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Listening to the Genes: How Transcriptomics Is Transforming Livestock Production

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Introduction:

Growing food demand, climate change, and the need for sustainable and welfare-focused farming systems are all posing challenges to livestock production. The biological processes that underlie animal variation in productivity, health, and stress resilience cannot be adequately explained by conventional breeding methods alone. A potent high-throughput method for examining the dynamics of gene expression and comprehending how genetic information is functionally regulated in various tissues and situations is transcriptomics. Researchers can find important genes and regulatory networks involved in growth, reproduction, disease resistance, and environmental adaptation by "listening to genes." The use of transcriptomic insights in breeding programs, precision livestock farming, and animal selection is growing.

What Does It Mean to "Listen" to Genes:

"Listening to genes" refers to the study of gene expression patterns to understand how livestock respond to environmental conditions, health challenges, and production demands. Gene expression governs how genetic information is translated into functional molecules that drive cellular activities. Through precise regulation of when and how genes are expressed, cells adapt, function efficiently, and respond to internal and external influences such as genetics, nutrition, and management practices. These processes can be investigated using high-throughput molecular approaches, including transcriptomics and proteomics (Cassar-Malek et al., 2008).

Understanding Transcriptomics:

Transcriptomics focuses on the comprehensive analysis of the transcriptome, defined as the complete set of RNA molecules expressed in a particular cell, tissue, or organism at a specific developmental stage or under defined physiological conditions (Dong & Chen, 2013). This field primarily examines gene expression at the RNA level. Common techniques used to study the transcriptome include microarrays and RNA sequencing (Lowe et al., 2017). These techniques are broadly based on hybridization

and sequencing methods (Parreira & de Sousa Araujo, 2018). Whole-transcriptome analysis plays a vital role in elucidating genome organization, gene function, and regulatory networks, as well as in identifying molecular biomarkers associated with disease states and environmental responses (Jiang et al., 2015).

Why Gene Expression Matters More Than Genes Alone:

A gene's presence does not ensure that it will always function. Where, when, and the degree of gene expression are what really count. Gene expression in livestock explains why animals with equivalent genes may differ in terms of stress tolerance, disease resistance, growth rate, or milk production. For instance, a study by Bhat et al. (2019) compared gene expression patterns in mammary epithelial cells of Kashmiri and Jersey cattle across different stages of lactation and reported higher expression of milk production-related genes in Jersey cattle, which accounts for their superior milk yield. Similarly, Pires et al. (2019) demonstrated that physiological responses and heat shock protein (HSP) expression patterns indicated lower thermal stress adaptation in Caracu cattle, a tropically adapted taurine breed, compared to Nelore cattle, a zebuine breed.

Application of Transcriptomics:

1. Predicting the Role of Genes:

Transcriptomic approaches have been widely used to identify gene functions and genes underlying important phenotypic traits (Lowe et al., 2017). Liver transcriptome analysis has revealed breed-specific differentially expressed genes, such as CYP genes in Holstein and GIMAP genes in Jersey cattle, which are associated with feed efficiency, immune function, and metabolic processes (Salleh et al., 2017). Additionally, pituitary transcriptome studies have identified key candidate genes, including SLC38A1, SLC38A3, GNAQ, DGKH, GNB4, ESR1, NPY, and GAL, that may regulate growth-related hormone secretion in Yunling and Leiqiong cattle (Lu et al., 2020).

2. Improving Animal Production through Transcriptomics:

Transcriptomics helps identify genes and regulatory networks associated with key production traits, including disease resistance, lactation performance, muscle development, meat quality, and reproductive efficiency (Parreira & de Sousa Araujo, 2018). This information can be effectively applied in animal selection and breeding programs to improve productivity and overall herd performance.

3. For Assessing Environmental Stress Tolerance in Livestock:

Transcriptomics enables the discovery of genes and pathways that respond to and fight environmental stresses. Transcriptomics' nontargeted nature allows for the discovery of novel transcriptional networks in complex systems (Lowe et al., 2017). Studies in indigenous breeds such as Sahiwal cattle have revealed that heat stress triggers the activation of key genes, including *SHH*, *GRK1*, *CHRM3*, *CAMK2A*, and *HSPB7*, along with metabolic pathways such as pyruvate metabolism that support cellular energy balance under thermal stress (Das et al., 2025). Similarly, research in Holstein

cattle has shown that heat tolerance is closely linked to immune regulation, with genes such as *OAS2*, *MX2*, *IFIT5*, and *TGFB2* playing central roles in immune effector processes during heat exposure (Liu et al., 2020). Together, these findings illustrate how transcriptomic studies across diverse cattle breeds are unraveling the molecular strategies animals use to cope with heat stress.

