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Integrating omics approaches in livestock biotechnology: innovations in production and reproductive efficiency

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Current achievements in omics technologies have modernized livestock biotechnology, offering extraordinary comprehension of animal productivity, health, and reproduction. This extensive study examines the integration and implementation of the omics approaches, genomics, transcriptomics, proteomics, metabolomics, and epigenomics in livestock production systems. We reconnoitered how genomic novelties redesign breeding strategies with marker-assisted selection and CRISPR-based gene editing. Together, transcriptomic analyses indicate key insights into gene expression patterns governing economically essential traits such as muscle growth and milk production. This study also shows the role of proteomics in identifying biomarkers for health surveillance and product quality improvement along with metabolomics, which contributes to understanding feed efficiency and disease resistance. Particular attention is given to epigenomics studies exploring DNA methylation and histone modifications in reproductive efficacy, underlining their importance in fertility and embryonic development. Integrating multi-omics data through systems biology approaches is discussed, demonstrating its perspective in evolving precision livestock production. We also observed how omics technologies improve assisted reproductive technologies (ART) by better understanding of molecular mechanisms underlying fertility and embryo development. While acknowledging the potential of these technologies, we discuss critical challenges, data integration complications, and ethical respect for genetic modification. This review outlines prospect directions and potential novelties in livestock biotechnology, highlighting the crucial role of omics approaches in addressing global food security contests through better livestock productivity and reproductive efficiency. This study suggests that continuous improvement in omics technologies might be the underlying cause of the determination of the future of sustainable livestock production.

KEYWORDS

omics, biotechnology, genomics, reproduction, proteomics

1 Introduction

Livestock production is key to global agriculture, providing significant resources such as meat, milk, wool, and leather (Krostitz, 1993; Rout et al., 2021). Livestock products are projected to increase considerably, prompting the need for more effective and supportable agricultural practices (Röös et al., 2017). Traditional livestock breeding, management, and productivity improvement approaches have relied on phenotypic selection and basic genetic approaches, contributing to substantial achievements over the past few years (van Arendonk, 2011). However, modern biotechnology has reformed this field, offering new ways to enhance livestock productivity, health, and reproductive efficiency (Sharma et al., 2021; Das et al., 2022).

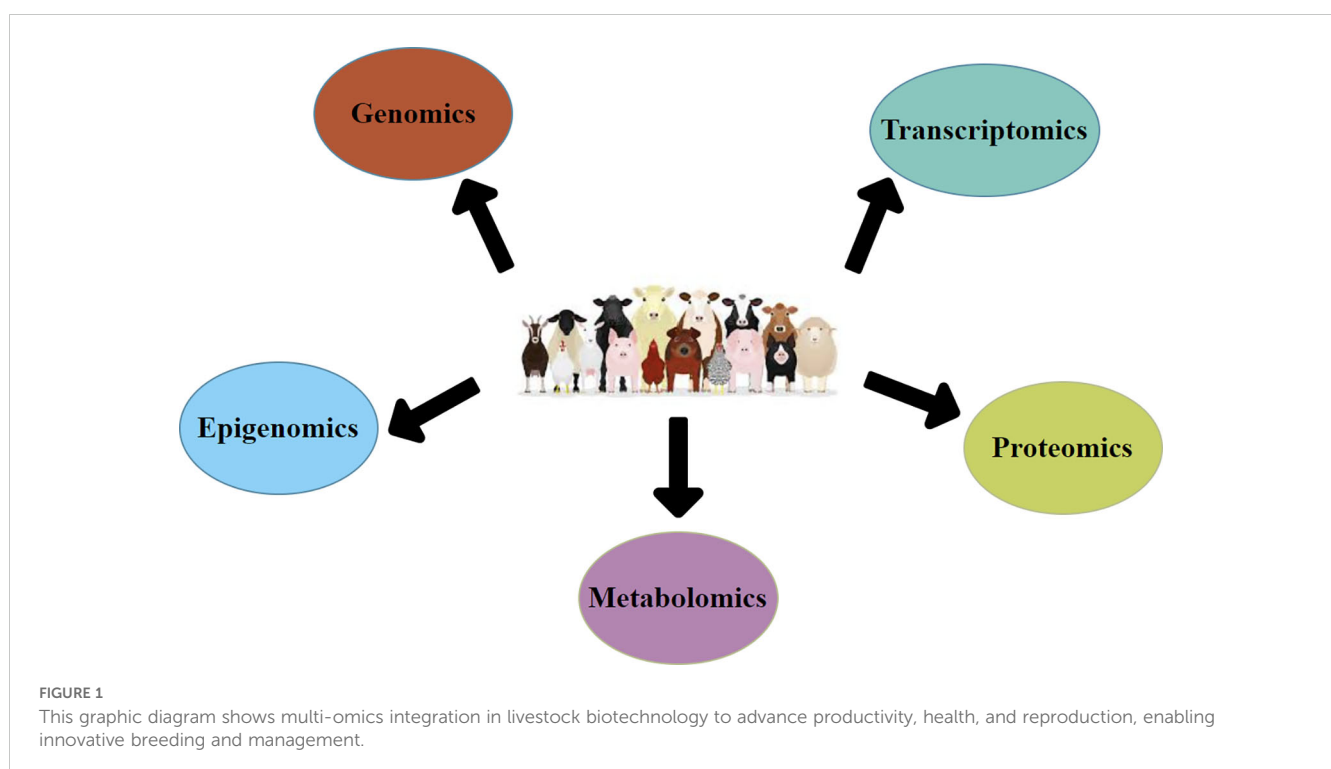
Integrating omics technologies like genomics, transcriptomics, proteomics, metabolomics, and epigenomics into livestock biotechnology signifies a paradigm shift in how we procedure livestock production and reproductive management (Chakraborty et al., 2022). These omics tools assist an inclusive approach to the molecular and cellular mechanisms prevailing key traits such as growth, milk production, feed efficiency, disease resistance, and fertility (Maru and Kumar, 2024). The capability to arrest vast amounts of data at multiple biological levels provides unique insights into the complex collaborations between genes, proteins, and metabolites (McCue and McCoy, 2017). This integrated approach, often called systems biology, can optimize livestock breeding programs, enhance animal welfare, and improve the permanence of livestock farming systems (Brito et al., 2020).

Genomics has contributed to advancing livestock biotechnology (ASLAM et al., 2024). Sequencing livestock genomics has opened up new provisions for understanding the genetic basis of

economically key traits. Genomic selection, a method that influences dense marker information across the genome, permits the prediction of the genome perspective of animals with better precision (Eggen, 2012; Chakraborty et al., 2022). This has contributed to further rapid genetic improvement, particularly in traits that are difficult to measure directly, such as disease resistance and reproductive productivity (Xu et al., 2017). Genomics is also instrumental in isolating genes and regulatory regions related to desirable traits, which can be directed for precision breeding through innovative gene-editing technologies such as CRISPR-Cas9 (Bohra et al., 2020).

Transcriptomics, which comprises the study of RNA transcripts, is another layer of complexity to knowing livestock biology (Lowe et al., 2017). By studying gene expression patterns in several tissues and growing stages, transcriptomics describes insights into how genes are synchronized in response to environmental, nutritional, and physiological changes (Chandhini and Rejish Kumar, 2019). This information is valuable for improving traits associated with growth, lactation, and reproductive enactment (Long, 2020). Identifying differentially expressed genes and non-coding RNAs offers new goals for genetic and nutritional involvements that can improve animal productivity and health (Jilo et al., 2024).

Proteomics is a comprehensive study of proteins and their functions, and associated genomics and transcriptomics provide information about biological effectors in cells and tissues (Satrio et al., 2024). Meanwhile, proteins are the primary molecules responsible for cellular functions. Understanding its abundance, modifications, and interactions is crucial for revealing the mechanisms underlying key traits in livestock (Wang and Ibeagha-Awemu, 2021). Proteomics has been applicable to



identify biomarkers for disease resistance, meat and milk quality, and reproductive traits (Ribeiro et al., 2020). Post-translational modifications, like phosphorylation, acetylation, and glycosylation, have revealed key regulatory pathways influencing cellular processes such as muscle growth, immune response, and reproductive efficiency (Nissa et al., 2021).

Metabolomics studies identify small molecules or metabolites in biological processes, offering an exclusive approach to the metabolic processes associated with livestock growth and reproduction (Goldansaz et al., 2017). Profiling the metabolome can increase insights into animals' nutritional and physiological status and identify biomarkers allied to feed efficiency, energy metabolism, and health (Marina et al., 2024). Metabolomics can improve livestock production by optimizing diets, finding metabolic bottlenecks, and selecting more efficient animals to convert feed into valuable products (Sun et al., 2019). Metabolomics studies can develop our understanding of metabolic adjustments during pregnancy, lactation, and growth, leading to targeted involvements that improve animal reproduction (Choudhary et al., 2024).

Epigenomics, exploring the heritable changes in gene expression that do not involve modifications in the DNA sequence, signifies an emerging frontline in livestock biotechnology (Ibeagha-Awemu and Zhao, 2015). Epigenetic modifications, such as DNA methylation and histone modifications, are key in regulating gene expression during growth and responding to environmental dynamics such as nutrition, stress, and disease (Kumar et al., 2020). Livestock epigenomics will likely improve reproductive efficiency, as epigenetic mechanisms impact fertility and embryonic development (Wang and Ibeagha-Awemu, 2021). Understanding the epigenetic role of livestock species may lead to new approaches

for managing reproductive tasks, such as embryonic loss, low fertility rates, and early embryonic death (Zhu et al., 2021) (Figure 1).

