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BIOTECHNOLOGY

Proteomic profiling: A tool to unlock the potential of Nigerian indigenous goats

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ABSTRACT. Nigeria possesses a rich diversity of indigenous goats (predominantly the West African Dwarf, Sokoto Red and Sahel goats), that are superbly adapted to local environment but often underperform compared to improved breeds. Proteomic profiling emerges as a powerful avenue to bridge this gap. This approach examines the protein content of an organism, providing insights into its genetic potential. In the case of Nigerian indigenous goats, this method can reveal valuable information about their unique traits, disease resistance, and potential for improvement through selective breeding. This review underscores how integrating proteomic profiling into breeding programs can unlock genetic potential of Nigerian indigenous goats. It is however concluded that with the use of technologies involved in proteomic profiling, strategies can be formulated for Nigerian indigenous goat breeds to improve their productivity, health, and product quality. With strategic application of these technologies, supported by ongoing research and investment, proteomics can empower Nigerian goat farmers to tap into the vast potential of their indigenous breeds thus offering a powerful approach to unlocking the genetic diversity and adaptive potential of Nigerian indigenous goats. Ultimately, proteomic profiling can boost productivity, animal health and product quality, empowering Nigerian goat producers to leverage the full spectrum of their breeds' adaptive diversity.

Keywords: Breeds; diversity; improvement; indigenous; proteome.

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Introduction

Despite improvements in livelihoods and economic development, the role of goats in Nigeria's agricultural sector remains indispensable. Goats supply meat, milk, hides, and other products that enhance food security and boost the socio-economic status of rural households. They also help maintain ecosystem health by consuming unwanted plants and shrubs. Accordingly, goat production is drawing increasing interest across Nigeria, yet the overall productivity remains well below its potential, largely because farmers rely on unimproved breeds, traditional husbandry systems and limited genetic potential of indigenous goats (Daramola et al., 2010; Nwachukwu and Berekwu, 2020; Akintunde et al., 2024).

It is interesting to note that native goat breeds however, exhibit remarkable resilience across diverse production systems, from agro-pastoral to fully pastoral settings, thanks to traits such as extended walking range, ability to thrive on low-quality fodder, effective use of marginal environments, and low capital requirements. Goats typically possess unique qualities like resistance to disease, heat tolerance, short generation intervals, and high rates of reproduction (Oguoma, 2003; Lebbie, 2004).

Goats are a versatile livestock, supplying meat, milk, hides, skins, and manure rural communities and commercial market alike. Their by- products support food security, household incomes, and a variety of small-scale industries. Goats contribute approximately 17% of Africa's total meat and 12% of its milk output, playing a vital role in human nutrition and rural livelihoods (Lebbie, 2004; Adam et al., 2010). Although goat milk has historically been underutilized, its nutritional and therapeutic benefits are gaining wider appreciation. 60% of goats are kept primarily for milk, 35% for meat, and 5% for skin and hide production.

Compared to cattle, sheep, and buffaloes, goats have a higher feed conversion efficiency that results in meat and milk. In addition, goat milk surpasses sheep milk in global production and consumption. Goat dung remains a vital organic fertilizer, enhancing soil fertility for smallholder farms (Karbo et al., 1999). Beyond economics, goats hold deep cultural significance in many Nigerian communities. They feature prominently in marriage rites, funerals and other traditional ceremonies (Lebbie, 2004; Ajala et al., 2008). Over 95% of rural households rear goats, making them second only to cattle in generating income and meeting family (Duku et al., 2011). Farmers in rural areas own goats of all ages and genders.

In Nigeria, extensive and semi-extensive small ruminant production systems have been studied using household kitchen waste as supplements with fodder in goat production. The traditional free-range system is the main method used to raise indigenous goats, which contributes to high morbidity, mortality and low productivity. Small ruminant especially, goat production systems in tropical climates are typified by poor performance when compared to breeds from temperate regions due in part to prolonged grazing hours, confinement stress and limited nutritional management (Ajala et al., 2008).

