as coughing or vocal stress; and thermal images into temperature characteristics with interpretable biological meaning. PLF therefore contains an analytical layer between sensing and decision-making in which raw measurements are progressively transformed into information.

A central challenge within this analytical layer is establishing a valid relationship between the variable that can be measured technically and the biological condition that is actually of interest. A variable that is easy to measure is not necessarily biologically informative, and the fact that a biologically relevant characteristic can be detected by a sensor does not guarantee that the measurement is sufficiently reliable for management purposes. Reduced activity, for example, may represent an early sign of disease, but it may also reflect environmental temperature, age, physiological stage, circadian rhythm, or normal individual variation. The objective is therefore not merely to detect change, but to determine whether an observed deviation falls within expected biological variation or represents an event requiring intervention. This distinction is particularly important in early-warning systems. Excessively sensitive systems may produce large numbers of false-positive alarms and reduce farmer confidence, whereas insufficiently sensitive systems may fail to detect important events. Measurement accuracy and biological decision accuracy should consequently be regarded as related but distinct characteristics of PLF performance.

The next layer of smart-farm architecture transforms processed information into decision support. Contemporary PLF frameworks can therefore be conceptualized as a sequence connecting sensing, communication, data storage, analytical processing, biological interpretation, and decision-making (Fotos et al., 2026). Continuous measurement of temperature and relative humidity, for

example, is not itself a management decision. The measurements acquire management value when they are interpreted in relation to the thermal load experienced by animals, a critical condition is identified, and an appropriate response such as modifying ventilation or cooling is considered. Similarly, a change in activity or milk characteristics becomes actionable only when it is interpreted as indicating an increased probability of a biologically relevant event and translated into an appropriate management response.

An important conceptual distinction must also be made between decision support and automated intervention. Some systems generate an alert and leave the final decision to the farmer or veterinarian, whereas others directly control physical equipment according to predefined rules or model outputs. Identifying a cow with an increased risk of mastitis or lameness and placing that animal on an inspection list represents decision support. In contrast, automatically activating ventilation or cooling when environmental and animal-based indicators exceed defined thresholds approaches closed-loop control. More advanced architectures may measure the biological response following an intervention and feed the resulting information back into the system. Monitoring and intervention then become components of a dynamic feedback mechanism rather than independent processes. From an engineering perspective, the most advanced PLF systems are therefore not simply capable of sensing; they can interpret measurements, identify an appropriate response, implement or recommend that response, and subsequently evaluate its biological consequences.

This architecture also clarifies the relationship between precision livestock farming and the broader concept of the smart farm. PLF primarily focuses on precise measurement and management of animals and animal-related production processes, whereas smart farming integrates these functions within the wider digital infrastructure of the farm. Animal sensors, environmental sensors, automated feeding and milking systems, robots, ventilation and energy-management systems, databases, and farm-management software may operate within the same information ecosystem. From this perspective, PLF can be regarded as the biological measurement and decision-making core of the smart livestock farm, while Internet of Things (IoT) technologies provide much of the communication infrastructure connecting its physical and digital components. Integration of sensors, communication networks, data-processing platforms, and decision-support systems transforms conventional farm equipment into interconnected components capable of generating and responding to information (Mokashi et al., 2026).

The technological sophistication of a smart farm should therefore not be evaluated simply according to the number of devices it contains. A farm may contain numerous sensors while remaining poorly integrated if individual systems cannot exchange information, measurements cannot be associated with

a common animal identity, or the resulting data do not influence management decisions. Conversely, a simpler architecture containing fewer sensors may constitute a more advanced PLF application when those sensors measure biologically appropriate variables, their data are reliably integrated, and the resulting information serves a clearly defined management objective. Technological complexity and management value are therefore not synonymous. The critical characteristic is continuity across the information chain.

This distinction is particularly relevant to the increasing use of the term digital twin in livestock research. An IoT-based monitoring platform or dashboard displaying sensor data should not automatically be classified as a digital twin. Neethirajan (2026) emphasized that systems limited to data acquisition and anomaly detection are more appropriately regarded as advanced monitoring platforms, whereas architectures approaching a genuine digital twin require a dynamic relationship between the physical system and its virtual representation. Fotos et al. (2026) similarly identified the capacity to simulate how an animal or production environment may respond to future conditions or alternative interventions as an important distinction between digital twins and conventional decision-support systems. Genuine livestock digital twins remain at a relatively early stage of technological maturity. Their potential and limitations will therefore be examined later in this chapter rather than using the term to describe all digitally connected monitoring systems.

Conceptually, PLF architecture can thus be understood as a continuous chain extending from the biological event to sensing, digital measurement, data transmission and processing, biological interpretation, management decision, and, where appropriate, physical intervention followed by renewed measurement. Weakness at any point in this chain may limit the value of the entire system. A highly accurate sensor provides little benefit if it measures an inappropriate biological indicator; an accurate measurement loses value if it cannot be reliably transmitted; correctly transmitted data are of limited use if they are interpreted incorrectly; and even a valid alarm has little practical value if it cannot be translated into an appropriate management response. The technologies discussed in the following sections should therefore be evaluated not simply according to their technical specifications, but according to where they operate within this information chain, which biological dimension they measure, and how effectively the resulting information can contribute to livestock management

3. Animal Identification, Wearable Sensors, and Location Tracking

Individual-level precision management requires measurements to be reliably associated with the animal from which they originate. Electronic identification (EID) therefore represents one of the fundamental infrastructural components of PLF. Its importance lies not merely in assigning a digital identity to an animal, but in enabling measurements of feed intake, body weight, milk production,

health, movement, and behavior from different systems to be integrated within a continuous individual record. Radio Frequency Identification (RFID) is among the most widely used technologies for this purpose. A typical RFID system consists of a transponder or electronic tag carried by the animal and an antenna-reader system that detects the stored identity when the animal enters its reading range. When integrated with feeders, drinkers, milking units, weighing platforms, or sorting gates, electronic identification allows each event to be automatically assigned to the appropriate animal. In pigs, for example, RFID systems have been used to associate individual identity with feeding and drinking events, thereby transforming simple identification into a component of continuous behavioral and intake monitoring (Buonaiuto et al., 2026).

The technical configuration of electronic identification varies according to species, production system, and management objective. Electronic ear tags are widely applicable in cattle, sheep, goats, and pigs, while electronic boluses retained within the reticulorumen provide an alternative in ruminants. RFID systems also differ in operating frequency and reading range. Low-frequency systems are well established where animals pass close to a defined reading point, whereas Ultra-High Frequency (UHF) systems may provide longer reading distances and the potential to detect multiple tags within the same area. Nevertheless, tag orientation, animal position, reading distance, and the simultaneous presence of several animals can influence identification performance (Buonaiuto et al., 2026). EID also extends beyond on-farm management. Linking a persistent electronic identity with movement, health, transport, and slaughter records can support traceability throughout the production chain, thereby connecting PLF with broader biosecurity and food-safety systems (Gresse and van Marle-Köster, 2026; Peng et al., 2025).

The scientific value of electronic identification increases substantially when identity is connected with continuously measured phenotypes. RFID itself generally indicates which animal is present, whereas accelerometers, temperature sensors, GPS devices, automated feeders, weighing systems, and other sensors provide information about what the animal is doing or how its biological state is changing. Combining these layers enables longitudinal phenotypic records to be constructed for individual animals. Feed intake, feeding frequency, body weight, activity, milk production, health interventions, and reproductive events can consequently be linked through time. Such high-frequency phenotyping is relevant not only to routine farm management but also to animal breeding, because traits that are difficult or expensive to measure conventionally may become available at much greater temporal resolution. Integration of electronic identity, performance records, and genomic information may therefore contribute to the characterization of genotype–phenotype relationships and future genomic selection strategies (Peng et al., 2025).

Wearable sensors extend this framework by continuously recording behavioral or physiological characteristics. Devices may be attached to the ear, neck, leg, or other body regions, while rumen boluses can provide internal measurements in ruminants. Depending on sensor type, movement, orientation, temperature, and other variables can be recorded at high frequency. Accelerometers are particularly important because patterns in their signals can be associated with activities such as walking, resting, feeding, and rumination. Longitudinal monitoring can then establish an individual's normal behavioral pattern and identify deviations potentially associated with estrus, parturition, disease, welfare impairment, or environmental stress. However, sensor output depends strongly on device placement. A neck-mounted accelerometer and a leg- or ear-mounted device may represent the same behavior differently, while temperature measured within the reticulorumen has a different physiological interpretation from temperature measured at the skin or ear. Sensor placement should therefore be determined by the biological variable of interest rather than technical convenience alone.

The measurement device itself must also remain biologically acceptable. Weight, dimensions, attachment method, durability, and retention can influence both data quality and animal behavior, particularly in young animals and small-bodied species. A sensor cannot be assumed to be biologically neutral simply because it successfully records data. Similarly, long-term monitoring requires continuity of both identity and measurement. Tag loss, incorrect readings, battery depletion, communication failures, and incorrect matching of records from multiple devices may introduce gaps or errors that become increasingly important as population size and monitoring duration increase. These limitations are particularly relevant when systems developed under controlled experimental conditions are transferred to commercial farms, where environmental exposure, connectivity, equipment integration, and maintenance requirements are substantially more variable (Dao et al., 2026).

Location tracking adds a spatial dimension to individual monitoring. Information on where an animal is located, how far it moves, which areas it prefers, how closely it remains associated with the herd, and how long it spends near resources such as feed, water, shade, or resting areas can provide indicators of behavior, health, welfare, and environmental use. Global Positioning System (GPS) and other Global Navigation Satellite System (GNSS) technologies are particularly valuable in extensive systems, where continuous visual observation is impractical. Sequential location records can be transformed into movement distance, speed, home range, resource-use patterns, and grazing distribution. When spatial data are integrated with topography, vegetation, water availability, shade, or other environmental layers, they can provide information not only on where animals are located but also on how animals interact with heterogeneous landscapes (Mason et al., 2026; Ben Souf et al., 2026). Such measurements may

reveal individual differences in grazing strategies and environmental adaptation that are poorly represented by conventional production records.

Spatial information becomes more biologically informative when combined with movement sensors. GPS identifies where movement occurs, whereas accelerometers provide higher-frequency information on its intensity and characteristics. Their integration can therefore improve behavioral interpretation by distinguishing, for example, high activity associated with grazing from movement toward water or separation from the herd (Mason et al., 2026). Changes in daily movement distance, spatial isolation, grazing patterns, or resource use may also contribute to the detection of lameness, disease, heat stress, injury, or approaching parturition. However, these changes should not be interpreted independently of environmental conditions and normal individual variation, particularly in extensive systems where behavioral variability is naturally high (Zhao et al., 2026).

Location technology can also shift from passive monitoring to active management. Virtual fencing systems use digitally defined geographical boundaries and GPS-enabled collars to influence animal movement without conventional physical fences. Animals approaching a virtual boundary may first receive an acoustic warning followed, if movement continues, by a controlled electrical stimulus. With appropriate learning, animals may respond predominantly to the acoustic cue. Such systems can support rotational grazing, dynamic pasture allocation, and exclusion from environmentally sensitive areas (Gresse and van Marle-Köster, 2026). Their evaluation, however, must extend beyond technical containment efficiency to include individual differences in learning, frequency of electrical stimulation, system failure, and potential consequences for animal welfare.

Satellite-based positioning is less effective inside enclosed buildings, where roofs and structural materials interfere with satellite signals. Indoor systems may therefore use RFID, Bluetooth, Wi-Fi, or Ultra-Wideband (UWB) technologies. UWB can provide relatively high spatial resolution and has been explored for individual tracking even in poultry. Mekonnen (2026), for example, described a pilot application combining inertial measurement units with UWB sensors for monitoring individual activity and location in broiler flocks, illustrating the potential extension of individual spatial monitoring beyond large animals. Nevertheless, increasing spatial and temporal resolution also increases energy demand, data volume, communication requirements, and cost. In GPS-based systems, frequent sampling improves characterization of short-term movement but reduces battery life, while real-time transmission may be constrained by limited network coverage in remote grazing areas (Zhao et al., 2026).

Electronic identification, wearable sensing, and location tracking should therefore be viewed as complementary rather than independent components of

PLF. Electronic identity provides the stable reference linking measurements to the individual; wearable sensors describe changing behavioral and physiological characteristics; and location technologies add the spatial context in which these changes occur. Their value does not depend primarily on the volume of data generated, but on whether reliable longitudinal records can be translated into biologically meaningful information and practical management decisions. This principle also establishes the transition toward contactless monitoring technologies, which seek to obtain comparable phenotypic information without requiring a device to be physically attached to each animal.

4. Computer Vision, Thermal Imaging, and Acoustic Monitoring

Contactless monitoring technologies provide an alternative to systems that require a device to be attached to each animal. Cameras, thermal sensors, and microphones placed within the production environment can continuously collect information from individuals or groups without direct physical interaction. Their importance in PLF derives not from recording images, temperature patterns, or sounds alone, but from converting these signals into measurable phenotypes related to performance, health, behavior, and welfare. Such systems are particularly attractive in poultry and pig production, where large numbers of animals occupy a shared environment and individual wearable sensors may be technically or economically impractical.

Computer vision also faces substantial challenges under commercial conditions. Variable illumination, shadows, dust, dirty lenses, changing camera angles, differences in animal appearance, and occlusion when animals overlap can reduce performance. Maintaining individual identity across successive video frames is particularly difficult in dense groups. Models developed in one housing system or population may also perform less accurately when transferred to different genotypes, ages, stocking densities, camera configurations, or environmental conditions. Consequently, high accuracy reported from a restricted experimental dataset should not be interpreted as evidence of general commercial validity. The practical criterion is whether a system can maintain biologically meaningful performance over time under variable farm conditions.

Infrared thermography (IRT) provides a complementary form of contactless phenotyping by detecting infrared radiation emitted from the body surface and converting it into spatial temperature information. Changes in surface temperature may accompany alterations in peripheral blood flow, inflammation, fever, environmental heat load, or physiological stress. IRT therefore offers the possibility of repeated temperature assessment without capturing or restraining the animal. This is particularly relevant because conventional contact measurements may require handling, limit measurement frequency, and potentially alter the physiological state being assessed. Thermal imaging has consequently been investigated for applications including heat-stress assessment,

inflammatory conditions, mastitis, lameness, and other health-related changes across livestock species.

