

PROTEOMIC PROFILING OF HETEROGENEOUS RABBIT POPULATIONS IN NIGERIA: A REVIEW

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Abstract

In Nigeria, rabbit farming is a big livestock industry that supports the nation's economy and food security. On the other hand, little is known about the proteome profiles and genetic diversity of Nigerian rabbit populations. The analysis of all the proteins in a biological sample, known as proteomic profiling, has proven to be an effective method for determining the molecular foundations of rabbit traits. This review identifies the prospects and challenges of proteomic profiling of heterogeneous rabbit populations in Nigeria. It can however be concluded that proteomic profiling will aid in the improvements of rabbit stocks in Nigeria. By applying this knowledge to develop more efficient breeding techniques, rabbit farming in Nigeria can become more sustainable and productive overall. By combining proteomic data with other omics technologies, researchers can better understand the biology of rabbits and develop targeted strategies to improve rabbit farming in Nigeria.

Description of Problem

Rabbits can be raised on grain-free diet because food prices are rising and the demand for grains is rising, it is advantageous to be able to raise a good protein on garden fodder in developing countries. Rabbits are noted for their early maturity, high fecundity, rapid growth rates, and high feed conversion rates. Compared to a calf for a cow and up to two kids for a goat, when given the right care, rabbits can yield over forty kits annually (1). Furthermore, according to (2), rabbits are odorless, noiseless, and able to adapt to a wide range of habitats, unlike many larger ruminants.

According to several authors (3, 4, 5), rabbit farming, also referred to as cuniculture, is a type of mini-livestock production that can help farmers increase their income and boost agricultural productivity while also meeting the recommended level of animal protein intake by humans. Compared to other meat sources, rabbit meat has a reduced cholesterol content, making it a rich source of animal protein (6). Compared to other livestock, they require less space and

money to raise, and because they can use a variety of forages and household waste as feed, feeding them is less expensive. Additionally, because they are extremely prolific, farmers can easily grow their flock quickly (7). Since rabbit manure is a good source of organic manure and has been utilized to increase plant production (8), it can be considered an organic fertilizer. Improving breeding techniques, disease resistance, and overall productivity require an understanding of the genetic diversity and proteomic profiles of rabbit populations (9). The research on proteomic profiling of heterogeneous rabbit populations in Nigeria is summarized here, and its implications for rabbit farming are discussed.

According to (10), proteomics is the study of protein interactions, functions, compositions, and structures as well as how they affect cellular processes. Compared to genomics, proteomics offers a deeper understanding of the structure and function of the organism. But because the expression of proteins varies with time and environment, it is far more complex than genomics (11). A thorough understanding of the proteins expressed in the various tissues and

organs of rabbits can be obtained through proteomic profiling, which also sheds light on the molecular processes underlying significant characteristics like growth, reproduction, and disease resistance. The present status of proteome research on African rabbit populations is outlined in this review, along with its implications for rabbit farming in the area.

Proteomic Profiling of Rabbit Populations

Proteomics is the comprehensive analysis of the structure and function of proteins to comprehend the nature of an organism (12). Among the most important instruments for analyzing protein profiles in cells is mass spectrometry. However, due to their complexity and dynamic nature, biomarker discovery continues to be the primary challenge in proteomics. Thus, an understanding of biological systems and how diseases alter them can be achieved by combining the proteomics approach with genomics and bioinformatics. But only a small portion of the blood's proteins have been examined in the majority of studies (13).

Numerous proteomics techniques exist, such as gel-free high-throughput screening technologies like multidimensional protein identification technology (14), stable isotope labeling with amino acids in cell culture (15), isotope-coded affinity tag, and isobaric tagging for relative and absolute quantitation (16). One-dimensional (1D) and two-dimensional (2D) gel electrophoresis (2-DE) (17). Tissues, organelles, and cells can be studied using shotgun proteomics (18), 2D difference gel electrophoresis (2D-DIGE) (19), and protein microarrays (20). High-throughput processing methods include label-free quantification of high mass resolution liquid chromatography (LC)-tandem mass spectrometry (MS), large-scale western blot assays (21), and multiple reaction monitoring assays (22). (23) 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 PTMs of expressed proteins under various

environmental or disease states can be achieved through protein expression mapping (23). 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 (24).