Three indigenous goat breeds are recognized across Nigeria: the Sahel, the West African dwarf, and the Red Sokoto (Osinowo et al., 1992; Butswat, 1998). According to Ngere et al. (1984), the West African dwarf breed is widespread in the humid forest zone of southern Nigeria, while the Red Sokoto and Sahel breeds are primarily found in Northern Savannah and Sahel regions, respectively (Adamu et al., 2021). Indigenous goat breeds in Nigeria are mainly raised for their meat; they have not been improved or selected for the production of both meat and milk. To unlock their full genetic potential in Nigeria, modern breeding science and technology must be introduced, specifically in the area of livestock genetic improvement. By identifying superior individuals within local populations and using them as the foundation for selective mating programs, it is possible to modify the genetic makeup of the population towards higher growth rates, enhanced disease resistance and overall greater productivity, thereby ensuring sustainable advancement in Nigeria's goat sector.

Proteomic analysis offers a powerful means to uncover the genetic potential for individual goats for key production traits such as growth rate, disease resistance, and milk yield (Chen et al., 2019; Di Gerlando et al., 2019; Rexroad et al., 2019; Zhao et al., 2023). The term "proteome" refers to the entire complement of proteins that can be expressed in a particular tissue or organism at a given time. Thus, proteomics is the study of the proteome of an organism as a way to identify all the proteins present and to understand the functions of these proteins in the life of an organism (Cho, 2007; Toscano et al., 2017). Recently, proteomic studies in various farm animals have successfully discovered protein biomarkers linked to economically important traits, or identified genomic markers associated with the expression of target proteins. (Doherty et al., 2004; Kjaersgard et al., 2006; Martins et al., 2012; Souza et al., 2012).

The knowledge of the protein complement in goats may not only enhance basic understanding of the biology of this species but also serve as a channel to discover new diagnostic biomarkers and therapeutic targets for the goat industry. With the advances in biomedical sciences, proteomics has become an invaluable tool in accelerating the discovery of new diagnostic tools and medicines for a range of diseases. The field of proteomics usually begins with the identification of differentially expressed proteins. These data are then integrated into on a large scale in the field of "functional genomics," which is the study of the relationship between the proteins that are made and the genes that control the proteins' synthesis (Carpenter & Conlan, 2021). Despite its promise, goat proteomics remain underexplored.

Nigeria is home to a rich diversity of indigenous goat breeds, highly adapted to the local environment, yet underperforming compared to genetically enhanced counterparts (Food and Agriculture Organization of the United Nations [FAO], 2007). As the livestock sector seeks ways to increase productivity sustainably, proteomic profiling has emerged as a transformative tool capable of unlocking latent genetic potential in these valuable animals. Significant advancements in the field of proteomics now present biotechnologists with a more systematic avenue of biological and genetic research. The 21st century has ushered in the era of immense progress in the development of a sophisticated study of proteins and their functions, and thus proteomics offers the biological scientist a new dimension for addressing questions and challenges. The laws of inheritance laid down by Mendel in the mid-nineteenth century still hold true today; the field of genetics has undergone nothing short of a revolution in the past decade with the Human Genome Project and the advent of bioinformatics.

However, the significance of proteins, which are translated from the coding regions of nucleic acids, has always been paramount in the study of trait inheritance, biomolecular function, and disease causation. With the sequencing of many genomes now complete, including that of *Homo sapiens*, proteomics, as a global analysis of expressed proteins in a given cell or tissue type, surely offers a tantalizing way forward in understanding biological and genetic processes at a molecular level. Profiling the proteome of an organism in health and under defined conditions or stresses can lead not only to a more precise identification of gene function but more realized therapeutic strategies for diseases that are caused at the protein level (Bergendahl et al., 2019).

The development of tissue-specific and disease-specific protein "fingerprints" could now be achieved in a fraction of the time and thus, worldwide, the forensic uses of proteomics in disease identification and classification are moving toward mainstream adoption. As such, this scientific literature review provides a basic understanding of the major themes and studies in the dynamic and burgeoning field of proteomics as a potential tool in the improvement of Nigerian indigenous goat breeds.