Thermal measurements nevertheless require careful biological interpretation. Surface temperature is not equivalent to core body temperature and is influenced by anatomical site, ambient temperature, humidity, air movement, distance and angle of measurement, surface contamination, hair or feather coverage, and physiological variation. McManus et al. (2022) showed that thermography has been investigated across numerous species and health conditions, but substantial variation exists among studies in anatomical regions, measurement protocols, and diagnostic thresholds. Such heterogeneity limits the transferability of fixed threshold values between populations and production environments. IRT should therefore be considered primarily as a complementary screening technology rather than an unconditional substitute for clinical examination or direct measurement of core temperature. Its strongest PLF application may be the detection of deviations from an individual or group thermal pattern, followed by integration with behavioral, environmental, production, or other physiological information.

Acoustic monitoring provides a third contactless information stream. Animal sounds contain information associated with respiratory function, social communication, fear, pain, hunger, and environmental stress. Microphone-based systems can collect these signals continuously and quantify characteristics that would otherwise depend on the presence and experience of a human observer. Unlike cameras, acoustic systems can operate independently of visible light, and a single microphone may monitor multiple animals simultaneously. These characteristics make acoustic sensing particularly relevant to intensive pig and poultry systems, although interpretation becomes more difficult when multiple animals vocalize simultaneously or when ventilation equipment and other farm machinery generate substantial background noise.

Respiratory monitoring represents one of the clearest applications of acoustic PLF. Coughing and other respiratory sounds can be detected and classified to provide continuous surveillance for changes potentially associated with respiratory disease. Acoustic monitoring has also been explored in poultry, where vocalization patterns and acoustic characteristics have been associated with age and time of day, responses to environmental stressors, and changes in health status (Mahdavian et al., 2021). However, as with image analysis, classification accuracy alone does not establish clinical usefulness. Background noise, microphone position, housing acoustics, animal density, overlapping vocalizations, and differences among populations can affect performance. Systems intended for early disease detection must therefore be validated against appropriate biological or clinical reference measures and assessed in independent commercial populations.

Computer vision, thermal imaging, and acoustic sensing consequently provide different but complementary representations of the animal. Cameras primarily describe visible morphology, movement, posture, and spatial behavior; thermal systems characterize patterns of surface heat distribution; and microphones capture respiratory and vocal signals. None of these information streams necessarily identifies the biological cause of an abnormal pattern when used in isolation. Reduced movement detected by a camera, altered surface temperature, or increased coughing may each indicate a relevant change, but interpretation depends on the animal, environment, production stage, and associated measurements. The greatest potential of contactless monitoring therefore lies not simply in replacing human observation with cameras or microphones, but in generating continuous digital phenotypes that can be combined with other animal- and environment-based data to support more reliable biological interpretation and earlier management intervention.

5. Automated Monitoring of Feed Intake, Water Consumption, and Body Weight

Feed intake, water consumption, and body weight are among the most fundamental variables describing animal performance, yet conventional recording methods generally provide only intermittent information. PLF technologies allow these traits to be monitored repeatedly or continuously, transforming isolated measurements into longitudinal phenotypes. Their principal contribution is therefore not simply the automation of weighing or recording, but the ability to characterize intake and growth trajectories, detect deviations from expected patterns, and relate resource use to individual performance.

Individual feed intake can be recorded through electronic feeding systems that combine RFID-based identification with load cells or other weighing mechanisms. When an identified animal accesses the feeder, the system records the amount of feed present before and after the visit together with the time and duration of access. Repeated visits can then be aggregated to estimate daily intake and feeding characteristics such as meal frequency, duration, and size. In feedlot cattle, such systems enable individual feed intake to be evaluated together with body weight and growth, providing a basis for more precise assessment of feed efficiency (Gresse and van Marle-Köster, 2026). Similar principles are well established in pigs, where automated feeders can additionally support precision-feeding strategies in which nutrient supply is adjusted according to individual body weight, intake, and estimated requirements. However, the technical possibility of individual feeding does not imply that it is economically optimal in every production system. Infrastructure cost and management complexity may favor group-level precision strategies under some commercial conditions (Giannico et al., 2026).

Automated feeding records also contain behavioral information. Changes in feeding frequency, meal duration, or the timing of feeder visits may precede obvious reductions in total daily intake and may therefore contribute to health or welfare surveillance. Nevertheless, the feeder itself can influence the behavior being measured. Social competition, dominance, adaptation to new equipment, and individual temperament can affect access to automated stations. Animals that use a station less frequently may consequently be underrepresented, while RFID errors, simultaneous access by multiple animals, feed loss, load-cell drift, and communication failures can introduce additional measurement error. Calibration, identification of missing records, and detection of biologically implausible intake values are therefore essential components of data quality control.

Water intake can be monitored using comparable principles. Flow meters combined with electronic identification can record individual water consumption, drinking frequency, and visit duration, particularly in cattle and pigs. Water and feed intake are physiologically interdependent, and disruptions in water availability can rapidly affect feed consumption and production. Changes in drinking behavior may also provide information related to heat stress, health disturbances, or malfunctioning equipment. For this reason, feed and water monitoring are increasingly better understood as complementary components of resource-use phenotyping rather than independent measurements. In contrast, direct measurement remains substantially more difficult in grazing systems. GPS and accelerometers may estimate grazing activity, while remote sensing may characterize pasture availability, but such indicators should not be presented as equivalent to direct measurement of dry matter intake. Distinguishing measured traits from proxy indicators or model-derived estimates remains an important methodological principle in PLF.

Automated body-weight monitoring similarly changes the temporal resolution of performance recording. Walk-over weighing systems place load cells in locations that animals routinely cross when accessing water, feed, milking areas, or other resources. When combined with electronic identification, repeated weight records can be assigned to individual animals without manual restraint. Such systems have been applied in cattle and small ruminants and can reduce both labor requirements and disturbance associated with conventional weighing (Alawneh et al., 2011; Mura et al., 2026). Instead of obtaining body weight at intervals of several weeks, repeated measurements make it possible to describe growth as a continuous trajectory and to identify departures from expected development.

The major challenge is that weighing a freely moving animal differs fundamentally from weighing a stationary animal on a conventional scale. Partial loading of the platform, movement during measurement, variable crossing speed, and the simultaneous presence of another animal can produce substantial noise.

Automated systems therefore require algorithms that identify valid records and extract stable weight estimates from repeated measurements. Masiello et al. (2026), for example, demonstrated this principle using the SenseMat platform, in which repeated measurements were filtered according to loading and behavioral conditions before daily body-weight estimates were derived. Importantly, the very large number of measurements produced by such systems should not be confused with biological sample size. Their proof-of-concept study generated thousands of weight records from only two buffalo calves; the large number of sensor observations increased temporal resolution but did not increase the number of independent experimental animals.

High-frequency body-weight data also require biological interpretation. Short-term variation may reflect gastrointestinal fill, feed and water consumption, excretion, or measurement conditions rather than changes in tissue mass. This is particularly important in ruminants, where daily fluctuations can be substantial. The objective is therefore to separate the underlying growth signal from short-term biological and technical noise. Once this is achieved, longitudinal records may provide information beyond absolute body weight, including growth rate, growth stability, responses to environmental disturbances, and recovery following adverse events. Such phenotypes may eventually have applications in both management and genetic improvement, although repeated measurements from the same individual must be analyzed using statistical approaches appropriate for longitudinal data.

Automated monitoring of feed intake, water consumption, and body weight therefore represents more than a labor-saving replacement for conventional recording. Its principal value lies in converting traits traditionally observed at discrete intervals into dynamic phenotypes describing resource use and performance over time. The usefulness of these systems ultimately depends on measurement validity, appropriate quality control, and the biological interpretation of longitudinal patterns rather than on the sheer number of records generated.

6. Environmental Monitoring and Smart Housing Systems

The production environment is a major determinant of animal health, welfare, and performance, and environmental sensing therefore constitutes an essential component of PLF. Unlike wearable or imaging technologies, environmental sensors do not directly measure the animal; they quantify the conditions to which animals are exposed. This distinction is important because identical environmental conditions do not necessarily produce identical biological responses. Genotype, age, production level, health status, body covering, and previous adaptation can modify the response to environmental stress. Environmental measurements should therefore be interpreted primarily as

indicators of exposure or risk and, where possible, combined with animal-based responses (Lee et al., 2026).

Air temperature and relative humidity are the most widely monitored environmental variables. Their combined evaluation, commonly through indices such as the temperature–humidity index (THI), provides a more informative representation of thermal load than temperature alone and is particularly established in dairy cattle management. Continuous sensing enables periods of potentially adverse thermal conditions to be identified at substantially higher temporal resolution than occasional manual measurements. However, THI remains an environmental index rather than a direct measurement of heat stress in the animal. Animals differing in metabolic heat production, age, genotype, or physiological state may respond differently to the same THI. Integrating environmental indices with respiratory rate, body or surface temperature, activity, feed intake, and production records can therefore distinguish potential thermal exposure from the biological response that actually occurs (Lee et al., 2026).

Air-quality monitoring provides another important environmental information layer. Ammonia (NH_3) is particularly relevant in intensive housing because its concentration is influenced by manure or litter characteristics, temperature, moisture, pH, air movement, and ventilation. Continuous monitoring can identify both persistent deterioration in air quality and spatial or temporal patterns that may be missed by occasional measurements. Carbon dioxide (CO_2) can also provide information related to occupancy and ventilation dynamics, while methane (CH_4) monitoring has relevance to environmental assessment in ruminant production. Nevertheless, gas concentration and emission rate are not equivalent measurements. Converting a measured concentration into an emission estimate requires information on ventilation rate and air exchange; a sensor reading expressed as a concentration should therefore not be interpreted directly as the quantity emitted by the animals (Lee et al., 2026). Similar caution applies to other gases, including hydrogen sulfide, for which short-duration concentration peaks may be biologically or occupationally important even when daily average exposure appears acceptable.

Environmental monitoring is particularly important in poultry production because large numbers of animals share the same air volume and housing conditions. Metabolic heat, moisture, CO_2, NH_3, particulate matter, litter condition, and ventilation interact within a highly dynamic environment, and relatively small failures in environmental control can simultaneously affect a large proportion of the flock. Continuous monitoring of temperature, relative humidity, gas concentrations, and air movement can therefore provide information relevant to both production and welfare. Mekonnen (2026) emphasized that the value of these environmental data increases when they are integrated with flock behavior and production indicators. For example, a given

temperature accompanied by normal spatial distribution may represent a different biological condition from the same temperature associated with clustering, panting, reduced activity, or changes in feed and water consumption.

The location of environmental sensors is consequently as important as the variables measured. Conditions within a livestock building are rarely spatially uniform. Temperature, air velocity, humidity, gas concentrations, and particulate matter may differ according to distance from air inlets and exhausts, animal density, manure accumulation, litter moisture, or building geometry. A single centrally located sensor may therefore fail to represent the microenvironment actually experienced by animals. Distributed sensor networks can characterize this spatial heterogeneity more effectively, but increasing sensor density also increases calibration, maintenance, communication, and data-quality requirements. Sensor drift, cross-sensitivity, inappropriate placement, loss of calibration, and network interruptions may compromise long-term measurements (Lee et al., 2026; Rawdhan et al., 2026). The objective should therefore be reliable environmental characterization rather than simply maximizing the number of sensors.

Environmental monitoring becomes a smart housing system when measurement is connected to active environmental control. Sensors provide the perception layer, control rules or algorithms constitute the decision layer, and fans, air inlets, heaters, cooling systems, lighting, or other equipment provide the physical intervention layer. When environmental conditions are measured again following an intervention, a feedback loop is created in which the housing system can respond dynamically to changing conditions (Losacco et al., 2025; Lee et al., 2026). The objective is not necessarily to maintain a single fixed environmental value, but to keep conditions within biologically appropriate ranges while responding to changes in animal age, stocking density, production stage, weather, and internal heat and moisture loads.

The development of smart housing also creates an opportunity to move beyond control based exclusively on environmental thresholds. Conventional automation may activate fans when air temperature exceeds a predetermined value. A more advanced PLF architecture can combine environmental measurements with animal-based indicators such as activity, spatial distribution, surface temperature, respiratory responses, feed and water intake, or production performance. Environmental control can then respond not only to what the building sensors report but also to evidence of how the animals are responding. Such integration is particularly relevant because environmental thresholds derived from population averages cannot fully represent differences among animals or production stages.

Environmental monitoring and smart housing should therefore be regarded as a progression from measurement to biological interpretation and finally to

adaptive control. Continuous sensing makes the production environment quantitatively visible; integration with animal-based data establishes whether environmental exposure is producing a biologically relevant response; and automated control provides the mechanism for intervention. The scientific and practical value of a smart housing system ultimately depends not on the number of connected devices, but on whether this feedback process maintains a more appropriate environment for the animals while using ventilation, heating, cooling, and other resources efficiently.

7. Automation, Robotics, and Closed-Loop Control

The progression from monitoring to intervention represents an important stage in the development of PLF. Sensors may detect a decline in feed intake, deterioration in air quality, or an animal requiring inspection, but the management cycle remains incomplete if every physical response depends on subsequent human action. Automation and robotics extend digital monitoring into the physical production environment by allowing information generated by sensors and decision-support systems to influence feeding, milking, cleaning, environmental control, animal movement, and other farm operations. Their significance therefore extends beyond labor substitution: they provide a mechanism through which digitally generated management decisions can be implemented consistently and repeatedly (Mata, 2026; Zhou et al., 2026).

Automation and robotics should nevertheless be distinguished conceptually. A feeding line operating at predetermined times or a ventilation fan activated when temperature exceeds a fixed threshold represents automation, but not necessarily robotics. Robotic systems generally combine sensing, localization, movement, physical interaction, and some capacity to respond to changing conditions. This distinction is increasingly important as livestock systems move from fixed sequences toward adaptive operation. A cleaning robot directed toward areas identified as contaminated, a feeding robot modifying distribution according to measured consumption, or a mobile platform investigating an environmental anomaly detected by stationary sensors represents a closer integration of sensing and physical action than equipment following a predefined schedule.