Integrating these omics methodologies into livestock biotechnology presents significant challenges. A key issue is the enormous amount of data produced by omics technologies, which requires advanced bioinformatics tools for practical analysis, interpretation, and integration (Fillinger et al., 2019). Integrating data from various omics tools, including genomics, transcriptomics, proteomics, metabolomics, and epigenomics, can reveal complex regulatory networks and molecular pathways underlying key traits. However, this process demands careful consideration of data compatibility and robust statistical analysis (Canzler et al., 2020; Graw et al., 2021). Developing computational models and machine learning algorithms is key for harnessing the full potential of omics technologies in livestock biotechnology (Koltes et al., 2019; Chakraborty et al., 2022). These models must consider the dynamic interactions between genes, proteins, and metabolites across different tissues, developmental stages, and environmental stresses.

Even though integrating omics into cattle biotechnology has several advantages, many studies have not fully examined the variety of uses across various species. Other significant livestock, like sheep, goats, poultry, and even aquaculture species, have the potential to advance livestock biotechnology in addition to more conventional species like cattle and pigs (Prasad et al., 2023). Because of these differences in species-specific biological systems, customized strategies that consider each species' distinct genetic composition and physiological traits are required (Council et al., 2002). In this regard, one example of the technological developments in the field is the function of non-coding RNAs (ncRNAs), a crucial area of genomics

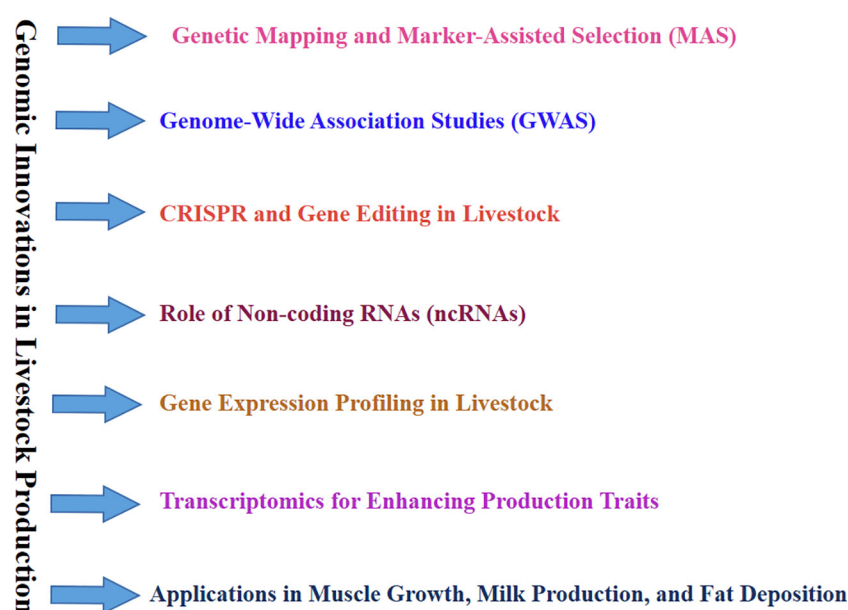


FIGURE 2

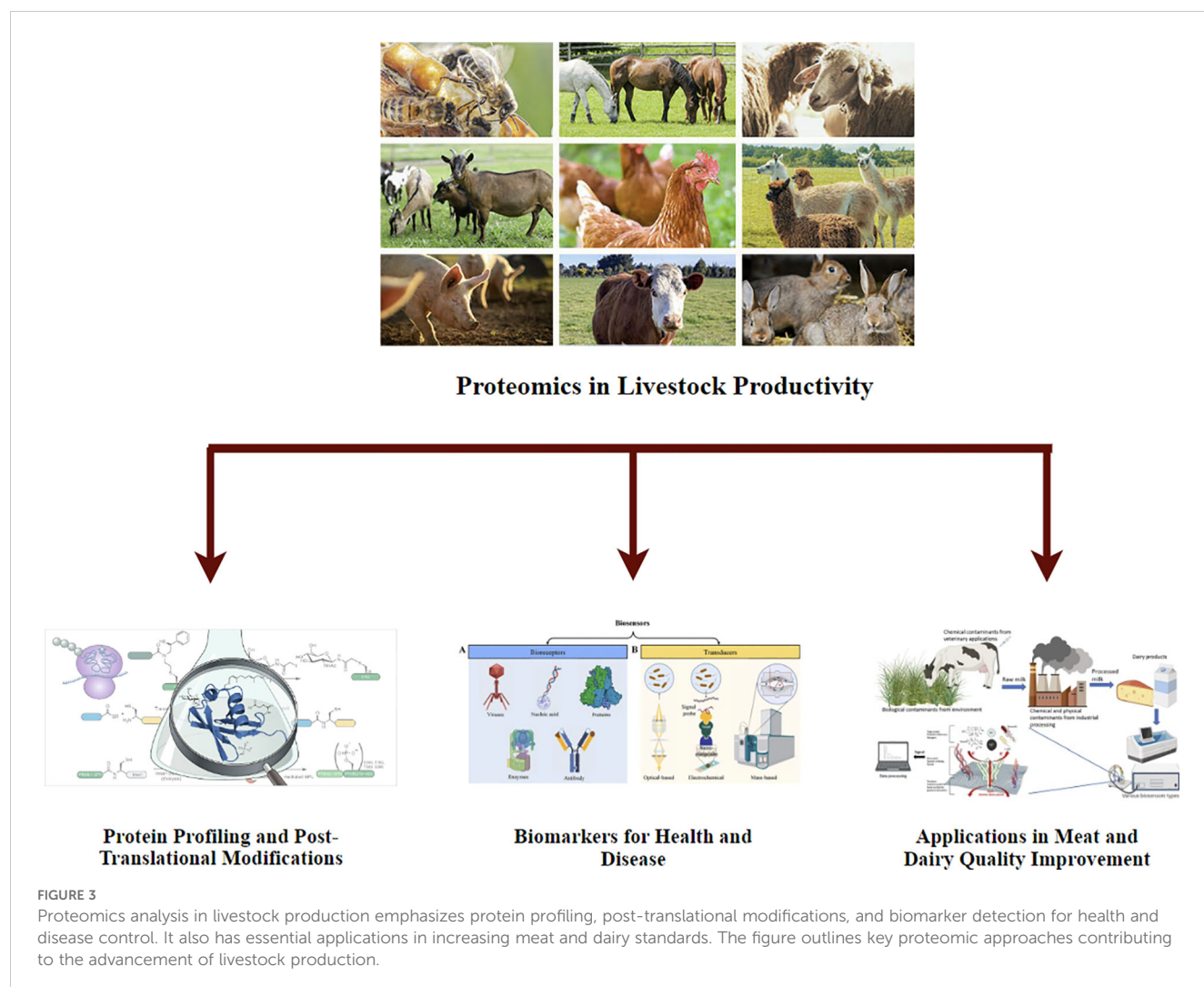
Overview of Genomic Innovations in Livestock Biotechnology. The flow diagram outlines key genomic approaches, including genetic mapping, marker-assisted selection (MAS), genome-wide association studies (GWAS), CRISPR and gene editing, and transcriptomics. These approaches are pivotal in improving production traits and exploring gene expression, aiming at muscle growth, milk production, and fat deposition. Integrating these technologies depicts advancements in livestock breeding, productivity, and reproductive proficiency.

study. Although most ncRNA research has been on cattle, studies on the functional roles of ncRNAs in other species, such as pigs, sheep, and poultry, are gaining popularity (Gong et al., 2023). ncRNAs that regulate gene expression during essential physiological processes like immunological responses, growth, and reproduction include long non-coding RNAs, circular RNAs, and microRNAs (Yadav et al., 2024). It has been discovered that several miRNAs influence sheep follicular development, providing insight into how to improve reproductive success (Yang et al., 2019). Additionally, miRNAs have been shown to modify poultry's immune responses, which could be utilized to enhance disease resistance and vaccine efficacy (Do et al., 2021).

Reproductive management and animal breeding are changing due to omics technologies other than ncRNAs. Cattle and pig breeding operations now rely heavily on genomic selection, which uses genomic data to forecast an animal's genetic potential (Misztal et al., 2020). However, genomic selection also spreads to other species, such as poultry, where genomics increases meat yield and egg production, and goats, where genome-wide association studies (GWAS) are used to find loci linked to disease resistance features

(Ren et al., 2024). Furthermore, proteomics and metabolomics provide fresh perspectives on the metabolic processes that control development and fertility in different species (Panner Selvam et al., 2021). Researchers are finding biomarkers that predict fertility and feed efficiency by examining the proteome profiles of dairy cows and pigs (Aranciaga et al., 2020; Mills, 2021). This could lessen the environmental effect of livestock farming (Figure 2).

The potential assistance of integrating omics approaches in livestock biotechnology is enormous. Understanding the molecular mechanisms, growth, reproduction, and health, we can develop more accurate and targeted strategies for improving livestock production (Singh et al., 2014). For instance, genomic selection with transcriptomic and proteomic data can improve the accuracy of breeding programs, leading to more practical selection for traits such as feed efficiency, disease resistance, and reproductive performance (Gutierrez-Reinoso et al., 2021). Additionally, metabolomics and epigenomics insights can apprise nutritional interventions that enhance animal growth and fertility while reducing the environmental stress of livestock farming (Loor, 2022) (Figure 3).