Nigeria harbors a diverse population of indigenous goat breeds; each uniquely adapted to varying ecological zones. Their resilience to diseases and harsh environment makes them invaluable assets to small holder farmers. However, their productivity often falls short compared to improved breeds. Proteomic profiling emerges as a transformative tool to bridge this gap and unlock the genetic potential slumbering within Nigerian indigenous goats. Proteomic profiling is an advanced technique that allows for the detailed examination of the protein content of an organism, providing insights into its genetic potential. In the case of Nigerian indigenous goats, this approach can uncover valuable information about their unique traits, disease resistance, metabolic pathways, and potential for improvement through selective breeding.

Nigerian indigenous goats are known for their adaptability to local environments and disease resistance, making them an essential livestock resource in Nigeria. However, to fully unlock their genetic potential, it is necessary to understand the protein expressions that underpin these valuable traits. Genetic traits are passed down from parent to offspring, and genome studies offer powerful pathways for unlocking the productivity of livestock species. In recent years, there has been increasing interest in goat genomics due to the economic and agricultural importance of this livestock species. Though genomic studies in Europe, America, and Asia have advanced goat breeding significantly, research in African breeds remains limited. Nigerian goats are typically raised under extensive systems and contribute to rural livelihoods. In contrast, limited data exists on the genetic diversity and structure of African indigenous goats, including those in Nigeria.

In Nigeria, goats are mainly kept under extensive farming systems and serve as critical assets for many rural households (Nwachukwu & Berekwu, 2020). However, goat productivity remains low due to many factors such as infectious diseases, parasites, poor quality feeds, and limited access to improved livestock. These constraints have exacerbated the poverty and day-to-day hardship, particularly in rural areas where goat farming is the main source of livelihood (Bamaiyi, 2013). It is thought that identifying the genetic make-up of Nigerian indigenous goats and the underlying genes that control important production and adaptation traits will open new opportunities for molecular breeding and better conservation strategies. This work marks a pivotal step, investigating the gene products - the proteins - of Nigerian indigenous goats, that regulate genetic function in Nigerian indigenous goats in order to understand the functional make-up of their genetic resource.

Importance of Nigerian indigenous goats

While the push toward commercialization and the use of exotic goat breeds has gained momentum in Nigeria, financial limitations have slowed its adoption. Indigenous goats remain indispensable, not just for their meat, milk and hides but for their nutritional contributions to rural households, economic significance across informal sectors and cultural value in ceremonies and traditions. For most insemination and artificial reproduction studies, protocols obtained from studies using exotic breeds are being adopted thus risking the potential benefits that could be derived from using Nigerian indigenous goats which are naturally endowed to withstand the environmental and ecological constraints in the country such as trypanotolerance. A deeper understanding of the reproductive physiology of Nigerian goats is essential for reversing the downward trends in productivity (Daramola et al., 2010; Jesuyon et al., 2023).

Materials and methods

Proteomic profiling as a research tool

Proteomic profiling relies on the idea that the proteome (the whole association of proteins produced by the genome) is drastically more relevant than both the genome and the transcriptome when it comes to defining the phenotype of an organism at any given time (Feussner & Polle, 2015). The proteome is far more complicated than the genome or the transcriptome, due to the huge quantity of potential variations among protein species; dealing with this complexity is a chief mission and proteomics studies have the possibility, if successful, to increase the functional knowledge of the genome by a significant amount (Al-Amrani et al., 2021; Holman et al., 2013). Figure 1 showed the overview of genes in the human genome, transcripts in the human transcriptome and proteoforms in the human proteome.

Modern proteomic technologies can simultaneously detect and analyze hundreds of proteins, in a single experiment and this has important applications in biotechnology and biomedical research (Cho, 2007; Al-Amrani et al., 2021), allowing researchers to define the classical and alternative proteomes in unique tissues and stages of development, investigate responses to disease and environmental changes, identify functions of unique proteins in biological processes and develop quantitative datasets for drug and diagnostic development (Verrills, 2006; Al-Amrani et al., 2021).