Automatic milking systems (AMS) provide one of the most mature examples of this integration. Their importance lies not only in mechanizing milk removal but in combining electronic identification, repeated measurements, robotic physical interaction, and individual management within the same system. A cow entering an AMS can be identified automatically, milked without continuous human intervention, and associated with records describing milking frequency, milk yield, and selected milk characteristics. These data can subsequently contribute to health and production management. Automatic milking therefore illustrates the PLF sequence of identifying the animal, collecting biological and

production information, performing a physical intervention, and recording the subsequent response within a continuous management system (John et al., 2016; Cogato et al., 2021; Losacco et al., 2025).

Robotic applications increasingly extend beyond milking. Automated or autonomous systems can distribute or push feed, remove manure, inspect livestock facilities, collect eggs, assist animal movement, and perform other repetitive tasks. Mobile monitoring robots may also carry cameras, thermal sensors, microphones, or environmental sensors through areas that would otherwise require multiple fixed sensing units. The potential advantage is not simply automation of movement but the capacity to direct sensing or intervention toward locations where the digital monitoring system indicates that attention is required. In this configuration, the robot becomes a physical actuator of the farm's broader digital architecture.

However, the technological maturity of livestock robots varies considerably. Automatic milking and some feeding and manure-removal systems are established commercial technologies, whereas autonomous health inspection, individualized robotic intervention, and several veterinary applications remain largely at prototype or limited validation stages (Mata, 2026; Zhou et al., 2026; Fang et al., 2026). A robot that performs successfully under controlled experimental conditions cannot be assumed to maintain the same performance around animals whose movement and behavior are inherently variable. Commercial validation must therefore consider reliability over extended periods, different housing conditions, mechanical durability, contamination, maintenance requirements, and the capacity to operate safely when animals behave unpredictably.

Animal–robot interaction introduces an additional biological dimension that distinguishes livestock robotics from conventional industrial automation. Animals may avoid, investigate, habituate to, or interact unpredictably with autonomous equipment. Robot dimensions, speed, movement trajectory, noise, proximity, and operating frequency may influence behavior and potentially welfare. Technologies should consequently be adapted to animal biology rather than requiring the production environment or animals to be modified primarily to facilitate robotic operation. A technically efficient robot that disrupts resting, feeding, social behavior, or safe movement would represent poor integration regardless of its mechanical performance.

The most advanced form of automation is closed-loop control, in which sensing, interpretation, intervention, and subsequent measurement form a continuous feedback process. Environmental control provides a straightforward example: sensors detect changing conditions, the control system modifies ventilation or cooling, and subsequent measurements determine whether the intervention achieved the intended result. The same principle can theoretically be

extended to feeding and other management processes. The defining characteristic is that intervention is not the endpoint; its biological or environmental consequences are measured and used to inform the next decision. Closed-loop systems therefore shift PLF from periodic adjustment toward continuous adaptive management.

Greater autonomy, however, also increases the consequences of technical failure. Failure of a passive monitoring sensor may result primarily in missing data, whereas failure of ventilation, cooling, feeding, or milking equipment can directly affect animal health, welfare, and production. Critical systems therefore require fail-safe operation, backup power, manual override, and the capacity to maintain essential functions during network or software failure. Human oversight also remains important, particularly when automated outputs concern health and welfare. The appropriate objective is not the removal of the stockperson from livestock management, but a redistribution of human effort from repetitive physical tasks toward supervision, interpretation, maintenance, and decisions requiring biological judgment.

Automation and robotics thus represent the physical intervention layer of PLF. Their greatest potential emerges when actions are linked dynamically to information from animals and their environment rather than performed according to fixed schedules alone. The transition from automated equipment to adaptive closed-loop management also illustrates a broader principle of smart livestock production: technological sophistication should be judged not by the degree of autonomy itself, but by whether automation produces reliable, safe, biologically appropriate, and practically useful improvements in farm management.

8. Data Integration, Multimodal Sensing, and Digital Twins

Individual PLF technologies generally measure only a limited dimension of the animal or production environment. Accelerometers characterize movement, cameras describe visible morphology and behavior, thermal sensors measure surface temperature patterns, microphones capture acoustic signals, electronic feeders quantify intake, and environmental sensors describe the conditions surrounding the animal. Biological states, however, are multidimensional. Reduced activity may be associated with disease, heat stress, reproductive status, social interactions, or normal behavioral variation. The interpretation of a single sensor signal is therefore frequently ambiguous. Multimodal sensing addresses this limitation by combining complementary information sources to provide a more complete representation of the animal and its environment.

The principal value of multisensor integration is increased biological specificity rather than simply increased data volume. A decline in activity becomes more informative when accompanied by reduced feed intake, altered body temperature, or changes in milk production. Similarly, abnormal flock distribution detected by cameras may have different interpretations depending on

simultaneous measurements of temperature, air velocity, or gas concentrations. Each information source constrains the range of plausible biological explanations generated by the others. In this sense, multimodal PLF seeks to transform several partially informative signals into a more coherent description of biological state. The objective is not to maximize the number of sensors but to combine measurements that contribute genuinely complementary information.

Data integration requires observations from different systems to be associated correctly in time, space, and, where appropriate, with the same individual animal. Electronic identification provides a particularly important reference for individual-level integration, whereas synchronized timestamps and spatial information become essential when combining cameras, environmental sensors, feeding systems, and other devices. Differences in sampling frequency also create practical challenges. An accelerometer may produce measurements several times per second, body weight may be recorded only when an animal crosses a platform, feed intake may be summarized by feeding event, and production measurements may be available once or several times per day. Integrating these data therefore requires alignment at biologically meaningful temporal scales rather than assuming that all measurements represent equivalent time points.

Interoperability is one of the major constraints on this process. A contemporary farm may use electronic identification from one manufacturer, activity sensors from another, an automatic milking or feeding system from a third, and environmental control equipment from yet another. When these systems use proprietary data formats, communication protocols, and software platforms, they may coexist physically while remaining digitally isolated, creating data silos that restrict multisensor integration (Mura et al., 2026; Zhao et al., 2026). Interoperability also has a semantic dimension. Two systems may both report a variable called “activity” while measuring fundamentally different characteristics, or may define a “feeding event” using different thresholds. Technical compatibility therefore does not guarantee biological comparability. Common data definitions, metadata, standardized timestamps, and open communication interfaces are increasingly important components of integrated PLF architecture.

Multimodal systems also introduce new sources of uncertainty. Sensor failure, missing observations, asynchronous measurements, incorrect animal identification, and differences in measurement precision can propagate through an integrated system. Adding a poorly performing sensor may contribute noise rather than useful information. Multimodality should therefore not be assumed to improve performance automatically. Each additional information stream should provide biologically relevant information, remain sufficiently reliable under farm conditions, and justify the additional cost and complexity of integration. The purpose of data fusion is ultimately to derive a more reliable biological

interpretation from uncertain and complementary signals, not simply to construct larger datasets.

Digital twins represent a more advanced extension of this integration. The concept refers to a dynamic relationship between a physical system and its virtual representation rather than merely a digital database containing sensor measurements. In livestock production, electronic identification, wearable sensors, cameras, microphones, automated weighing and feeding systems, and environmental sensors can collectively provide the information required to construct increasingly detailed digital representations of animals and their production environment. A genuine digital twin, however, requires more than monitoring. The virtual representation must remain dynamically connected with its physical counterpart and be updated as the biological system changes (Neethirajan, 2026).

This distinction is important because the term digital twin is increasingly applied to systems that are more accurately described as monitoring platforms or digital dashboards. A platform that displays current temperature, activity, body weight, and feed intake provides an integrated representation of the present state but does not necessarily constitute a digital twin. More advanced digital-twin architectures should be capable of using continuously updated information to represent the current system, estimate its future development, and evaluate the potential consequences of alternative management interventions before they are applied physically (Neethirajan, 2026; Fotos et al., 2026). A livestock digital twin could, for example, combine current body weight, feed intake, environmental conditions, and previous performance to evaluate expected growth under alternative feeding or environmental scenarios. In principle, management could then progress from describing what is currently occurring toward evaluating what may occur under different future conditions.

Livestock systems nevertheless present particular challenges for digital-twin development because animals are dynamic biological entities rather than mechanically deterministic objects. Growth, metabolism, health, behavior, and responses to environmental conditions vary among individuals and over time. Welfare creates an additional difficulty because many of its dimensions cannot be represented directly by a single sensor output. Activity, lying behavior, feed intake, or surface temperature may contribute useful information, but they do not constitute complete measurements of affective state or positive welfare. Increasing the complexity of the virtual representation therefore does not remove the need for biological interpretation.

Reliable synchronization between the physical and virtual systems is another fundamental challenge. Under commercial conditions, sensors fail, batteries are depleted, devices are lost, cameras become contaminated, and network connections are interrupted. A digital twin must therefore recognize uncertainty

and missing information rather than continuing to generate apparently precise outputs after its connection with the physical system has deteriorated. Interoperability becomes even more important in this context because data originating from different manufacturers and platforms must be integrated without losing their technical or biological meaning. Neethirajan (2026) identifies limited interoperability among livestock sensor platforms as a major barrier to the transition from digital-twin prototypes toward practical implementation.

Digital twins should consequently be regarded as an emerging PLF architecture rather than an established commercial endpoint. Many of their required components already exist, including continuous sensing, automated feeding and milking, computer vision, environmental control, biological models, and decision-support systems. The remaining challenge is to integrate these components reliably, maintain synchronization with the physical animal or production system, represent uncertainty appropriately, and demonstrate that the resulting system improves decisions under long-term commercial conditions. The scientific significance of digital twins will therefore depend less on producing increasingly detailed virtual images of farms and more on whether dynamic digital representations can support biologically valid evaluation of future states and alternative interventions.

Data integration thus represents the transition from isolated digital measurements toward system-level PLF. Multimodal sensing can reduce the ambiguity inherent in individual sensor signals, while digital twins extend integration toward continuously updated representations capable of supporting prospective management. Neither approach gains value merely through technological complexity. Their usefulness depends on biologically meaningful integration, reliable data exchange, explicit treatment of uncertainty, and demonstrable improvement in management decisions.

9. Precision Health, Reproduction, and Welfare Management

The practical value of PLF becomes most evident when continuously collected data are translated into management decisions concerning animal health, reproduction, and welfare. These applications share a common principle: biologically important events are often preceded by subtle changes that occur before they become sufficiently pronounced for conventional observation. Alterations in activity, feeding and drinking behavior, rumination, body temperature, spatial distribution, vocalization, body weight, or production may therefore provide early indications of changing biological status. PLF does not eliminate the need for clinical, reproductive, or welfare assessment; rather, it increases the temporal resolution of observation and can identify animals or groups that require closer attention.

Precision health management is particularly concerned with the transition from clinical detection toward earlier risk identification. Conventional disease

recognition frequently occurs after visible symptoms, substantial reductions in feed intake, or measurable production losses have developed. Continuous monitoring creates the possibility of detecting deviations from an individual's previous pattern before these changes become clinically obvious. Activity sensors, automated feeding systems, cameras, thermal imaging, acoustic monitoring, milk measurements, and other technologies can each contribute signals associated with health disturbances. Respiratory disease illustrates this principle clearly. Continuous acoustic monitoring can identify changes in coughing or respiratory sounds even when human observers are absent, potentially providing an earlier indication of emerging respiratory problems (Garrido et al., 2023; Sharifuzzaman et al., 2026). Similarly, changes in locomotion, posture, or activity can contribute to lameness surveillance, while thermal and production data may provide complementary information for inflammatory or metabolic disturbances.

The interpretation of these signals nevertheless requires caution because most sensor-derived indicators are not disease-specific. Reduced activity can accompany lameness, systemic disease, heat stress, reproductive events, or normal variation. Reduced feed intake is similarly a general biological response rather than a diagnosis. The appropriate role of PLF is therefore often risk stratification: identifying animals whose current pattern differs sufficiently from expectation to justify inspection, clinical examination, or additional measurement. A system that identifies a cow as having an increased probability of mastitis or a pig as showing abnormal respiratory activity should not automatically be interpreted as having established a clinical diagnosis. The distinction between screening, early warning, and diagnosis is essential for both scientific validation and responsible commercial use.

Multimodal monitoring can improve this process because health disturbances frequently affect several biological functions simultaneously. An animal showing reduced activity, declining feed intake, altered body temperature, and abnormal production is more biologically informative than an isolated change in any one of these variables. The same principle applies at group level. In poultry, simultaneous changes in flock activity, spatial distribution, water or feed consumption, vocalization, and environmental conditions may indicate an emerging health or management problem even when continuous identification of individual birds is impractical. Precision health management should therefore use the biologically appropriate observational unit—individual, group, flock, or herd—rather than assuming that individual monitoring is always superior.

Reproductive management represents another major application of high-frequency monitoring. Reproductive events are accompanied by behavioral and physiological changes that can be captured digitally. Alterations in activity, rumination, feeding behavior, temperature, and spatial behavior may contribute

to estrus detection, while changes in movement and isolation from the group may provide information related to approaching parturition. In dairy systems, activity-based estrus detection has become one of the more established applications of wearable monitoring, allowing reproductive surveillance to continue throughout the day rather than depending solely on periodic visual observation. Integration with electronic identification and production records can further support decisions concerning insemination timing and reproductive follow-up.

The usefulness of reproductive monitoring depends on the same principles that apply to health surveillance. Biological events vary among individuals, and a fixed threshold may not perform equally well across parity, production level, housing system, breed, or environmental conditions. Increased activity may indicate estrus but can also result from regrouping, disturbance, or other behavioral events. Similarly, isolation or altered movement near parturition is biologically plausible but not necessarily specific. Longitudinal systems that compare an animal with its own previous pattern may therefore provide advantages over approaches based exclusively on population-wide thresholds. In extensive sheep and goat systems, where direct observation is less frequent, combinations of location and activity data may be particularly useful for identifying animals showing movement patterns associated with parturition, injury, illness, or separation from the flock. Mura et al. (2026) identified reproduction, health, feeding, grazing management, and welfare as important areas in which PLF-based decision support may contribute to small-ruminant management.

