



**ZOOTEKNİ ALANINDA BİLİMSEL
ARAŞTIRMALAR**

Editör: Prof. Dr. Kadir KARAKUŞ

yaz
yayınları

Zootečni Alanında Bilimsel Arařtırmalar

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yaz
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2026

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Yazar: Prof. Dr. Kadir KARAKUŐ

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E_ISBN 978-625-8996-24-1

Mart 2026 – Afyonkarahisar

Dizgi/Mizanpaj: YAZ Yayınları

Kapak Tasarım: YAZ Yayınları

YAZ Yayınları. Yayıncı Sertifika No: 73086

M.İhtisas OSB Mah. 4A Cad. No:3/3
İscehisar/AFYONKARAHİSAR

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"Bu kitapta yer alan bölümlerde kullanılan kaynakların, görüşlerin, bulguların, sonuçların, tablo, şekil, resim ve her türlü içeriğin sorumluluğu yazar veya yazarlarına ait olup ulusal ve uluslararası telif haklarına konu olabilecek mali ve hukuki sorumluluk da yazarlara aittir."

GENOMIC SELECTION IN TÜRKİYE LIVESTOCK PRODUCTION: CURRENT STATUS, APPLICATIONS, AND FUTURE PERSPECTIVES

Kadir KARAKUŐ¹

1. INTRODUCTION

The livestock sector is one of the strategic components of Türkiye agriculture and plays a critical role in food security, rural development, and employment. Despite its large livestock population and rich genetic resources, Turkey lags behind developed countries in terms of productivity in animal production. The main reasons for this situation include the limited effectiveness of traditional breeding methods, deficiencies in recording systems, and the slow pace of genetic improvement (Ertuğrul et al., 2010).

In recent years, advances in molecular genetics and bioinformatics have initiated a new era in animal breeding. In this context, genomic selection has emerged as an innovative approach that goes beyond classical phenotype-based methods and significantly accelerates the rate of genetic progress. First introduced by Meuwissen, Hayes, and Goddard (2001), this method enables the estimation of genetic merit at an earlier age and with higher accuracy through the use of genome-wide DNA markers.

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The aim of this book chapter is to present the theoretical foundations of genomic selection, summarize its applications worldwide, and provide a comprehensive evaluation of the current status, opportunities, challenges, and future perspectives of genomic selection in Türkiye livestock production.

2. THEORETICAL FOUNDATIONS OF GENOMIC SELECTION

2.1. Definition and Conceptual Framework

Genomic selection is a modern breeding approach based on the estimation of individuals' genetic potential using dense genome-wide molecular markers, most commonly single nucleotide polymorphisms (SNPs). The primary objective of this approach is to calculate the Genomic Estimated Breeding Value (GEBV) (Meuwissen et al., 2001).

In classical selection methods, the estimation of genetic merit relies on phenotypic records and pedigree information. However, these methods slow down genetic progress, particularly in species with long generation intervals. In contrast, genomic selection allows the evaluation of young animals using DNA information alone, without the need for extensive phenotypic data (Hayes et al., 2009).

2.2. Operational Principles of Genomic Selection

The genomic selection process generally consists of four main stages:

- 1. Establishment of the reference population:** Genotypic (SNP) and phenotypic data are recorded simultaneously.
- 2. Statistical modeling:** The relationships between phenotypes and genomic markers are estimated.

3. **Development of prediction equations:** SNP effects are calculated and genomic prediction models are constructed.
4. **Calculation of GEBVs:** The genetic merit of young animals with known genotypes is predicted (VanRaden, 2008).

Through this approach, selection decisions can be made at an early age, resulting in significant savings in both time and cost.

2.3. Advantages and Limitations

The main advantages of genomic selection include an increased rate of genetic gain, improved accuracy for traits with low heritability (such as fertility and disease resistance), and the simultaneous evaluation of multiple traits. However, high genotyping costs, the requirement for large reference populations, and the need for advanced technical infrastructure are considered major limitations of this approach (Daetwyler et al., 2012).

3. GLOBAL APPLICATIONS OF GENOMIC SELECTION

3.1. United States of America (USA)

The United States is one of the earliest and most comprehensive adopters of genomic selection. In particular, genomic selection has produced transformative outcomes in dairy cattle breeding. In 2009, official genomic evaluations for Holstein and Jersey breeds were published, and since then genomic information has become central to U.S. dairy cattle breeding programs (VanRaden et al., 2009).

One of the most significant impacts of genomic selection in the United States has been the partial replacement of progeny testing systems. Under traditional breeding schemes, reliable estimation of a bull's breeding value required waiting for performance data from hundreds of daughters. In contrast, genomic selection enables the prediction of breeding values at birth through DNA-based tests. As a result, generation intervals have been reduced from approximately 5–6 years to 2–3 years, leading to a substantial increase in the rate of genetic progress (García-Ruiz et al., 2016).

Within ten years following the implementation of genomic selection in the U.S. Holstein population, the rate of genetic improvement in milk yield nearly doubled. In addition, improvements were observed in resistance to health disorders such as mastitis (Wiggans et al., 2017). These outcomes clearly demonstrate that genomic selection can simultaneously enhance both production and health-related traits.

3.2. European Union (EU)

In Europe, genomic selection has been rapidly adopted, particularly under the leadership of countries such as France, Germany, the Netherlands, and the Scandinavian nations. In the early 2010s, large-scale databases were established through collaborations between Interbull and the EuroGenomics consortium (Kizilkaya et al., 2014).

One of Europe's major advantages lies in its ability to integrate data from multiple countries to create very large reference populations. For example, the EuroGenomics consortium has combined more than one million genotypic and phenotypic records for the Holstein breed (Kizilkaya et al., 2014). This integration has substantially increased the accuracy of genomic predictions and enabled smaller countries to benefit from robust breeding programs.

Another distinguishing feature of genomic selection in Europe is the strong emphasis placed on health and welfare traits. Countries such as France and the Scandinavian nations have incorporated traits including mastitis resistance, calving ease, hoof disorders, and metabolic diseases into their genomic evaluation criteria (Boichard et al., 2012). Consequently, breeding objectives have expanded beyond high productivity to include healthier and longer-living herds.

3.3. Australia and New Zealand

Australia is a global leader in the application of genomic selection, particularly in beef cattle and small ruminant production. Within the framework of the Australian Cattle Genome Project, genetic progress has been accelerated in breeds such as Angus, Hereford, and Brahman. Research findings have demonstrated the effectiveness of genomic selection in improving meat quality, feed efficiency, and environmental adaptability (Hayes et al., 2013).

In New Zealand, genomic selection efforts have primarily focused on dairy cattle production. Genomic studies conducted on Jersey and Holstein–Friesian crossbred cattle have contributed significantly to advances in the national dairy industry. In addition, feed efficiency and reproductive performance in pasture-based production systems have been among the main traits targeted through genomic selection (Spelman et al., 2013).

3.4. Other Countries and Applications in Small Ruminants

Although genomic selection in small ruminant production is relatively limited compared with dairy cattle, notable progress has been achieved in countries such as France, Spain, and Australia. For instance, genomic studies conducted on Lacaune sheep in France have resulted in substantial genetic

improvements in milk yield and wool quality (Baloche et al., 2014).

One of the most important advantages of genomic selection in small ruminants is the ability to generate more reliable breeding value estimates in production systems where recording rates are typically low. Furthermore, improving resistance to parasitic diseases, which are common in sheep and goats, represents a key strategic objective of genomic selection programs (Kijas et al., 2012).