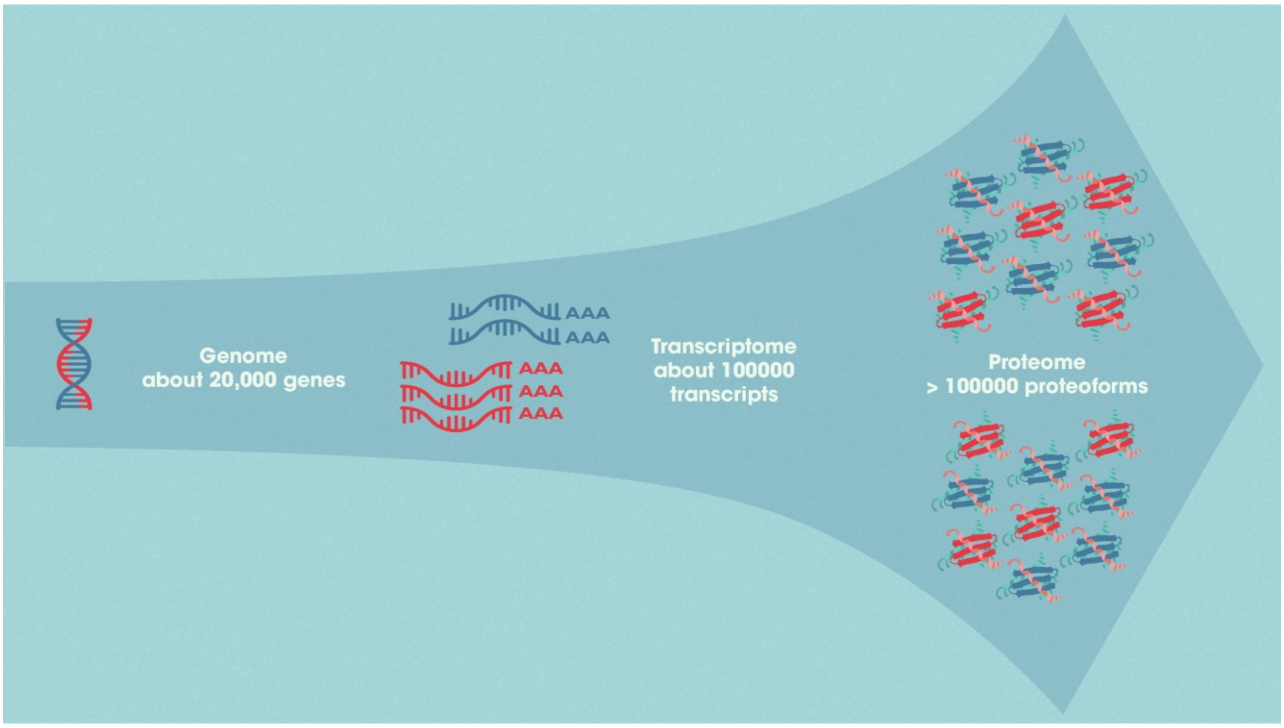

Figure 1. There are approximately 20,000 genes in the human genome, ~100,000 transcripts in the human transcriptome and over > 1000000 proteoforms in the human proteome.

Source: Beeton-Kempen (2020).

Profiling of the embryonic proteome in extensive gene silencing research and characterizing the stall proteome in terms of cellular senescence and disease mechanisms are also good examples of areas where proteomics has contributed to understanding of the biology and pathology of living organisms (Shekari et al., 2014; Delfarah et al., 2021). Proteomics plays an increasingly important role in understanding molecular mechanisms underlying self-renewal and pluripotency of embryo stem cells and their applications in cell therapy and developmental biology studies. As the function of a protein is strongly associated with its localization in cell, a complete and accurate picture of the proteome of embryo stem cells cannot be achieved without knowing the subcellular locations of proteins (Shekari et al., 2014). It also provided insight into tracking proteins that shuttle between different compartments.

The three primary milestones that catalyzed the development of proteomics were the 1985 discovery of the polymerase chain reaction (PCR), which allowed the development of large quantities of unique DNA for sequencing (Kadri, 2019); the development of the first mass spectrometer capable of sequencing proteins (Yates, 2013); and the third in 1995 with the sequencing of the first complete genome of a free-living organism (Rasko & Mongodin, 2005). The technological advances in fast sequence analysis of large quantities of DNA and the development of mass spectrometry (to detect and characterize proteins) ultimately gave rise to the field known today as proteomics.

