Review Article

Prospects of Proteomics in Goat Breeding in Nigeria: A Narrative Review

Babatunde Olatunji[1*] Ajayi Bababunmi Alaba[1] Akintunde Adeyinka Oye[2] Akinsola Kafayat Funmi[1] Osunkeye Jacob Olumuyiwa[1]

[1]Department of Animal Science, Faculty of Agricultural Production and Management, College of Agriculture and Renewable Natural Resources, Osun State University, Osun State, Nigeria
[2]Department of Agriculture and Industrial Technology, School of Science and Technology, Babcock University, Ilishan-Remo, Ogun State, Nigeria

[*]Corresponding author, E-mail address: olatunji.babatunde@pgc.uniosun.edu.ng

Received: 5 June 2025; Revised: 13 July 2025; Accepted: 14 July 2025

Abstract

Proteomics, the large-scale study of proteins and their functions, is emerging as a transformative tool in animal breeding and genetics. This narrative review explores the prospects of proteomics in enhancing goat breeding programs in Nigeria, with a focus on improving productivity, disease resistance, and adaptation to environmental stressors in indigenous breeds such as the West African Dwarf, Sokoto Red, and Sahel goats. Although these breeds are rich in genetic diversity and important for local economies, they remain underexploited in terms of targeted genetic improvement. Proteomics offers a pathway to understand the complex biological processes underlying economically important traits by identifying key protein biomarkers associated with growth, reproduction, lactation, and resistance to endemic diseases. Integrating proteomic data into conventional and molecular breeding strategies can enable more precise selection, resulting in improved herd performance and sustainability. In addition, proteomic profiling can aid in characterizing breed-specific responses to nutrition and climate variability, thereby contributing to resilience in the face of climate change. Despite its potential, proteomics remains underutilized in Nigerian livestock research due to limited infrastructure, funding, and technical expertise. This review highlights the need for strategic investments in proteomics research facilities, capacity building, and collaborative networks among academic institutions, government agencies, and the private sector. Myostatin (MSTN), Myogenic regulatory factors (MRFs), Insulin-like growth factor 1 (IGF-1), actin, and myosin have been studied to regulate muscle growth and development thus vital for meat animals. The adoption of proteomics in Nigerian goat breeding holds significant promise for advancing animal productivity and food security while preserving the genetic integrity of indigenous breeds. Emphasizing a multidisciplinary approach, this paper advocates for the inclusion of proteomics in future breeding programs to drive sustainable genetic improvement in Nigeria's goat population.

Keywords: Proteomics, Goat, Breeding, Nigeria

Introduction

Goats play a crucial role in Nigeria's agricultural economy, serving as key sources of meat, milk, hides, and financial security for millions of smallholder farmers. Among the indigenous breeds, the Red Sokoto (RS) goats, shown in Figure 1, and West African Dwarf (WAD) goat, shown in Figure 2, are particularly important due to their exceptional adaptability to tropical environments and their significant contributions to meat and milk production. These resilient breeds are vital small ruminant genetic resources across tropical regions, often serving as economic lifelines for resource-poor rural households (Ayoola et al., 2025).



Figure 1. Red Sokoto goats. Photo credit: Babatunde O.



Figure 2. West African Dwarf goat. Photo credit: Babatunde O.