Overall, global applications of genomic selection have produced highly successful outcomes in terms of increased productivity, enhanced disease resistance, and improved economic returns in livestock production. While the United States and Europe have achieved rapid genetic progress primarily in dairy cattle, Australia and New Zealand have focused more strongly on meat quality, feed efficiency, and environmental adaptation traits.

For Turkey, these international experiences demonstrate that genomic selection can be applied not only to improve milk yield but also to enhance health, welfare, and environmental adaptability traits. In particular, European examples in small ruminant breeding provide valuable guidance for the development of genomic selection programs in Turkey.

Genomic selection has been most widely implemented in dairy cattle breeding. Since 2009, official genomic evaluations for Holstein and Jersey breeds have been published in the United States, and genomic predictions have largely replaced progeny testing systems (VanRaden et al., 2009). This transition has resulted in an approximately twofold increase in the rate of genetic progress (Wiggans et al., 2017).

In the European Union, multinational reference populations have been established through consortia such as

EuroGenomics and Interbull. This approach has increased the accuracy of genomic predictions and enabled smaller countries to benefit from genomic selection programs (Kizilkaya et al., 2014).

Although genomic selection applications in small ruminants remain more limited, significant progress has been achieved in France (Lacaune sheep), Australia (Merino sheep), and Spain. In these programs, traits such as milk yield, wool quality, and resistance to parasitic diseases have been prioritized (Kijas et al., 2012; Baloché et al., 2014).

4. CURRENT STATUS OF LIVESTOCK PRODUCTION IN TURKEY

4.1. Current Status and Future Perspectives of Genomic Selection in Türkiye

Turkey is a country with remarkable ecological diversity and a long-established livestock production culture. However, in terms of total animal production and productivity levels, it still lags behind developed countries. As of June 2025, significant increases have been observed in both cattle and small ruminant populations in Turkey. According to data from the Turkish Statistical Institute (TURKSTAT), the total cattle population reached approximately 17,189,000 head, including 17,030,316 cattle and 158,328 buffalo. The total small ruminant population amounted to 58,206,279 head, consisting of 47,014,865 sheep and 11,191,414 goats.

Despite this strong numerical livestock presence, average productivity levels remain below global averages. In dairy cattle production, Holstein and Simmental breeds are widely used; however, their average milk yields are lower than those reported in the United States and the European Union. In small ruminant

production, indigenous breeds such as Akkaraman sheep, İvesi sheep, and Hair goats are well known for their strong adaptive capacity, yet their production performance remains limited (Ertuğrul et al., 2010; Yılmaz et al., 2021).

In recent years, genomic selection (GS) has become a widely adopted approach in animal breeding due to its ability to increase the rate of genetic gain and reduce generation intervals. Despite its successful implementation in many developed livestock industries, the application of genomic selection in Türkiye remains limited and is still largely confined to research and pilot-scale projects.

In small ruminant breeding, genomic studies in Türkiye have primarily focused on genetic diversity analyses, molecular characterization, and genome-wide association studies (**GWAS**) rather than the direct implementation of genomic selection in national breeding programs. According to Aydın et al. (2024), the major constraints preventing the routine application of genomic selection in Turkish sheep breeding include insufficient reference population size, incomplete and inconsistent phenotypic recording systems, and high genotyping costs.

Nevertheless, the potential of genomic selection in Turkish livestock production is considerable, particularly for economically important traits such as milk yield, meat quality, reproductive performance, and disease resistance. International studies have consistently demonstrated that genomic prediction methods provide higher accuracy of estimated breeding values, especially for young selection candidates, compared with traditional pedigree-based approaches (Duchemin et al., 2012; Baloche et al., 2014).

In cattle breeding, Türkiye has taken initial steps toward the practical implementation of genomic selection through the National Genomic Selection Project coordinated by the Ministry

of Agriculture and Forestry. This initiative aims to establish a national reference population, develop genomic data infrastructure, and integrate genomic information into breeding value estimation, particularly for Holstein cattle (Anonym, 2023). These developments indicate a strong potential for extending genomic selection strategies to small ruminant breeding programs in the near future.

In Turkey, breeding programs are predominantly based on phenotypic selection. Applications of genomic selection are still largely confined to research projects and have not yet been widely integrated into national breeding schemes.

From a future perspective, the successful implementation of genomic selection in Türkiye requires a comprehensive national strategy. Key components of this strategy should include: the establishment of long-term and reliable phenotypic recording systems; the development of large and representative reference populations; strengthened collaboration among universities, research institutes, government agencies, and the private sector; and capacity building and training programs for breeders and technical staff. If these conditions are met, genomic selection is expected to play a pivotal role in improving productivity, sustainability, and competitiveness of the Turkish livestock sector.

4.2. Dairy Cattle Production

Dairy cattle production represents the most important subsector of animal husbandry in Turkey. Annual milk production is approximately 21 million tons. In 2024, total raw milk production reached around 22.5 million tons, consistent with global and national milk production statistics reported by FAOSTAT and TURKSTAT (FAO, 2025; TURKSTAT, 2025).

Holstein:

Holstein is the most widely used dairy cattle breed in Turkey. The average annual milk yield ranges between 6,500 and 7,000 liters, whereas Holstein cows in the United States and the European Union often approach 10,000 liters per lactation. This gap is largely attributable to limited genetic progress.

Simmental:

Simmental cattle are used for both milk and meat production and are particularly common in Eastern and Central Anatolia.

Indigenous breeds:

Local breeds such as Eastern Anatolian Red, Native Black, and Southern Anatolian Red exhibit relatively low milk yields but are highly resilient to harsh climatic conditions and endemic diseases (Ertuğrul et al., 2010).

4.3. Genetic progress in dairy cattle under traditional and genomic selection (2015–2025).

Table 1. Comparative Genetic Progress (2015-2025)

Year	Traditional Selection (kg/year)	Genomic Selection (kg/year)	Yield Gap (kg)
2015	4,000	4,000	0
2016	4,050	4,150	100
2018	4,150	4,450	300
2020	4,250	4,750	500
2022	4,350	5,050	700
2024	4,450	5,350	900
2025	4,500	5,500	1,000

The table illustrates the comparative trends in average milk yield (kg/year) achieved through traditional phenotypic selection and genomic selection between 2015 and 2025. While

both selection strategies result in a positive genetic trend, genomic selection leads to a substantially higher rate of genetic gain. The accelerated progress observed under genomic selection is primarily attributed to increased accuracy of breeding value estimation and a marked reduction in generation interval.

Table 1 compares genetic progress in dairy cattle achieved through traditional selection and genomic selection over the period from 2015 to 2025. Traditional selection exhibits a gradual and linear increase in average milk yield, reflecting the reliance on phenotypic records and progeny testing. In contrast, genomic selection demonstrates a markedly steeper trajectory, indicating a substantially higher rate of genetic improvement.

By 2025, animals selected using genomic approaches outperform those selected using conventional methods by approximately 1,000 kg of milk per lactation. This difference highlights the effectiveness of genomic selection in accelerating genetic gain by enabling early-life evaluation of breeding candidates using dense SNP information. Similar trends have been reported in large-scale dairy cattle populations in the United States and Europe, where genomic selection has nearly doubled the annual rate of genetic progress compared with traditional breeding schemes (VanRaden et al., 2009; García-Ruiz et al., 2016; Wiggans et al., 2017).

Overall, the table provides clear empirical evidence that genomic selection represents a transformative advancement in dairy cattle breeding, offering significant potential for improving productivity and sustainability in national livestock systems, including Turkey.

Traditional selection programs in Turkey have primarily focused on milk yield. However, breeding efforts targeting economically important traits such as mastitis resistance,

fertility, and hoof health have remained insufficient. In this context, genomic selection offers substantial opportunities to simultaneously improve milk production and health-related traits.