Animal welfare monitoring extends PLF into a more complex domain because welfare is multidimensional and cannot be represented adequately by a single production or behavioral variable. Sensors can quantify activity, lying, locomotion, feeding, social proximity, spatial distribution, vocalization, thermal responses, and other animal-based characteristics relevant to welfare assessment. Continuous monitoring may reveal changes that would be difficult to identify during short observational periods and can substantially increase the frequency with which welfare-related information is collected. In poultry, for example, cameras may characterize flock distribution, movement, crowding, use of resources, or selected behavioral patterns, while acoustic systems may provide complementary information on flock vocalization. In extensive sheep production, wearable and location technologies can provide information on movement, resource use, isolation, and behavioral changes that would otherwise be difficult to observe continuously (Ben Souf et al., 2026).

However, measurement of behavior should not be equated automatically with measurement of welfare. A camera may accurately classify lying, walking, feeding, or social behavior without determining whether the animal is experiencing a positive or negative affective state. Similarly, reduced movement

may reflect disease or pain but may also represent normal resting behavior. Production performance presents the same conceptual limitation: high growth rate or milk yield cannot by itself demonstrate good welfare, just as a temporary decline in production does not define poor welfare. PLF can therefore provide objective and high-frequency welfare indicators, but these indicators must be interpreted within established biological and welfare frameworks rather than treated as direct digital measurements of the complete welfare state (Papakonstantinou et al., 2024; Akinyemi et al., 2026).

This limitation is particularly important for positive welfare. Many current PLF systems are better suited to detecting deviations, disease, reduced activity, abnormal behavior, or environmental stress than to identifying positive experiences. Traits such as play, exploration, affiliative behavior, environmental engagement, or positive social interaction are more difficult to quantify reliably, especially under commercial conditions. A future welfare-oriented PLF system should therefore move beyond the absence of negative indicators and investigate whether digital technologies can characterize opportunities for positive behavioral expression. Such development will require close integration between sensor engineering, ethology, veterinary science, and animal welfare research.

Precision health, reproduction, and welfare management consequently represent different applications of the same underlying information architecture. Continuous measurements allow deviations from expected biological patterns to be detected earlier and can prioritize animals or groups requiring attention. Their value, however, depends on maintaining a clear distinction between a measured signal, a biologically relevant indicator, an early-warning event, and a confirmed biological condition. PLF is most defensible when it strengthens observation and decision-making without overstating what a sensor-derived phenotype can demonstrate. In this role, digital monitoring can complement rather than replace veterinary examination, reproductive expertise, welfare assessment, and experienced stockmanship.

10. Species-Specific Applications of Precision Livestock Farming

Precision livestock farming does not have a single technological configuration that can be transferred unchanged among animal species and production systems. The biological unit being monitored, economic value of the individual animal, herd or flock size, housing system, production cycle, availability of electronic identification, communication infrastructure, and type of management decision all influence which technologies are practically useful. Consequently, the meaning of “precision” varies among production systems. In dairy cattle it frequently refers to individual-animal monitoring, whereas in commercial poultry the biologically and economically appropriate unit may be the flock or a specific area within the house. In extensive ruminant production, location and behavioral information may be more valuable than continuous measurements of production.

Species-specific PLF should therefore be understood as the selection of an appropriate measurement and management resolution rather than the universal pursuit of individual monitoring (Fotos et al., 2026; Mata, 2026).

Dairy cattle production represents one of the most technologically mature applications of PLF. Individual animal value is relatively high, production cycles are long, animals can be electronically identified, and dairy farms have generated individual digital records for decades. Milk yield, milking frequency, reproductive records, activity, rumination, body weight, feeding behavior, and selected milk characteristics can therefore be linked longitudinally to the same animal. Automatic milking systems further integrate identification, repeated production measurements, and physical intervention. Wearable sensors can contribute to estrus and health surveillance, while automated weighing and feeding technologies allow performance and resource use to be monitored over time. The central feature of dairy PLF is consequently the ability to construct an increasingly detailed longitudinal phenotype for an identified individual and use deviations from that animal's expected pattern to support management.

Beef cattle production requires a more differentiated approach because intensive feedlot and extensive grazing systems present fundamentally different monitoring problems. In feedlots, electronic identification, automated feed-intake recording, repeated body-weight measurement, computer vision, thermal monitoring, and environmental sensors can be incorporated into relatively structured facilities. Individual feed intake and growth can consequently be evaluated together to characterize feed efficiency and performance (Fotos et al., 2026; Gresse and van Marle-Köster, 2026). Walk-over weighing can further increase the frequency of body-weight recording without repeated handling. Under extensive conditions, however, fixed infrastructure becomes less useful because animals are distributed across large areas. GPS/GNSS tracking, accelerometers, remote sensing, virtual fencing, and strategically located walk-over weighing systems consequently become more relevant. In this context, knowing where animals are located, how they use grazing resources, and whether their movement pattern has changed may be more immediately valuable than obtaining high-frequency measurements from fixed equipment.

Sheep and goat production illustrates even more clearly how production system and economics influence PLF architecture. Intensive dairy sheep or goat farms can use electronic identification, milk records, automated weighing, activity and rumination sensors, and other technologies resembling those used in dairy cattle. Mura et al. (2026) identified applications including automated body-weight and body-condition monitoring, biometric identification, wearable sensors, positioning technologies, thermal monitoring, virtual fencing, and decision-support systems in dairy sheep production. In extensive systems, however, GPS and accelerometers may become more important because direct

human observation is infrequent and animals occupy large grazing areas. Changes in location and activity can provide information relevant to grazing, separation from the flock, illness, injury, or approaching parturition. Ben Souf et al. (2026) similarly identified considerable potential for wearable, imaging, and environmental technologies in extensive sheep welfare and health management.

The economic constraint is particularly important in small ruminants. A sensor cost that is acceptable for a high-value dairy cow may not be economically defensible when multiplied across hundreds of sheep or goats. Communication coverage and battery life also become critical when animals spend long periods in remote grazing areas. The optimal solution may therefore involve monitoring selected animals, using group-level indicators, processing information locally, or combining individual location data with remotely sensed information on the grazing environment. The technological objective is not to reproduce dairy-cattle PLF at lower cost, but to design a system appropriate to the biology and economics of small-ruminant production.

Pig production provides favorable conditions for several forms of intensive PLF because animals are generally maintained within controlled housing where feeding, environmental conditions, behavior, and sound can be monitored continuously. Electronic feeding systems can measure individual intake and support precision-feeding strategies, while cameras can quantify posture, locomotion, body dimensions, social interactions, and selected behavioral changes. Acoustic monitoring has particular relevance to respiratory surveillance because cough and other respiratory sounds can be recorded continuously at group level. Environmental monitoring is also important because temperature, humidity, ventilation, and air quality interact strongly with animal density and housing conditions. Reproductive applications include monitoring behavioral changes associated with estrus and farrowing, although these applications differ in technological maturity and should not be assumed to have the same level of validation as established feeding systems (Halachmi et al., 2019).

Poultry production represents a substantially different PLF paradigm. Commercial broiler and layer houses contain large numbers of animals whose individual economic value is relatively low, making the attachment of sophisticated sensors to every bird impractical in most commercial situations. Technologies capable of observing many animals simultaneously are therefore more attractive. Cameras can characterize flock activity, spatial distribution, movement, crowding, or resource use; microphones can capture flock-level acoustic changes; automated feeding and drinking systems provide group-level resource-use information; and environmental sensors continuously describe temperature, humidity, air movement, CO_2, NH_3, and other characteristics of the house environment (Fotos et al., 2026; Mekonnen, 2026). Precision in poultry

production may consequently involve identifying an abnormal region or an emerging flock-level deviation rather than identifying a specific bird.

This group-level architecture has important biological advantages rather than representing merely a compromise caused by low individual animal value. A ventilation problem, thermal disturbance, failure of a drinking line, or emerging respiratory challenge may initially produce changes in spatial distribution, activity, water consumption, or flock vocalization. Detecting such collective changes can provide an actionable warning before the identity of individual affected birds becomes the primary management question. In laying hens, the transition toward cage-free and aviary systems additionally creates opportunities for monitoring nest use, movement between levels, perching, crowding, and other resource-use patterns. However, the complexity of these environments also increases problems of occlusion and individual tracking, and many poultry PLF technologies remain at prototype or limited commercial-validation stages.

Aquaculture represents a further extension of precision animal monitoring, but the source material provides substantially less species-specific coverage than for terrestrial livestock. The chapter source identifies aquaculture as one of the sectors in which several precision-feeding applications remain experimental or pilot-scale compared with the stronger evidence base in dairy cattle and pigs (Giannico et al., 2026). It would therefore be inappropriate to present aquatic PLF in this chapter at the same level of detail or technological maturity without introducing additional literature. The broader principle nevertheless remains applicable: sensor architecture and management resolution must be adapted to the biological and production environment rather than transferred directly from terrestrial systems.

Across species, technological feasibility should therefore not be confused with practical usefulness. Under experimental conditions, individual broilers can be tracked, sheep can carry multiple sensors, and cattle can generate extremely high-frequency measurements. Commercial production imposes constraints related to cost, battery life, connectivity, maintenance, animal behavior, staff capacity, and system reliability. The optimal PLF system is consequently not the one that generates the largest amount of data, but the one that produces sufficiently reliable information to alter a meaningful management decision with acceptable technical and economic burden.

Species-specific PLF applications ultimately share a common measurement–decision–intervention framework but differ in the biological scale at which this framework is most useful. Dairy cattle currently provide the clearest model of intensive individual-level monitoring; feedlot cattle emphasize growth, intake, and efficiency; extensive cattle and small ruminants emphasize location, grazing, and remote surveillance; pigs provide strong applications in feeding, environmental control, imaging, and acoustic health monitoring; and poultry

increasingly relies on flock-level visual, acoustic, and microclimatic information. These differences should not be interpreted as unequal progress toward a single ideal technological system. They reflect the biological, structural, and economic diversity of animal production itself. The success of PLF therefore depends on identifying the appropriate animal or group, the appropriate measurement intensity, and the management decision for which additional information has genuine value.

11. Validation, Reliability, and Biological Interpretation of PLF Technologies

One of the central challenges in evaluating PLF technologies is defining what it means for a system to "work." An accelerometer may detect movement, a camera may locate an animal within an image, a microphone may classify a cough, and a thermal camera may measure surface temperature accurately, yet none of these achievements alone demonstrates that the technology is a reliable management tool under commercial conditions. Validation should therefore be viewed as a sequence extending from accurate measurement of a physical signal to correct interpretation of a biological event, generalization across animals and farms, and ultimately improvement of a meaningful management decision. High performance reported in the PLF literature frequently represents only one stage of this evidence chain (Mason et al., 2026; Ghazy & Abu El-Naser, 2026).

The first level is measurement validation. When a sensor measures a physical variable such as body weight, temperature, location, acceleration, or gas concentration, its output should be compared with an appropriate reference method. Automated body-weight measurements may be compared with calibrated static scales, thermal measurements with suitable reference temperature measurements, and environmental gas sensors with reference analyzers. Bias, absolute error, root mean square error, variability, and agreement between methods can then be quantified. Correlation alone is insufficient. Two methods may rank animals similarly and consequently show a high correlation while maintaining a substantial systematic difference in the actual values recorded. Validation of a new measurement technology therefore requires evaluation of agreement with the reference method rather than simply demonstration of a statistical association.

Accuracy and precision must similarly be distinguished. A sensor is accurate when its measurements are close to the reference value and precise when repeated measurements are close to one another. A device may consistently overestimate the true value and therefore demonstrate high repeatability but poor accuracy. Conversely, measurements may average close to the reference value while showing substantial random variation. Both characteristics matter in PLF. A small and stable systematic bias may sometimes be corrected through calibration,

whereas large irregular variation can obscure genuine biological change and reduce the value of longitudinal monitoring.

Reliability must also be demonstrated over the time scale for which the technology is intended to operate. Livestock sensors are exposed for weeks or months to moisture, dust, ammonia, temperature fluctuations, mechanical impact, animal contact, and other conditions rarely reproduced fully during short laboratory evaluations. Gas sensors may drift, wearable devices may change position, camera lenses may become contaminated, electronic tags may loosen, and wireless communication may become intermittent. Mason et al. (2026) emphasized that reported sensor performance can be affected by placement, connectivity, animal morphology, environmental conditions, and duration of use. Short-term calibration performance and long-term field reliability should therefore be treated as distinct validation requirements.

A second level of validation concerns classification of biological states or events. Systems designed to identify feeding, rumination, lameness, estrus, coughing, or specific behaviors are commonly evaluated using true-positive, false-positive, true-negative, and false-negative classifications. Metrics such as sensitivity, specificity, precision, recall, and F1 score describe different aspects of this performance and should be interpreted according to the intended application. Overall accuracy can be particularly misleading when the biological event is uncommon. A system may achieve apparently high accuracy largely by correctly classifying the abundant negative observations while performing poorly on the relatively rare events that management actually needs to detect. Event prevalence and the practical consequences of false-positive and false-negative decisions must therefore be considered together with conventional performance metrics.

The quality of the reference standard is equally important. A disease-detection system should ideally be validated against appropriate veterinary diagnosis or laboratory testing, an estrus-detection system against relevant physiological or reproductive reference measures, and automated behavioral classifications against systematic ethological observations. Garrido et al. (2023) noted limitations in field validation and reference testing within studies using PLF technologies for respiratory disease detection. Behavioral reference data create an additional challenge because human annotation itself may contain uncertainty. If trained observers classify the same behavior differently, apparent disagreement between an algorithm and its reference labels may partly reflect uncertainty in the ground truth. Clearly defined ethograms, observer training, and assessment of inter- and intra-observer agreement are consequently important components of behavioral technology validation.

Independence of observations represents another major methodological issue. Thousands of video frames from one bird or millions of accelerometer

observations from one cow do not represent thousands or millions of independent biological subjects. Repeated observations from the same individual are correlated. If frames or time segments from the same animal are randomly distributed between training and test datasets, the system may encounter characteristics of the same animal, environment, camera position, or background during both model development and evaluation. Test performance may consequently appear substantially better than the ability of the system to generalize to genuinely new animals.