Despite their adaptability, indigenous goat breeds often exhibit lower reproductive performance and growth potential compared to exotic or improved breeds, which can limit productivity (Kubkomawa et al., 2017). WAD in southwestern, Nigeria showed Kidding interval of 261 ± 75 days and litter size 1.6 ± 0.5. Annual reproductive rate was 2.3 kids per doe (Adeoye 1985). Mean litter size for RS was 1.4 ± 0.06, annual reproductive rate was 2.1-2.3 kids per doe (Adu et al., 1979), the kidding interval for RS was not available at the time of writing this review. This is in contrast with their exotic counterpart such as Nubian goats with mean litter size of 2.9 (Marai et al., 2002), Osmanabadi goats with kidding interval of 195.09 ± 5.65 days (Rathod and Dixit 2021). In terms of growth, Kalahari Red (KR) was compared with WAD, KR kids exceeded WAD kids birth weight (2.30 ± 0.06 kg vs 1.56 ± 0.06 kg), at 3-month weaning (8.88 ± 0.57 kg vs 3.88 ± 0.20 kg) and at 6-month post-weaning (13.97 ± 0.86 kg vs 5.05 ± 0.37 kg). Corresponding pre-weaning average daily gain (ADG) estimates were 84.44 ± 2.44 g and 31.73 ± 1.16 g and post-weaning ADG were 61.88 ± 1.81 g and 24.84 ± 1.21 g (Omotosho et al., 2020). In another study, when raised under similar conditions, average birth weight of the Sahelian (2.2 ± 0.23 kg) was significantly higher than the Red Sokoto kids (1.0 ± 0.17). At weaning age, the average kid weight of the Sahelian (5.6 ± 0.42 kg) was significantly higher than the Red Sokoto (3.9 ± 0.44 kg) (Makun et al., 2008).

Common traditional goat breeding practices in Nigeria, includes uncontrolled Natural mating where goats mate freely during communal grazing or in household compounds, controlled natural mating/selective mating where selected bucks are kept separate and introduced to does during breeding seasons, unintentional inbreeding in village and pastoral systems often due to ignorance of inbreeding consequences (Okpeku et al., 2019). Selection practices, where practiced, is usually based on health status and fecundity for bucks and does respectively. Official intervention on breeding and improvement was nil (Jesuyon et al., 2023). In addition to the main goals, Breeders utilize offspring testing, pedigree keeping, and social restrictions on selling genetically valuable animals to influence herd composition and performance (Bitrus et al., 2023). Goat keepers in north central Nigeria primarily utilize semi-intensive management systems, focusing on traits like disease resistance, survival, and fertility, while also considering growth and cultural importance in their traditional breeding practices (Yakubu and Aachapu 2011). These traditional breeding and selection strategies have yielded only modest gains, with progress frequently constrained by environmental and socio-economic challenges. For instance, larger herd sizes have been associated with reduced repeatability in litter size, likely due to genetic dilution and management inefficiencies that compromise the effectiveness of selection (Akpa et al., 2010).

Recent advances in molecular biology have provided novel opportunities to enhance animal breeding strategies. Among these, proteomics (the comprehensive study of protein structures, functions, interactions, and abundances) has emerged as a powerful tool for understanding the molecular mechanisms that govern phenotypic traits. This approach involves the systematic analysis of the entire protein complement expressed by a cell, tissue, or organism under specific conditions (Zhang et al., 2021; Aebersold and Mann 2003; Smith et al., 2023). By identifying protein biomarkers associated with traits such as growth, immunity, and fertility, proteomics offers a valuable complement to genetic and genomic methods, potentially accelerating the pace and precision of animal breeding.

For example, Lamri et al. (2023) identified 10 proteins associated with muscle structure in male goats using proteomics. Also Wani et al. (2021) identified Interferon-Stimulated Gene 15 (ISG15) and Interferon Regulatory Factor 7 (IRF7) suggesting as key biomarkers of goat's antiviral and immunomodulatory response to Peste des Petits ruminants virus (PPRV).

This review explores the current landscape and prospects of proteomic applications in Nigerian goat breeding. It examines how proteomic technologies can be leveraged to address key challenges in the sector, support the conservation of indigenous breeds, and enhance the productivity and resilience of local goat populations.

Overview of Goat Breeding in Nigeria

Nigeria, as at 2022, has an estimated goat population of 88 million goats. (USDA 2025). These goats thrive in diverse agro-ecological zones and their production has emerged as a fundamental strategy for improving livelihoods, alleviating poverty, and achieving sustainable agriculture and food security (Aduba and Salako 2024). These animals demonstrate exceptional versatility, thriving across diverse environments from intensive dairy farms to arid landscapes. Their economic and social significance extends beyond mere agricultural production, encompassing cultural, religious, and environmental dimensions. Despite their economic significance, substantial knowledge gaps persist regarding the genetic and molecular foundations of the key phenotypic traits of these goat breeds. This limited understanding presents a considerable obstacle to developing effective breeding programs aimed at improving critical productivity traits such as growth rates, meat quality, milk yield, and reproductive efficiency, as well as resilience traits including environmental adaptability and disease resistance (Yakubu 2010; Okpeku et al., 2011).