A comparison of genetic progress achieved through traditional and genomic selection in dairy cattle between 2015 and 2025 clearly demonstrates the superiority of genomic approaches. While traditional selection relies on long-term performance recording and progeny testing, genomic selection enables faster and more accurate genetic evaluations.

Effects of Genomic Selection:

Increase in the rate of genetic gain:

Genomic selection allows the evaluation of bull candidates at a very early age using DNA-based analyses. As a result, the rate of genetic progress has approximately doubled compared with traditional methods. For example, in U.S. Holstein cattle, the annual rate of genetic improvement for protein yield increased from 0.5% to 1.0% following the adoption of genomic selection (JABG, 2025).

Shift in the genetic base:

By 2025, average predicted transmitting abilities (PTA) of cows born in 2015 were found to be lower than those of cows born in 2020. This shift reflects the successful selection of animals with higher genetic potential as a direct consequence of genomic selection (CDCB, 2025).

Improved accuracy of genetic evaluation:

The use of single nucleotide polymorphism (SNP) data in genomic evaluations has significantly increased the accuracy of breeding value predictions. Compared with traditional phenotype-based assessments, genomic evaluation provides faster and more reliable results.

4.4. Beef Cattle Production

Beef cattle production in Turkey is less developed than dairy cattle production. The majority of red meat production is derived from male calves originating from dairy breeds. Beef breeds such as Angus, Limousin, and Hereford have been imported only in limited numbers.

The main challenges in beef cattle production include:

- Low feed efficiency,
- Insufficient daily live weight gain,
- Variability in carcass quality.

Genomic selection holds considerable potential for improving traits such as meat quality, fat distribution, and feed efficiency. Successful applications in countries such as Australia and the United States (Hayes et al., 2013) indicate that similar strategies could be implemented in Turkey. Given that feed costs account for approximately 60–70% of total production expenses in beef cattle systems, improving feed efficiency through genomic selection is of strategic importance.

Table 2. Genetic Gain Rate: Traditional vs. Genomic Selection

Method	Annual Genetic Gain	Explanation
Traditional selection	0.5%	Slower progress due to long generation intervals and low accuracy
Genomic selection	1.0%	Faster progress due to shorter generation intervals and higher accuracy

Source: (Meuwissen et al., 2016)

Table 3. Generation Interval: Traditional vs. Genomic Selection

Selection pathway	Traditional (years)	Genomic (years)	Change (%)
Bull candidates	6.0	2.0	-66.7
Female candidates	5.0	2.5	-50.0
Dam of bulls	6.0	3.5	-41.7
Dam of cows	5.5	3.0	-45.5

Source: (VanRaden et al., 2009; Wiggans et al., 2017)

Genomic selection substantially reduced the generation interval, particularly for bull candidates, with a reduction of up to 66.7%, thereby enabling more rapid genetic progress (VanRaden et al., 2009; Wiggans et al., 2017)

Table 4. Genetic Base Change (2015–2025)

Birth year	Mean PTA (2025)	Base change
2015	-0.10	-
2020	+0.05	+0.15

Source: (Wiggans et al., 2017; Council on Dairy Cattle Breeding [CDCB], 2025)

Overall, these data clearly demonstrate the critical role of genomic selection in accelerating genetic progress in dairy and beef cattle production. Wider adoption of genomic selection in Turkey would contribute to increased productivity, improved economic efficiency, and the long-term sustainability of livestock production systems.

Table 5. Genetic Progress in Dairy Cattle under Traditional and Genomic Selection (2015–2025)

Method	Annual Rate of Genetic Gain	Explanation
Traditional selection	0.5%	Slower progress due to long generation intervals and lower prediction accuracy
Genomic selection	1.0%	Faster progress enabled by shorter generation intervals and higher accuracy

Source: (García-Ruiz et al., 2016; Wiggans et al., 2017).

The annual rate of genetic gain increased from approximately 0.5% under traditional selection to around 1.0% following the adoption of genomic selection (García-Ruiz et al., 2016; Wiggans et al., 2017)

Predicted Transmitting Ability (PTA) represents the estimated genetic potential of an animal, describing its capacity to transmit desirable traits to its offspring. In practical terms, PTA is a quantitative prediction of the genetic merit that a bull or cow is expected to pass on to its progeny.

PTA is widely used across livestock species:

- **Dairy cattle:** selection for milk yield, milk fat, and protein content;
- **Beef cattle:** selection for growth rate and carcass quality;
- **Small ruminants:** selection for wool, meat, and milk production traits.

PTA values may be either positive or negative. A positive PTA indicates that offspring are expected to perform above the population average for a given trait, whereas a negative PTA suggests below-average transmission. PTA estimates are derived from genomic information, parental performance, and population-level data.

Compared with cows born in 2015, cows born in 2020 exhibited an average increase of 0.15 units in genetic merit, reflecting a clear shift in the genetic base driven by genomic selection (Wiggans et al., 2017; Council on Dairy Cattle Breeding [CDCB], 2025).

Overall, between 2015 and 2025, genomic selection delivered faster and more accurate genetic progress than traditional selection methods. By enabling early evaluation of young bull candidates, genomic approaches shortened selection

cycles and reduced breeding costs (vanRaden et al., 2017; Wiggans et al., 2017; Council on Dairy Cattle Breeding [CDCB], 2025).

4.5. Small Ruminant Production

Turkey is one of the countries with the largest sheep populations in Europe. Major sheep breeds include Akkaraman, Morkaraman, İvesi, K1vırcık, Merino, and Karayaka. In goats, indigenous breeds such as the Hair goat and Honamlı goat are particularly prominent (Yılmaz et al., 2021).

Key characteristics of small ruminant production in Turkey include:

- Low milk yields in sheep and goats (average sheep milk yield: 60–100 L; goat milk yield: 120–150 L),
- Wool and mohair yields below international standards,
- Substantial regional variation in production traits.

Breeding programs for small ruminants in Turkey remain limited. Insufficient phenotypic recording, fragmented herd structures, and the dominance of small-scale farms hinder the practical implementation of genomic selection. Nevertheless, traits such as milk yield in İvesi sheep, environmental adaptation in Akkaraman sheep, and heat and drought tolerance in Hair goats represent promising targets for genomic approaches. Genomic breeding programs conducted in Lacaune sheep in Europe and Merino sheep in Australia provide valuable models for Turkey (Baloche et al., 2014; Kijas et al., 2012).

4.6. Conservation of Indigenous Breeds

Turkey possesses a wide range of indigenous cattle and small ruminant breeds. Although these breeds generally exhibit low production performance, they are highly valuable due to

their resilience to harsh climatic conditions, disease resistance, and ability to survive on limited feed resources.

Examples include:

- **Native Black cattle:** low milk yield but high tolerance to heat stress;
- **Southern Anatolian Red cattle:** strong survival capacity under challenging environmental conditions;
- **Hair goats:** exceptional adaptability to hot and arid environments.

Genomic selection can be applied not only to improve productivity but also to preserve adaptive traits in indigenous breeds. According to FAO (2025), the conservation of animal genetic resources, supported by genomic tools, represents a strategic approach in the context of climate change.

In summary, despite Turkey's large livestock population, the sector is characterized by relatively low productivity. The main contributing factors include:

- Limited effectiveness of traditional selection methods,
- Inadequate phenotypic and pedigree recording systems,
- Predominance of small-scale farming systems,
- Limited use of modern biotechnological tools.

Nevertheless, Turkey holds substantial potential for the implementation of genomic selection. Its large livestock population, combined with a gradually strengthening biotechnology infrastructure, provides a solid foundation for significant progress in genomic-based breeding programs.

