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Genome-Wide Association Studies to Optimize Indigenous Chickens Production in Tropical Countries: A Review

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ABSTRACT

Indigenous chickens in tropical countries are characterized by remarkable adaptability to harsh environmental conditions, disease resilience and suitability for low-input scavenging production systems, however, they exhibit relatively low productivity compared to commercial breeds. Genome-wide association studies (GWAS) have emerged as powerful tools for unraveling the genetic architecture of complex traits in these populations offering new opportunities for genetic improvement. This review synthesizes current genomic findings on indigenous chicken populations in tropical regions focusing on GWAS applications for production traits, disease resistance, heat tolerance and adaptation. Key findings reveal moderate to high heritabilities for body weight (0.50-0.69), antibody responses to major pathogens (0.11-0.79) and heat tolerance traits with numerous significant single nucleotide polymorphisms (SNPs) and candidate genes identified. Notable candidate genes include *ATP1A1*, *PLCB4*, *RYR2* and *AKT3* for thermotolerance, *MX1*, *CDC16*, *TOLLIP* and *ROBO2* for Newcastle disease and infectious bursal disease resistance, and *PBX1*, *LDB2* and *NCAPG* for growth performance. The review highlights the feasibility of genomic selection for simultaneous improvement of productivity and resilience in indigenous chicken ecotypes. Challenges including limited phenotyping infrastructure, small population sizes and genotype-by-environment interactions are discussed alongside recommendations for integrating genomic tools into sustainable breeding programs in tropical countries.

1. Introduction

The global poultry sector is the fastest-growing livestock subsector, driven by rising demand for animal protein particularly in developing countries (FAO, 2023). In tropical regions, indigenous chickens constitute a significant proportion of poultry populations and play a vital role in rural livelihoods providing high-quality protein, income and cultural value. In sub-Saharan Africa, approximately 80% of poultry production occurs on smallholder village farms where chickens are typically reared outdoors under free-ranging conditions. These indigenous ecotypes are well adapted to local environments and raised in scavenging production systems demonstrating resilience to disease challenges despite the near absence of routine vaccination and biosecurity measures (Wong et al., 2017). However, indigenous chickens are generally less productive than commercial breeds with slower growth rates, lower egg production and smaller body sizes (Kebede, 2024). Management and genetic improvement programs have been hampered by a lack of routine data recording which is essential for conventional selective breeding. The genetic architecture of production traits in indigenous African chickens remains poorly characterized limiting the design of effective breeding strategies (Kanlisi et al., 2024).

Recent advancement in genomic technologies offers a transformative opportunity to overcome the limitations of traditional breeding in indigenous chicken populations. GWAS enables the identification of genetic markers associated with traits of economic importance providing a basis for marker-assisted selection (MAS) and genomic selection (GS). These approaches can accelerate genetic gain while preserving the adaptive characteristics that make indigenous chickens valuable in tropical production systems (Zhou et al., 2024). Therefore, the objective of this review was to synthesize current genomic findings related to GWAS applications in indigenous chicken populations of tropical countries with emphasis on production traits, disease resistance, heat tolerance and adaptation. The review also discusses methodological considerations, challenges and future directions for integrating genomic tools into sustainable breeding programs.

2. Methodology

2.1 Literature Search Strategy

A comprehensive literature search was conducted using databases including PubMed, Web of Science, Scopus, AGRIS, and Google Scholar. Peer-reviewed articles published between 2010 and 2026 were prioritized with seminal earlier works included where relevant. Only studies that focused on (i) indigenous or locally adapted chicken populations in tropical or sub-tropical countries, (ii) employed GWAS, selection signature analysis or genomic prediction methodologies and (iii) reported significant SNP-trait associations or candidate genes were included while studies on commercial broiler or layer lines without relevance to indigenous populations were excluded unless they provided comparative insights.

2.2 Data Extraction and Synthesis

For each included study, information was extracted on population characteristics, sample size, genotyping platform, statistical methods, traits analyzed, significant SNPs and candidate genes. Findings were synthesized thematically according to trait categories such as growth and

production, disease resistance, heat tolerance and adaptation. Tables were constructed to summarize key GWAS findings and candidate genes.