Proteomic profiling is an important breakthrough in translational research as the genome or the transcriptome do not provide information directly or even indirectly about the state or function of a cell or tissue, both of which can be described by the proteome. Also, the near complete sequences of many important genomes and the rapid accumulation of numerous expressed sequence tags have set the stage for high-throughput mapping and identification of proteins since databases of sequenced genomes and transcripts are now available.

Genetic diversity, adaptive potential of Nigerian indigenous goats and proteomic profiling

Nigerian goats thrive in diverse and often harsh ecological areas, contributing to both nutrition and rural economies. Their milk offers low cholesterol and high digestibility, making them valuable for diary development. (Ajala et al., 2008; ALKaisy et al., 2023; Navamniraj et al., 2023). With increased recognition of its nutritional and commercial value, recent advancements in goat milk proteomics hold promise for boosting the diary sub-sector in Nigeria.

Proteomic profiling has emerged as a transformative approach to decode the rich genetic diversity and environmental adaptability of Nigerian indigenous goats, as demonstrated by studies on genetic diversity in Southern Nigeria (Okpeku et al., 2011), landscape genomics in South African indigenous goat populations (Mdladla et al., 2017), and genetic analysis of Nigerian indigenous goat populations (Ojo et al., 2015; Ojo et al., 2018). These studies have revealed significant genetic variation within and between goat populations, suggesting the need for conservation and improvement programs. This variation reflects the adaptive potential of these goats, allowing them to thrive in diverse environmental conditions across Nigeria. The use of proteomic profiling can further enhance the understanding of the unique genetic traits and adaptive potential of these indigenous goats, which can be harnessed for sustainable livestock production.

Proteomic profiling, the large-scale study of proteins, has emerged as a powerful tool in the field of livestock genetics, offering insights into the genetic diversity and adaptive potential of indigenous goat populations.

Methods and techniques for proteomic profiling

Proteomic profiling involves several key methodologies. The conventional techniques for purification of proteins are chromatography based such as ion exchange chromatography (IEC), size exclusion chromatography (SEC) and affinity chromatography (Jungbauer & Hahn, 2009; Voedisch & Thie, 2010; Hage et al., 2012). For analysis of selective proteins, enzyme-linked immunosorbent assay (ELISA) and western blotting can be used. These techniques may be restricted to analysis of few individual proteins but also incapable to define protein expression level (Lequin, 2005; Kurien & Scofield, 2006).

Other proteomics techniques exist, such as gel-free high-throughput screening technologies like multidimensional protein identification technology (Steel et al., 2005), stable isotope labeling with amino acids in cell culture (Ong et al., 2002), isotope-coded affinity tag, and isobaric tagging for relative and absolute quantitation (Butler et al., 2010), One-dimensional (1D) and two-dimensional (2D) gel electrophoresis (2-DE) (Al-Amrani et al., 2021). Tissues, organelles, and cells can be studied using shotgun proteomics (Haynes and Roberts, 2007), 2D difference gel electrophoresis (2D-DIGE) (Minden, 2012), and protein microarrays (Cutler, 2003; Liotta et al., 2003). High-throughput processing methods include label-free quantification of high mass resolution liquid chromatography (LC)-tandem mass spectrometry (MS), large-scale western blot assays (Schulz et al., 2007; Al-Amrani et al., 2021), and multiple reaction monitoring assays (Stahl-Zeng et al., 2007).

Yoithapprabhunath et al. (2015) have classified proteomics into two categories in the past ten years: protein expression mapping and protein interaction mapping. The former technique measures the quantitative expression of the proteome in tissues, bodily fluids, or cells by combining 2-DE and MS. Understanding the post-translational modifications (PTMs) of expressed proteins under various environmental or disease states can be achieved through protein expression mapping (Yoithapprabhunath et al., 2015). To identify the interaction partners for the encoded proteins in each cell and at the proteome-wide scale, protein-protein interaction mapping employs the yeast two-hybrid system in conjunction with mass spectrometry (Pandey & Mann, 2000).