5. OPPORTUNITIES FOR GENOMIC SELECTION IN TURKEY

5.1. Potential for Genetic Progress

One of the major challenges in both cattle and small ruminant production in Turkey is the slow rate of genetic progress. Selection programs based on traditional breeding methods have achieved limited success, particularly in cattle, due to long generation intervals and low accuracy of breeding value estimation.

Genomic selection offers several key opportunities:

- **Reduction of generation interval:** In dairy cattle, the genetic merit of bulls can be estimated without the need for progeny testing, thereby substantially accelerating the rate of genetic progress.
- **Improvement of low-heritability traits:** Traits such as fertility, resistance to mastitis, and tolerance to heat stress can be selected with higher accuracy using genomic information (Hayes et al., 2009).
- **Simultaneous improvement of multiple traits:** Productivity and adaptive traits can be jointly evaluated within genomic prediction models.
- **Evaluation of local breeds:** Genomic selection enables a clearer assessment of the genetic potential of indigenous breeds that exhibit strong environmental adaptation but relatively low production performance.

Genomic studies conducted in Turkey, particularly on Holstein dairy cattle and Akkaraman sheep, suggest that the rate of genetic progress could be increased by approximately 30–

40% through the implementation of genomic selection (Yılmaz et al., 2021).

5.2. National Databases and Breeding Programs

Several national livestock databases currently in use in Turkey have the potential to serve as a foundation for genomic selection:

- **TURKVET:** A system for animal identification and movement recording;
- **E-Improvement:** A national platform for pedigree and performance recording;
- **Breeding projects:** Regional improvement programs implemented by TİGEM and universities.

These databases facilitate the accumulation of large-scale phenotypic records. With the integration of genotypic data, reference populations suitable for genomic selection could be rapidly established.

Although international data sharing initiatives similar to those in Europe are not yet feasible for Turkey, the creation of an integrated national database represents a realistic and necessary short-term goal. Projects supported by TÜBİTAK and TAGEM have already taken important steps in this direction.

5.3. Role of Research Institutions and Universities

The feasibility and expansion of genomic selection in Turkey largely depend on the infrastructure and project development capacity of universities and research institutions.

• Universities:

Institutions such as Ankara, Selçuk, Ege, Atatürk, and Uludağ universities host molecular genetics laboratories capable of supporting genomic research.

- **Research institutes:**

The Lalahan Livestock Research Institute, Karakoyun Research Station, and the GAP International Agricultural Research and Training Center conduct studies focused on the conservation of genetic resources in indigenous breeds.

- **International collaborations:**

Turkey participates in projects coordinated by FAO and ICAR (International Committee for Animal Recording), particularly in the area of animal genetic resource conservation (Ertuğrul et al., 2010).

The existing infrastructure of these institutions provides a strong starting point for the wider adoption of genomic selection. However, further integration of bioinformatics and artificial intelligence tools into academic research is essential to enhance genetic data processing capacity and predictive accuracy.

Table 6. Comparison of Genomic Selection Implementation in Türkiye and Selected Livestock-Producing Regions

Aspect	Türkiye	European Union (EU)	Australia
Stage of implementation	Early / pilot stage	Fully implemented	Fully implemented
Main livestock species	Cattle (Holstein), limited sheep studies	Dairy cattle, beef cattle, sheep	Sheep, beef cattle
Reference population size	Limited and under development	Large, well-established	Large, breed-specific
Phenotypic recording systems	Incomplete and heterogeneous	Long-term, standardized	Long-term, standardized
Use of genomic breeding values	Mainly research-oriented	Routine use in national breeding programs	Routine use in breeding decisions
Genotyping density	Medium-density SNP arrays	Medium- to high-density SNP arrays	Medium- to high-density SNP arrays
Institutional	Developing (public-	Strong (breeding	Strong (industry-

Aspect	Türkiye	European Union (EU)	Australia
coordination	led initiatives)	organizations, industry-driven)	research partnerships)
Economic impact	Potential, not yet quantified	Proven increase in genetic gain	Proven increase in genetic gain
Major constraints	Cost, data availability, infrastructure	Mainly maintenance costs	Mainly maintenance costs
Future prospects	High, with national strategy	Stable and optimized	Stable and optimized

Table 6; comparison of the current status and implementation level of genomic selection in Türkiye, the European Union, and Australia, based on published literature and official reports (Duchemin et al., 2012; Baloché et al., 2014; Hayes et al., 2009; Aydın et al., 2024; Anonym, 2023).

5.4. Sectoral Needs and Economic Opportunities

The livestock sector in Turkey faces significant challenges, including high feed costs and dependence on imported semen and breeding stock. Genomic selection offers economically viable solutions to these issues:

- **Reduced dependence on imported breeding material:**

National genomic selection programs can improve the quality of domestic breeding stock, thereby decreasing reliance on imports.

- **Increased milk and meat production:**

Even small-scale farms can benefit from genetically improved herds with higher productivity.

- **Reduction of disease-related losses:**

Genetically improved resistance to mastitis, hoof disorders, and parasitic infections can substantially reduce economic losses.

- **Export potential:**

High-quality breeding materials developed through genomic selection could be exported to Middle Eastern and Central Asian countries.

These opportunities demonstrate that genomic selection represents not only a scientific advancement but also a strategic economic tool capable of strengthening the sustainability and competitiveness of livestock production in Turkey.

6. CHALLENGES AND CONSTRAINTS

Although genomic selection has substantial theoretical potential in Turkey, its practical implementation remains limited due to a range of structural, economic, and institutional constraints. These challenges can be broadly categorized into five main groups.

6.1. Economic Constraints

Genomic selection is a cost-intensive process, particularly during the initial implementation phase.

- **Genotyping costs:**

Single nucleotide polymorphism (SNP) arrays and whole-genome sequencing technologies remain relatively expensive in Turkey. The establishment of large reference populations requires the genotyping of thousands of animals, creating a considerable financial burden (Boichard et al., 2012).

- **Small-scale farm structure:**

More than 70% of livestock production in Turkey is carried out by small family farms (TURKSTAT, 2025). These enterprises generally lack the financial capacity to invest in genomic testing.

- **Dependence on imports:**

Genetic materials and bioinformatics software are largely imported. Fluctuations in exchange rates further constrain the affordability and sustainability of genomic technologies.

6.2. Technical Infrastructure Limitations

The success of genomic selection depends on robust technical infrastructure and advanced bioinformatics capacity.

- **Data management:**

Although milk recording systems such as E-Islah and TURKVET are relatively well developed, phenotypic data remain incomplete and inconsistently recorded. While milk yield is regularly monitored in some regions, reproductive performance and health traits are often poorly documented.

- **Laboratory capacity:**

The number of laboratories capable of conducting large-scale genotyping analyses is limited, and most existing facilities primarily focus on research rather than routine breeding applications.

- **Shortage of bioinformatics expertise:**

The analysis of genomic data requires complex statistical models and high-performance computing infrastructure. Turkey currently faces a shortage of specialists in bioinformatics and quantitative genomics (Ertuğrul et al., 2010).

6.3. Institutional and Governance Challenges

Multiple institutions are involved in livestock breeding programs in Turkey; however, coordination among these stakeholders is often insufficient.

- **Unclear allocation of responsibilities:**

The roles of the Ministry of Agriculture and Forestry, breeder associations, universities, and the private sector are not always clearly defined.

- **Lack of a national strategy:**

There is no comprehensive, long-term national roadmap specifically dedicated to genomic selection. Existing breeding initiatives are largely implemented at regional or project-based levels.

- **Data-sharing barriers:**

Data collected by different institutions are often fragmented and not integrated into a centralized national database.