3. Results

3.1 GWAS for Growth and Production Traits

Growth performance is a primary target for genetic improvement in indigenous chickens. A GWAS of Rwandan indigenous chickens identified four significant SNPs (rs74098018, rs13792572, rs314702374 and rs14123335) associated with body weight on chromosomes 8, 11, and 19. Putative candidate genes in the vicinity of these SNPs included pre-B-cell leukemia homeobox 1 (*PBX1*), *GPATCH1*, *MPHOSPH6* and *MRM1*. *PBX1* is involved in skeletal muscle differentiation through regulation of canonical Wnt signaling making it a plausible candidate for growth regulation (Habimana et al., 2021).

A large-scale study of 2,573 dual-purpose Sasso chickens raised under smallholder farm conditions in Ethiopia identified 15 distinct markers significantly associated with growth, carcass traits, NDV titres, IgA levels and chicken survival following quality assurance with 2.9 million SNP markers used in genomic analyses (Morris et al., 2024). Results revealed a largely polygenic mode of genetic control for all phenotypic traits suggesting that genomic selection may be more effective than marker-assisted selection for growth improvement.

Similarly, a comprehensive GWAS of 1,113 Ghanaian local chickens from three agro-ecological zones using imputed Affymetrix Axiom® 600K SNP-chip genotypes identified 58 1-Mb SNP windows on chromosomes 1, 2, 4, 5, 6, 7, 8, 9, 13, 18 and 33 each explaining more than 1% of the genetic variance for at least one growth, carcass or internal organ trait. Heritabilities for body weight at week 22 (BW22), average daily gain (ADG), dressed weight, breast weight, thigh weight, wing weight, drumstick weight and neck weight ranged from 0.50 to 0.69 while head weight, shank weight and gizzard weight were moderate (0.31-0.35). Candidate genes included *EMX2*, *CALCUL1*, *ACVR1B*, *CACNB1*, *RB1*, *MLNR*, *FOXO1*, *NCAPG*, *LCORL*, *LAP3*, *LDB2*, *KPNA3* and *CAB39L* (Kanlisi et al., 2024).

In Eritrea, indigenous chickens raised in low-input village systems exhibit marked variation in body size including a reduced body size phenotype associated with reduced feed consumption, thermotolerance, disease resistance and adaptability to resource-limited environments. Genetic variants associated with this phenotype have been identified through genomic analyses offering insights into the genetic basis of adaptation to tropical production systems (Gheyas et al., 2026).

3.2 GWAS for Disease Resistance

Infectious diseases remain a major constraint to indigenous chicken production in tropical countries. A landmark GWAS of two distinct indigenous Ethiopian chicken ecotypes investigated the genetic architecture of antibody response to four major infectious diseases—infectious bursal disease (IBDV), Marek's disease (MDV), fowl typhoid (SG), and fowl cholera (PM)—along with resistance to *Eimeria* and cestode parasitism, and two production traits (body weight and body condition score). The study derived significant moderate to high heritabilities for IBDV, MDV, and PM antibody titres, cestode infestation, body weight, and body condition score, with heritability estimates ranging from 0.11 to 0.79. Genome-wide significant SNPs were identified for each trait, and selective sweep analyses revealed a locus on chromosome 18 associated with viral antibody titres and resistance to *Eimeria* parasitism within a positive selection signal. Importantly, no significant genetic correlations were found between production, immune, and disease traits, implying that selection for enhanced antibody response and disease resistance will not adversely affect production (Psifidi et al., 2016).

A subsequent joint analysis of the two Ethiopian ecotypes confirmed the presence of genetic variability and identified SNPs significantly associated with immune, disease and production traits with candidate genes including *TOLLIP*, *ANGPTL5*, *BCL9*, *THEMIS2* for IBDV, *GRM7* for MDV and *MAP3K21* for SG (Banos et al., 2020; Psifidi et al., 2016).

For Newcastle disease (ND), a continuing global threat to domestic poultry, a study of three popular Tanzanian chicken ecotypes challenged with a lentogenic NDV strain estimated moderate heritabilities (0.18-0.35) for various host response phenotypes. Five quantitative trait loci (QTL) associated with growth and/or response to NDV were identified by single-SNP analyses with immune-related genes such as *ETS1*, *TIRAP* and *KIRREL3* located in regions associated with viral load at 6 days post-infection. These findings indicate that NDV response traits may be improved through selective breeding to enhance NDV resistance and vaccine efficacy in Tanzanian local ecotypes (Walugembe et al., 2019).