Traditional breeding practices among smallholder goat farmers in Nigeria remain largely unstructured, often marked by uncontrolled mating, inadequate record-keeping, and minimal adoption of reproductive technologies. Line breeding and cross breeding are practiced in some research farms but it is largely challenged by poor adaptability of exotic breeds to local climates, diseases and high cost of management. Assisted reproductive technologies (ART) such as artificial insemination using normal-saline diluent has been used in goat breeding in Nigeria (Ihejirika and Ewuola 2024). However this is not widely spread because of the high technical skill, equipment and finance required. Also, frozen semen and embryo transfer are rare due to inadequately trained personnel, cost of equipment, cost of hormone synchronization and power instability in Nigeria.

These limitations contribute to persistently low productivity, particularly in meat yield, milk production, and reproductive performance. Fakoya and Oloruntoba (2009) reported 7.55% of farmers in Osun State using intensive systems, more survey data suggests that extensive system is still high with more goat keepers gradually adopting semi-intensive system. Oni et al. (2022) in Ondo State study reported 60.5% using semi-intensive systems, with virtually no intensive farmers recorded, indicating that intensive production in southwestern Nigeria remains uncommon. Similarly, Girei and Ayoola (2017) found that merely 10% of goat farmers in Adamawa State adopted intensive management practices, further highlighting the widespread reliance on traditional, low-input systems.

Efforts to improve goat performance have focused on phenotypic selection, limited crossbreeding programs and recently, using microsatellite markers to discriminate breeds of goats (Okpeku et al., 2011; Awobajo et al., 2015; Ojo et al., 2024). To achieve sustainable

improvement, integration of molecular tools like proteomics is essential to uncover the biological basis of desirable traits and facilitate precision breeding. For example, if proteomic profiling of ovarian follicular fluid in WAD does with high kidding rates reveals elevated levels of proteins like Zinc-α2-glycoprotein, Annexin A1, and Complement C3, all linked to follicle quality and oocyte competence. These proteins could be used to screen young females for reproductive potential before first kidding, early culling or selection. It can also serve for an enhanced artificial insemination programme where these proteins can be used in timing for optimal success or tailor hormone treatments for lower-performing animals. Similar research has been carried out in Canindé goats where levels of zinc α2-glycoprotein-type proteins, complement factor B, and complement C3 were significantly higher in large follicles compared to medium or small ones (Junior et al., 2018).

Fundamentals of Proteomics

Proteomics refers to the large-scale study of the proteome-the entire complement of proteins expressed by a cell, tissue, or organism under specific conditions. Since proteins execute most of the biological functions encoded by genes, proteomics offers direct insights into cellular physiology and molecular mechanisms. As a branch of biotechnology, proteomics integrates techniques from molecular biology, biochemistry, and genetics to analyze protein structure, function, interactions, and dynamics (Tamang 2023).

According to Omics Tutorials (2025), proteomics can be categorized into several subfields based on its specific applications. Expression proteomics examines differences in expression of proteins, quantities in which they are expressed and how their expressions differ across different tissues, developmental stages and even changes in environmental conditions. It also study expression levels across different physiological or pathological states (example, healthy versus diseased tissues). utilizing techniques such as two-dimensional polyacrylamide gel electrophoresis (2D-PAGE), mass spectrometry and label-free quantification or isotopic labeling (e.g., iTRAQ, SILAC). Expression is very important in identification of trait-associated proteins, uncovering molecular pathways, biomarker discovery, precision breeding and selection, validating genomic prediction and species-specific insights in understudied livestock (Kajin et al., 2025). For instance, research can be carried to determine differential expression of Myosin light chain 1 (MYL1) in muscle tissue of goats with varying meat tenderness.