Proteomic methods including mass spectrometry, 2D gel electrophoresis, and bioinformatics analysis have not been widely employed in studies examining the proteomes of African rabbit populations (25, 26). However, proteins linked to a number of physiological functions, such as metabolism, immunity, and stress response, have been found through these investigations. Proteomic analysis of rabbit skeletal muscle, for instance, has revealed proteins essential to meat production that are involved in muscle growth and development.

Implications for Rabbit Farming

There are various ramifications for rabbit farming from the proteomic profiling of Nigeria's heterogeneous rabbit populations. Firstly, it offers useful data for creating molecular markers linked to desired characteristics like growth rate, resistance to disease, and quality of meat. It also advances our knowledge of the molecular mechanisms that underpin key physiological processes in rabbits, which can help us design more focused breeding programs. Thirdly, it can aid in the creation of nutritional strategies that are specifically targeted at enhancing the productivity and well-being of rabbits in various environmental settings. Fourth, proteomic research can aid in the creation of vaccines and remedies for illnesses that afflict African rabbits.

Future Directions

Proteomic profiling of rabbit populations in Nigeria is still in progress as there are a number of obstacles to overcome. Among these are the requirements for more thorough research encompassing a larger spectrum of rabbit populations and the fusion of proteomic data with other omics technologies like metabolomics and genomics. In order to improve rabbit farming

practices in Nigeria and deepen our understanding of rabbit biology, future research should concentrate on tackling these issues.

Conclusion and Application

A valuable way to understand the genetic diversity and molecular mechanisms underlying key physiological processes in rabbits is to conduct proteomic profiling of heterogeneous rabbit populations in Nigeria. The overall productivity and sustainability of rabbit farming in Nigeria can be increased by using this information to create more effective breeding strategies. Through the integration of proteomic data with other omics technologies, scientists can enhance their comprehension of rabbit biology and devise focused approaches to ameliorate rabbit farming in Nigeria.

References

1. Dairo, F.A.S., Abi, H.M. and Oluwatusin, F.M. (2012). Social acceptability of rabbit meat and strategies for improving its consumption in Ekiti State, southwestern Nigeria. *Livestock Research for Rural Development*, 24(6).
2. Anthony, V. and Madu, I. (2015). Survey of the current status and seasonal problems associated with rabbit production in Kaduna metropolis. *Journal of Basic and Applied Research in Biomedicine*, 1(1): 36-39.
3. Biobaku, W.O. and Doumu, E O. (2003). Growth response of rabbits fed graded levels of processed and dehulled sunflower seed. Nigeria. *Journal of Animal Production*, 30(1): 32-36.
4. Ajala, M.K. and Balogun, J.K. (2004). Economics of rabbit production in Zaria, Kaduna State. *Tropical Journal of Animal Science*, 7(1): 1-10.
5. Oluwatusin, F. (2014). Determination of rabbit keeping in the tropics: Evidence from Nigeria. *Journal of Economics and Sustainable Development*, 5 (6): 57-62.
6. Nistor, E., Bampidis, V.A., Pacala, N., Pentea, M., Tozer, J. and Prundeanu, H. (2013). Nutrient content of rabbit meat as compared to chicken, beef and pork meat. *Journal of Animal Production Advances*, 3(4): 172-176.
7. Okpakpor, U. E., Adeleke, M. L., Adegbenro, M., & Onibi, G. E. (2021). Assessment of rabbit production value chain in South-West Nigeria. *Annals of Animal and Biological Research*, 1(1): 40-44.
8. Adi, I.P.T.S., Yuliartin, M.S. and Udayana, T. G. B. (2020). Effect of Rabbit compost and NPK on the growth and yield of Zucchini (*Cucurbita pepo* L.). *Sustainable Environment Agricultural Science*, 4(2): 151-156.
9. Oseni, S.O. and Lukefahr, S.D. (2014). Rabbit production in low-input systems in Africa: situation, knowledge and perspectives—A review. *World Rabbit Science*, 22(2): 147-160.
10. Wilkins, M.R., Sanchez, J.C., Gooley, A.A., Appel, R.D., Humphery-Smith, I., Hochstrasser, D.F. and Williams, K.L. (1996). Progress with proteome projects: why all proteins expressed by a genome should be identified and how to do it. *Biotechnology and Genetic Engineering Reviews*, 13(1): 19-50.
11. Holman, J.D., Dasari, S. and Tabb, D.L. (2013). Informatics of protein and posttranslational modification detection via shotgun proteomics. *Proteomics for Biomarker Discovery*, 1002: 167-179.
12. Babatunde, O., Ajayi, B.A., Akintunde, A.O., Akinsola, K.F. and Osunkeye, J. O. (2025). Prospects of Proteomics in Goat Breeding in Nigeria: A Narrative Review. *Journal of Applied Animal Science*, 18(1): 41–56.
13. Al-Amrani, S., Al-Jabri, Z., Al-Zaabi, A., Alshekaili, J., and Al-Khabori, M. (2021). Proteomics: Concepts and applications in human medicine. *World Journal of Biological Chemistry*, 12(5): 57.
<https://doi.org/10.4331%2Fwjbc.v12.i5.57>