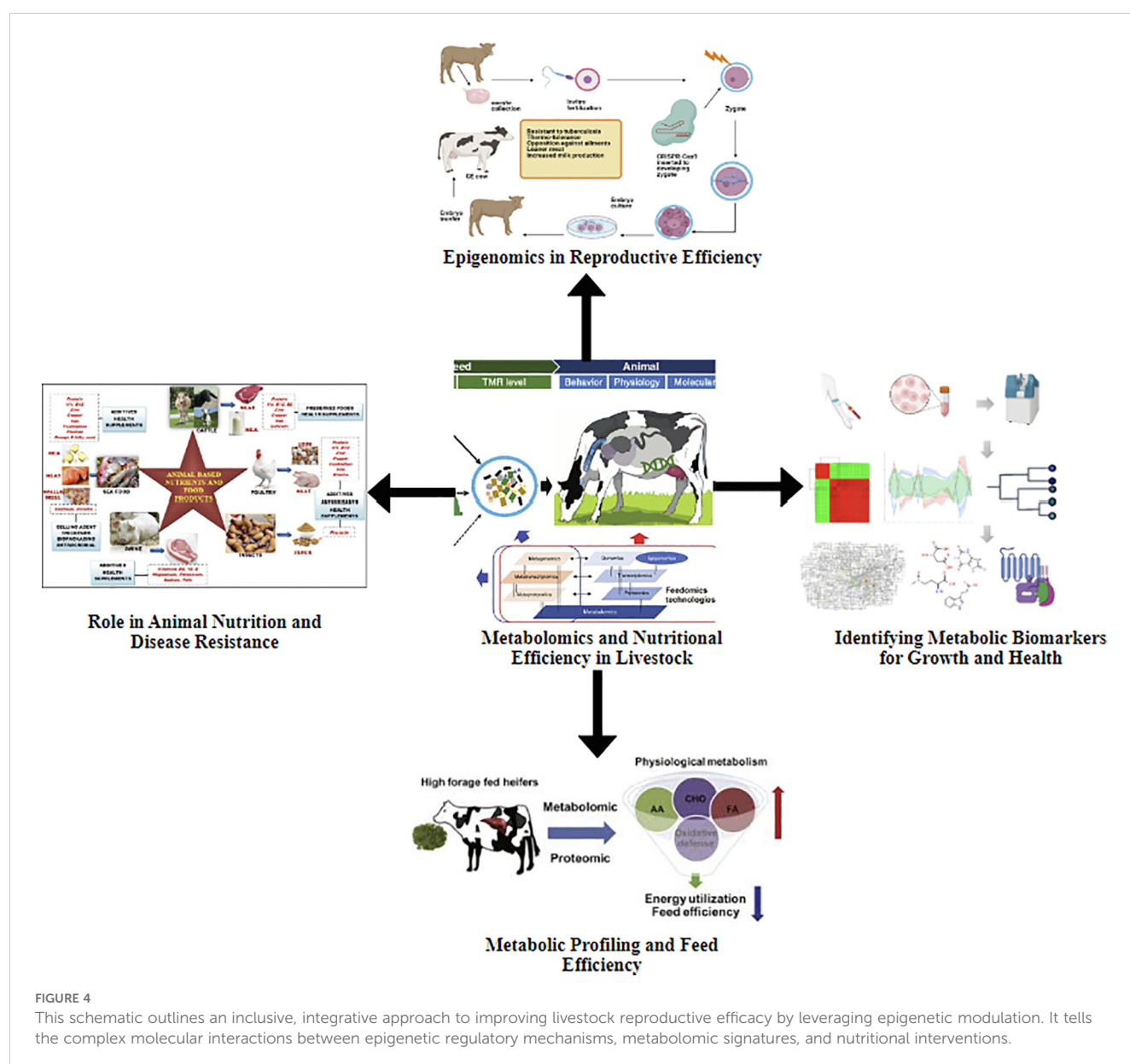
2 Genomic innovations in livestock production

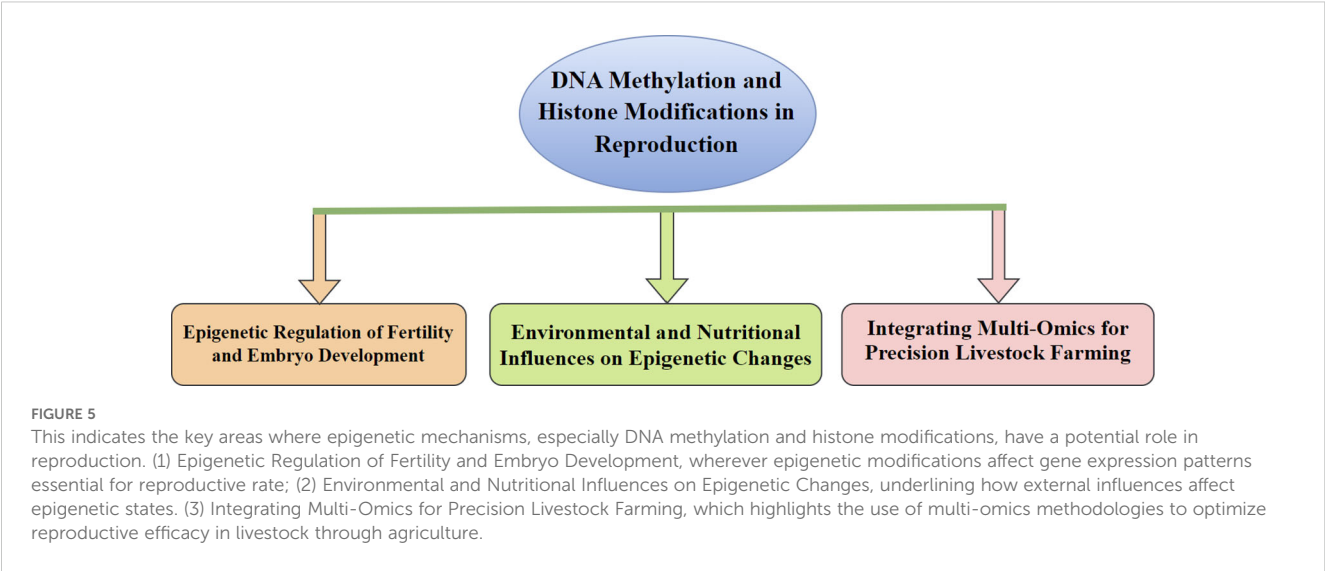
Genomic innovations have transformed livestock breeding and management, offering previously absent genetic improvement (Perisse et al., 2021). The integration of genomic technologies like genetic mapping, marker-assisted selection (MAS) (Boopathi, 2013), genome-wide association studies (GWAS) (Uffelmann et al., 2021), and CRISPR-Cas9 gene editing (Singh et al., 2017), with transcriptomics and gene expression profiling (Kumar et al., 2016) has enabled a more detailed understanding of the genetic basis of complex traits (Ribeiro et al., 2020)s. This has significantly improved growth, reproductive performance, disease resistance, and production traits such as muscle development and milk yield (Islam et al., 2020). Furthermore, the expanding repertoire of non-coding RNAs (ncRNAs) has revealed

regulatory mechanisms that govern gene expression, providing deeper insights into the molecular networks that shape livestock phenotypes (Velez, 2023; Jilo et al., 2024) (Figure 4).

2.1 Genetic mapping and marker-assisted selection

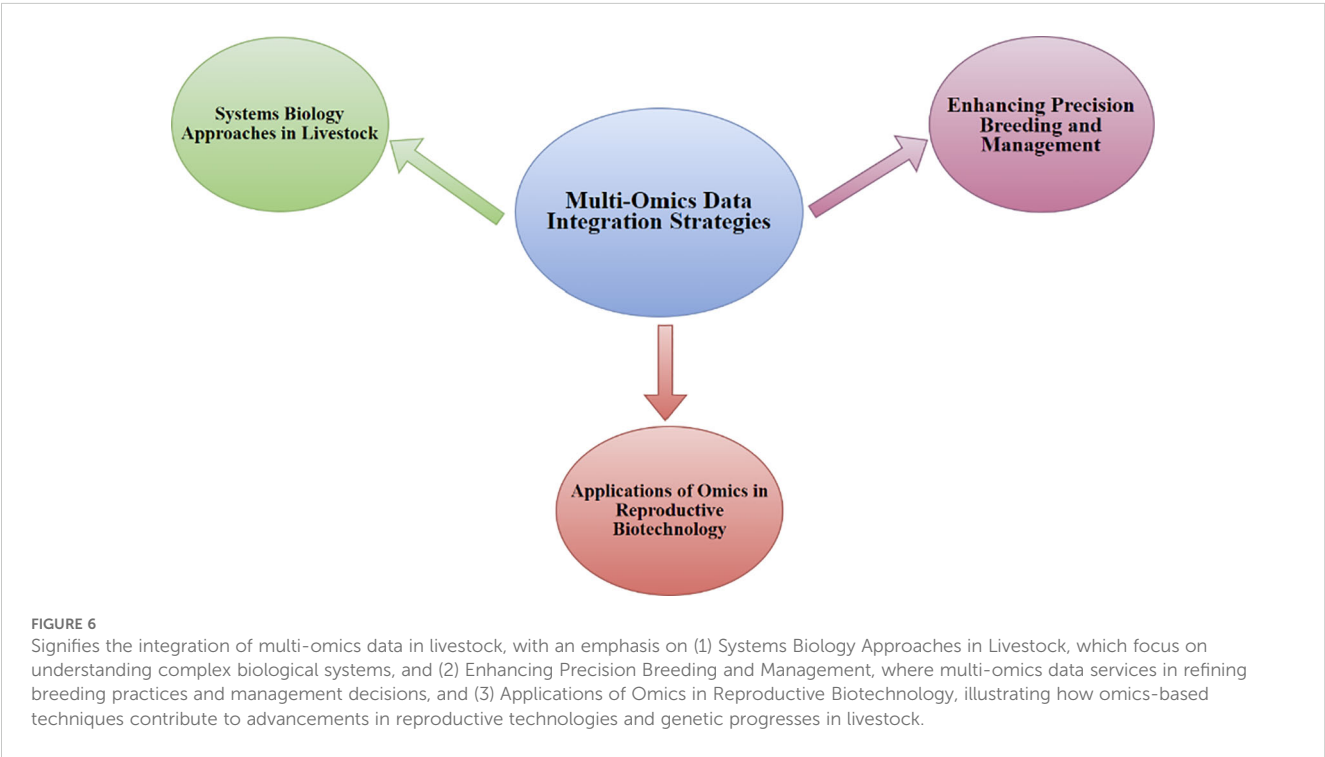
Genetic mapping discusses identifying the relative positions of genes and other genetic components within a genome (Council et al., 1988; Boopathi, 2013). High-resolution genetic maps have been recognized for livestock species, including cattle, pigs, sheep, and chickens, consenting to their recognition of quantitative trait loci (QTLs) with economically essential traits (Cockett and Kole, 2008; Stinckens et al., 2010; Hu et al., 2020). These findings of QTLs are vital for finding molecular markers for breeding, such as growth





rate, milk yield, disease resistance, and reproductive productivity (Khalil, 2020). Advances in next-generation sequencing (NGS) tools have improved the accuracy of genetic maps, providing more profound attention to the genetic architecture of livestock traits (Ghosh et al., 2018). In cattle, high-density single nucleotide polymorphism (SNP) arrays have been used to identify QTLs with milk production, fertility, and meat quality (Ibeagha-Awemu et al., 2016). Genetic mapping in poultry indicates loci associated with growth rate, egg production, and resistance to infectious diseases like Marek’s disease and avian influenza (Churchil, 2023) (Figure 5).