6.4. Farmer Education and Awareness Gaps

The effectiveness of genomic selection is closely linked to active participation by livestock producers. However, awareness of modern breeding technologies remains limited among Turkish farmers.

- **Limited awareness:**

Many producers are unfamiliar with genomic selection and its potential economic benefits.

- **Short-term economic perspective:**

Small family farms tend to prioritize immediate cash flow, often overlooking long-term genetic investment opportunities.

- **Insufficient training programs:**

Training activities organized by agricultural chambers and breeder associations typically focus on nutrition and disease management, with limited emphasis on genetics and genomics.

6.5. Ethical and Biodiversity Concerns

The intensive application of genomic selection may also raise ethical and environmental concerns.

- **Loss of genetic diversity:**

Selection focused exclusively on high-performing animals may accelerate genetic erosion, particularly in indigenous breeds.

- **Reduced environmental adaptation:**

Replacing locally adapted breeds with high-yield but environmentally sensitive genotypes may decrease resilience to climate change (FAO, 2015).

- **Consumer perception:**

In some consumer segments, skepticism toward genomic technologies may negatively affect product acceptance and marketability.

Table 7. Comparison of Traditional BLUP and Genomic GBLUP Methods

Feature	BLUP (Traditional)	GBLUP (Genomic)
Data used	Phenotype + pedigree	Phenotype + SNP genotypes
Age at selection	Late (progeny testing)	Early (calf/lamb stage)
Accuracy in young animals	Low	High
Generation interval	Long	Short
Performance in low-heritability traits	Limited	High

Table 7 presents a comparison of traditional BLUP (Best Linear Unbiased Prediction) and genomic GBLUP (Genomic BLUP) approaches across key characteristics. While BLUP relies on phenotypic records and pedigree information, GBLUP

incorporates genome-wide SNP data into the prediction model. This integration substantially improves the accuracy of breeding value estimation, particularly in young animals. Moreover, GBLUP demonstrates superior performance in low-heritability traits such as fertility and disease resistance. Shortened generation intervals and early selection capability represent major advantages of genomic selection in modern breeding programs (VanRaden, 2008; Goddard, 2012; Meuwissen et al., 2016).

Table 8. Priority Genomic Selection Targets for Livestock Production in Turkey

Species	Breed	Priority traits	Regional suitability
Dairy cattle	Holstein	Milk yield, mastitis resistance, fertility	Marmara, Aegean
Dual-purpose cattle	Simmental	Milk and meat yield, hoof health	Central Anatolia
Beef cattle	Angus (crossbred)	Feed efficiency, carcass quality	Eastern Anatolia
Sheep	Akkaraman	Adaptation, fertility	Central Anatolia
Sheep	İvesi	Milk yield	Southeastern Anatolia
Goat	Hair goat	Heat and drought tolerance	Mediterranean

Table 8 summarizes priority traits targeted for genomic selection in major livestock breeds raised in Turkey, along with their regional suitability. The table reflects Turkey's ecological diversity and emphasizes not only productivity but also environmental adaptation and sustainability. For instance, mastitis resistance and fertility are critical traits for Holstein dairy cattle in intensive production regions such as the Marmara and Aegean regions. In Akkaraman sheep, adaptation and reproductive performance are strategically important for semi-arid conditions in Central Anatolia. This region-specific

approach highlights the potential of genomic selection to support tailored breeding programs across diverse production environments (Ertuğrul et al., 2010; FAO, 2015).

In conclusion, the main barriers to the widespread adoption of genomic selection in Turkey include high genotyping costs, a shortage of bioinformatics expertise, institutional coordination challenges, and low awareness among livestock producers. The dominance of small-scale farming systems further complicates field-level implementation. Addressing these constraints through integrated national strategies will be essential for the successful integration of genomic selection into Turkey's livestock sector.

7. FUTURE PERSPECTIVES AND POLICY RECOMMENDATIONS

The successful implementation of genomic selection in Turkey requires a comprehensive, nationally coordinated strategy. Priority policy areas include the establishment of a centralized genomic database, the development of robust reference populations, the expansion of farmer education and extension programs, and the support of genomic projects aimed at the conservation and sustainable use of indigenous breeds.

In addition, strengthening university–industry partnerships and increasing participation in international consortia will enhance Turkey's capacity in genomic breeding and facilitate knowledge transfer and technological integration (Meuwissen et al., 2016).

8. CONCLUSION

Genomic selection is widely recognized as a transformative approach in animal breeding, extending beyond

traditional methods based on phenotypes and pedigree information by substantially increasing the rate of genetic progress. This approach, which relies on dense genome-wide marker information, improves the accuracy of breeding value estimation—particularly in young animals—and enables selection decisions to be made at an early age. Consequently, the reduction in generation interval leads to increased annual genetic gain, positioning genomic selection as a core component of modern livestock production systems (Meuwissen et al., 2016; Hayes et al., 2023).

The findings and evaluations presented in this book chapter demonstrate that genomic selection is not only effective in high-performing commercial breeds but also serves as a powerful tool for the sustainable improvement of indigenous and locally adapted genetic resources. In countries such as Turkey, characterized by high ecological diversity and rich native breed resources, genomic selection plays a strategic role in balancing productivity gains with environmental adaptation. In particular, the genomic characterization of stress-resilient genotypes—such as Akkaraman sheep and Hair goats—has the potential to mitigate the adverse impacts of climate change on animal production systems (FAO, 2015; Brito et al., 2021).

From the perspective of Turkish livestock production, the benefits of genomic selection extend beyond accelerated genetic improvement in economically important traits such as milk yield, feed efficiency, fertility, and disease resistance. This technology also contributes to the scientific grounding of breeding programs, the development of indigenous breeds without genetic erosion, and the enhancement of international competitiveness. However, realizing this potential is directly dependent on the establishment of strong reference populations, sustainable recording systems, and the adoption of long-term national breeding policies.

Recent integration of genomic selection with artificial intelligence and machine learning–based prediction models signals a paradigm shift in animal breeding. Big data analytics enables the joint evaluation of genetic and environmental variables, allowing more accurate estimation of genotype \times environment interactions. These advances indicate that genomic selection will play a central role not only in genetic improvement but also in the design of climate-resilient and sustainable livestock production systems in the future (Van Eenennaam et al., 2023; Misztal et al., 2020).

In conclusion, genomic selection should be regarded not merely as an option but as an inevitable transformation tool for the Turkish livestock sector. With the adoption of a coordinated national genomic breeding strategy, strengthened collaboration among universities, the private sector, and public institutions, and increased awareness among livestock producers, genomic selection has the potential to deliver long-term and sustainable gains in productivity, resilience, and the conservation of animal genetic resources in Turkey.

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CATTLE BREEDS IN TÜRKİYE IN THE CONTEXT OF CLIMATE CHANGE: GENETIC ADAPTATION AND BREEDING STRATEGIES

Kadir KARAKUŞ¹

1. INTRODUCTION

Climate change poses a significant threat to global livestock production systems through rising temperatures, altered precipitation patterns, and increased frequency of extreme weather events. Cattle production is particularly vulnerable to climate-induced stressors such as heat stress, water scarcity, and feed shortages, which negatively affect animal welfare, productivity, and reproductive performance (IPCC, 2021; Godde et al., 2021).

In this context, developing climate-resilient cattle populations has become a priority for sustainable livestock production. Genetic adaptation strategies, including the conservation of indigenous breeds, controlled crossbreeding, and genomic selection, play a crucial role in mitigating the adverse effects of climate change (FAO, 2018; Hayes et al., 2009).