14. Washburn, M. P., Wolters, D. and Yates, J. R. (2001). Large-scale analysis of the yeast proteome by multidimensional protein identification technology. *Nature Biotechnology*, 19(3): 242-247.
15. Ong, S.E., Blagoev, B., Kratchmarova, I., Kristensen, D.B., Steen, H., Pandey, A. and Mann, M. (2002). Stable isotope labeling by amino acids in cell culture, SILAC, as a simple and accurate approach to expression proteomics. *Molecular and Cellular Proteomics*, 1(5): 376-386.
16. Ross, P.L., Huang, Y.N., Marchese, J.N., Williamson, B., Parker, K., Hattan, S., Khainovski, N., Pillai, S., Dey, S., Daniels, S. and Purkayastha, S. (2004). Multiplexed protein quantitation in *Saccharomyces cerevisiae* using amine-reactive isobaric tagging reagents. *Molecular and Cellular Proteomics*, 3(12): 1154-1169.
17. Vercauteren, F. G., Bergeron, J. J., Vandesande, F., Arckens, L. and Quirion, R. (2004). Proteomic approaches in brain research and neuropharmacology. *European Journal of Pharmacology*, 500(1-3): 385-398.
18. Wolters, D.A., Washburn, M.P. and Yates, J.R. (2001). An automated multidimensional protein identification technology for shotgun proteomics. *Analytical Chemistry*, 73(23): 5683-5690.
19. Klose, J., Nock, C., Herrmann, M., Stühler, K., Marcus, K., Blüggel, M., Krause, E., Schalkwyk, L.C., Rastan, S., Brown, S.D. and Büsow, K. (2002). Genetic analysis of the mouse brain proteome. *Nature Genetics*, 30(4): 385-393.
20. Cutler, P. (2003). Protein arrays: The current state-of-the-art. *Proteomics*, 3(1): 3-18.
21. Schulz, T.C., Swistowska, A.M., Liu, Y., Swistowski, A., Palmarini, G., Brimble, S.N., Sherrer, E., Robins, A.J., Rao, M.S. and Zeng, X. (2007). A large-scale proteomic analysis of human embryonic stem cells. *BMC Genomics*, 8(1): 1-16.
22. Stahl-Zeng, J., Lange, V., Ossola, R., Eckhardt, K., Krek, W., Aebersold, R. and Domon, B. (2007). High sensitivity detection of plasma proteins by multiple reaction monitoring of N-glycosites. *Molecular and Cellular Proteomics*, 6(10): 1809-1817.
23. Yoithapprabhunath, T.R., Nirmal, R.M., Santhadevy, A., Anusushanth, A., Charanya, D., Chinthu, K.S. and Yamunadevi, A. (2015). Role of proteomics in physiologic and pathologic conditions of dentistry: Overview. *Journal of Pharmacy & Bioallied Sciences*, 7(Suppl 2): S344.
24. Pandey, A. and Mann, M. (2000). Proteomics to study genes and genomes. *Nature*, 405(6788), 837-846.
25. Miller, I., Rogel-Gaillard, C., Spina, D., Fontanesi, L. and M de Almeida, A. (2014). The rabbit as an experimental and production animal: from genomics to proteomics. *Current Protein and Peptide Science*, 15(2): 134-145.
26. Ribeiro, D.M., Bandarrinha, J., Nanni, P., Alves, S.P., Martins, C.F., Bessa, R.J.B., Falcão-e-Cunha, L. and Almeida, A.M. (2020). The effect of *Nannochloropsis oceanica* feed inclusion on rabbit muscle proteome. *Journal of Proteomics*, 222:103783.