MAS leverages the association between molecular markers and desirable traits to accelerate breeding (Cobb et al., 2019). By selecting animals based on their genetic profiles rather than solely on phenotypic performance, MAS improves the accuracy and efficiency of breeding programs (Beuzen et al., 2000; Brito et al., 2020). MAS has been widely adopted in dairy cattle to enhance milk yield, fat and protein content, and somatic cell count (a measure of mastitis resistance) (Alhussien and Dang, 2018). MAS has been used in beef cattle to select traits like feed efficiency, marbling, and carcass weight (Hozáková et al., 2020). Identifying markers linked to the myostatin gene (MSTN), which regulates muscle development, has



enabled the selection of animals with increased muscle mass and reduced fat deposition (Ayuti et al., 2024). Despite its success, MAS effectiveness depends on the strength of the linkage between the marker and the target trait, which can vary between populations and environments (Podlich et al., 2004). Additionally, MAS is more effective for traits controlled by a few significant genes (oligogenic traits) than polygenic traits influenced by multiple genes (Singh et al., 2015; Boopathi and Boopathi, 2020). As a result, MAS with genomic selection and GWAS capture a broader spectrum of genetic variation to develop complex traits (Tam et al., 2019) (Figure 6).

2.2 Genome-wide association studies

GWAS is an effective tool for identifying the genetic variants for complex traits by scanning the entire genome for connotations (Xiao et al., 2022). Unlike MAS, which has pre-identified markers, GWAS permits the discovery of novel loci related to traits of interest (Korte and Farlow, 2013). This method has been instrumental in uncovering the genetic basis of complex traits in livestock, with growth, reproduction, disease resistance, and product quality (Te Pas et al., 2017). In cattle, GWAS has identified genetic variants with milk yield, fat composition, fertility, and resistance to mastitis (Devani et al., 2020). In pigs, GWAS has revealed loci related to feed efficiency, meat quality, and susceptibility to diseases such as porcine reproductive and respiratory syndrome (PRRS) (Lunney

and Chen, 2010). In sheep and goats, GWAS has been identified in study traits like wool quality, carcass composition, and resistance to gastrointestinal parasites (Arzik et al., 2022; Carracelas et al., 2022). A critical success of GWAS in livestock is the discovery of the DGAT1 gene in dairy cattle, which shows a key role in milk fat synthesis (Khan et al., 2021). Identifying this gene has enabled the selection of animals with improved milk fat content, significantly enhancing dairy production (Barillet, 2007). Another example is identifying the FTO gene associated with fat deposition in cattle and pigs, providing opportunities to manipulate body composition for improved meat quality (Óvilo et al., 2022).

While GWAS has important innovations in livestock genetics, it also has challenges. The genetic architecture of complex traits mainly includes small effect sizes, making it challenging to identify all the contributing loci (McCarthy et al., 2008; Korte and Farlow, 2013; Tam et al., 2019). The accuracy of GWAS relies on the quality and size of the datasets in some livestock species (Zhang et al., 2014). Another task is population stratification, where genetic differences between subpopulations can confuse the results (Marigorta et al., 2018). To address these tasks, scientists use multi-omics approaches integrating genomic, transcriptomic, and epigenomics data to gain an extensive understanding of trait variation (Akiyama, 2021). Advances in computational techniques and machine learning also educate the power and accuracy of GWAS, permitting the identification of subtler genetic effects (Okser et al., 2014; Prabhod, 2022). As sequencing costs continue

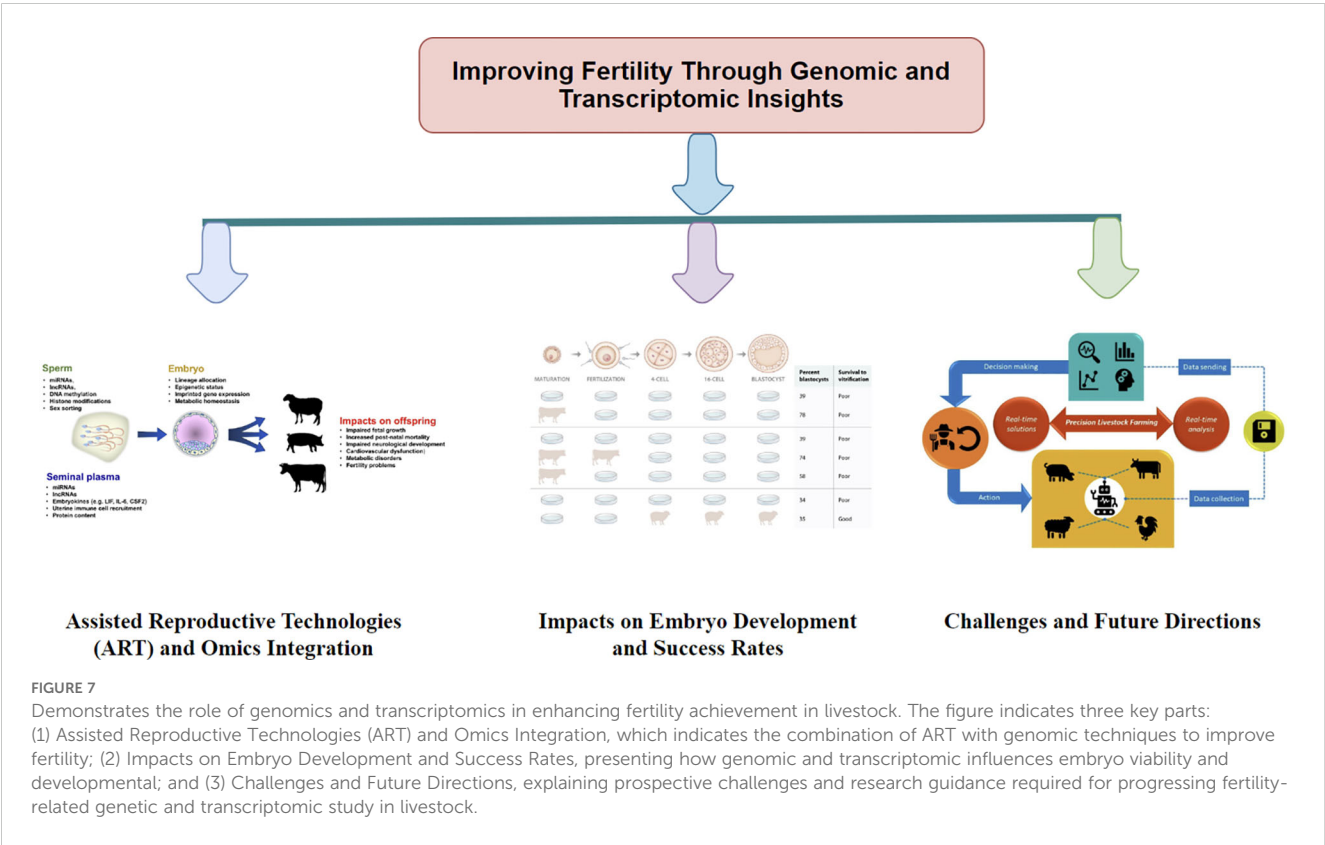


FIGURE 7 Demonstrates the role of genomics and transcriptomics in enhancing fertility achievement in livestock. The figure indicates three key parts: (1) Assisted Reproductive Technologies (ART) and Omics Integration, which indicates the combination of ART with genomic techniques to improve fertility; (2) Impacts on Embryo Development and Success Rates, presenting how genomic and transcriptomic influences embryo viability and developmental; and (3) Challenges and Future Directions, explaining prospective challenges and research guidance required for progressing fertility-related genetic and transcriptomic study in livestock.

to decrease, the whole-genome sequence data in GWAS is becoming more feasible for enhancing genetic mapping resolution (Fuentes-Pardo and Ruzzante, 2017) (Figure 7).

2.3 CRISPR and gene editing in livestock

CRISPR-Cas9 is an innovative genome editing technique that allows precise modifications to the DNA sequence at specific loci (Gupta et al., 2019). This can potentially revolutionize livestock productivity by enabling the introduction, deletion, or alteration of genes linked with desirable traits (Quétier, 2016). Unlike traditional breeding methods, which depend on natural variation, CRISPR enables targeted genome manipulation, introducing beneficial alleles that may be rare or absent in the population (Scheben et al., 2017).

One of the most prospective implementations of CRISPR in livestock is the development of disease-resistant animals (Lamas-Toranzo et al., 2018). Scientists used CRISPR to produce pigs resistant to PRRS by editing the gene encoding the CD163 receptor, which the virus uses in the host cells (Burkard et al., 2017) and exhibits resistance to PRRS. CRISPR has improved chickens' resistance to avian influenza and cattle's resistance to bovine tuberculosis, providing new avenues for strengthening animals (Pal and Chakravarty, 2019; Gao et al., 2023). CRISPR has also been used to improve production in cattle by editing the myostatin gene (MSTN) to make animals with better muscle mass, resulting in higher meat yield (Kalds et al., 2023). In pigs, CRISPR has been used to modify genes linked with growth performance and feed efficiency, leading to animals that are highly productive and environmentally sustaining (Wu and Bazer, 2019). CRISPR has been used in dairy cattle to present enhanced milk production and composition alleles, offering new opportunities to strengthen dairy production (Yang, 2024).