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2. EFFECTS OF CLIMATE CHANGE ON CATTLE PRODUCTION

2.1. Heat Stress

The thermal comfort zone for cattle generally ranges between 5 and 20 °C. When the temperature–humidity index (THI) exceeds 72, significant reductions in feed intake, milk yield, and reproductive performance are observed (West, 2003). Prolonged exposure to heat stress disrupts endocrine regulation, immune responses, and metabolic balance, leading to substantial economic losses in cattle enterprises (Bernabucci et al., 2010; Collier et al., 2017).

2.2. Drought and Feed Scarcity

Drought reduces pasture productivity and forage crop yields, leading to a negative energy balance in cattle. Breeds with high metabolic demands, such as **Holstein**, are particularly vulnerable to these conditions due to their elevated requirements for energy and nutrients (Godde et al., 2021).

3. INDIGENOUS CATTLE BREEDS IN TÜRKİYE AND THEIR ADAPTIVE CAPACITY

3.1. Adaptation Strategies

Various strategies have been developed to enhance the adaptation of cattle breeds in Türkiye to climate change. These strategies include the following:

- **Conservation and Improvement of Indigenous Breeds:**

Indigenous cattle breeds are generally more resilient to climate change; therefore, the conservation and genetic improvement of these breeds are of great importance. Preserving the genetic diversity of indigenous breeds enables the

development of animals capable of adapting to future climatic conditions and contributes to long-term sustainability in cattle production systems (Ertuğrul et al., 2010; FAO, 2018).

- **Environmental Management:**

Environmental management strategies such as increasing shaded areas in cattle housing, improving ventilation, ensuring the efficient use of water resources, and installing cooling systems have been reported to significantly reduce heat stress and improve animal welfare and productivity in cattle production systems (Mader et al., 2006; West, 2003).

- **Nutritional Strategies:**

Drought and the reduction of feed resources caused by climate change necessitate the reassessment of cattle feeding strategies. The utilization of locally available feed resources and the preference for high-nutritional-value feeds have been shown to be effective in meeting the nutritional requirements of cattle and maintaining productivity under stress conditions (Renaudeau et al., 2019).

Cattle farming in Türkiye is a sector that is highly vulnerable to the adverse effects of climate change. However, adaptation strategies such as the conservation of indigenous breeds, the development of environmental management practices, and the improvement of nutritional strategies may help mitigate these negative impacts. In the future, breeding cattle breeds capable of adapting to climate change and supporting research in this field will be of great importance (Godde et al., 2021).

3.1.1. Breeding Programs in Indigenous Cattle Breeds

Indigenous cattle breeds in Türkiye have adapted to the climatic conditions of their regions over many years through natural selection. However, due to ongoing climate change,

various breeding programs are currently being conducted to further enhance the resilience and adaptive capacity of these breeds.

Methods Used in Breeding Programs

Both traditional and modern methods are employed in cattle breeding programs in Türkiye. These methods include:

- **Genetic Selection:**

Selection and breeding of individuals that exhibit higher resistance to climate-related stress factors, including heat stress, feed scarcity, and water limitation.

- **Crossbreeding:**

Crossing indigenous breeds with exotic breeds to obtain animals that combine enhanced environmental adaptability with improved productivity.

- **Genomic Selection:**

Identification of genetically superior individuals using modern biotechnological approaches based on dense SNP marker information and genomic estimated breeding values (GEBVs) (Meuwissen et al., 2001; Hayes et al., 2009).

- **Embryo Transfer:**

Rapid multiplication of genetically superior individuals to accelerate genetic improvement while maintaining adaptive traits.

Breeding Programs in the Boz Breed: The Boz breed is an indigenous cattle breed raised mainly in Central Anatolia and Eastern Anatolia. This breed is well known for its resistance to drought and cold climatic conditions. Breeding programs conducted on the Boz breed focus on increasing productivity while maintaining resistance to climate change. In this context,

genetic selection methods are widely used to identify and breed individuals with superior adaptive performance (Ertuğrul et al., 2010).

Breeding Programs in the Native Black Breed: The Native Black breed is primarily raised in the Black Sea region and has adapted to humid climatic conditions. Breeding programs for this breed mainly focus on increasing resistance to heat stress, improving disease resistance, and maintaining robustness under variable environmental conditions (Ertuğrul et al., 2010).

Native Black × Simmental Crossbreed: Crossbreeding programs combining the metabolic robustness and feed-efficiency traits of the Native Black breed with the superior meat productivity of the Simmental breed have been reported to result in animals that perform well under challenging climatic and management conditions (Rauw et al., 1998; Nardone et al., 2010).

Breeding Programs in Eastern Anatolian Red and Southern Anatolian Red Breeds: Eastern Anatolian Red and Southern Anatolian Red cattle are indigenous breeds adapted to hot and arid climatic conditions. Breeding programs for these breeds primarily focus on increasing water-use efficiency, enhancing heat tolerance, and improving resistance to environmental stressors (Hansen et al., 2020; FAO, 2018).

Eastern Anatolian Red × Jersey Crossbreed: Eastern Anatolian Red cattle exhibit genetic adaptations to hot and arid environments. Variants of the **AQP1 (Aquaporin 1)** gene contribute to improved water-use efficiency and dehydration tolerance, while **TLR4 (Toll-like receptor 4)** gene variants play an important role in strengthening immune responses under heat stress conditions (Hansen et al., 2020; Collier et al., 2017).

Southern Anatolian Red Breed: The Southern Anatolian Red is an indigenous cattle breed raised in the Mediterranean and Southeastern Anatolia regions. This breed is highly resistant to high temperatures and prolonged drought conditions. Genetic studies have identified adaptive variations related to energy metabolism and thermal tolerance, particularly involving **LEP (leptin)** gene polymorphisms, which support survival and productivity under hot environments (Sejian et al., 2015; Ertuğrul et al., 2010).

Boz × Holstein Crossbreed: Crossbreeding programs combining the adaptive traits of the Boz breed with the high milk yield potential of the Holstein breed aim to produce animals capable of efficiently utilizing energy reserves during drought periods and under thermal stress (Bernabucci et al., 2010; Nardone et al., 2010).

Indigenous cattle breeds in Türkiye have been shaped by long-term natural selection pressures and possess significant adaptive traits that confer resilience against environmental stress factors.

Table 1. Climate Adaptation Characteristics of Indigenous Cattle Breeds in Türkiye

Breed	Adaptive Trait	Dominant Environmental Factor
Native Black	Low metabolic rate	Cold-humid climate
Boz Breed	Tolerance to water and feed scarcity	Arid-semi-arid climate
Eastern Anatolian Red	Resistance to cold and drought	High altitude
Southern Anatolian Red	Heat tolerance	Hot-arid climate

Source: (FAO, 2018; Ertuğrul et al., 2010; Anonymous, 2023; TÜBİTAK, 2023).

4. GENETIC ADAPTATION MECHANISMS

4.1. Heat Shock Proteins (HSPs)

Heat shock proteins, particularly **HSP70** and **HSP90**, play a critical role in protecting cells against thermal stress by preventing protein denaturation, facilitating proper protein folding, and maintaining cellular homeostasis. Increased expression of these proteins has been consistently observed in cattle exposed to heat stress conditions. Indigenous and tropically adapted cattle breeds exhibit higher basal and inducible expression levels of HSP genes, which contributes significantly to their enhanced tolerance to elevated ambient temperatures and prolonged heat exposure (Sejian et al., 2015; Bernabucci et al., 2010).

HSP-mediated cellular protection is considered one of the most important molecular mechanisms underlying thermal tolerance in cattle, particularly under climate change scenarios characterized by frequent heat waves and increased temperature variability.