4. Growth, Muscle Development, and Meat Quality:

Transcriptomics has been widely applied to investigate muscle growth and meat quality traits. In Yunling and Leiqiong cattle, transcriptomic analysis of the pituitary gland identified candidate genes, including *SLC38A1*, *SLC38A3*, *DGKH*, *GNB4*, *GNAQ*, *ESR1*, *NPY*, and *GAL*, that may regulate growth by influencing the secretion of growth-related hormones, thereby supporting improved selection strategies in zebu cattle (Lu et al., 2020). Similarly, in Tibetan sheep, genes such as *LIPE*, *LEP*, *ADIPOQ*, *SCD*, and *FASN* were associated with the AMPK signaling pathway and shown to influence muscle development and muscle fiber type transformation, ultimately affecting meat quality (Wen et al., 2022).

5. In Breeding and Precision Livestock Farming:

Information generated through transcriptomic analyses can be effectively utilized in animal selection and breeding programs to improve economically important traits, including production performance, reproductive efficiency, and stress tolerance.

6. Integration with other omics:

The integration of multi-omics data, including genomics, transcriptomics, and epigenomics, provides comprehensive systems-level insights that support sustainable animal production, welfare, and health (Suravajhala et al., 2016). Such integrative approaches facilitate the identification of robust biomarkers associated with animal health and improve the accuracy of biological interpretations (Choudhary et al., 2024). For instance, a study on Sanhe cattle investigating cold stress demonstrated that combined transcriptomic and metabolomic analyses revealed the activation of key metabolic pathways involved in maintaining energy homeostasis under low-temperature conditions (Hu et al., 2021).

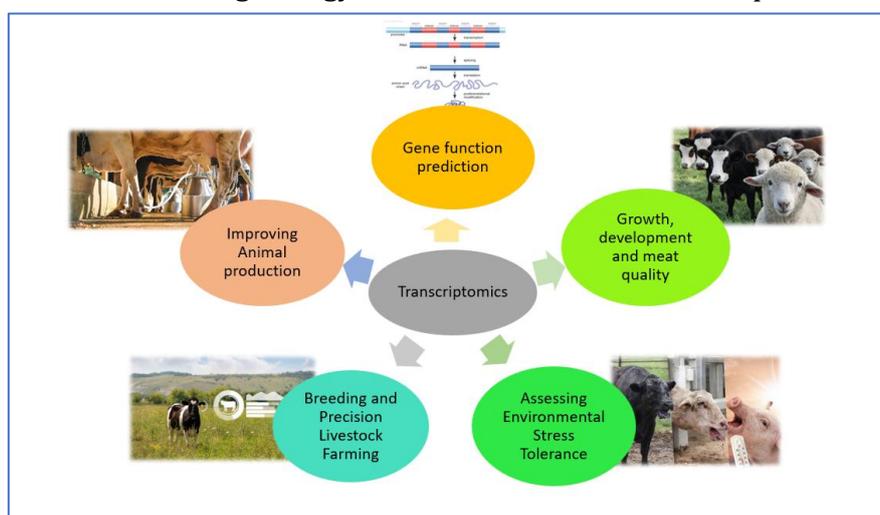


Figure 1. Applications of Transcriptomics in Livestock Improvement

Challenges in Transcriptomics Studies:

- One of the primary challenges in transcriptomic studies is RNA extraction, as obtaining RNA of sufficient quantity and high quality is critical. RNA is highly unstable and degrades rapidly, making sample collection, handling, and storage crucial steps in the workflow.
- Another major limitation is the availability of high-quality reference genome assemblies and annotations. For many livestock species, incomplete or inaccurate reference genomes can restrict data analysis and interpretation due to assembly errors and insufficient functional annotation.
- Transcriptomic datasets are highly complex and high-dimensional, often containing expression data for thousands of genes. This complexity necessitates the use of dimensionality reduction and advanced statistical approaches, such as Principal Component Analysis (PCA), to extract biologically meaningful patterns.
- Despite declining costs, high-throughput sequencing and advanced techniques such as spatial transcriptomics remain expensive, particularly for studies requiring large sample sizes to achieve adequate statistical power.
- The integration of transcriptomic data with other omics datasets, including genomics, proteomics, and metabolomics, poses significant computational and analytical challenges, requiring advanced bioinformatics expertise and substantial computing resources.

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