The role of gene-edited animals in the food supply focused on strict regulatory consent and people's perception of genetically modified organisms (GMOs) may upset the acceptance of this technology (Brookes and Smyth, 2024). We must also address ethical apprehensions regarding animal welfare, biodiversity, and food safety. Moreover, the potential for unplanned off-target effects, where CRISPR introduces changes in unintentional genome regions, requires careful checking to ensure the safety and efficacy of gene-edited animals (Cook et al., 2017; Wienert and Cromer, 2022).

2.4 Transcriptomics for enhancing production traits

Transcriptomics is a tool for understanding the gene expression patterns related to production traits in livestock (Salleh et al., 2017). In dairy cattle, transcriptomic analyses have recognized key genes involved in milk production associated with milk-protein synthesis, fat metabolism, and immune response (Zhou et al., 2019). These results have delivered valuable information for improving milk quality and productivity through selective breeding (Wang et al., 2018). In beef cattle, transcriptomics has been used to identify

muscle development and meat quality. By analyzing gene expression in muscle tissues, we recognized genes linked with muscle growth, fat deposition, and meat tenderness (Wang et al., 2009). These understandings have knowledgeable breeding strategies to increase carcass quality and meat yield (Guo and Dalrymple, 2022).

2.5 Gene expression profiling in livestock

Gene expression describes accompaniments transcriptomics to allow a more focused examination of gene activity under different biological circumstances (Wolf, 2013; Kumar et al., 2016). Through techniques like RNA sequencing (RNA-Seq) and microarrays, the expression levels of thousands of genes advance a deeper understanding of the molecular networks for phenotypic traits (Singh and Singh, 2024). In livestock production, gene expression profiling has helped identify regulatory pathways for essential traits like growth, reproduction, and immune function (Loor et al., 2005). For example, gene expression profiling has elucidated key genes intricate in skeletal muscle development in cattle and pigs, enhancing meat quality and yield through targeted breeding (Karisa, 2013; Zeng and Du, 2023). The dynamic nature of the transcriptome challenges livestock production, as gene expression patterns can be affected by several environmental factors such as diet, stress, and disease (Parreira and de Sousa Araújo, 2018). While gene expression profiling offers valuable insights into trait variation, it must be taken within the broader context of other molecular data, such as epigenomics and proteomics, to recognize its full effect on livestock traits (Triantaphyllopoulos et al., 2016).

2.6 Role of non-coding RNAs

Non-coding RNAs (ncRNAs), including microRNAs (miRNAs), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs), have emerged as crucial regulators of gene expression in livestock (Do and Suravajhala, 2023; Suravajhala, 2023). ncRNAs do not encode proteins but regulate gene expression at the transcriptional and post-transcriptional (Szymanski et al., 2003) and are associated with diverse biological processes, including development, metabolism, and immune response located ncRNAs as key players in determining complex traits in livestock (Huang et al., 2021).

New studies have implicated the ncRNAs in regulating traits like muscle growth, fat deposition, and reproductive performance (Yang et al., 2023). miRNAs have been shown to regulate muscle development by targeting genes in muscle hypertrophy (Horak et al., 2016). The lncRNAs have been linked with fat metabolism, inducing traits such as fatty tissue development (Cheng et al., 2021). ncRNAs have also been associated with milk production and composition in cattle (Lu et al., 2021). For example, specific miRNAs regulate genes related to milk protein synthesis, and others are related to lactation and immune function in the mammary gland (Hue-Beauvais et al., 2021). By modulating the expression of key genes through ncRNA-based involvements,

production traits such as muscle growth, milk yield, and reproductive efficiency may be improved (Hu et al., 2022). Despite the developing interest in ncRNAs, little is known about their functions in livestock. The ncRNA-mediated regulation and the trouble of precisely measuring ncRNA expression levels present challenges for integration in the breeding programs (Ramesh, 2013). However, progress in RNA sequencing technologies and bioinformatics techniques is expected to enable the finding of new ncRNAs and their roles in livestock production.

2.7 Applications in muscle growth, milk production, and fat deposition

Muscle growth is a significant characteristic of livestock production, mainly for meat-producing animals such as cattle, pigs, and poultry (Wang et al., 2024). Genomic tools have determined numerous genes and regulatory pathways intricate in muscle development, with myogenesis, muscle hypertrophy, and protein synthesis (Yang et al., 2024). The myostatin gene (MSTN) has been specified as an essential regulator of muscle growth in cattle and pigs (Aiello et al., 2018). Animals with mutations in MSTN show better muscle mass and reduced fat deposition, enhancing carcass quantity and meat quality (Ceccobelli et al., 2022). Gene editing technologies, like CRISPR-Cas9, have been utilized to have mutations in MSTN and other muscle-related genes, causing significant muscle growth and feed efficiency in animals (Zhao et al., 2022).

Milk production is a complicated trait involving multiple genes in lactation, metabolism, and immune function (Golan and Assaraf, 2020). Genomic technologies have identified various QTLs and SNPs related to milk yield, fat and protein content, and lactation (Ma et al., 2021). The DGAT1 gene, which signifies a potential role in milk fat synthesis, has been recognized as a major contributor to milk composition in dairy cattle (Khan et al., 2021; Tian et al., 2022). MAS and genomic selection have been adopted in dairy breeding programs to improve milk production and traits like somatic cell count and mastitis resistance (Brito et al., 2021). Transcriptomics and gene expression profiling have also delivered valuable understandings of the molecular mechanisms for lactation, leading to new approaches for improving milk quality and production efficiency (Sikka et al., 2023).

Fat deposition is significant in livestock production, influencing meat quality and reproductive performance (Schumacher et al., 2022). Genomic studies have discovered several genes intricate in fat metabolism, including those related to adipogenesis, lipogenesis, and fatty acid oxidation (Ladeira et al., 2016). The FTO gene has been linked with fat deposition in cattle and pigs, giving opportunities to influence body composition for better meat quality and reproductive efficiency (Dvořáková et al., 2012; Jevsinek Skok et al., 2016). Transcriptomics and gene expression profiling have identified livestock fat deposition regulatory networks (Huang et al., 2017). Studies have shown that miRNAs and lncRNAs have critical roles in regulating adipogenesis and

lipid metabolism, offering new targets for genetic progress (Lorente-Cebrián et al., 2019).

3 Proteomics in livestock productivity

Developments in molecular biology have delivered powerful techniques to attain these goals, with proteomics developing as one of the most transformative methodologies (Misra et al., 2019). Proteomics, the large-scale study of proteins and their role, offers an extraordinary prospect to comprehend the molecular tools causing important physiological and productive traits in livestock (Gao et al., 2024). It complements genomic and transcriptomic approaches by focusing on proteins that indicate cellular functions (Sobti et al., 2022). This is important because proteins are the functional products of genes, and their expression, modification, and interactions are significant to cellular processes, with metabolism, growth, reproduction, and immune responses (Udenwobe et al., 2017).

3.1 Protein profiling and post-translational modifications

In livestock, protein describing maps the proteome, or the complete set of proteins, having different tissues, phases of development, and physiological conditions (Jamwal et al., 2023). This method delivers insights into the molecular mechanisms of heavy growth, reproduction, and disease resistance (Ribeiro et al., 2020). Protein profiling has been functional extensively in livestock species, including cattle, pigs, sheep, goats, and poultry (Almeida et al., 2015). In cattle, proteomic analyses of muscle tissues have recognized proteins intricate in muscle growth, energy metabolism, and meat quality (Picard et al., 2010). In dairy cows, protein profiling of milk and mammary tissues has shown key proteins complicated in milk production, fat synthesis, and immune responses (Dai et al., 2018). Poultry protein profiling has provided insights into muscle development, egg production, and disease resistance (Kanakachari et al., 2022).

Mass spectrometry (MS) is an extensive livestock protein profiling technique (Soler et al., 2020). MS-based proteomics identifies and quantifies thousands of proteins in a single experiment (Taverna and Gaspari, 2021). MS can map protein interactions and pathways, providing a systems-level understanding of cellular processes (Richards et al., 2021). Other tools, such as two-dimensional gel electrophoresis (2D-GE) and protein microarrays, are also applied for protein profiling (Meleady, 2018), although they are less extensive than MS.

PTMs are chemical modifications that follow proteins after synthesis (Barber and Rinehart, 2018). These modifications can change protein function, stability, localization, and relations and are essential for regulating cellular processes (Karve and Cheema, 2011). PTMs regulate animal growth, reproduction, metabolism, and immune responses (Fan et al., 2024). In dairy cows, PTMs have

been associated with mastitis resistance, with phosphorylated proteins identified as critical regulators of the immune response in the mammary gland (Adnane et al., 2024). The study of PTMs in livestock is still in its initial stages, but advances in proteomics technologies enable the identification of PTMs on a larger scale (Almeida et al., 2021). MS-based approaches help study PTMs, as they can identify modifications at specific amino acid residues and quantify changes in PTMs in response to different situations (Doll and Burlingame, 2015). The role of post-translational modifications (PTMs) in livestock productivity presents a promising avenue for identifying novel genetic targets. By elucidating how PTMs regulate key biological processes, researchers can enhance breeding strategies to improve traits such as growth efficiency, reproductive performance, and disease resistance.

3.2 Biomarkers for disease and health

Proteomics biomarkers are crucial as they offer real-time insights into an animal's physiological state and response to environmental and biological challenges (Raposo de Magalhães et al., 2020). Proteomic technologies are compatible with biomarker discovery because they enable the inclusive analysis of proteins and their modifications through tissues and biofluids (Dayon et al., 2022). These biomarkers can be used to identify diseases initially, expect disease susceptibility, monitor the effectiveness of treatments, and assess animal health (Xu and Veenstra, 2008; Reinhart et al., 2012). Biomarkers have been identified for various livestock conditions, including metabolic disorders, infectious diseases and reproductive (Zachut et al., 2020).