Functional proteomics focuses on illustrating the biological roles of specific proteins through protein isolation, purification, and functional assays. It uncovers how proteins interact, assemble, and carry out molecular activities within living systems thus revealing mechanism behind biological function. It also reveals protein roles and signaling pathways by mapping out protein-protein interactions within complexes thereby revealing how unknown proteins contribute to specific biological processes. It employs affinity purification or immuno-precipitation coupled with mass spectrometry thus allowing reconstruction of cellular machinery and signal transduction networks. It also interprets the functional relevance of proteins discovered in genomic studies. Lastly, it accelerates discovery of therapeutic or productivity targets (Yanagida 2002). A hypothetical research can be a study on Catalase (CAT) protein to reveal activity, especially under stress or disease.

Interaction proteomics investigates protein-protein interactions to construct interaction networks that help clarify

complex biological pathways. Common methods include yeast two-hybrid screening and affinity purification coupled with mass spectrometry. Interaction proteomics is wellestablished, with highthroughput MS methods enabling large-scale interaction mapping which is crucial for complex traits like fertility or disease resistance. Interaction proteomics reveals how proteins work within networks, helping to map key biological pathways, validate biomarkers, and identify targets for precise breeding, health, or management interventions (Veenstra 2024). An example of interaction proteomics research is the study of Heat Shock Protein 70 (HSP70) to identify protein-protein interactions (PPIs) and network associations helps map pathways of immunity or stress adaptation, critical for resilience traits.

Structural proteomics aims to determine the three-dimensional structures of proteins using techniques like X-ray crystallography and nuclear magnetic resonance (NMR) spectroscopy. Structural proteomics is important for understanding function of protein because it makes the 3D structures of proteins visible. It is this structure that determine how they interact, respond to mutations, and perform biological functions. it helps in drug and vaccine design, improves protein annotation in under-characterized species like native goats, and encourages logical breeding by linking protein structure to desirable traits like disease resistance or heat tolerance. X-ray crystallography has been used to demonstrate the three-dimensional structure of caprine beta-lactoglobulin (this is a major protein found in goat milk). This reveals how its folding affects digestibility and allergic tendency in goats (Crowther 2018).

Post-translational modification (PTM) proteomics analyzes chemical modifications such as phosphorylation, glycosylation, and acetylation, which can significantly alter protein function. Post-translational modifications like phosphorylation, glycosylation, and acetylation have been used in the following ways: act as dynamic switches that regulate protein activity, structure, interactions, localization, and stability, enable cells to rapidly respond to changing stimuli through reversible modifications by kinases, phosphatases, transferases, or deacetylases, Create PTM crosstalk, where one modification influences another, allowing complex regulation of pathways and they are also crucial for identifying active biomarker forms, understanding disease mechanisms, and designing targeted interventions in both human medicine and livestock productivity. Phosphoproteomics has been used by researchers to track dynamic changes in phosphorylation across hundreds of proteins to reveal how signal transduction pathways are rapidly activated or suppressed, such as when kinases alter enzyme activity or trigger stress responses (Mumby and Brekken 2005).

Comparative proteomics explores interspecies or inter-strain variations in protein profiles to infer evolutionary trends and functional divergence. Comparative proteomics explores interspecies or inter-strain variations in protein profiles to infer evolutionary trends and functional divergence. It comes handy in identifying conserved and divergent protein expression patterns across species or strains, it also reveals how different organisms utilize cellular resources under natural or stress conditions such as, metabolism or growth mechanisms. It is used to discover species-specific proteins linked to key traits, like stress tolerance or disease resistance. Knowledge acquired from this informs targeted breeding or therapeutic strategies. Lastly, it can be used to unravel the evolutionary history of gene duplication, dosage compensation, and adaptive innovation through comparative abundance and turnover profiling. Comparative proteomics was used by Han et al. (2022) to perform label-free comparative proteomic analysis on milk whey from bovine, goat, and camel, identifying 840

whey proteins and revealing quantitative differences. Cystatin C (CST3), cathepsin B (CTSB), and SERPING1 were found to significantly differentiate these species while myostatin (MSTN), myogenic regulatory factors (MRFs), Insulin-like growth factor 1 (IGF-1), actin and myosin are vital for growth and development of meat animals.