Figure 2 showed an overview of proteomic techniques. Proteomic profiling techniques, such as mass spectrometry and protein microarrays, enable the identification and quantification of proteins in goat tissues and fluids. These techniques provide valuable information on protein expression patterns associated with specific traits, such as disease resistance, reproduction, and environmental adaptation. Bioinformatics tools for analyzing proteomic data, understanding protein functions, and identifying potential biomarkers are also of high significance. Proteomic methods including mass spectrometry, 2D gel electrophoresis, and bioinformatics analysis have not been widely employed in studies examining the proteomes of Nigerian indigenous goat populations.

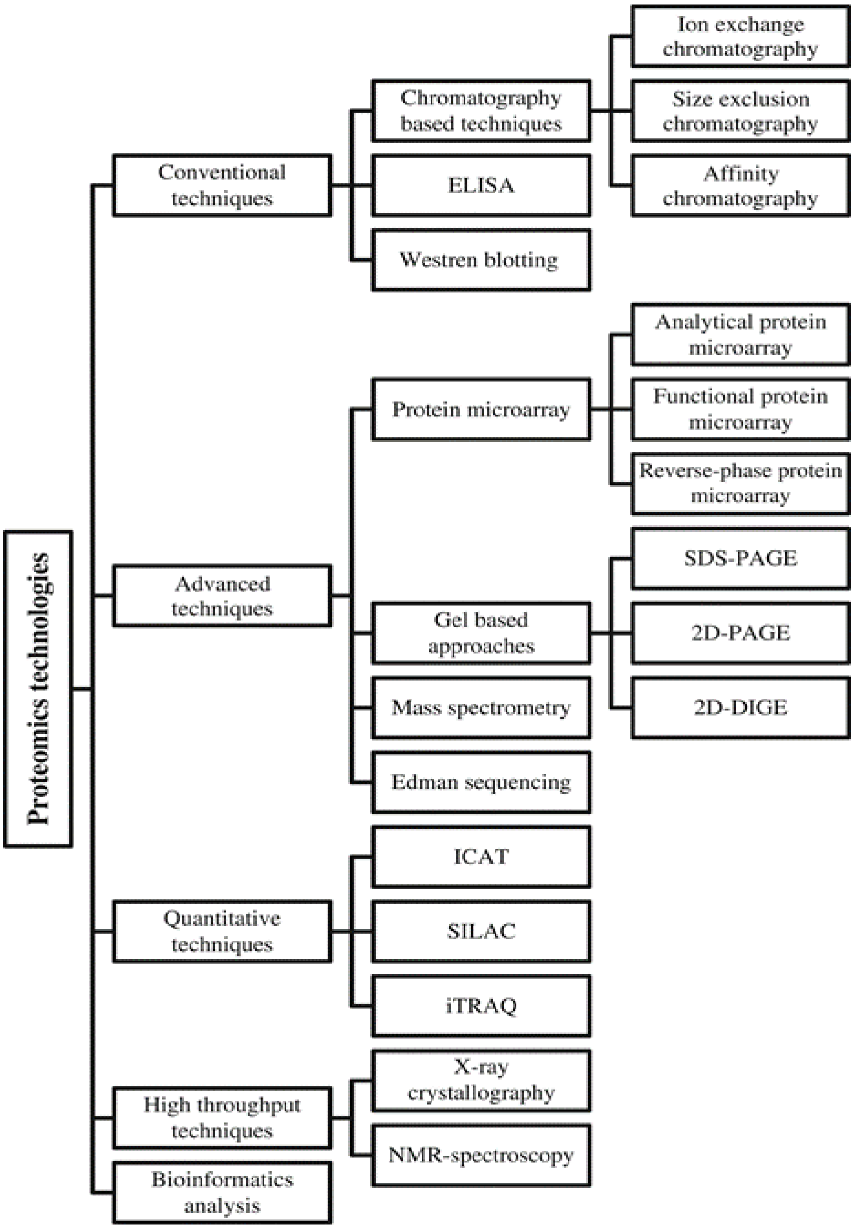

Figure 2. An overview of proteomics techniques. Source: Aslam et al. (2017)

Results and discussion

Applications of proteomic profiling in Nigerian indigenous goats

By applying proteomic profiling to Nigerian indigenous goats, researchers can:

- Identify protein markers associated with beneficial traits such as growth rate, meat quality, and milk production.
- Explore the molecular basis of disease resistance, which can lead to the development of targeted therapies or vaccines.
- Understand the nutritional metabolism that allows these goats to thrive in challenging environments.