Validation design should therefore reflect the intended claim of generalizability. If a system is expected to perform on new animals, evaluation should include animals that were absent from model development. If it is intended for new flocks or herds, separation should occur at the group level; if it is intended for deployment across farms, independent farms should be represented in the evaluation. Internal approaches such as cross-validation or training–validation–test partitioning remain useful for model development, but validation conducted within the same farm, genotype, housing environment, or underlying population should not be described as external validation. Stronger evidence is obtained when the final system is tested in animals, production periods, populations, or farms that contributed no data to its development (Zhao et al., 2026; Sharifuzzaman et al., 2026).

This requirement is particularly important because PLF systems frequently interact directly with the production environment. Camera performance may change with illumination, camera angle, flooring, animal color, stocking density, or occlusion. Wearable-sensor relationships may differ among breeds, ages, body sizes, and production stages. Acoustic systems may be affected by building characteristics, ventilation equipment, animal density, and background noise. Environmental sensors may behave differently across temperature and humidity ranges. Ghazy and Abu El-Naser (2026), for example, reported that many studies in the recent small-ruminant PLF literature relied on single-farm datasets and that independent external validation was performed in fewer than half of the studies they reviewed. Similar generalizability concerns occur in imaging, acoustic, and behavioral-monitoring applications across other livestock species.

Technical or statistical performance must subsequently be separated from biological validity. A camera may measure a gait characteristic with high repeatability, but the association between that characteristic and clinically meaningful lameness still requires validation. A thermal camera may measure surface temperature accurately without that measurement being sufficiently specific for a particular disease. A microphone may detect coughing accurately without identifying the etiology of the cough. Similarly, an algorithm may classify lying or feeding behavior correctly without those behaviors alone

providing a valid measure of welfare. Success at one stage of the measurement chain therefore cannot be assumed to establish validity at the next stage.

Early-warning systems add a temporal dimension to validation. An alarm is useful not only when it identifies the correct event but when it provides sufficient time for an effective intervention. A disease alert generated shortly before conventional clinical recognition may be statistically accurate yet offer little management advantage. A somewhat less accurate system that identifies increased risk sufficiently early to permit inspection, treatment, separation, or environmental correction may have greater practical value. Lead time, alarm duration, and the number of alarms generated per event should therefore complement conventional classification metrics when evaluating early-warning technologies.

False alarms also have an operational meaning that can be obscured by percentages. A low false-positive rate applied continuously across thousands of animals may still generate numerous unnecessary inspections each day. Repeated irrelevant warnings can produce alarm fatigue, reducing the likelihood that farmers or staff respond appropriately when a genuinely important alarm occurs. Reporting false alarms per animal-day, per hundred animal-days, or as the number of unnecessary checks generated per farm may consequently provide more interpretable measures of operational burden than a percentage alone. The acceptable balance between false positives and false negatives will also differ according to the biological and economic consequences of the event being monitored.

The final stages of validation concern management and commercial performance. A technically accurate system may still have little value if its output does not alter a decision, if the warning arrives too late, if the recommended action cannot be implemented, or if maintenance and data loss make continuous operation unrealistic. Validation should therefore progress from physical measurement to biological classification, independent external testing, management impact, and long-term performance under commercial conditions. Success at one stage does not guarantee success at the next. A proof-of-concept study can provide valuable evidence that a principle is technically feasible, but it should not be interpreted as equivalent to validation across multiple farms and production cycles.

A rigorous PLF evidence chain can consequently be expressed as: accurate and repeatable measurement → valid biological interpretation → independent external validation → stable long-term field performance → actionable management information → measurable biological or operational benefit. Economic feasibility and adoption subsequently determine whether this validated benefit can be sustained in practice. From this perspective, accuracy, precision, recall, or F1 score may be necessary descriptors of particular stages, but none is

sufficient as a stand-alone measure of PLF success. The scientific maturity of precision livestock farming will depend increasingly on demonstrating that performance observed under controlled conditions is maintained across independent animals, genotypes, environments, production periods, and commercial farms.

12. Economic, Operational, and Adoption Challenges

Scientific validation does not guarantee adoption of a PLF technology. A sensor may measure accurately, a camera system may classify behavior reliably, or an early-warning system may identify risk before conventional observation, yet its impact remains limited if farmers do not invest in the technology, cannot operate it consistently, or do not incorporate its outputs into routine management. The transition from technological capability to effective farm use is therefore influenced by economic feasibility, operational reliability, infrastructure, technical support, digital skills, trust, and compatibility with existing management practices (Kallioniemi et al., 2024; Gouroubera et al., 2026).

Economic evaluation should extend beyond the initial purchase price. PLF systems may require sensors, cameras, gateways, communication networks, installation, software licenses, cloud services, modifications to existing housing, and integration with other equipment. After installation, batteries, calibration, replacement devices, cleaning, software subscriptions, data storage, connectivity, technical service, spare parts, and system updates generate continuing expenditure. The relevant economic concept is therefore the total cost of ownership rather than capital expenditure alone. This distinction is particularly important for technologies involving large numbers of individual sensors, where relatively small per-device costs can become substantial at herd or flock scale (Mura et al., 2026; Zhao et al., 2026).

The economic return is often more difficult to quantify than the cost. Benefits may arise through reduced labor, earlier disease detection, improved reproductive performance, lower mortality, more efficient feeding, reduced resource use, or avoidance of production losses. Some of these outcomes are indirect or probabilistic. An early-warning system, for example, generates economic value only if the warning leads to an intervention that changes the subsequent biological or production outcome. Similarly, automation may reduce repetitive physical labor while increasing requirements for technical supervision, maintenance, and data interpretation. Return on investment should therefore be evaluated from the management changes generated by the technology rather than from its technical capabilities alone.

Farm scale and production system strongly influence this balance. Fixed infrastructure such as cameras or environmental sensor networks can monitor large numbers of animals in intensive systems, reducing the cost per animal. In extensive systems, large areas, limited connectivity, battery requirements, and

lower individual animal value may make the same technological architecture economically inappropriate. Small farms may also face greater difficulty distributing fixed costs across production units. Consequently, technologies that are economically viable in large dairy, pig, or poultry enterprises cannot automatically be assumed to provide equivalent returns in small-ruminant or extensive production systems.

Operational burden is equally important. Ease of use should not be reduced to the simplicity of a software interface. Attaching sensors, replacing batteries, cleaning cameras, recalibrating equipment, restoring network connections, troubleshooting devices, interpreting outputs, and maintaining data systems are all components of technology use. A well-designed mobile interface cannot compensate for devices that repeatedly fail under barn conditions. Likewise, a highly accurate system requiring frequent manual data transfer may become impractical in a large commercial enterprise. Kallioniemi et al. (2024), examining adoption of animal-welfare technologies on Finnish dairy farms, identified financial constraints, farmer workload and coping capacity, and equipment performance under barn conditions among important factors influencing adoption.

Interoperability can add substantially to this operational burden. Farms commonly acquire technologies incrementally, and equipment purchased from different manufacturers may use incompatible communication protocols, data formats, or software platforms. A technically effective sensor can therefore lose practical value if its information cannot be integrated with the existing herd-management, feeding, milking, or environmental-control system. Proprietary platforms may also constrain future expansion by limiting the ability to incorporate new equipment. Open interfaces, standardized data structures, and modular architectures consequently have economic as well as technical importance because they influence the long-term flexibility of the investment.

Technology acceptance adds a human dimension to these constraints. The Technology Acceptance Model emphasizes perceived usefulness and perceived ease of use as major determinants of users' attitudes and behavioral intentions. Broader approaches additionally incorporate trust, social influence, self-efficacy, and facilitating conditions. In a meta-analysis incorporating 33 studies, 17 countries, and 13,660 farmers, Gouroubera et al. (2026) showed that acceptance of agricultural digital technologies is associated not only with technical characteristics but also with perceived usefulness and ease of use within a broader social and institutional context. For PLF, this distinction is important because the benefit valued by a farmer may differ from the performance metric emphasized by a researcher. A classification accuracy of 95% may be scientifically impressive, whereas the farmer's practical questions concern whether the system

saves time, identifies problems earlier, reduces losses, or improves production management.

Acceptance, adoption, and effective use should also be distinguished. A farmer may regard a technology positively but decide not to purchase it because of investment constraints or inadequate technical support. Conversely, a farm may purchase a technology but use only a small proportion of its functions. Activity sensors may be installed while alarms are rarely reviewed, or environmental sensors may collect continuous data while ventilation continues to be managed through conventional fixed thresholds. Technology ownership is therefore not equivalent to digital transformation. The relevant endpoint is sustained integration of the technology into routine decision-making.

This distinction also explains the potential intention–use gap. Positive attitudes toward digitalization do not necessarily translate into actual use when infrastructure, financial resources, technical support, or organizational capacity are insufficient. Regional differences in internet coverage, electricity reliability, service networks, access to financing, training, and advisory services can therefore influence adoption as strongly as characteristics of the technology itself (Zhao et al., 2026). Limited access to these resources may also create a digital divide in which larger and better-capitalized farms capture productivity and management advantages more rapidly than smaller enterprises.

The economic, operational, and adoption challenges of PLF are consequently interconnected. Increasing sensor density may improve information resolution while increasing investment, maintenance, and energy requirements. Cloud-based processing may expand analytical capacity while creating dependence on connectivity. Automation may reduce repetitive labor while increasing demand for technical expertise. Greater technological complexity can improve functionality but may simultaneously reduce robustness and usability. PLF design should therefore be treated as an optimization problem rather than a pursuit of maximum technological sophistication. The objective is to achieve sufficient biological and management value with an acceptable balance among cost, reliability, maintenance burden, infrastructure requirements, and user capacity. When this balance is not achieved, digitalization risks becoming an expensive and fragile technological layer; when it is achieved, PLF can become a functional component of everyday livestock management.

13. Data Ownership, Privacy, Ethics, and Governance

Privacy extends beyond the animals being monitored. Cameras, location systems, access records, and automated equipment may also generate information concerning farm employees and their activities. Technologies installed for animal monitoring can therefore become indirect systems of workplace observation. Appropriate governance should distinguish between data required for legitimate animal-management purposes and unnecessary collection of information about

people. Data minimization, clearly defined access permissions, and appropriate local processing can reduce some of these concerns without eliminating the information required for livestock management.

Cybersecurity becomes particularly important when digital systems control physical processes. Network-connected feeding, milking, ventilation, cooling, and environmental-control systems are not merely information technologies; they are cyber-physical components of livestock production. Software failure, corrupted sensor information, loss of connectivity, or unauthorized access can therefore affect animal health, welfare, and production continuity rather than only compromise digital records. Critical PLF systems should consequently incorporate safe operating modes, backup systems, manual override, and clear procedures for maintaining essential functions during network or software failure. Cybersecurity in livestock production must be understood as part of biological and operational safety.

Ethical evaluation should also consider the relationship between technology and the animal. A fundamental principle is that technology should be adapted to animal biology rather than requiring animals to adapt to poorly designed technological systems. Wearable devices may impose physical burdens, robots can alter movement or behavioral patterns, and automated housing systems can affect animals even when their technical performance is satisfactory. A system should therefore be evaluated not only according to measurement accuracy or production efficiency but also according to whether its physical presence and interventions alter behavior, health, or welfare.

Automation additionally changes the human–animal relationship. Automated feeding, milking, weighing, and health monitoring can reduce the need for some routine interactions. This may reduce disturbance during certain procedures, but it can also reduce opportunities for stockpersons to develop the experiential knowledge obtained through regular contact with animals. The objective of PLF should therefore not automatically be the elimination of human involvement. Continuous digital monitoring can extend the limited observational capacity of farmers, veterinarians, and animal-care staff, but biological interpretation and responsibility remain particularly important when decisions concern health and welfare.

A human-in-the-loop approach is consequently appropriate for many high-consequence applications. A system may identify an animal as being at increased risk of mastitis, lameness, or respiratory disease, but the clinical significance of that warning and the appropriate intervention may still require human assessment. At the same time, retaining a human operator does not guarantee responsible automation itself. Persistent system accuracy may encourage excessive reliance on automated recommendations, creating automation bias, whereas repeated false alarms may produce alarm fatigue and eventual disregard of valid warnings

(Mekonnen, 2026). Effective oversight therefore requires users who understand both the capabilities and limitations of the system rather than simply retaining nominal authority over the final decision.

Governance provides the framework connecting these issues. Sustainable PLF requires transparent definitions of data origin, access rights, permitted uses, portability, security responsibilities, and decision accountability. It should also clarify what happens when algorithms are updated, when a farmer changes technology providers, or when automated recommendations contribute to an adverse outcome. Greater data availability can support research and technological development, but data sharing should not eliminate farmer control, employee privacy, or legitimate commercial confidentiality (Tedeschi et al., 2026).

The development of PLF therefore creates responsibilities alongside technological opportunities. Unclear data rights can reduce farmers' digital autonomy; inadequate cybersecurity can threaten production continuity and animal welfare; poorly designed technologies can interfere with normal behavior; and excessive automation can obscure human responsibility for biological decisions. The future smart farm should consequently be defined not only by the quantity of data it generates or the sophistication of its automation, but also by transparent data governance, secure infrastructure, appropriate human oversight, and technologies designed around the biological needs of the animals they monitor.

14. Future Research Areas

Research in precision livestock farming has progressed beyond the stage at which the principal objective was simply to develop new sensors. Electronic identification, activity monitoring, cameras, microphones, thermal imaging, automated weighing and feeding, robotic milking, and environmental sensing are already technically feasible for many applications. The more important research challenge is now to determine how high-frequency measurements can be converted into biologically meaningful information, how that information can support reliable decisions, and whether those decisions produce measurable benefits under commercial conditions. Current limitations therefore increasingly concern validation, generalizability, interoperability, biological interpretation, economic feasibility, and governance rather than sensor availability alone (Klingström et al., 2025; Tedeschi et al., 2026; Neethirajan, 2026).

A major priority is the transition from short-term proof-of-concept studies toward multicenter and longitudinal commercial-farm validation. Technologies developed in one population, production cycle, housing system, climate, or farm cannot be assumed to maintain equivalent performance elsewhere. Future studies should therefore incorporate independent farms, production periods, genotypes, ages, and environmental conditions that reflect the intended population of use. Long-term studies are also required to quantify sensor drift, equipment failure,

changing animal characteristics, seasonal effects, and changes in system performance over time. The research pathway should increasingly progress from prototype to pilot testing, independent multicenter validation, and ultimately sustained commercial evaluation rather than treating technical feasibility as evidence of deployment readiness.