4.2. Genes Regulating Water Balance

Genes involved in water balance regulation play a key role in adaptation to dehydration stress. Among these, the **aquaporin (AQP)** gene family, particularly **AQP1**, is essential for facilitating transmembrane water transport and maintaining osmotic balance at the cellular level. Enhanced expression and functional polymorphisms of AQP1 have been associated with improved water-use efficiency and dehydration tolerance in cattle raised under arid and semi-arid environmental conditions (Collier et al., 2017; Nardone et al., 2010).

Efficient regulation of cellular water balance is a crucial adaptive trait for cattle exposed to drought and limited water

availability, which are expected to intensify under future climate change scenarios.

Table 2. Major Genes Associated with Climate Adaptation in Cattle

Gene	Function	Type of Adaptation
HSP70	Cellular heat tolerance	Temperature
AQP1	Water balance regulation	Dehydration
LEP	Energy metabolism	Starvation
IGF1	Metabolic balance	Feed scarcity

Source: (Sejian et al., 2015; Collier et al., 2017; Bernabucci et al., 2010)

5. EXOTIC BREEDS AND BREEDING STRATEGIES

Cattle Breeds with High Adaptive Capacity to Climate Change

Although indigenous breeds represent the primary genetic resource for climate adaptation, several exotic cattle breeds have also demonstrated notable resilience to environmental stressors.

- **Brahman:** Brahman cattle are highly resistant to hot climates. Their loose and thick skin, well-developed sweat glands, and efficient thermoregulatory mechanisms provide protection against heat stress. In addition, their immune system exhibits enhanced resistance to environmental and pathogenic stressors (Sejian et al., 2018; Hansen, 2004).

- **African Nguni:** Nguni cattle are well adapted to the hot and arid climates of Southern Africa. Their durable skin structure, resistance to parasites, and high reproductive efficiency enable successful adaptation to harsh environmental conditions (Nardone et al., 2010).

- **Zebu (*Bos indicus*):** Zebu cattle are widely raised in hot climates across India, Africa, and Asia. This breed is characterized by high tolerance to elevated temperatures, strong adaptation to water scarcity, and the ability to survive under low nutritional conditions (Hansen, 2004).

- **Hereford:** Hereford cattle exhibit adaptability across a wide range of climatic conditions, from cold to moderately warm environments. Their capacity to tolerate cold stress and variable humidity conditions makes them suitable for diverse production systems (Mader et al., 2006; Hansen, 2004; Sejian et al., 2018).

Although high-yielding exotic breeds such as Holstein and Simmental dominate modern dairy and beef production systems, they are generally more sensitive to heat stress. Therefore, under climate change conditions, the integration of genomic selection and controlled crossbreeding programs has become increasingly important to enhance resilience while maintaining productivity (Hayes et al., 2009).

5.1. Breeding Programs in Exotic Cattle Breeds

Exotic cattle breeds are widely raised in Türkiye due to their high productivity. However, their increased sensitivity to climate change has emphasized the importance of breeding programs aimed at improving environmental resilience through both conventional and genomic approaches.

Heat tolerance and climate resilience in cattle are complex traits regulated by multiple genes involved in thermoregulation, water balance, and endocrine responses. Variants in **ATP1A1**, which encodes the Na⁺/K⁺-ATPase enzyme, have been associated with cellular ion balance and heat stress tolerance in dairy cattle. Similarly, polymorphisms in **NR3C1**, the glucocorticoid receptor gene, influence stress responsiveness and cortisol regulation under thermal stress

conditions. Genes related to water transport and energy metabolism, such as **AQP1** and **LEP**, have also been reported to play key roles in adaptation to hot environments by affecting hydration status, feed intake, and metabolic efficiency. The integration of these functional candidate genes into genomic selection programs enhances the accuracy of breeding values for climate resilience traits (Dikmen et al., 2012; Collier et al., 2017; Hayes et al., 2016; Misztal et al., 2020).

5.1.1. Breeding Programs in Holstein

The Holstein breed is the most widely used dairy cattle breed worldwide due to its superior milk yield. However, Holstein cattle are highly sensitive to hot climatic conditions. Breeding programs conducted in Türkiye and other regions with rising temperatures focus on increasing heat tolerance through genetic selection, genomic selection, and controlled crossbreeding with more resilient indigenous breeds (Bernabucci et al., 2010; Hayes et al., 2009).

Studies have demonstrated that **HSP90** and **HSP70** gene expression plays a protective role against heat stress in Holstein cattle. Selection strategies aimed at enhancing the expression of these stress-related genes, as well as introgression of adaptive alleles through crossbreeding, are increasingly applied to improve thermotolerance (Sejian et al., 2015; Collier et al., 2017).

5.1.2. Breeding Programs in Simmental

The Simmental breed is preferred for both milk and meat production. Breeding programs in this breed focus on improving adaptation to increasing temperatures caused by climate change, while simultaneously enhancing disease resistance and maintaining productivity (Hayes et al., 2022).

Genetic analyses conducted in Simmental cattle have identified several candidate genes associated with thermal tolerance and stress response. Among these, **ATP1A1**, which is involved in cellular ion transport and heat stress response, and **NR3C1**, which regulates glucocorticoid-mediated stress adaptation, have been reported to contribute to improved resilience under thermal stress conditions (Bernabucci et al., 2010; Collier et al., 2017).

5.2. Resilience-Related Genes in Exotic Cattle Breeds

Exotic cattle breeds are generally preferred for their high productivity; however, they are more sensitive to heat stress and water scarcity. Nevertheless, these breeds also possess resilience-related genes that can be enhanced through targeted breeding, crossbreeding, and genomic selection strategies. Identifying and selecting favorable alleles associated with thermoregulation, immune function, and metabolic efficiency will play a critical role in improving the sustainability of exotic cattle production systems under climate change conditions (Hayes et al., 2009; Sejian et al., 2018).

6. CROSSBREEDING AND GENOMIC SELECTION STRATEGIES

The negative effects of climate change on cattle production are too complex to be addressed solely through environmental management practices. Consequently, genetics-based adaptation strategies have become a fundamental component of sustainable production systems in modern livestock farming. In this context, **controlled crossbreeding and genomic selection** have emerged as two of the most effective approaches for developing climate-resilient and economically efficient cattle genotypes (Hayes et al., 2009).

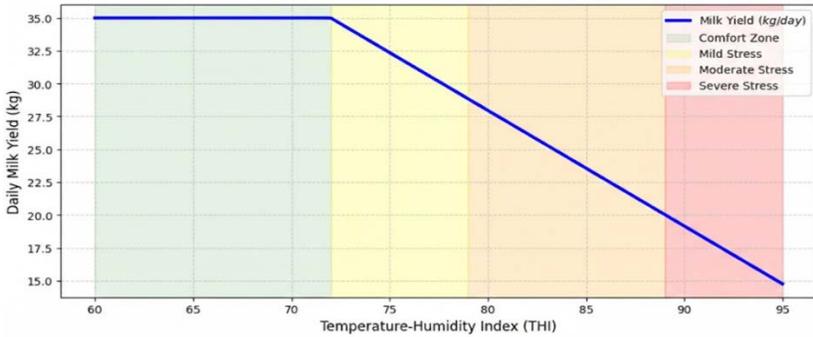
6.1. Crossbreeding Approach

Crossbreeding is a classical yet still highly relevant breeding method that aims to exploit heterosis by mating cattle breeds with different genetic backgrounds. Under the increasing pressures of heat stress, feed scarcity, and water limitation driven by climate change, combining the adaptive capacity of indigenous breeds with the high production potential of exotic breeds offers a strategic and sustainable solution.