In Rwanda, GWAS identified four significant SNPs (rs314787954, rs13623466, rs13910430 and rs737507850) on chromosome 1 strongly associated with antibody response to ND. The closest genes to these SNPs included cell division cycle 16 (*CDC16*), zinc finger BED-type containing 1 (*ZBED1*), myxovirus resistance 1 (*MX1*) and growth factor receptor bound protein 2 related adaptor protein 2 (*GRAP2*). *MX1* is particularly notable as it encodes a GTPase with antiviral activity against a broad range of RNA viruses making it a strong candidate for ND resistance (Habimana et al., 2021).

In Cameroon, a genome-wide association study identified two SNPs in and around the *ROBO2* gene as being involved in modulating antibody response to NDV in native chickens. Similarly, in Ethiopia, genomic markers associated with antibody response to NDV in Sasso chickens identified SNPs including rs316795557 (*FOXP2*), rs313761644 (*CEP170B*) and rs733628728 providing further evidence for the genetic basis of NDV response (Berihulay et al., 2026). These findings collectively demonstrate the feasibility of genetic improvement for disease resistance in indigenous chicken populations.

3.3 GWAS for Heat Tolerance and Adaptation

Heat stress is a critical constraint to poultry production in tropical regions. Indigenous chickens routinely survive high environmental temperatures (40-45°C) that cause significant mortality and production loss in commercial breeds, however, the genetic mechanisms of thermotolerance remain poorly understood (Nawaz et al., 2021). Genomic analysis of Nigerian indigenous chickens from different agro-climatic conditions identified several candidate genes for adaptation, particularly in relation to thermotolerance and immune response including *cytochrome P450 2B4-like*, *TSHR*, *HSF1*, *CDC37*, *SFTPB*, *HIF3A*, *SLC44A2* and *ILF3*. The *TSHR* (thyroid stimulating hormone receptor) gene variant has been suggested to enhance the ability to tolerate and adapt to hot environmental circumstances in tropical climates (Rachman et al., 2025).

A recent integrative genomic analysis across 14 geographically and climatically diverse chicken breeds identified 25 high-confidence genes under selection with *ATP1A1*, *PLCB4*, *RYR2* and *AKT3* forming a regulatory hub coordinating cardiovascular, calcium and survival signaling. These genes converge on interconnected adrenergic, calcium and GnRH signaling pathways with coordinated expression across heart, hypothalamus and liver forming an integrated thermoregulatory axis. Transcriptome-wide association study (TWAS) analysis linked *ATP1A1* to 145 gene-trait associations across 13 tissues and 14 trait categories and cross-species phenome-wide association study (PheWAS) validated conserved roles in cardiovascular function (*RYR2*) and ionic homeostasis (*ATP1A1*) (Xu et al., 2026).

Furthermore, a study examining selective sweeps in indigenous chickens from Saudi Arabia and Sri Lanka identified 12 genes under positive selection involved in adaptations to both tropical desert and tropical monsoon island climates. Additionally, selection signatures detected in Sri Lankan, Brazilian and Egyptian chickens implicated genes such as *TRMTIL*, *SOCS2* and *NFKB1* in adaptation to hot environments (Xu et al., 2022).

A genome-wide scan for selection signatures in domestic chickens from tropical and temperate regions of Asia identified 34 genes with signatures of positive selection including *FABP2*, *RAMP3*, *SUGCT* and *TSHR*, and genes related to vascular smooth muscle contractility (*CAMK2*) (Guo et al., 2022). Whole-genome analyses also revealed *SLC33A1* and *TSHR* genes exhibiting stronger signatures for positive selection in tropical chicken genomes providing insights into how environmental temperature stress can lead to advantageous genomic adaptations (Xu et al., 2022).

3.4 Selection Signatures

Beyond GWAS, selection signature analyses have provided complementary insights into the genomic basis of tropical adaptation. An integrated environmental and genomic analysis of African indigenous chickens applied ecological niche modeling combined with genome-wide selection signature analyses (XPEHH and Fst) and genotype-environment association (redundancy analysis) to identify genomic signatures of adaptation in African village chickens. These regions harbor several gene clusters including regulatory genes suggesting a predominantly oligogenic control of environmental adaptation (Kebede et al., 2024).