Continuous digital monitoring also creates new opportunities for phenotyping. Conventional livestock phenotypes are frequently based on measurements obtained at discrete ages or production stages, whereas PLF can generate longitudinal descriptions of growth, feed intake, activity, behavior, environmental response, and recovery from disturbance. These time-series data can support the development of dynamic phenotypes describing not only average performance but also biological stability, variability, adaptability, and resilience. An animal's response to heat, regrouping, disease challenge, feed change, or another disturbance may be characterized through the magnitude of deviation from its previous trajectory, the duration of the response, and the rate of recovery. Such phenotypes may provide biologically meaningful information that is largely absent from conventional endpoint measurements.

This development also creates opportunities to connect digital phenotyping with animal breeding and genetics. High-frequency phenotypes may reveal individual differences in environmental sensitivity and recovery that are obscured when animals are characterized only by periodic production records. Future research can investigate the genetic basis of these longitudinal responses and their relationships with production, health, welfare, and efficiency. Genotype × environment interactions are particularly relevant because continuous environmental sensing allows the conditions experienced by individual animals or groups to be described with much greater temporal resolution. The combination of pedigree or genomic information with longitudinal animal and environmental data could therefore extend selection objectives from performance under average conditions toward robustness and resilience across variable production environments.

Multimodal phenotyping will be another important research direction. No single sensor adequately represents the biological state of an animal, and simply increasing the number of devices does not guarantee better information. Future studies should determine which combinations of behavioral, physiological, production, spatial, acoustic, visual, and environmental measurements provide genuinely complementary information and which merely introduce redundancy, cost, and noise. The objective should be parsimonious multisensor systems that retain biological information while reducing unnecessary technological complexity. This is particularly important for commercial implementation, where every additional sensor introduces requirements for energy, maintenance, calibration, data transmission, and integration.

Interoperability will consequently remain a major research and standardization priority. Closed data formats and incompatible platforms restrict integration among technologies from different manufacturers and create barriers to longitudinal data use. Digital twins will intensify this requirement because continuously updated virtual representations depend on reliable information exchange across multiple systems. Common data dictionaries, open application programming interfaces, synchronized timestamps, standardized metadata, and explicit definitions of the biological meaning of variables will therefore be important components of future PLF infrastructure (Neethirajan, 2026). Adaptation of FAIR principles—making data findable, accessible, interoperable, and reusable—may further improve scientific reproducibility and data reuse, although complete openness will not always be compatible with farmer control, privacy, or commercial confidentiality.

Digital-twin research should focus on these functional requirements rather than applying the term to increasingly sophisticated dashboards. Key questions include how accurately physical and virtual systems can be synchronized, how biological models can be updated for an individual animal or group, how uncertainty should be represented, and whether alternative interventions can be simulated reliably before implementation in the physical system (Neethirajan, 2026). Integration of mechanistic biological models with continuously updated sensor information represents a particularly promising direction. Mechanistic models can provide biological structure, while longitudinal observations can continuously update the state of the animal or production system. The scientific value of such systems will depend on whether simulated interventions predict subsequent biological responses under independent real-world conditions.

This development also requires a transition from prediction toward stronger causal understanding. Observational PLF datasets can identify relationships between reduced feed intake, altered activity, environmental conditions, and disease, but prediction alone does not establish whether one variable causes another. Farm management frequently requires an answer not only to “what is likely to happen?” but also to “what will happen if this management factor is changed?” Large observational datasets therefore do not eliminate the need for experimental research. Controlled and randomized animal experiments can test whether relationships identified through continuous monitoring are causal, while PLF data can improve experimental design by identifying sensitive periods, generating longitudinal phenotypes, and detecting responses that conventional measurements may miss. Continuous farm data and classical experimentation should consequently be viewed as complementary rather than competing research approaches.

Environmental assessment provides another opportunity for integration. Conventional life cycle assessment commonly relies on period-level or annual

average inputs, whereas PLF systems can generate continuous information on feed consumption, growth, mortality, environmental conditions, and energy use. Future research could integrate these data streams into more dynamic LCA frameworks in which environmental performance is updated during production rather than calculated only retrospectively. Carbon footprint, nutrient-use efficiency, or other environmental indicators could then become variables available to management rather than solely outcomes reported after production has ended. Such approaches should nevertheless evaluate the environmental burden of the digital infrastructure itself, including devices, batteries, communication networks, data processing, and electronic waste.

Research standards must evolve alongside these technological developments. PLF studies should report the number of biologically independent animals and farms, data-partitioning procedures, external validation, event prevalence, missing-data management, sensor specifications, sampling frequency, and relevant software or algorithm versions sufficiently clearly to permit critical evaluation. Reproducibility should also be strengthened through transparent analytical protocols and, where commercial restrictions permit, sharing of anonymized example data, code, model parameters, or validation procedures. Technology readiness should be reported explicitly because a laboratory prototype, a proof-of-concept study on one commercial farm, and a technology validated across thousands of animals in multiple production systems represent fundamentally different levels of evidence.

Future research should also address the socio-technical dimensions of PLF more directly. Data ownership, portability, cybersecurity, algorithmic transparency, human oversight, and farmer trust are not secondary issues to be considered after technology development; they influence whether the technology can function sustainably within livestock production. Cyber-physical systems controlling feeding, milking, ventilation, or other essential processes require research on safe failure modes, network interruption, corrupted sensor information, backup control, and recovery. Similarly, human–machine collaboration should be evaluated empirically to determine when automation improves decisions and when it introduces automation bias, alarm fatigue, or loss of important stockperson knowledge.

The future of PLF will therefore require increasingly transdisciplinary research. Animal scientists, veterinarians, ethologists, geneticists, engineers, data scientists, economists, environmental scientists, and social scientists address different components of the same biological–digital system. Technology-centered research asking whether a sensor or algorithm can perform a task must increasingly be complemented by system-centered research asking whether the resulting intervention improves animal health, welfare, resource-use efficiency, economic viability, environmental performance, or resilience under actual farm

conditions. The long-term scientific importance of PLF will not arise simply from measuring animals more frequently. It will arise from converting continuous digital phenotypes into biologically interpretable, externally validated, economically feasible, ethically governed, and actionable knowledge for livestock management.

15. Conclusion

Precision Livestock Farming represents a transition from periodic and largely retrospective livestock management toward continuous measurement, earlier detection, and data-informed decision-making. Its defining feature is not the presence of sensors, cameras, robots, or other digital technologies, but the functional integration of measurement, biological interpretation, management decisions, and, where appropriate, intervention. PLF should therefore be understood as an integrated management system rather than as a collection of digital devices.

The appropriate form and resolution of PLF depend on species, production system, and management objective. Individual-level monitoring may be particularly valuable in dairy cattle and other systems with high-value, long-lived animals, whereas flock- or house-level monitoring may be more appropriate in poultry and location-based technologies more relevant in extensive production systems. Precision should therefore not be equated with individualization; the appropriate level of precision is that at which additional information can meaningfully improve a management decision.

Continuous monitoring also creates opportunities to move from discrete measurements toward longitudinal digital phenotypes describing growth, intake, activity, environmental responses, disease-related deviations, and recovery. Such information may contribute not only to routine management but also to welfare assessment, physiology, and genetic improvement through the characterization of robustness, resilience, and genotype × environment interactions. However, greater data volume does not necessarily translate into better management. Technical accuracy must be distinguished from biological validity and practical usefulness, and digital signals should generally be regarded as decision-support information rather than automatic diagnoses or complete assessments of health and welfare.

The practical value of PLF therefore depends on reliable measurement, biological interpretation, independent validation, economic feasibility, interoperability, and integration into existing farm management. Adoption also requires attention to total ownership costs, usability, farmer trust, data ownership, cybersecurity, and appropriate human oversight. Digitalization should extend rather than replace human observational and decision-making capacity, particularly where animal health and welfare are concerned.

Ultimately, the success of PLF should not be measured by the number of sensors installed, the volume of data generated, or the degree of automation achieved. Its scientific and practical maturity will depend on whether digital technologies can convert reliable measurements into biologically meaningful and actionable information that produces demonstrable improvements under commercial conditions. Future progress will therefore depend less on technological complexity itself and more on validated integration of animals, environments, data, and management to improve health, welfare, production efficiency, resource use, and the resilience of livestock production systems.

References

Akinyemi, B. E., Akaichi, F., Turner, S. P., Johnson, A. K., & Siegford, J. M. (2026). Precision livestock farming and farm animal welfare: A scientometric analysis of research trends and technological innovations. Computers and Electronics in Agriculture, 255, 112341. https://doi.org/10.1016/j.compag.2026.112341

Alawneh, J. I., Stevenson, M. A., Williamson, N. B., Lopez-Villalobos, N., & Otley, T. (2011). Automatic recording of daily walk-over liveweight of dairy cattle at pasture in the first 100 days in milk. Journal of Dairy Science, 94, 4431–4440. https://doi.org/10.3168/jds.2010-4002

Ben Souf, I., Darej, C., Najjar, A., & M'Hamdi, N. (2026). Precision livestock farming technologies for sheep welfare in extensive systems: A comprehensive review. Veterinary Medicine and Science, 12, e71207. https://doi.org/10.1002/vms3.71207

Buonaiuto, G., Nannoni, E., Sardi, L., Belperio, S., Sanzò, C., & Martelli, G. (2026). Invited review: Precision livestock farming technologies in swine intensive production. Applied Animal Science, 42, 175–202. https://doi.org/10.15232/aas.2025-02699

Cogato, A., Brščić, M., Guo, H., Marinello, F., & Pezzuolo, A. (2021). Challenges and tendencies of automatic milking systems (AMS): A 20-years systematic review of literature and patents. Animals, 11, 356. https://doi.org/10.3390/ani11020356

Dao, S. D., Khodadadian Gostar, A., Tennakoon, R., Chuah, W. Q., & Bab-Hadiashar, A. (2026). Modernizing livestock operations: Smart feedlot technologies and their impact. Animals, 16, 1244. https://doi.org/10.3390/ani16081244

Fang, Y., Liu, Y., Gu, J., Feng, W., & Zhang, T. (2026). Design and laboratory validation of an automatic vaccination robot for sheep. AgriEngineering, 8, 313. https://doi.org/10.3390/agriengineering8080313

Fotos, L., Papakonstantinou, G. I., Pourlis, A., Valasi, I., Michailidis, G., Tsiropoulos, Z., Kaimakamis, I., & Papatsiros, V. G. (2026). Precision livestock farming as a strategic tool for mitigating and adapting to the consequences of climate change in farm animals. Sci, 8, 247. https://doi.org/10.3390/sci8090247

Garrido, L. F. C., Sato, S. T. M., Costa, L. B., & Daros, R. R. (2023). Can we reliably detect respiratory diseases through precision farming? A systematic review. *Animals, 13*, 1273. https://doi.org/10.3390/ani13071273

Ghazy, A. A., & Abu El-Naser, I. A. (2026). A systematic review of artificial intelligence in small ruminant production systems: Applications, performance outcomes, and reported implementation challenges. *BMC Veterinary Research, 22*, 485. https://doi.org/10.1186/s12917-026-05806-z.

Giannico, F., Carbonara, C., Caputi Jambrenghi, A., Ragni, M., Salem, A. Z. M., Tarricone, S., Selvaggi, M., & Colonna, M. A. (2026). Sensor-based precision feeding systems in animal production: Technologies and applications. Animals, 16, 1333. https://doi.org/10.3390/ani16091333

Gouroubera, M. W., Gouthon, M., Segnon, A. C., Dosso, F., Togbévi, Q. F., Moumouni-Moussa, I., & Zougmoré, R. B. (2026). Understanding farmers' acceptance of digital technologies: A meta-analytic structural equation modeling approach based on the technology acceptance model. Frontiers in Sustainable Food Systems, 10, 1723715. https://doi.org/10.3389/fsufs.2026.1723715

Gresse, A. U., & van Marle-Köster, E. (2026). Precision livestock farming technologies to support sustainable beef cattle production: A South African perspective. *South African Journal of Animal Science, 56*(6), 226–240. https://doi.org/10.17159/sajas.v56i06.01.

Halachmi, I., Guarino, M., Bewley, J., & Pastell, M. (2019). Smart animal agriculture: Application of real-time sensors to improve animal well-being and production. Annual Review of Animal Biosciences, 7, 403–425. https://doi.org/10.1146/annurev-animal-020518-114851

John, A. J., Clark, C. E. F., Freeman, M. J., Kerrisk, K. L., Garcia, S. C., & Halachmi, I. (2016). Review: Milking robot utilization, a successful precision livestock farming evolution. Animal, 10(9), 1484–1492. https://doi.org/10.1017/S1751731116000495

Kallioniemi, M. K., Kymäläinen, H.-R., & Niemi, J. K. (2024). Enabling factors and constraints for the adoption of animal welfare-enhancing technologies among Finnish dairy farmers. Frontiers in Animal Science, 5, 1332525. https://doi.org/10.3389/fanim.2024.1332525

Klingström, T., Zonabend König, E., & Zwane, A. A. (2025). Beyond the hype: Using AI, big data, wearable devices, and the internet of things for high-throughput livestock phenotyping. Briefings in Functional Genomics, 24, elae032. https://doi.org/10.1093/bfgp/elae032

Lee, M., Tedeschi, L. O., & Seo, S. (2026). Biosensors in precision livestock farming in dairy production: Decoding animals' needs. Animal Bioscience, 39(4), 260154. https://doi.org/10.5713/ab.260154

Losacco, C., Pugliese, G., Forte, L., Tufarelli, V., Maggiolino, A., & De Palo, P. (2025). Digital transition as a driver for sustainable tailor-made farm management: An up-to-date overview on precision livestock farming. Agriculture, 15, 1383. https://doi.org/10.3390/agriculture15131383

Mahdavian, A., Minaei, S., Marchetto, P. M., Almasganj, F., Rahimi, S., & Yang, C. (2021). Acoustic features of vocalization signal in poultry health monitoring.