Proteomics workflow typically involves protein precipitation and digestion, where samples are diluted with a denaturing buffer to unfold proteins present. The proteins are then digested into peptides using proteolytic enzymes such as trypsin (Aebersold and Mann 2016). After this, the sample is cleaned up by solid-phase extraction (SPE) techniques to remove impurities and concentrate the peptides (Zhang et al., 2013).

Next, LC-MS analysis is performed using liquid chromatography (LC) coupled with mass spectrometry (MS), which is widely used for high-throughput proteomic studies (Domon and Aebersold 2006). The LC-MS system is equipped with an appropriate mass analyzer such as a time-of-flight (TOF) or orbitrap detector. MS parameters such as ionization mode, collision energy, and scan range are optimized for specific proteins being analyzed (Michalski et al., 2011).The acquired MS data is processed using appropriate software to identify and quantify plasma proteins. Typically, ProteoWizard is adopted for raw data conversion and compound identification, and the UniProt database is used to match and annotate identified proteins (Chambers et al., 2012; UniProt Consortium 2023). The identified proteins are then quantified in concentration (μg/μL), and their corresponding retention times (in minutes) are obtained.

Applications of Proteomics in Livestock Breeding

Proteomics has found widespread application in livestock species such as cattle, sheep, pigs, and poultry, where it has contributed significantly to the understanding of traits related to growth, reproduction, immunity, and milk production. These applications are equally relevant and promising in goat breeding, offering a molecular-level perspective that can inform precision breeding and management strategies.

a. Understanding Genetic and Molecular Mechanisms

Proteomics has emerged as a powerful tool for identifying key proteins and regulatory networks underlying complex traits in livestock, including growth performance, reproductive efficiency, and disease resistance. Proteomic analyses have been used in pigs to investigate feed efficiency revealed enzymes such as glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and acyl-CoA dehydrogenase as critical to glycolysis and fatty acid oxidation pathways, respectively. This has revealed energy metabolism as central to feed conversion (Xiang et al., 2024). Similarly, in beef cattle, heat shock proteins (e.g., HSP70) and tropomyosin have both been linked to meat quality properties such as tenderness and postmortem proteolysis, thus demonstrating the biochemical basis of meat palatability (Hwang et al., 2023; Tian et al., 2024). These insights provide a foundation for marker-assisted selection and targeted genetic improvement.

b. Integration with Multi-Omics Approaches

The integration of proteomics with other omics platform such as genomics, transcriptomics, and metabolomics has enabled a more holistic understanding of trait expression and regulation. In sheep, multi-omics studies combining proteomics with transcriptomics have been used to identify

keratin-associated proteins (KAPs), which play a structural role in determining wool fineness and strength (Wang et al., 2023; Li et al., 2024).

Poultry feed efficiency improvement studies have revealed the relevance of ATP synthase subunits and elongation factor Tu, which are involved in energy metabolism and protein biosynthesis, respectively. These were discovered through integrative analysis with QTL mapping and metabolite profiling (Urgessa and Woldesemayat 2023). This type of integration improves interpretation and enhances breeding accuracy.

c. Applications in Animal Health and Welfare

Proteomics also plays a critical role in improving animal health and disease resilience. For instance, in male fertility assessments, proteins like tektin-4, which is involved in sperm flagellar structure and calmodulin, which is a calcium-binding messenger protein essential for sperm motility and capacitation, have been identified as biomarkers for semen quality and cryopreservation outcomes (Allai et al., 2024; Tiwari et al., 2024).

With respect to disease resistance, annexin A1 and S100 calcium-binding proteins have been found to regulate inflammatory responses and innate immunity during bacterial and parasitic infections (Choudhary et al., 2024). These discoveries offer new avenues for health-related genetic selection and vaccine development.

d. Advancements in Meat and Dairy Science

In the domains of meat and dairy science, proteomics has contributed to quality enhancement and process optimization. For example, desmin, a cytoskeletal protein, has been associated with tenderness development, while myosin light chain and enolase are involved in energy depletion and water-holding capacity (Wang et al., 2023; Hwang et al., 2023) In dairy cattle, proteomics has helped identify proteins such as β-casein, α-lactalbumin, and lactoferrin, that influences milk composition, coagulation properties, and udder immune defense, respectively (Proteomics-Based Advancements in Research toward Sustainable Production of Dairy Livestock 2022). These applications support the development of value-added animal products and enhance production sustainability.