Proteomics is a robust approach for identifying biomarkers related to infectious diseases in livestock, such as bovine tuberculosis, mastitis, foot-and-mouth disease, and avian influenza, enabling early diagnosis and optimizing disease control strategies (Suminda et al., 2022). In dairy cows, milk proteomic analyses have known key protein biomarkers related to mastitis, an inflammatory condition of the mammary gland that badly impacts milk production and quality (Giagu et al., 2022). These biomarkers contain acute-phase proteins, enzymes, and immune-related proteins upregulated due to infection (Bathla et al., 2020). Monitoring these biomarkers allows early mastitis detection, enabling timely interventions to mitigate damage to the mammary gland. Proteomics has also been used in pigs to find biomarkers for porcine reproductive and respiratory syndrome (PRRS), a viral disease associated with reproductive failure in sows and respiratory distress in piglets, aiding disease management (Genini et al., 2012). Proteomic studies have specified proteins intricate in the immune response to PRRS, which could be used to improve diagnostic tests and vaccines (Wu et al., 2022).

Besides infectious diseases, metabolic disorders like ketosis and fatty liver disease are common in high-producing livestock, particularly dairy cows (Wu, 2020). Proteomics has been used to find protein biomarkers for metabolic health in livestock, allowing primary detection and intervention (Abdelnour et al., 2019). In dairy cows, proteomic analyses of blood and milk have known biomarkers for ketosis, a metabolic disorder that occurs when cows mobilize

excess fat during early lactation (Cecilian et al., 2018). These biomarkers contain enzymes intricate in lipid metabolism, such as acyl-CoA synthetases and fatty acid-binding proteins, raised in cows with ketosis (Soares et al., 2021). Proteomics has also been used to find biomarkers for reproductive performance in livestock. For example, in cattle, proteomic studies of follicular fluid and uterine secretions have known proteins involved in ovarian function, fertilization, and early embryo development (Ferrazza et al., 2017). These biomarkers could predict fertility and develop reproductive management in dairy and beef herds (Fu et al., 2016). While proteomics has an outstanding prospective for biomarker discovery in livestock, several tasks must be addressed. One of the main tasks is the complexity of the proteome, as protein expression can differ extensively between tissues, developmental stages, and environmental conditions (Kumar et al., 2016). Another task is the need for large-scale validation of biomarkers in varied populations and environments (Trapp et al., 2014). Therefore, comprehensive validation is required before biomarkers can be implemented in routine diagnostic tests or management practices. Developing high-throughput proteomics platforms, like targeted MS and multiple reaction monitoring (MRM), facilitates the validation of biomarkers in large-scale research (Colangelo et al., 2013). As these tools develop, protein biomarkers in livestock management will likely increase, improving disease detection, animal welfare, and productivity.

3.3 Applications in meat and dairy quality development

Meat quality is a key factor in livestock production, determining market value. The biochemical composition of muscle tissues initially identifies characteristics such as tenderness, flavor, juiciness, and color (Clinquart et al., 2022). Proteomics offers valuable insights into the molecular mechanisms essential to these attributes, allowing the identification of proteins and pathways that influence meat quality (Wu et al., 2015). Postmortem muscle glycolysis expressively affects meat quality by pH, water-holding capacity, and tenderness (Stajkovic et al., 2019). Proteomic studies have known key enolase and creatine kinase proteins related to glycolysis and muscle contraction, which affect meat quality traits in cattle, pigs, and poultry (Picard et al., 2010). Proteomics has also been used to study the effect of stress on meat quality (Xing et al., 2019). Stress during transport and slaughter can yield pale, soft, and exudative (PSE) meat that is less desired by consumers. Proteomic investigations of muscle tissues have identified stress-associated proteins, like heat shock proteins and enzymes involved in oxidative stress, that are upregulated in animals related to stress (Kim et al., 2010). These proteins could be utilized as stress-resistant biomarkers, allowing us to less susceptible animals to stress and produce higher-quality meat (Gagaoua et al., 2021).

Milk quality is an essential feature of livestock productivity, with proteomics having a prospect of understanding the molecular factors that affect milk composition and yield. Proteomic analyses of milk and mammary gland tissues have recognized proteins involved in milk production, secretion, and immune function, regulating

milk production and quality (Bhat et al., 2020). The proteomic studies have identified caseins, whey proteins, and enzymes intricate in fat and lactose synthesis as key contributors to milk composition (Bhat et al., 2020). Proteomics has been used to study mastitis's effects on milk quality (Reinhardt and Lippolis, 2020). Proteomic analyses of milk from mastitis cows have known proteins involved in the immune response, such as lactoferrin and serum albumin, which are raised during infection (Abdelmegid et al., 2017). These proteins may serve as biomarkers for early mastitis discovery, allowing timely treatment to inhibit impacts on milk productivity (Libera et al., 2021).

4 Metabolomics and nutritional efficiency in livestock

Metabolomics, the inclusive study of small molecules, is a powerful tool for revealing metabolic pathways that govern livestock growth, health, and productivity. Metabolic profiling contains the detailed analysis of metabolites in biological samples such as blood, urine, tissues, and ruminal fluid, providing insights into physiological and pathological states (Saleem et al., 2013). This allows the identification of key metabolites and pathways that affect feed efficiency, growth performance, and animal health (Kaur et al., 2023). In livestock, feed efficiency is a key factor of productivity and sustainability. Animals having to convert feed into body mass efficiently reduces production costs and minimizes environmental effects, thus improving the sustainability of livestock production (Taiwo, 2023). Several factors affect feed efficiency, including genetics, gut microbiota, nutrient absorption, and metabolic activity (Li et al., 2019). Metabolomics studies have helped unravel these complexities by identifying metabolic pathways that differentiate efficient from inefficient animals (Singh et al., 2023).

Studies on cattle, pigs, and poultry have confirmed that metabolic pathways associated with energy, amino acid, and lipid metabolism are key in determining feed efficiency (Zampiga et al., 2021). Healthy animals tend to have lower nitrogenous waste metabolites and higher metabolites related to better energy utilization (Ferket et al., 2002). These results deliver potential biomarkers that can be used for the genetic selection of animals with superior feed conversion ratios (FCR). Metabolomics also allows the monitoring of nutrient absorption and utilization, providing information on how different feeds affect metabolic processes (Roques et al., 2020). We can improve feed efficiency and reduce waste by optimizing feed composition based on metabolomics data.

4.1 Identifying metabolic biomarkers for growth and health

Metabolomics has allowed the identification of biomarkers correlating substantial growth and health traits in livestock

(Wang and Kadarmideen, 2019). Biomarkers are signs that reveal physiological states and can be used to monitor growth rates, disease susceptibility, immune responses, and animal welfare (Staley et al., 2018). In beef cattle, metabolites such as plasma glucose, creatinine, and urea have been associated with faster growth rates and better feed efficiency (Gómez et al., 2022). These biomarkers could find animals with superior growth potential early, enabling precision breeding and management (Karisa et al., 2014). In dairy cattle, metabolites related to energy balance and lactation performance, like ketone bodies, have been known as potential biomarkers for milk production and health status (Gross and Bruckmaier, 2019).

The detection of health-related biomarkers has also progressive disease resistance research. In poultry, metabolic biomarkers associated with oxidative stress and immune function have allied to resistance against coccidiosis (Ducatelle et al., 2018). By identifying animals with better metabolic profiles, we can breed for better disease resistance, reducing antibiotic dependence and improving animal welfare (Pal and Chakravarty, 2019). Additionally, metabolic biomarkers can support the early diagnosis of subclinical diseases, which are frequently hard to detect through traditional clinical methods (Martins et al., 2021). For example, metabolomics analyses have shown distinct metabolic signatures with mastitis in dairy cows, allowing earlier intervention and more efficient treatment (Haxhijaj et al., 2022).

4.2 Role in animal nutrition and disease resistance

The application of metabolomics in livestock nutrition delivers a comprehensive understanding of how dietary mechanisms influence animal metabolism and productivity (Fontanesi, 2016). By evaluating different diets' metabolic changes, metabolomics can help improve feed formulations to increase performance and health (Roques et al., 2020). Diets supplemented with omega-3 fatty acids have increased livestock's metabolic profile, leading to healthier growth rates and better meat quality (Alagawany et al., 2019). Metabolomics also offers insights into how animals respond to dietary challenges, such as nutrient deficiencies (Jones et al., 2012). By understanding the metabolic variations in response to these challenges, we can modify nutritional involvements to moderate their effects (Verma et al., 2018). Metabolomics also shows that animals suffering from heat stress have altered carbohydrate and lipid metabolism (Sammad et al., 2020).

Metabolomics permits finding metabolic pathways that contribute to immune function and pathogen resistance. Elevated systemic antioxidant metabolite profiles correlate with enhanced immunological resilience, reducing susceptibility to pathogenic defies, with mastitis in bovine and respiratory infections in swine (Castro-Moretti et al., 2020). These findings show that controlling dietary antioxidant interventions may improve host immune resilience and pathogen resistance.

4.3 Epigenomics in reproductive efficiency

Epigenomics studies have revealed that environmental factors, such as nutrition, stress, and disease, can induce epigenetic alterations that affect reproductive performance (Ho et al., 2017). Maternal nutrition in gestation can alter the DNA methylation patterns in offspring, leading to modifications in growth, metabolism, and reproductive performance (Zheng et al., 2014). These results significantly affect breeding and management practices, as they advocate optimizing the maternal environment, which might develop reproductive efficiency in livestock (Greenwood and Bell, 2014). Moreover, epigenomics modifications show a crucial role in embryo development and the formation of pregnancy. Epigenetic alterations of vital reproductive genes regulate embryonic implantation, placental morphogenesis, and fetal development, contributing to reproductive success (Palini et al., 2011; Choux et al., 2015). Elucidating epigenetic modulators of reproductive initiation allows strategic interventions to optimize fertility and reproduction.