Applied Acoustics, 175, 107756. https://doi.org/10.1016/j.apacoust.2020.107756

Masiello, A., Galante, I., Spagnuolo, A., Vetromile, C., Sorrentino, M. L., Costanzo, G., Marotta, A., De Cristofaro, F., Lubritto, C., & di Cicco, M. R. (2026). From recycled end-of-life tires to smart circular livestock infrastructures: Development and proof-of-concept validation of the SenseMat platform. Applied Sciences, 16, 9062. https://doi.org/10.3390/app16189062

Mason, S. P., Wang, N., & Salak-Johnson, J. L. (2026). Smart animal welfare: A review of sensing technologies, deployment challenges, and AI-driven insights. Sensors, 26, 5387. https://doi.org/10.3390/s26175387

Mata, F. (2026). The impact of precision livestock farming technologies on productivity, animal welfare, and environmental sustainability. J, 9, 13. https://doi.org/10.3390/j9020013

McManus, R., Boden, L. A., Weir, W., Viora, L., Barker, R., Kim, Y., McBride, P., & Yang, S. (2022). Thermography for disease detection in livestock: A scoping review. *Frontiers in Veterinary Science, 9*, 965622. https://doi.org/10.3389/fvets.2022.965622

Mekonnen, G. B. (2026). Precision housing dynamics in poultry: AI-driven predictive systems. Poultry Science and Management, 3, 10. https://doi.org/10.1186/s44364-026-00025-6

Mokashi, U., Rohouma, W., Refaat, S. S., Benlamri, R., Abdullah, A. K. M., Reaz, M. B. I., Ayari, M. A., Haq, M. F. U., & Reza, R. A. (2026). A systematic review on real-time monitoring of cattle: Leveraging IoT, wearables, and cloud platforms for sustainable farming practices. In M. Trabelsi et al. (Eds.), Proceedings of the 2nd Symposium on Smart, Sustainable, and Secure Internet of Things (Lecture Notes in Electrical Engineering, Vol. 1513). Springer. https://doi.org/10.1007/978-981-95-5136-1_27

Mura, M. C., Trimasse, O., Carcangiu, V., & Luridiana, S. (2026). Precision livestock farming for dairy sheep: A literature review of IoT and decision-support systems for enhanced management and welfare. AgriEngineering, 8, 58. https://doi.org/10.3390/agriengineering8020058

Neethirajan, S. (2026). Digital twins for cows and chickens: From hype cycles to hard evidence in precision livestock farming. Agriculture, 16, 166. https://doi.org/10.3390/agriculture16020166

Papakonstantinou, G. I., Voulgarakis, N., Terzidou, G., Fotos, L., Giamouri, E., & Papatsiros, V. G. (2024). Precision livestock farming technology: Applications and challenges of animal welfare and climate change. Agriculture, 14, 620. https://doi.org/10.3390/agriculture14040620

Peng, W., Liu, Z., Cai, J., & Zhao, Y. (2025). Research and application progress of electronic ear tags as infrastructure for precision livestock industry: A

review. Intelligence & Robotics, 5(2), 433–449. https://doi.org/10.20517/ir.2025.22

Qiao, Y., Kong, H., Clark, C., Lomax, S., Su, D., Eiffert, S., & Sukkarieh, S. (2021). Intelligent perception-based cattle lameness detection and behaviour recognition: A review. Animals, 11, 3033. https://doi.org/10.3390/ani11113033

Rawdhan, S. A., Abdelhamid, M. A., Anwer, A. A., & Shaaban, F. M. (2026). An IoT and machine learning approach for predicting air quality parameters in poultry houses. Journal of Biosystems Engineering, 51, 15. https://doi.org/10.1007/s42853-026-00300-8

Sharifuzzaman, M., Mun, H.-S., Lagua, E. B., Hasan, M. K., Kang, J.-G., Kim, Y.-H., Mehtab, A., Park, H.-R., & Yang, C.-J. (2026). Advances in audio classification and artificial intelligence for respiratory health and welfare monitoring in swine. Biology, 15, 177. https://doi.org/10.3390/biology15020177

Tedeschi, L. O., Guarnido-Lopez, P., Menendez III, H. M., & Seo, S. (2026). Advancing precision livestock farming: Integrating artificial intelligence and emerging technologies for sustainable livestock management. Animal Bioscience, 39(4), 250289. https://doi.org/10.5713/ab.25.0289

Zhang, X., Li, B., & Xue, X. (2026). Lightweight fine-tuning for pig cough detection. Animals, 16, 253. https://doi.org/10.3390/ani16020253

Zhao, X., Liao, Q., Wang, D., Meijering, E., Brosnahan, C., Keeling, S., Tian, R., Li, W., Sutherland, M., & Kang, J. (2026). Multimodal animal health monitoring in extensive livestock production systems. Frontiers in Veterinary Science, 13, 1832869. https://doi.org/10.3389/fvets.2026.1832869

Zhou, L., Hao, L., Xiong, Y., Qin, H., Bao, A., & Chen, Z. (2026). Research progress of robotic technologies and applications in smart pig farms. Agriculture, 16, 334. https://doi.org/10.3390/agriculture16030334

CHAPTER 17

Licensed Storage System for Maintaining Sustainable Quality in Olives After Harvest

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1. INTRODUCTION

Storage is defined as the preservation of a product's quality over a specific period. The objective of storage is to minimize factors that could adversely affect product quality (Dizlek, 2012). From a historical perspective, humanity observed that agricultural produce obtained through the agricultural revolution would spoil if not consumed within a certain timeframe. To prevent this, methods such as storing agricultural products beneath snow, inside caves, or underground were adopted (Rezaei et al., 2020). With technological advancements, mechanical cold storage facilities began to be used for agricultural products in the United States in the early 1900s, marking the beginning of a period of rapid technological progress in storage practices (Türk and Karaca, 2015). In Turkey, technological development in storage accelerated following World War II, driven by rising commercial demand for the storage of agricultural products (Nizamlıoğlu and Gökmen, 2017).

Increasing agricultural production depends on obtaining a higher yield per unit area. However, the proper handling and utilization of the harvested produce are also crucial. In practice, only a small fraction of agricultural products is consumed immediately after harvest; the vast majority is stored for a certain period. Consequently, storage often becomes a necessity for agricultural products. Storage can be defined as holding products for a specific duration under optimal conditions while preserving their characteristics and freshness (Özocak and Şişman, 2015).

When determining the physical properties of agricultural products, it is crucial to have prior knowledge of storage areas, conditions, and durations. Given the short shelf life of agricultural products, it is necessary to select appropriate methods and strategies; otherwise, product losses or return processes are inevitable (Memiş and Keskin, 2015).

Storage under unsuitable conditions leads to losses in both the quality and quantity of agricultural products—though the extent varies by variety (Şişman and Albut, 2010). The objective of storage is to minimize the impact of harmful microorganisms, insect activity, adverse climatic conditions, and water loss on the produce, thereby slowing down the ripening process and preserving freshness (Ekmekyapar, 2001). Even when agricultural products are harvested at the optimal time, failure to store them in facilities that meet technical requirements results in physiological disorders such as spoilage and decay. This leads to economic losses alongside the deterioration of the produce itself. Storing agricultural products in specialized agricultural facilities helps minimize these adverse effects (Polat, 1994).

Under current conditions, product storage structures can be designed with capacities ranging from as little as 1 ton up to 100,000 tons (Kibar et al., 2014). Volumetric adequacy, material and construction quality, insulation materials,

natural and mechanical ventilation, and heating and cooling systems are key design parameters for ensuring optimal conditions in product storage structures (Polat, 2015).

The olive (Olea europaea L.) is an agricultural product of immense strategic and economic value in the Mediterranean basin. However, the phenomenon of periodicity inherent to the olive tree's physiology, where a year of high yield (the "on-year") is followed by a year of low yield (the "off-year") leads to significant market instability (Tan, 2021).

2. Environmental Conditions in Storage

Climatic conditions must be controlled to preserve the freshness of stored agricultural products until consumption. This requirement varies depending on the type of stored product, the climatic characteristics of the storage region (such as temperature, relative humidity, and atmospheric composition), in-storage ventilation conditions, and microbiological development (Alkan, 2013). The climatic environmental conditions that must be considered during storage are listed below as sub-headings.

2.1. Relative Humidity

Relative humidity is a critical factor in preventing water loss during the storage of agricultural products; therefore, it must be maintained at specific levels within storage environments. Failure to maintain adequate humidity levels leads to water loss, resulting in product deterioration and losses (Özdemir, 1993). Furthermore, inadequate relative humidity by slowing down respiration and metabolic processes contributes to fungal diseases and a decline in product quality (Karaçalı, 1993).

Even when a uniform moisture balance is maintained within an enclosed storage facility for agricultural products, signs of spoilage due to high moisture levels may still appear by the end of the storage period. This phenomenon arises from the transfer of moisture generated by the respiration of the products (Özocak and Şişman, 2015). In the case of grains, heat transfer between kernels occurring via conduction and the upward movement of heated, moisture laden air leads to a process known as moisture migration (Şişman, 2003). Consequently, the resulting moisture movement and the subsequent increase in product moisture content trigger the deterioration of the agricultural products (Kendirli, 2006).

2.2. Temperature

Temperature must be maintained at a specific level during storage to preserve product quality and prevent spoilage. Temperature is the most critical factor among storage conditions. The required temperature level varies depending on the characteristics of the products stored in the warehouse. Furthermore, the ideal

temperature must be maintained throughout the storage period (Karaman and Cemek, 2007).

After harvest, agricultural products undergo a ripening process. While ripening consists of various distinct events, each of these proceeds under optimal conditions. Deviations in the ripening process occur when temperatures exceed these optimal levels, whereas temperatures below the optimum result in a slowdown of the process. Low temperatures cause a reduction in the rate of respiration. If such temperature fluctuations occur during storage, they lead to product losses, alterations in chemical composition, loss of flavor, and a decline in quality. Therefore, optimal storage temperature conditions must be maintained throughout the ripening process (Karaçalı, 2009).

2.3. Air Movements and Ventilation

To establish and maintain optimal humidity and temperature conditions during the storage of agricultural products, mechanical cooling systems are used in conjunction with suitable in-storage ventilation systems. The purpose of ventilation within the storage facility is to ensure temperature and relative humidity levels that are appropriate for the agricultural product; this also facilitates proper airflow. Furthermore, optimal ventilation allows for the removal of unwanted odors from the storage environment. Ventilation under optimal conditions ensures the supply of necessary oxygen for the agricultural product. These systems help keep the stored products cool, minimize losses, and maintain the presence of aroma compounds essential for the product's ripening process (Karaman and Cemek, 2007).

Agricultural products are affected by the composition of the surrounding air during storage. The gases present in the air that influence the products' metabolism are oxygen and carbon dioxide; conversely, nitrogen—which makes up 79% of the air—is inert regarding the products. The optimal characteristics of agricultural products are preserved by leveraging the effects of low oxygen and high carbon dioxide levels within the storage atmosphere. Beyond these gases, another environmental factor determining the quality of the stored product is the air pressure inside the storage facility. A drop in internal air pressure reduces both the quantity of gases present and their respective partial pressures. For instance, a reduction in air pressure to 10% of atmospheric levels corresponds to a drop in oxygen concentration to approximately 2% (Karaçalı, 1993).

To maintain optimal conditions for agricultural products during storage, it is essential to ensure adequate and balanced air circulation within the storage facility. Insufficient air circulation leads to the formation of localized zones known as "micro-ecologies." In these zones, heat transfer fails to reach the desired level, causing temperatures to rise and humidity to drop. Under these unfavorable conditions, the ripening and senescence of agricultural products accelerate, and quality losses increase rapidly (Karaçalı, 1990).

3. The Concept Of A Licensed Storage

Licensed warehouses are vital agricultural facilities that enable the preservation of agricultural products under optimal post-harvest conditions and facilitate year-round product supply, while also ensuring that trade is formally recorded. Furthermore, licensed warehousing fosters stability in agricultural product markets (Ergin and Bal, 2020). These facilities contribute significantly to the transparency and clear traceability of agricultural markets. Particularly in both developed and developing nations, licensed warehousing helps maintain the balance between supply and demand for agricultural products and prevents price fluctuations (Doğan and Bulut, 2021; Sezal, 2017).

The licensed warehousing system consists of agricultural facilities operated by joint-stock companies whose operating principles are established by public authorities that provide optimal conditions for preserving the quality characteristics of agricultural products after harvest. By ensuring optimal storage conditions, these facilities manage storage processes that preserve agricultural products such as grains, olives, and cotton in a manner consistent with their quality specifications (Memiş and Keskin, 2016).

The harvested quantities of agricultural products and consequently their prices do not exhibit regularity; this irregularity stems from the nature of agricultural markets. The primary cause of price fluctuations is the variation in harvest volumes resulting from natural conditions. In this context, minimizing price fluctuations caused by climatic conditions during post-harvest operations is achieved through storage systems that maintain optimal conditions (Peker, 2019).

Licensed warehouses used for storing agricultural products are required to maintain a maximum moisture level of 14%; in practice, however, the level maintained is often lower than this limit. These facilities consist of reinforced concrete or steel silos that meet international standards and are equipped with drying systems for products with high moisture content. Products accepted for licensed storage are received by expert warehouse personnel. Following delivery and weighing, the products are continuously monitored via sensors. In-warehouse ventilation is managed by experts, either manually or automatically. Ambient temperature is constantly monitored to mitigate the risk of heating within the stored agricultural products. Storage duration varies depending on the specific characteristics of the agricultural product and market demand (Abdullah et al., 2019).

There are certain conditions that must be met to ensure optimal storage conditions and efficient operations in licensed warehousing. First and foremost, the licensed warehouse must be capable of accommodating the volume of agricultural products intended for storage. Producers and traders need to be confident that the licensed warehouse to which they deliver their products possesses adequate capacity; insufficient capacity not only creates serious

problems but also undermines trust in the licensed warehousing system (Peker, 2019).

The Licensed Warehousing system was developed in 2005 by the Ministry of Trade of the Republic of Türkiye to establish a reliable national standard for the post-harvest storage of agricultural products, and the resulting legislation was published in the Official Gazette that same year. The legislation enacted in this context is the Agricultural Products Licensed Warehousing Law No. 5300. This law aims to ensure the secure storage of agricultural products, the preservation of product quality during the storage period, and the objective execution of all associated processes. Furthermore, it guarantees that licensed warehouses accept agricultural products from both producers and traders without discrimination while also promoting the use of product receipts. By ensuring optimal storage conditions, the law fosters the development of agricultural trade and establishes sustainable transparency (Ministry of Trade of the Republic of Türkiye, 2005).