Comparative Analysis with Other Biotechnologies

In livestock research and breeding, several omics technologies-genomics, transcriptomics, metabolomics, and proteomics-offer complementary insights into the molecular basis of economically important traits. Understanding the comparative strengths of proteomics relative to other biotechnologies highlights its unique role and potential in advancing goat breeding in Nigeria.

Proteomics vs. Genomics

Genomics has significantly advanced the identification of genetic markers and quantitative trait loci (QTLs) associated with desirable traits. It remains the most mature omics technology in terms of throughput, standardization, and cost-efficiency. However, genomics provides only a blueprint of potential biological outcomes. In contrast, proteomics offers a functional readout by identifying and quantifying proteins that are actively involved in trait manifestation. For example, proteomic analyses have been used to investigate protein-level changes linked to beef quality traits, effectively complementing genomic studies (Hwang et al., 2023; Tian et al., 2024).

Proteomics vs. Transcriptomics

Transcriptomics focuses on gene expression at the mRNA level, offering insights into transcriptional regulation and the genes potentially involved in trait development. However, mRNA abundance does not always correlate with protein levels due to post-transcriptional regulation, degradation, or translational control. Proteomics bridges this gap by characterizing the actual proteins executing cellular functions. In pig studies, for instance, proteomic data have revealed proteins associated with feed efficiency, providing functional validation of transcriptomic findings (Xiang et al., 2024).

Proteomics vs. Metabolomics

Metabolomics investigates the small molecules and metabolic intermediates that reflect the end products of cellular processes. It provides a snapshot of the organism's biochemical state. Proteomics complements this by identifying the enzymes and regulatory proteins driving these metabolic pathways. Integrated proteomic and metabolomic analyses have been used in sheep and goat studies to identify biomarkers related to meat tenderness and flavor (Wang et al., 2023; Hwang et al., 2023), illustrating the synergy between these approaches.

Proteomics within Multi-Omics Approaches

Multi-omics approaches aim to integrate genomics, transcriptomics, proteomics, and metabolomics to provide a systems-level understanding of complex traits. Within this framework, proteomics plays a critical role by connecting gene expression to phenotypic outcomes through the functional molecules-proteins. In poultry research, multi-omics strategies that include proteomic data have successfully identified biomarkers related to feed efficiency and disease resistance, demonstrating the power of integration (Dehau et al., 2022; Urgessa and Woldesemayat 2023). Such approaches hold strong promise for application in goat breeding, particularly for unraveling the genetic and functional basis of traits relevant to productivity and adaptation.

From the comparative analysis above, proteomics offers unique advantages that fill crucial gaps left by genomics, transcriptomics, and metabolomics. Proteomics provides essential functional insight, especially when transcriptomic data is inconclusive, genomic variants need validation, and phenotypic traits are complex and environmentally influenced.

Prospects of Proteomics in Goat Breeding in Nigeria

Proteomics can significantly enhance the genetic makeup of goat breeds in Nigeria by providing insights into the genetic diversity and functional traits of these animals. This approach involves analyzing the protein expressions and variations that correlate with desirable phenotypic traits, thereby facilitating targeted breeding programs. By integrating proteomics with genomic data, researchers can identify specific proteins and genes associated with traits such as disease resistance, productivity, and adaptability, which are crucial for improving indigenous goat breeds in Nigeria.

Akintunde et al. (2024) reviewed that the low production and productivity of goats in Nigeria is caused by the inability to conserve and adequately characterise the indigenous breeds. Molecular tools are also underutilised, thereby limiting the capacity to apply characterised information and molecular tools to goat breeding programmes. The review also suggested that conservation techniques, such as livestock preservation and the use of molecular markers, are essential for enhancing their traits, including adaptability and disease resistance. Proteomics can

complement genomic studies by providing functional insights into how specific proteins influence these traits, thereby guiding selective breeding efforts (Qureshi et al., 2014). The integration of next-generation sequencing (NGS) with proteomics allows for a comprehensive analysis of the goat genome, facilitating the identification of genetic markers for improved breeding strategies (Qureshi et al., 2014).