4.4 Metabolic profiling and feed efficiency

Current advances in metabolomics have developed our understanding of feed efficiency in livestock production through inclusive metabolic profiling approaches (Artegoitia et al., 2019). Incorporating high-throughput metabolomics technologies with traditional phenotypic extents has explained the complex biochemical networks underlying feed conversion efficiency (Alfaro and Young, 2018). Metabolic profiling, mainly through mass spectrometry and nuclear magnetic resonance spectroscopy, discloses significant relations between specific metabolic signs and feed efficiency phenotypes, with residual feed intake (RFI) and feed conversion ratio (FCR) (Taiwo, 2023). High-yield animals show unique metabolic features that reveal variations in energy metabolism, protein conversion, and lipid utilization pathways (Cantalapiedra-Hijar et al., 2018). These metabolic traits indicate the physiological adaptations of these proficient animals and suggest potential biomarkers for finding superior genetics (Gaughan et al., 2019; Nawaz et al., 2024). Additionally, applying metabolomics in livestock production has added to our understanding of the interaction between host metabolism, rumen microbiota, and feed efficiency, enabling the development of targeted nutritional involvements to enhance production efficiency while minimizing environmental influence (Rawal et al., 2024).

5 DNA methylation and histone modifications in reproduction

5.1 Epigenetic regulation of fertility and embryo development

Epigenetic modifications, mainly DNA methylation and histone modifications, modulate reproductive proficiency, with abnormal

epigenetic signs in gametogenesis associated with low fertility and embryonic development (Jambhekar et al., 2019; Zhang et al., 2023). Histone modifications regulate key genes intricate in early embryo development, such as cell differentiation and organogenesis (Brunmeir et al., 2009). Epigenetic alterations of reproductive developments critically underpin the efficacy of assisted reproductive technologies, with *in vitro* fertilization and embryonic transfer strategies (Canovas et al., 2017). ART techniques can induce epigenetic changes in embryos, leading to altered gene expression and reduced developmental potential (DeAngelis et al., 2018). By understanding the epigenetic mechanisms that control fertility and embryo development, we can improve strategies to optimize ART results and increase reproductive efficiency in livestock.

5.2 Environmental and nutritional influences on epigenetic modifications

Heat stress has been revealed to change DNA methylation patterns in sperm, resulting in low fertility and reduced embryo development (Rahman et al., 2018). Maternal nutrition during gestation can increase epigenetic modifications in offspring that affect their growth, metabolism, and reproduction (Gu et al., 2015). Nutritional values can also affect epigenetic modifications in livestock. Diets rich in methyl donors, such as folate and methionine, can expand DNA methylation and enhance reproductive efficacy (Diniz et al., 2024). Likewise, diets with antioxidants can lower oxidative stress and protect against epigenetic damage, increasing fertility and embryo development (Torres-Arce et al., 2021). Understanding the environmental and nutritional influences on epigenetic modifications is key for regulating breeding and management practices in livestock.

5.3 Integrating multi-omics for precision livestock farming

Multi-omics integration allows the inclusive analysis of biological processes, providing insights into the complicated interactions between genes, proteins, metabolites, and environmental factors that influence livestock productivity (Fonseca et al., 2018). Using genomic with metabolomics data, we can identify genetic variants regulating metabolic pathways and contribute to traits like feed efficiency, growth, and disease resistance (Suravajhala et al., 2016). Integrating transcriptomic with proteomic data can deliver insights into how gene expression is transformed into protein function, allowing the identification of key regulatory networks (Kumar et al., 2016). Integrating multi-omics data also has essential applications in reproductive biotechnology, such as embryo selection and artificial insemination, by linking epigenomics with genomic data to find epigenetic markers that indicate embryo viability and reproductive values (Hernández-Vargas et al., 2020; Zhu et al., 2021; Wadood and Zhang, 2024).

6 Multi-omics data integration strategies

6.1 Systems biology approaches in livestock

Systems biology approaches have been employed to model the regulatory networks governing feed efficiency in cattle (Woelders et al., 2011). Integrating multi-omics data allows us to find the genetic and molecular aspects causing disease susceptibility and resistance (Hasin et al., 2017). These findings are used to develop targeted interventions, such as vaccines and nutritional supplements, that improve disease resistance and increase animal welfare (Colditz, 2002).

6.2 Enhancing precision breeding and management

Integrating multi-omics data can enable precision breeding and management practices in livestock production (Suravajhala et al., 2016; Gao et al., 2024). These results are applied to improve more accurate selection standards for breeding programs, leading to better productivity and sustainability. Using genomic and metabolomics data allows us to find genetic variants affecting metabolic pathways and serve traits such as feed efficiency, growth, and disease resistance (de Almeida Santana et al., 2016). Integrating the transcriptomic and proteomic data can deliver insights into how gene expression is interpreted into protein function, allowing the identification of key regulatory networks that regulate important traits (Haider and Pal, 2013). Integrating multi-omics data also has applications in reproductive biotechnology, such as embryo selection and artificial insemination (Rabaglino et al., 2021). Combining epigenomics and genomic data can reveal epigenetic markers that predict embryo viability and reproductive performance (Hernández-Vargas et al., 2020; Wu and Sirard, 2020).

6.3 Applications of omics in reproductive biotechnology

The omics techniques in reproductive biotechnology can revolutionize livestock breeding and management practices. Genomic selection assists precise identification of breeding individuals showing enhanced reproductive potential, including fertility, embryonic viability, and reproductive proficiency (Das et al., 2021). Epigenomics data can find epigenetic markers that expect reproductive values, permitting a more precise selection of animals for breeding programs (Wang et al., 2023). Transcriptomic and proteomic data can identify key genes and proteins' roles in reproductive processes, such as oocyte maturation, embryo development, and placental function (Zhang et al., 2009b).

7 Improving fertility of livestock production through genomics and transcriptomics

7.1 Assisted reproductive technologies and omics integration

Assisted reproductive techniques have been used in livestock production to improve reproductive performance and accelerate genetics. These techniques include artificial insemination (AI), *in vitro* fertilization (IVF), embryo transfer (ET), and somatic cell nuclear transfer (SCNT) (Bertolini and Bertolini, 2009). With genomic and transcriptomic insights, ART can enhance fertility and reproductive rates (Ducreux et al., 2024). Genomic selection has allowed us to find animals with superior reproduction, such as early puberty, higher conception rates, and shorter calving intervals (Granleese et al., 2015). Genome-wide association studies (GWAS) have identified loci associated with fertility traits, allowing the selection of animals with required genetics (Wu et al., 2014; Ma et al., 2019). Transcriptomics delivers valued information about gene expression dynamics during key stages of reproduction, with oocyte maturation, embryo development, and implantation (Sirard, 2012). Transcriptomic profiling of reproductive tissues discloses key molecular pathways of uterine receptivity, embryo implantation, and assisted reproductive technology efficiency (He et al., 2021).

7.2 Impacts on embryo development and success rates

Embryogenesis arises from complicated molecular processes involving transcriptional regulators, involved signaling pathways, and dynamic epigenetic modulation (Chan et al., 2011). Integrative omics analyses reveal molecular mechanisms of heavy embryogenesis, optimizing assisted reproductive technology practices (Feuer et al., 2013; Ducreux et al., 2024). Preimplantation genetic screening (PGS) and preimplantation genetic diagnosis (PGD) permit the identification of embryos with the best genetics, lowering the possibility of miscarriage and improving implantation rates (Chen et al., 2014). Transcriptomic profiling tells embryonic developmental proficiency, enabling precision embryo selection (Labrecque and Sirard, 2014). The integration of epigenomics with ART has shown the significance of epigenetic regulation during embryo development (Shi and Wu, 2009). Epigenetic changes, such as DNA methylation and histone modifications, are key in controlling gene expression in early development (Lim and Maher, 2010). Abnormal epigenetic patterns can lead to developmental abnormalities and decrease fertility rates (Boissonnas et al., 2013).

7.3 Challenges and future directions

Despite considerable developments in omics technologies and their integration with Assisted Reproductive Technologies (ART),

various key challenges still need to be discussed. A primary problem lies in these methodologies' complications and the high perspective of the data generated. Genomic, transcriptomic, proteomic, and epigenomic datasets are enormous and need advanced computational and bioinformatics techniques for practical analysis, understanding, and integration (Kaur et al., 2021). Regulating the computational capacity and expertise required to manage such complex data is possible, mainly for various livestock breeding programs (Berry et al., 2011; Ahmed, 2024). Moreover, the high expenses related to omics technologies present a critical barrier to their routine application on a broad scale.

Another task is rooted in the genetic architecture of fertility traits, which are polygenic and frequently modified by complex relations between genetic and environmental influences. This polygenic nature confuses the identification of pivotal genetic variants linked with fertility, as these traits are usually affected by many small-effect loci rather than single, efficiently identifiable genes (Montgomery et al., 2014). In species with long generation intervals and low reproductive rates, such as cattle, the ability to accurately map and validate fertility-related loci is further constrained by limited generational turnover, making longitudinal studies challenging (Li, 2017). Addressing these challenges is essential for advancing the application of omics-driven insights to improve reproductive efficiency in livestock.

8 Single-cell omics: a cutting-edge approach in livestock biotechnology

The most commonly used single-cell technologies include single-cell RNA sequencing (scRNA-seq), single-cell DNA sequencing (scDNA-seq), single-cell epigenomics (such as single-cell ATAC-seq and methylation profiling), and single-cell proteomics (Evrony et al., 2021). These methods allow for the high-throughput analysis of gene expression, genetic mutations, chromatin accessibility, and protein abundance at the resolution of individual cells (Lee et al., 2020). The ability to capture molecular heterogeneity within tissues is critical in livestock, where biological systems are complex and heterogeneous at the cellular level. The application of single-cell omics in livestock biotechnology enables the identification of rare cell populations, studying dynamic cellular processes, and unravelling cellular mechanisms that underpin key traits.