Proteomic profiling has transformative implications for Nigerian indigenous goat production through the following:

1. Understanding Physiology: Proteomics can provide information on the physiological differences between high-performing and low-performing goats. This knowledge can be used to develop targeted breeding programs to select for desirable traits such as increased milk yield or superior meat quality.
2. Disease Diagnosis: Proteomic analysis of blood or milk can aid in the early detection of diseases, allowing for prompt intervention and improved herd health. This empowers farmers to intervene promptly, minimizing herd health risks and economic losses.

3. Nutritional Optimization: By analyzing the protein profile of goats fed different diets, researchers can formulate diets that optimize growth, milk production, and fertility. This knowledge empowers the formulation of optimized diets that enhance growth, milk production, and fertility, ultimately maximizing the animals' genetic potential.

4. Product Quality Improvement: Proteomics can help identify proteins responsible for desirable qualities in meat and milk, enabling the development of targeted breeding or feeding strategies to enhance product quality. This information can be harnessed to develop targeted breeding or feeding strategies, leading to superior product quality that fetches premium market prices for Nigerian goat farmers.

5. Biomarker Discovery: Proteomic profiling can lead to the discovery of protein biomarkers associated with specific traits. These biomarkers can be used for rapid and non-invasive selection of breeding stock, significantly accelerating genetic improvement programs.

Advantages of proteomics over other genetic tools

Proteomic profiling offers several advantages over traditional genetic tools like genomics:

- It provides a dynamic view of an organism's functional molecules, not just static genetic information.
- It can detect changes in protein expression levels that govern phenotypic traits.
- It allows for the discovery of post-translational modifications that might affect protein function.

Implications for conservation and improvement programs

Proteomic profiling has the potential to identify protein markers linked to local environmental resilience, which can inform breeding strategies for enhancing desirable traits such as disease resistance, productivity, and adaptability. The information obtained from proteomic profiling of Nigerian indigenous goats can be used to develop breeding programs that enhance desired traits without compromising the genetic diversity and inform conservation efforts to protect these indigenous breeds from being displaced by commercial breeds.

Application in sustainable livestock production

Proteomic profiling can inform breeding programs aimed at enhancing desirable traits in Nigerian indigenous goats. By identifying proteins linked to productivity and adaptability, enabling breeders to develop associated with adaptation and productivity, breeders can selectively breed goats with superior traits, leading to more resilient and productive herds.

Challenges and future prospects

Despite its potential, proteomic profiling in Nigerian indigenous goats faces challenges such as cost, technical expertise, and the need for large-scale studies. There are several challenges that need to be addressed for effective proteomic profiling:

- The complexity of protein extraction and purification from goat tissues.
- The presence of high-abundance proteins can overshadow the detection of less abundant, yet potentially more informative, proteins.

Future research should focus on overcoming these challenges and further exploring the functional significance of proteins associated with adaptive traits.

Future directions

Moving forward, further research utilizing proteomic profiling should focus on elucidating the functional significance of genetic variation in indigenous goat populations. This includes understanding how specific proteins contribute to adaptive traits and how these traits can be enhanced through selective breeding and management practices. Additionally, efforts should be made to conserve and sustainably manage the genetic diversity of indigenous goat populations to ensure their long-term survival and contribution to sustainable livestock production.

Conclusion

Proteomic profiling stands at the frontier of livestock improvement in Nigeria. By decoding the expressed protein signatures of indigenous goats, researchers can uncover traits that matter most for productivity, resilience, and market value. With increased investment and collaboration, this tool can transform the diary and meat sectors, empowering farmers and preserving native breeds for generations to come. Proteomic profiling presents a powerful avenue for exploring the genetic diversity and adaptive potential of Nigerian indigenous goats. By leveraging this technology, researchers and breeders can gain valuable insights into the genetic traits of these goats, enabling the development of strategic approaches for sustainable livestock production in Nigeria.

Furthermore, proteomic analysis can inform breeding programs by identifying proteins associated with desirable traits, facilitating the selective breeding of goats enhanced genetic potential and improved performance.

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