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From Genes to Barns: Multi-omics in Livestock Production

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Introduction

The integration of omics approaches such as genomics, transcriptomics, proteomics, metabolomics, and epigenomics has numerous applications in livestock production and management. It provides information about the molecular and cellular mechanisms responsible for the key traits of animals, including growth, milk production, heat stress tolerance, disease resistance, feed efficiency, and fertility. Omics tools in veterinary research aid in disease surveillance and diagnosis, comprehend host-pathogen interactions, enhance breeding through genomic selection, uncover adaptive mechanisms and so on. Recently, the veterinary science field has experienced a substantial change due to the emergence and swift progress of omics technologies. These high-throughput, systems-level methods-including genomics, transcriptomics, proteomics, metabolomics, epigenomics, and metagenomics have transformed our capacity to comprehend the biology of animals at a molecular level. Initially developed and extensively utilized in human medicine, omics technologies are increasingly essential in animal health, disease diagnostics, vaccine development, nutrition, breeding, and welfare. The rising need for enhanced animal production, early disease identification, and efficient treatment options in livestock, pets, and wildlife underscores the necessity for deeper understanding of the intricate biological processes that regulate health and disease.

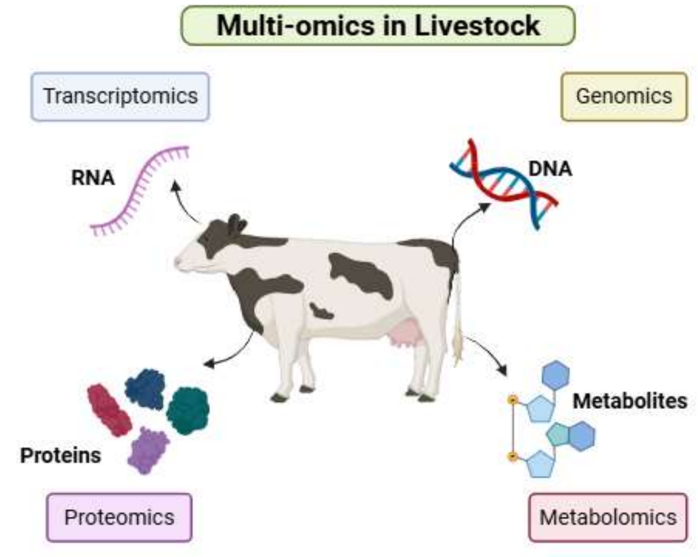

Fig.1: Multi-omics tools applied in Livestock (Created in Biorender)

1. Multi-omics data generation and integration

Multi-omics fata generation, integration and analysis involve the coordinated study o multiple biological data layers-such as genomics, transcriptomics, epigenomics, proteomics, metabolomics and microbiomics to achieve a comprehensive understanding of biological systems. Data generation begins with high-throughput technologies including next-generation sequencing for DNA and RNA, mass spectrometry for proteins and metabolites and array- or sequencing-based platforms for epigenetic and microbial profiling. Each omics layer captures distinct but complementary information, requiring careful experimental design, quality control, normalization and batch-effect correction to ensure data reliability and comparability across platforms.

Integration and analysis of multi-omics data aim to combine these heterogenous datasets to uncover molecular interactions, regulatory mechanisms and system-level phenotypes that cannot be fully explained by a single omics layer. Computational and statistical approaches such as correlation analysis, network-based methods, gene-ontology and pathway-based integration are commonly used to align data across different scales and dimensions. Through integrated analysis, multi-omics studies enable the identification of biomarkers, disease mechanisms and therapeutic target, supporting advances in systems biology, precision medicine and functional genomics.