8.1 Muscle biology and meat quality

Single-cell RNA sequencing has been used to explore the molecular landscape of muscle tissues in livestock species, revealing a greater cellular diversity than previously appreciated (Liu et al., 2019). Studies have identified distinct muscle fiber types and characterized gene expression patterns associated with muscle growth, fiber composition, and hypertrophy. By investigating gene expression in individual muscle cells, researchers can pinpoint

molecular pathways responsible for traits like meat tenderness, marbling, and muscle size, which are crucial for improving meat quality (Wu et al., 2023). Furthermore, single-cell technologies allow examining muscle tissue responses to various environmental and genetic factors (De Micheli et al., 2020). For example, muscle cells can be studied under different stress conditions, such as disease or extreme temperatures, to identify key genes influencing stress responses and growth patterns (Potter, 2018).

8.2 Immune system and disease resistance

Immune responses in livestock, such as those to infections or vaccinations, are complex and involve various types of immune cells that interact in a highly coordinated manner. Single-cell RNA sequencing identifies and characterizes different immune cell populations in tissues like blood, spleen, and lymph nodes (Zhao et al., 2020). Single-cell sequencing has been applied to study the immune response to infectious diseases such as mastitis in dairy cattle, avian influenza in poultry, and PRRS in pigs (Taxis and Casas, 2017). Single-cell level, scientists can uncover the molecular mechanisms behind immune activation, memory, and cellular plasticity, leading to a better understanding of how livestock animals defend against pathogens (Stubington et al., 2017). This knowledge is critical for developing more effective vaccines, improving disease resistance, and implementing precision medicine strategies in livestock populations. Additionally, single-cell technologies facilitate the discovery of rare immune cell subsets involved in pathogen recognition and immune regulation, offering new therapeutic targets for enhancing disease resistance in livestock (Yan et al., 2024).

8.3 Reproductive efficiency and fertility

Single-cell omics have proven helpful in examining the molecular mechanisms regulating gametogenesis, embryonic development, and fertility. Using single-cell RNA sequencing, researchers can analyze the gene expression profiles of individual cells within the ovary and testis, identifying key regulators of oocyte maturation, sperm development, and follicular growth (Gong et al., 2022; Dong et al., 2023). Single-cell technologies have investigated how specific gene networks control fertility in livestock species like cattle, pigs, and sheep. Single-cell RNA sequencing has provided insights into regulating follicular development, luteal function, and oocyte quality, all influencing fertility outcomes (Zhao et al., 2023). These studies have led to a better understanding of how hormonal signaling and cell-to-cell interactions govern reproductive success, which can help identify genetic and molecular markers for fertility traits. Moreover, single-cell approaches have been employed to study the early stages of embryonic development, identifying cellular pathways involved in blastocyst formation and implantation (Liu et al., 2022). This information is crucial for

improving reproductive technologies such as *in vitro* fertilization (IVF) and embryo transfer, which are integral to modern livestock breeding programs.

8.4 Milk production and lactation biology

Single-cell RNA sequencing has been applied to study the mammary gland at the single-cell level, revealing the complex cellular architecture and molecular pathways that regulate milk production. Scientists have identified specific gene sets involved in milk synthesis, secretion, and composition by profiling gene expression in lactating mammary epithelial cells (Martin Carli et al., 2020). Single-cell technologies have also been used to study the effects of environmental factors, such as diet, stress, and disease, on the mammary gland's function. Single-cell RNA sequencing has revealed how the mammary epithelium responds to changes in nutritional intake and how metabolic stress affects milk production (Becker et al., 2021). This information is crucial for developing strategies to optimize lactation performance, improve milk yield, and enhance the nutritional quality of milk.

8.5 Adipose tissue biology and fat deposition

Single-cell omics have enabled researchers to explore the molecular underpinnings of adipogenesis, fat distribution, and metabolic regulation at the level of individual adipocytes. By analyzing gene expression in single adipose cells, researchers have uncovered molecular pathways that control the differentiation of preadipocytes into mature adipocytes and the regulation of fat storage (Audano et al., 2022). Single-cell RNA sequencing has been used in species like cattle and pigs to study adipose tissue from different depots identifying genes associated with fat deposition and metabolic rate (Ford et al., 2023). This knowledge is essential for developing breeding programs to improve feed efficiency, reduce fat accumulation, and enhance the quality of meat products, such as lean cuts and marbling.

8.6 Genetic selection and precision breeding

Single-cell RNA sequencing allows identifying gene networks and regulatory pathways associated with these traits, providing more precise targets for genetic selection (Jackson et al., 2020). Single-cell technologies enable the identification of cellular markers for desirable traits, which can be used to inform selection decisions in breeding programs (Dumitrascu et al., 2021). Integrating single-cell omics with gene editing technologies such as CRISPR/Cas9, precision breeding strategies can be developed to enhance specific traits in livestock populations with minimal unintended consequences (Sindelar, 2024). By providing high-resolution insights into cellular diversity, gene expression, and functional

dynamics, single-cell technologies enable researchers to uncover novel molecular mechanisms that underpin key traits in livestock production and reproduction (Lyons et al., 2024). The applications of single-cell omics in livestock biotechnology, from muscle development and disease resistance to reproductive efficiency and milk production, pave the way for more efficient, sustainable, and resilient livestock farming systems. As these technologies evolve, their integration into breeding programs and biotechnology applications will be crucial for improving livestock productivity, health, and welfare.

9 Data analysis and integration complexities

The application of omics technologies in livestock breeding presents several ethical and regulatory challenges that require careful consideration. One prominent concern is the potential for unintended consequences, such as a reduction in genetic diversity or the inadvertent propagation of deleterious alleles (Singer et al., 2021). These possibilities highlight the need for approaches to observe and accomplish genetic variation in breeding populations to evade compromising overall herd resistance and suitability. Moreover, introducing gene-editing tools raises ethical questions about animal welfare and genetic variations' broader ecological influences. The long-term effects of gene editing in livestock remain unclear, particularly concerning animal health, behavior, and welfare in generations.

In addition to ethical concerns, regulatory challenges present significant hurdles to integrating gene editing and Assisted Reproductive Technologies (ART) in commercial livestock breeding (Soini et al., 2006). Regulatory frameworks governing these technologies vary widely among countries, with many imposing strict guidelines or outright prohibitions on using gene-editing tools in animals. Navigating these complex regulatory landscapes can impede the approval and application of these innovations in commercial breeding programs. Furthermore, the risk of public conflict with genetically modified animals has an additional hurdle, as public opinions about genetic modification may affect consumer approval and market capability. These ethical, regulatory, and social challenges will be vital for the responsible and maintainable progression of omics-based methodologies in livestock breeding.

10 Future innovations and potential impacts on the global livestock industry

There is creative potential for the future of livestock production due to the ongoing advancements in omics tools and their use in Assisted Reproductive Technologies (ART). These novelties have the potency to considerably strengthen reproductive efficiency, intensify genetic improvement, and assist in the overall

persistence of livestock systems. By application of genomic selection, we can find and transmit animals with better feed efficiency, thus reducing resource intake and minimizing the environmental factors related to livestock farming. Additionally, omics-based approaches allow a more comprehensive knowledge of the genetic aspects of health and disease resistance. This ability permits finding genetic markers associated with improved immune responses, supporting animals less vulnerable to disease. By decreasing the rate of illness in livestock populations, these policies reduce the dependency on antibiotics and other tonic procedures, thus contributing to global efforts to mitigate antimicrobial resistance.

Integrating multi-omics data, with genomics, transcriptomics, proteomics, and metabolomics, into livestock breeding programs also helps the introduction of precision livestock farming. This innovative approach allows the management of individual animals according to their exclusive genetic, physiological, and metabolic prominence, allowing for additional targeted and effective production rehearses. Precision-based management can improve key production characteristics, such as growth rates, reproductive efficiency, and product quality, alongside minimizing environmental influences. Integrating multi-omics in livestock breeding provides a data-driven, precision-oriented approach for assessment production with ecological viability, hopefully a new standard in global livestock management.

11 Summary of key findings

The application of omics technologies has significantly advanced livestock production by providing deep insights into the molecular mechanisms governing fertility, growth, and disease resistance. Genomic selection and transcriptomic profiling have played a crucial role in improving the success rates of assisted reproductive technologies (ART), allowing for more precise and data-driven breeding decisions. The integration of multi-omics approaches encompassing genomics, transcriptomics, proteomics, and metabolomics holds immense potential for further advancements in livestock reproduction. These approaches enhance reproductive efficiency, improve disease resistance, and boost overall productivity. By leveraging comprehensive molecular data, researchers can better understand the biological pathways influencing key traits, leading to more effective breeding strategies. Future advancements in livestock reproduction are expected to focus on refining precision breeding technologies. This includes the continued integration of genomic selection, transcriptomic profiling, and ART to optimize reproductive outcomes. Additionally, the development and application of gene-editing technologies, particularly CRISPR/Cas9, offer promising possibilities for directly modifying genetic traits associated with enhanced fertility, superior disease resistance, and greater resilience to environmental stressors. These innovations will contribute to more sustainable and efficient livestock production systems, ensuring long-term improvements in animal health and productivity. Furthermore,

bioinformatics, data integration, and machine learning inventions will support the creation of analytical models that can improve ART protocols and guide breeding policies. These models will improve reproductive management's precision, productivity, and sustainability of livestock systems. The extensive implementation of omics technologies in livestock production has the potential to play a significant role in global food security and the environment. By enhancing reproductive efficacy and decreasing the ecological footprint of livestock farming, these methodologies offer pathways to more resistant and sustainable livestock production systems, resolving the growing targets for food in an ecologically responsible manner.

Author contributions

AW: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Software, Validation, Writing – original draft, Writing – review & editing. FB: Data curation, Formal Analysis, Writing – review & editing. XZ: Conceptualization, Funding acquisition, Project administration, Resources, Supervision, Validation, Visualization, Writing – original draft.

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