Natural selection footprints among African chicken breeds and village ecotypes have been investigated revealing that high-altitude-adapted East African populations showed selection signatures with genes for angiogenesis, oxygen-heme binding, and transport (Elbeltagy et al., 2019). In Ethiopian indigenous chickens, landscape genomics revealed regions associated with adaptive phenotypic and genetic variation informing the design of genetic improvement programs that aim to increase productivity and resilience (Kebede et al., 2024). Also, South African indigenous chickens' genetic diversity has been explored through ecological niche modelling and landscape genomics as strategic conservation techniques. This review explores the impact of natural selection on indigenous chicken, genetic diversity, population size and the advancement of technologies in understanding local adaptation drivers (Dzomba et al., 2024).

3.5 Summary of Key GWAS Findings

Table 1: Summary of significant SNPs and candidate genes identified in GWAS of indigenous chickens in tropical countries

Trait Category	Population	Significant SNPs/Genes	Chromosome	Reference
Body weight	Rwanda indigenous chicken	rs74098018, rs13792572, rs314702374, rs14123335; *PBX1*, *GPATCH1*, *MPHOSPH6*, *MRM1*	8, 11, 19	Habimana et al. (2021)
Growth, carcass, internal organs	Ghanaian local chickens	58 SNP windows; *EMX2*, *CALCUL1*, *ACVR1B*, *CACNB1*, *RB1*, *MLNR*, *FOXO1*, *NCAPG*, *LCORL*, *LAP3*, *LDB2*, *KPNA3*, *CAB39L*	1, 2, 4, 5, 6, 7, 8, 9, 13, 18, 33	Kanlisi et al. (2024)
Growth, carcass, NDV, IgA, survival	Ethiopian Sasso chickens	15 distinct markers	Various	Morris et al. (2024)
IBDV, MDV, PM, *Eimeria*, cestodes	Ethiopian ecotypes	Genome-wide significant SNPs; locus on chromosome 18; *TOLLIP*, *ANGPTL5*, *BCL9*, *THEMIS2*, *GRM7*, *MAP3K21*	18	Psifidi et al. (2016); Banos et al. (2020)
NDV response	Tanzanian local ecotypes	QTL on multiple chromosomes; *ETS1*, *TIRAP*, *KIRREL3*	Various	Walugembe et al. (2019)

Trait Category	Population	Significant SNPs/Genes	Chromosome	Reference
NDV antibody response	Rwanda indigenous chicken	rs314787954, rs13623466, rs13910430, rs737507850; *CDC16*, *ZBED1*, *MX1*, *GRAP2*	1	Habimana et al. (2021)
Thermotolerance	Nigerian indigenous chickens	*cytochrome P450 2B4-like*, *TSHR*, *HSF1*, *CDC37*, *SFTPB*, *HIF3A*, *SLC44A2*, *ILF3*	Various	Rachman et al. (2025)
Heat adaptation	14 diverse breeds	*ATP1A1*, *PLCB4*, *RYR2*, *AKT3*	Various	Xu et al. (2026)
Heat stress resistance	White Leghorn	*PRKD1*, *CDH23*, *WIPF3*, *TRAT1*, *CACNB2*, *TRPV2*, *TRPV1*, *TRPV3*, *ATP2B4*, *CALM1*, *BDNF*, *SCIN*	Various	Hosseinzadeh et al. (2025)
Heat tolerance	Asian tropical/temperate chickens	*FABP2*, *RAMP3*, *SUGCT*, *TSHR*, *CAMK2*	Various	Guo et al. (2022)

4. Discussion

4.1 Genetic Architecture of Production Traits

The findings from GWAS in indigenous chicken populations reveal that production traits such as body weight and growth are largely polygenic, controlled by many loci of small effect. This is consistent with the genetic architecture of complex traits in other livestock species and has important implications for breeding strategy. While individual SNPs of large effect have been identified (e.g., *PBX1* for body weight in Rwandan chickens, *LDB2* and *NCAPG* in Ghanaian chickens), the polygenic nature of growth suggests that genomic selection which captures the effects of many markers simultaneously may be more effective than marker-assisted selection based on a few significant SNPs.