Indigenous cattle breeds are generally characterized by low maintenance requirements, enhanced disease resistance, and high tolerance to environmental stressors, whereas exotic breeds are distinguished by their superior milk and meat yields. However, decades of unidirectional selection focused primarily on productivity in exotic breeds have resulted in increased sensitivity to environmental stress, particularly heat stress and nutritional challenges (Godde et al., 2021; Bernabucci et al., 2010).

Within the context of Türkiye, crossbreeding combinations such as Boz Breed \times Holstein, Southern Anatolian Red \times Simmental, **and** Native Black \times Brown Swiss (Montbéliarde) have produced notable results in terms of both adaptive capacity and production performance under local production conditions (Ertuğrul et al., 2010).

Figure 1. Balance Between Productivity and Adaptation Through Crossbreeding (West. 2003; IPCC, 2021).



As illustrated in Figure 1, crossbred genotypes exhibit higher adaptive capacity compared with pure exotic breeds, while simultaneously demonstrating superior production performance relative to pure indigenous breeds. This outcome indicates that both biological and economic sustainability can be achieved concurrently under climate change conditions through well-designed crossbreeding strategies (Hayes et al., 2009; Ertuğrul et al., 2010).

6.2. Performance Effects of Crossbreeding Under Climate Stress

Under heat stress conditions, crossbred cattle have consistently been reported to exhibit:

- lower rectal temperature,
- more stable respiration rates, and
- reduced milk yield losses

when compared with purebred cattle populations (West, 2003; Sejian et al., 2015; Hansen, 2004).

These physiological advantages are primarily attributed to heterosis effects, which enhance immune system efficiency, thermoregulatory capacity, and metabolic flexibility. Crossbred animals are better able to regulate energy balance and experience less pronounced reductions in feed intake under heat stress conditions, thereby maintaining productivity in challenging environments conditions (Sejian et al., 2018; Nardone et al., 2010).

6.3. Fundamental Principles of Genomic Selection

Genomic selection is a modern breeding approach that enables the estimation of an animal's genetic potential at the DNA level, without the need to wait for phenotypic performance records. In this method, genomic estimated breeding values (GEBVs) are calculated using dense panels of single nucleotide polymorphisms (SNPs) distributed across the genome (Meuwissen et al., 2001; Hayes et al., 2009).

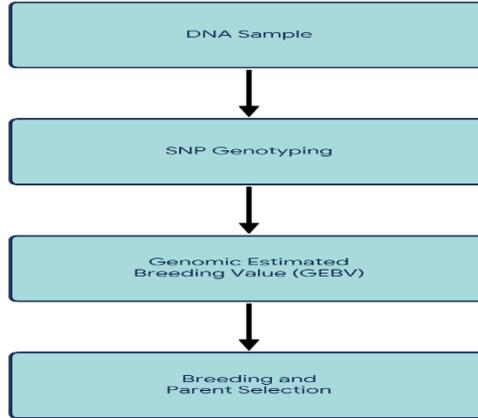
The most significant advantage of genomic selection in the context of climate change is its ability to identify adaptation-related traits at an early age with high accuracy, thereby accelerating genetic progress for resilience-related characteristics.

Schematic Representation of the Genomic Selection Process

The genomic selection process involves the analysis of DNA samples through SNP genotyping, the estimation of GEBVs using reference populations that include both genotypic and phenotypic data, and the implementation of breeding and selection decisions based on these estimates (Meuwissen et al., 2001; Hayes et al., 2009).

Through this approach, not only milk and meat yield traits but also heat tolerance, feed efficiency, immune response,

and water metabolism can be incorporated into selection criteria, thereby improving overall system resilience.



For the effective implementation of genomic selection in Türkiye, the following steps are essential:

1. Establishment of national reference populations,
2. Comprehensive genomic characterization of indigenous cattle breeds,
3. Integration of genomic data into structured crossbreeding programs.

Without these components, selection approaches based solely on phenotypic performance are unlikely to be sufficient under rapidly changing climate conditions.

Crossbreeding and genomic selection represent complementary breeding strategies. While crossbreeding delivers short- to medium-term gains in adaptive capacity, genomic selection enables the long-term development of climate-resilient and high-yielding cattle populations. The future sustainability of the Turkish livestock sector depends on the integrated, data-driven, and well-planned application of these approaches.

Crossbreeding programs aimed at transferring adaptive genes from indigenous breeds to exotic breeds play a critical role in establishing a balance between productivity and resilience, ensuring both biological robustness and economic viability.

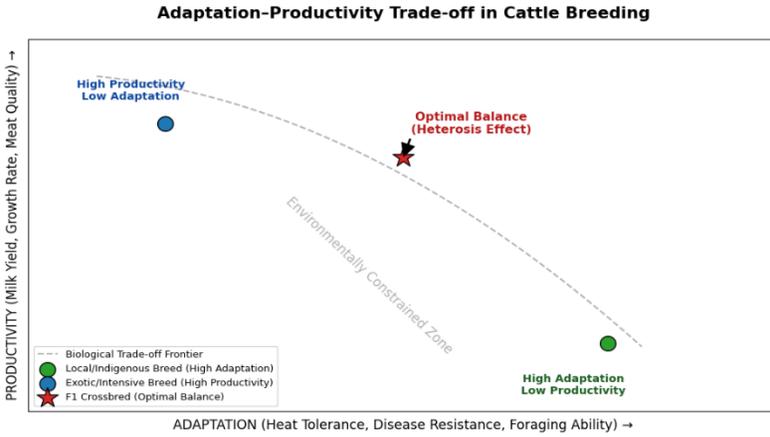


Figure 2. Conceptual Framework: Adaptation-Productivity Trade-off

In animal breeding, the Adaptation-Productivity Trade-off describes the inverse biological relationship between a breed's genetic potential for high production and its ability to withstand environmental stressors. While intensive exotic breeds (*Bos taurus*) offer superior milk yields and growth rates, they often lack sufficient heat tolerance and disease resistance under harsh climatic conditions. In contrast, indigenous breeds (*Bos indicus* and locally adapted *Bos taurus* populations) demonstrate remarkable resilience but lower commercial productivity.

Crossbreeding serves as a strategic intervention to optimize this trade-off by exploiting heterosis, resulting in genotypes that maintain high survival and adaptability while achieving substantial improvements in economic performance. This integrated breeding approach is therefore essential for

ensuring sustainable livestock production in the face of climate change (Hansen, 2004; Godde et al., 2021).

7. CONCLUSIONS AND RECOMMENDATIONS

The sustainability of cattle production in Türkiye is fundamentally dependent on the conservation and effective utilization of genetic resources that exhibit resilience to climate change. The genetic potential embodied within indigenous cattle breeds constitutes a strategic asset of not only national, but also global significance. These breeds represent irreplaceable reservoirs of adaptive traits shaped by long-term natural selection under diverse and often harsh environmental conditions.

Looking ahead, the expansion of breeding programs grounded in genomic selection, alongside the systematic conservation of indigenous cattle breeds within national and international gene banks, should be prioritized as central policy objectives. Such measures are essential for safeguarding genetic diversity while enabling the development of cattle populations capable of sustaining productivity under increasing climatic variability.

Rather than being marginalized or characterized solely by their relatively low production performance, indigenous cattle breeds in Türkiye should be recognized as critical sources of “**resilience genes**” that underpin adaptation to heat stress, drought, nutritional limitations, and disease pressure. These genetic resources provide the biological foundation upon which climate-resilient livestock systems can be built.

Consequently, the livestock production paradigm of the future should move beyond the traditional pursuit of maximum productivity and instead embrace a more balanced framework

centered on optimum productivity combined with maximum resilience. Integrating adaptive capacity into breeding objectives will be essential for ensuring the long-term biological, economic, and environmental sustainability of cattle production systems in the face of ongoing climate change.

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