The licensed warehousing system plays a prominent role in the trade of agricultural products. It enables the long-term storage of traded agricultural products under optimal conditions. This system serves as a mechanism that not only prevents price fluctuations but also supports the market development of agricultural products. Furthermore, licensed warehousing facilitates access to raw materials and ensures sustainability in agricultural production (Hekimoğlu & Altındeğer, 2006).

Licensed warehousing is not merely a physical storage facility but also a modern agricultural financing tool. An Electronic Product Certificate (ELÜS) is issued in exchange for olives delivered to the warehouse that meet established standards (Demirbaş, 2022). Producers can utilize these certificates as financial assets traded on platforms such as the Turkish Mercantile Exchange (TÜRİB) without being compelled to physically sell their products. ELÜS certificates are accepted as collateral by banks, enabling producers to easily access low-interest financing (Çetin, 2020).

Licensed warehouses will enable the prices of agricultural products in their respective markets to be determined under more favorable conditions. Furthermore, licensed warehousing will pave the way for new sources of financing and, indirectly, for new investments. In addition to creating new employment opportunities, this system will allow the marketing of agricultural products to be spread over a longer period. Licensed warehouses also provide agricultural producers with access to product prices throughout the entire season, thereby placing them in a position to determine the prices of their products (Karabaş and Zafer Gürler, 2010).

4. Olive And Licensed Storage System

The olive (Olea europaea L.) is an agricultural product of immense strategic and economic value in the Mediterranean basin. However, the phenomenon of periodicity inherent to the olive tree's physiology, where a year of high yield (the "on-year") is followed by a year of low yield (the "off-year") leads to significant market instability (Tan, 2021).

Global olive and olive oil production constitutes a fundamental pillar of agricultural economies, both in terms of employment and the value added it generates. Thanks to its geographical advantages and genetic resources, Turkey is a leading producer within the global olive corridor (Tan, 2022). However, the primary obstacle to the sector's macroeconomic sustainability is the year-to-year fluctuation in production volüme a phenomenon known as periodicity which can reach levels as high as 70% (Demirbaş & Çetin, 2021). Traditional storage infrastructure proves inadequate for preserving the olive's delicate physicochemical properties over extended periods; consequently, the product's commercial value rapidly declines due to oxidation, increased acidity, and microbiological spoilage (Garcia et al., 2020).

Olives are living tissue that continues to respire even after harvest; therefore, the climate control and atmospheric management implemented in licensed warehouses directly determine product quality (Clodoveo, 2022). Long-term storage of olives without loss of quality depends on the strict control of physical and chemical parameters within the storage facility. In traditional storage methods, olive acidity rises, and quality degradation occurs due to oxidation. In licensed warehouses, the temperature is maintained at a constant 15–18°C, and humidity levels are stabilized at 60–65% (Garcia et al., 2019). Furthermore, advanced engineering solutions—such as controlled atmosphere systems and nitrogen gas injection—are employed to prevent rancidity by eliminating contact between the olives and the air (Clodoveo, 2018).

There are several environmental factors for which optimal levels must be maintained during olive storage. Storage areas are kept within a constant temperature range of 4–8°C to inhibit cellular decomposition and mold growth (Ayton et al., 2019). Reducing the ambient oxygen (O_2) level to 2–3% and increasing the carbon dioxide (CO_2) level to 4–5% minimizes enzymatic reactions and the respiration rate (Garcia et al., 2020).

The Electronic Product Certificate (ELÜS) system, operating within the licensed warehousing framework, offers numerous benefits to agricultural producers and traders involved in the licensed storage of olives. Producers can access low-interest loans secured by warehouse receipts using their ELÜS holdings as collateral without being compelled to sell their olives immediately (Yılmaz, 2023). Meanwhile, industrial processors and exporters can hedge

against price risks by purchasing their future raw material requirements today through the ELÜS system (Demirbaş and Çetin, 2021).

The specifications required for licensed warehouses storing olives are clearly outlined in the Regulation on Licensed Warehousing for Olives. According to this regulation, the warehouse must be designed to prevent the ingress of foreign matter, contaminants, and moisture into the stored olives. Warehouses must be enclosed structures and feature areas that allow for the easy passage of transport vehicles. Storage practices must ensure that the quality of olives from different harvest periods and varieties does not deteriorate. Fire safety measures must be documented. The ventilation system must be adequate and possess the capacity to mitigate moisture-related damage. The facility design must facilitate the provision of ancillary services related to storage operations. Furthermore, the facility must meet appropriate quality and hygiene standards for the handling and discharge of the stored olives (Republic of Turkey Ministry of Trade, 2013).

Under current conditions in Turkey, there is only one company licensed for olive storage. Marmara Birlik Tarım Ürünleri Lisanslı Depoculuk A.Ş., which obtained its license in 2015, carries out licensed olive storage operations at its own facility. Apart from this licensed warehouse, there are currently no other enterprises in the country engaged in licensed olive storage activities. (Republic of Türkiye Ministry of Trade, 2026)

5. Conclusion

The inability to achieve consistent olive yields during the annual harvest season highlights the necessity of storage from the perspectives of agricultural production, market conditions, and consumers. In years of high supply, the harvest is abundant and prices drop, whereas in years of low supply, prices rise adversely affecting consumers. The licensed warehousing system is an institutional model developed to balance these fluctuations, ensure the product is preserved for extended periods without loss of quality, and provide financial security to producers. In this regard, olives must be stored in an organized and systematic manner under optimal conditions.

It can be argued that the widespread adoption of the licensed warehousing system for olives could enhance the competitiveness of the country's olive sector by ensuring quality preservation. In this context, it is advisable to initiate or expand efforts regarding the promotion of and support mechanisms for the licensed warehousing system for olives. Furthermore, research and development activities concerning licensed warehousing facilities are recommended for farmers, traders, and cooperatives.

In conclusion, expanding licensed warehousing facilities is essential for our country's olive sector, particularly regarding the preservation of product quality and price stability. This would yield positive outcomes for both producers and consumers. Furthermore, it would help elevate the global profile of our country's olive industry.

REFERENCE

Dizlek H. (2012). Physical and Chemical Changes Occurring in Cereals During Storage. Journal of Food and Feed Science-Technology, 12, 49-57.

Rezaei M, Talebi AA, Fathipour Y, Karimzadeh J, Mehrabadi M, Reddy GV. (2020). Effects of Cold Storage on Life-History Traits of Aphidius Matricariae. Entomologia Experimentalis et Applicata, 168(11): 800-807. doi: 10.1111/eea.12958

Türk R, Karaca H. (2015). Technical and Economic Characteristics of Cold Storage Facilities for Fresh Produce in Our Country. Teskon Conference Proceedings, 775-795.

Nizamlıoğlu NM, Gökmen S. (2017). Current Status, Problems, and Proposed Solutions Regarding Cold Storage Facilities in Karaman Province. Derim, 34(1): 43-50. doi: 10.16882/derim.2017.305442

Özocak, M. (2015). Licensed warehousing and its applications in the Thrace region. Namık Kemal University, Graduate School of Natural and Applied Sciences, Department of Biosystems Engineering. Tekirdağ, 69 p.

Memiş S, Keskin HD. (2015). Determination of the Perceptions of Hazelnut Product Exporting Enterprises Regarding Licensed Warehouse Site Selection Using Factor Analysis, Afyon Kocatepe University, Journal of Social Sciences, Vol. 18, No. 2, December 2016, 83-113.

Şişman, C. B. and Albut, S., (2010). Grain storage management, Proceedings of 3rd Annual International Symposium on Agricultural Research, 15-18.

Ekmekyapar, T. (2001). "Agricultural Structures" Atatürk University, Faculty of Agriculture Publications, No: 204, Erzurum, 2001.

Polat, R. (1994). "Research on Determining Cold Storage Conditions for Certain Apple Varieties." Gaziosmanpaşa University, Institute of Science, Master's Thesis, Department of Agricultural Machinery, Tokat, 73 pp.

Kibar H, Öztürk T, Temizel KE, (2014). Effective engineering properties in the design of storage structures of postharvest dry bean grain. Acta Scientiarum&Agronomy, 36(2): 147- 158.

Polat, H., (2015). Effects of different storage conditions on the nutritional qualities of barley and maize, Journal of Agricultural Sciences, 21 (2), 246-255.

Tan, S. (2021). The Problem of Periodicity in the Olive Sector and Price Stability Strategies. Proceedings of the National Olive Congress, 45-52.

Alkan, Ü. (2013). "Determination and Improvement of the Current Status of Cold Storage Facilities in Aydın Province." Master's Thesis, Adnan Menderes University Graduate School of Natural and Applied Sciences, Department of Agricultural Structures and Irrigation, Aydın, 78 pp.

Özdemir, A.E., (1993). “Studies on the storage of Amasya Starking and Golden Delicious apples grown in the Pozantı-Kamışlı Valley: I. Determination of the harvest time” Doğa, 16, 519-527, 1993.

Karaçalı, İ., (1993). “Storage and Marketing of Horticultural Products,” Ege University, Faculty of Agriculture Publications, No: 494, İzmir, 1993.

Şişman C.B. (2003). Location and Improvement Opportunities for Sunflower Warehouses in the Tekirdağ Region. Trakya University, Faculty of Agriculture, Tekirdağ, 135 pp.

Kendirli B (2006). Ventilation Systems in Agricultural Structures. Ankara University, Department of Agricultural Structures and Irrigation, Ankara.

Karaman, S. and Cemek, B. (2007). “Planning of apple storage structures suitable for the climatic conditions of the Tokat region.” V. National Horticultural Crops Congress, September 4–7, Erzurum.

Karaçalı, İ. (2009). “Storage and Marketing of Horticultural Products,” Ege University Faculty of Agriculture Publications, No: 494, Bornova, 486 pp.

Karaçalı, İ., (1990). Storage and Marketing of Horticultural Products. Ege University Faculty of Agriculture Publications No: 494, İzmir.

Ergin, A., Bal, E. Ç. (2020), Licensed Warehousing System, Electronic Product Certificate, and Turkish Specialized Commodity Exchange in Turkey, Journal of Social, Humanities and Administrative Sciences, 3(4), 261-272.

Doğan, H,G,, Bulut, A,(2021),A Research on Licensed Warehousing Activities in Turkey (Case of LİDAŞ in Mucur District of Kırşehir Province),Turkish Journal Of Agriculture-Food Science And Technology, 9(7), 1304-1311,https://doi,org/10,24925/turjaf,v9i7,1304-1311,4452

Sezal, L. (2017). The Licensed Warehousing System in Türkiye and State Incentives Provided, Journal of International Social Research, 10(52), 1146-1155.

Memiş, S., Keskin, D. (2016). The Role of the Licensed Warehousing System in Agricultural Products. Journal of Management and Economics, 22(2), 619-633.

Peker, G. İ. (2019). Inflation in Türkiye and the Licensed Warehousing System as a Proposed Solution. Master's thesis, Marmara University Institute of Social Sciences, Department of Economics, Istanbul. 100 pp.

Abdullah, MSM, Rahiman, MHF, Zakaria, A., Kamarudin, LM, & Mohamed, L. (2019). A review of moisture measurement techniques in agricultural silos. In IOP Conference Series: Materials Science and Engineering (Vol. 705, No. 1, p. 012001). IOP Publishing.

Republic of Turkey Ministry of Trade. (2005). Law on Licensed Warehousing for Agricultural Products https://mevzuat.gov.tr/mevzuat ?MevzuatNo=5300 &MevzuatT ur=1&MevzuatTertip=5

Hekimoğlu, B., Altındeğer, M. (2006). Licensed warehousing system for agricultural products and its effects. Samsun Governorship Provincial Directorate of Agriculture, Samsun.

Demirbaş, N. (2022). Institutionalization in Agricultural Marketing: Licensed Warehouses and the ELÜS Mechanism. Journal of Ege University Faculty of Agriculture, 59(1), 89-101.

Çetin, M. (2020). Licensed Warehousing and Producer Financing for Agricultural Products: The Case of Türkiye. Journal of Agricultural Economics, 26(2), 115-124.

Karabaş, S., Zafer Gürler, A. (2010). The functioning of the licensed warehousing system and its applicability in Turkey. Journal of Social Sciences Research, 5(1), 196-210.

Tan, S. (2022). Sustainable marketing strategies and periodicity management in olives and olive oil. Ege University Faculty of Agriculture Publications, No: 582, İzmir.

Demirbaş, N., Çetin, B. (2021). Development of the licensed warehousing system for agricultural products in Türkiye and its macroeconomic implications for the olive sector. Journal of Agricultural Economics, 27(2), 185-196.

Garcia, J. M., Yousfi, K., Mateos, R. (2020). Controlled atmosphere storage of olives: Preservation of physico-chemical parameters and bioactive compounds. Postharvest Biology and Technology, 163, 111-120.

Clodoveo, M. L. (2022). Modern technologies and atmosphere management in olive storage systems. Food Chemistry, 371, 131-142.

Garcia, J. M., Yousfi, K., Martinez, F. (2019). Technical Criteria for the Cold Storage of Virgin Olive Oils and Olives. International Olive Council (IOC) Technical Bulletin, 112, 14-22.

Clodoveo, M. L. (2018). Industrial Technologies for Extra Virgin Olive Oil Storage. Academic Press, 45-58.

Ayton, J., Gallagher, J., Mailer, R. (2019). The effect of storage conditions on the quality and shelf life of olive oil. International Journal of Food Science & Technology, 54(4), 1145-1153.

Yılmaz, M. (2023). The use of Electronic Warehouse Receipts (ELÜS) as collateral in agricultural finance and their legal framework. Journal of Banking and Capital Markets, 14(3), 45-62.

Republic of Turkey Ministry of Trade. (2013). Communiqué on Licensed Warehousing for Olives https://mevzuat.gov.tr/mevzua t?MevzuatNo= 17273 &MevzuatTur=9&MevzuatTertip=5

Republic of Türkiye Ministry of Trade. (2026). Licensed Warehouse Enterprises https://ticaret.gov.tr/ic-ticaret/lisansli-depoculuk/kurulus-ve-faaliyet-izinleri/lisansli-depo-isletmeleri