Proteomic research journey so far in Nigeria

Proteomics research in Nigeria is still in its infancy, yet it is increasingly contributing valuable insights into different aspects of human life, such as disease mechanisms, biomarker discovery, and therapeutic strategies. Some novel studies carried out with proteomics in Nigeria include those by Bachmann et al. (2014), Onile et al. (2017), and Ogunyinka et al. (2018), which demonstrated the application of proteomics in understanding cerebral malaria, schistosomiasis, and diabetes respectively, revealing key pathological pathways and potential diagnostic markers. Proteomic profiling of snake venom by Adamude et al. (2021) has enriched knowledge on local toxinology relevant for antivenom development. Some reviews have also exposed the importance of proteomics in the medical sector. Articles by Ogunjobi et al. (2024) and Funmilayo et al. (2024) laid bare the integrative role of proteomics in omics approaches for addressing chronic diseases and parasitology challenges. These efforts demonstrate the prospects of proteomics in advancing biomedical research in Nigeria. There is a need to explore this same power of proteomics in improving the productivity of indigenous breeds of goats through an integrated morphometric and proteomic approach in breeding.

Current Gaps and Research Challenges

While proteomics offers promising avenues for improving goat breeds, challenges such as the high cost of technology and the need for skilled personnel may limit its widespread adoption in Nigeria. Additionally, the integration of proteomic data with traditional breeding practices requires careful consideration to ensure the preservation of valuable genetic traits such as adaptability and disease resistance (Akintunde et al., 2024).

Future Directions and Recommendations

The synergy of multi-omics approaches is a powerful concept that can redefine goat breeding in Nigeria. However, tackling the challenges of data integration and interpretation requires deliberate investment in computational and bioinformatic capacity. Key steps include:

1. Data Integration and Systems Biology: Multi-omics generates complex datasets. Researchers need skills in network biology and tools like MOFA, DIABLO (mixOmics), and Cytoscape for integration and visualization. Proficiency in R, Python, and Bioconductor is essential.

2. Functional Annotation and Comparative Genomics: Due to poor annotation of local goat breeds, training in tools like BLAST2GO, InterProScan, and GO enrichment is critical. Researchers should also master orthology tools (OrthoFinder, eggNOG) and genome assembly software (SPAdes, Canu, MAKER).

3. Machine Learning and Predictive Modeling: To extract meaningful traits from noisy data, expertise in Random Forest, SVM, XGBoost, and deep learning is needed, along with platforms like scikit-learn, TensorFlow, and Keras-particularly for genomic prediction and selection index development.

4. QTL and GWAS Analysis: Linking omics markers to key traits requires competence in PLINK, GEMMA, TASSEL, and QTL tools like R/qtl and MapQTL.

5. Cloud Computing and Data Management: Given the size of multi-omics data, cloud and high-performance computing are essential to overcome local infrastructure limitations.

Recommendations for Nigeria:

a. Establish bioinformatics hubs in research-focused institutions such as, Osun State University, Nigeria.

b. Promote international training partnerships such as H3Africa, CGIAR, ILRI.

c. Develop national livestock omics databases.

d. Encourage cross-training in genomics, proteomics, statistics, and computer science for animal scientists.

e. High spirited individuals and philanthropic Non-Governmental Organizations can be encouraged to contribute to capacity building for multi-omics laboratory in Nigeria.

The integration of proteomics with conventional breeding approaches and other omics platforms holds great promise for revolutionizing goat breeding programs in Nigeria. By leveraging these technologies, breeding efforts can become more data-driven, targeted, and impactful, contributing to improved productivity, rural livelihoods, and national food security.

Conclusion

Proteomics has emerged as a transformative tool in livestock breeding, providing functional insights into the molecular basis of economically important traits such as growth, reproduction, immunity, and product quality. While genomics, transcriptomics, and metabolomics offer valuable layers of biological information, proteomics delivers a unique perspective by directly reflecting gene function through protein expression and interaction. This functional dimension is critical for advancing precision breeding and promoting sustainable livestock production systems.

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