2. Applications of multi-omics in Livestock sector

At the genomic level, technologies such as genetic mapping, marker-assisted selection (MAS), and genome-wide association studies (GWAS), have a crucial role in identifying and selecting the superior animal/calf with high accuracy at the earlier stage of development called genomic selection. For this, quantitative trait loci (QTL) associated with milk production, fertility, and meat quality in cattle and with egg production, growth rate, and disease resistance in poultry were identified through genetic mapping. By locating these loci, the animal that is having these traits can be selected at earlier stages before the development of its phenotypic characteristics. Apart from genetic mapping, MAS has been used to select trait like milk production, fat and protein content, and somatic cell count in dairy cattle and feed efficiency, marbling, carcass, and myostatin gene in beef cattle. Furthermore, GWAS also identified loci for milk yield, fat composition, fertility, mastitis resistance, feed efficiency, meat quality, wool quality, carcass composition, and gastrointestinal parasite resistance along with the DGAT1 and FTO genes, which are responsible for improved milk fat content and body fat deposition in livestock, respectively (Wadood et al., 2025). By genomic selection the breeding value of an animal can be estimated soon after birth, resulting in improved genetic gain of 60-120% in dairy cattle by reducing the genetic interval by 2 years (Chakraborty et al., 2022).

Omics analysis has also been used to study the factors affecting reproduction in livestock animals. RNA-seq and microbiome analysis showed a significant reduction in sperm viability and a rise in sperm abnormalities in cattle after feeding corn silage (Zhang et al., 2024). In addition to this, proteomics analysis of uterine secretion and follicular fluid of cattle detected proteins important for ovarian functions, fertilization, and development of embryo (Ferrazza et al., 2017). Furthermore, proteomics data of Tibetan pig sperm revealed 8 highly expressed fertility-related proteins (Zhao et al., 2021). Hence, these technologies can be used to identify markers related to fertility in order to improve the reproductive efficiency of animals.

RNA-seq-based transcriptomic studies are also used for the screening of disease-resistant animals. Differential gene expression analysis of purebred and crossbred cattle showed that the majorly affected pathways were related to inflammatory responses and the immune system. Additionally, the sensitivity or resistance to gastrointestinal nematodes depended on the T-cell receptor signaling pathway. Therefore, by applying omics approaches, disease-resistance animals can be selected, which improves the health status of the herd (Gao et al., 2024). Moreover, proteomics and metabolomics can also be used to detect biomarkers related to various infectious diseases in animals, such as mastitis, avian influenza, bovine tuberculosis, and foot-and-mouth disease. Early diagnosis can help in timely treatment and control of disease (Wadood et al., 2025).

Another aspect of livestock farming progress is the quality of meat and milk. The omics approaches are also helpful in assessing the quality of products obtained from animals. Protein profiling of muscle tissue, milk, and mammary glands has provided insights into muscle growth and development, meat quality, milk production and composition, fat synthesis, and egg production in livestock animals, including cattle, pigs, goats, sheep, and poultry. Moreover, proteomic analysis has also identified stress-associated proteins that were upregulated during stress and can be used as stress-resistant biomarkers for the selection of stress-resistant animals, eventually, contributing to the production of high-quality meat and milk (Wadood et al., 2025).

In recent years, research has identified several genes and pathways that play a crucial role in biological functions associated with adaptations to hypoxia. Recent studies indicate that the genes PPARA, EGLN1, and EPAS1 play a vital role in adapting to high altitudes (Haasl and Payseur, 2016; Heinrich et al., 2019). Investigating the molecular mechanisms that facilitate adaptation to hypoxia has consistently attracted interest. Yak (*Bos grunniens*), an indigenous animal of the Qinghai-Tibet Plateau and nearby areas provides meat and various essentials for the Tibetan people. Within mammalian cells, the HIF-α isoforms (HIF-1 α and HIF-2 α) are the most thoroughly researched and understood key players in the cellular adaptation to low oxygen levels. HIF1 α acts as a vital regulator of oxygen homeostasis, orchestrating the detection of oxygen and the cellular responses to hypoxia by managing the expression of numerous genes. Certain genes regulated by HIF1-α are involved in biological pathways related to energy metabolism, angiogenesis, erythropoiesis, iron homeostasis, and apoptosis.

3. Conclusion

Taken together, these findings highlight the application of multi-omics approaches in livestock research providing a powerful framework for understanding the complex biological mechanisms underlying economically important traits such as growth, reproduction, health, disease resistance and product quality. By integrating genomics, transcriptomics, proteomics, metabolomics and other omics technologies enable a system-level view of animal biology. This comprehensive understanding supports more accurate selection strategies, improved breeding programs and the development of precision livestock management practices. Ultimately, multi-omics approaches contribute to enhanced productivity, sustainability and animal welfare while also facilitating the development of resilient breeds adapted to changing environmental and production challenges.

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