The identification of moderate to high heritabilities for body weight (0.50-0.69) and body condition score in Ethiopian and Ghanaian ecotypes indicates that genetic improvement through selection is feasible (Kanlisi et al., 2024; Psifidi et al., 2016). Furthermore, the absence of significant genetic correlations between production and disease resistance traits suggests that simultaneous improvement of both productivity and resilience is achievable. This is a crucial finding for breeding programs in tropical countries where animals must be both productive and adaptable to local conditions. The Eritrean reduced body size phenotype represents an interesting case where reduced feed consumption, thermotolerance and disease resistance are associated with smaller body size. This suggests that selection for reduced body size may be a viable strategy for resource-limited environments although careful consideration of market preferences and production goals is necessary (Gheyas et al., 2026).

4.2 Disease Resistance: Opportunities and Challenges

The genetic architecture of disease resistance in indigenous chickens is characterized by moderate heritabilities and multiple significant SNP associations. The identification of *MX1* as a candidate gene for ND resistance is particularly promising given its known antiviral function (Habimana et al., 2021). Similarly, the association of *TOLLIP* with IBDV response highlights the role of innate immune pathways in disease resistance (Banos et al., 2020). However, translating these findings into breeding programs faces several challenges. First, disease resistance traits are often difficult and expensive to measure requiring controlled challenge experiments or extensive field recording. Second, the genetic correlations between different diseases traits are not well characterized as selection for resistance to one pathogen may not confer resistance to others. Third, genotype-by-environment interactions may modulate the expression of resistance genes particularly in the diverse agro-ecological zones of tropical countries.

The finding that selection for altered antibody response does not affect production traits is encouraging as it suggests that breeding goals can include both productivity and disease resistance without trade-offs (Psifidi et al., 2016). However, the long-term effects of selection on overall fitness and adaptation remain to be determined. The GIP IL program's development of a genetic selection platform focusing on NDV resistance and productivity traits demonstrates the practical application of these findings (Zhou et al., 2024).

4.3 Heat Tolerance

Heat tolerance is arguably the most important adaptive trait for indigenous chickens in tropical countries particularly in the context of global climate change. The identification of a cardio-neuroendocrine calcium signaling network involving *ATP1A1*, *PLCB4*, *RYR2* and *AKT3* provides a mechanistic understanding of heat adaptation (Xu et al., 2026). These genes coordinate cardiovascular function, calcium signaling and survival pathways across multiple tissues forming an integrated thermoregulatory axis. The convergence of selection signatures on genes involved in oxidative stress response, heat shock response and cellular stress pathways

(e.g., *HSF1*, *HIF3A*) suggests that natural selection has shaped the genomic architecture of heat tolerance in indigenous chickens over millennia. The *TSHR* gene which regulates thyroid function and metabolic rate has emerged as a consistent candidate for heat adaptation across multiple populations (Rachman et al., 2025; Guo et al., 2022; Xu et al., 2022). The identification of genes such as *TRPV1*, *TRPV2*, *TRPV3*, and *CDH23* that are involved in thermosensation provides additional insights into the sensory mechanisms of heat detection and response. These findings suggest that heat tolerance is a polygenic trait involving multiple physiological systems and that genomic selection may be the most effective approach for improving this trait.

4.4 Integrating Genomic Tools into Breeding Programs

The translation of GWAS findings into practical breeding programs requires careful consideration of several factors. First, the validation of SNP-trait associations in independent populations is essential as initial discoveries may be population-specific. Second, the development of low-cost genotyping platforms such as small SNP panels is necessary for implementation in resource-limited settings. Third, breeding objectives must balance productivity with adaptation, disease resistance and heat tolerance. The African Chicken Genetic Gains (ACGG) programs now known as Tropical Poultry Genetic Solutions (TPGS) has pioneered the selection and use of indigenous chicken strains with high productivity in semi-scavenging systems in the tropics (Dessie et al., 2024). The integration of genomic information into these programs could accelerate genetic gain while preserving the adaptive characteristics that make indigenous chickens valuable. Optimization of response to selection using genomic selection in indigenous chicken breeding programs has been investigated with results showing that genomic selection produced 38.7% greater genetic gain, 27% lower rate of inbreeding and 21.0% higher accuracy of selection compared to conventional selection (Mrode et al., 2026). These findings support the implementation of genomic selection in indigenous chicken breeding programs.

Furthermore, the development of the INDICHICK SNP chip with 74k to 75k markers represents a collaborative effort between ILRI and ICAR-DPR serving as a specialized genomic tool for native chicken breeds. During development, around 7 million SNPs were identified across ten indigenous breeds and two exotic lines with 75,192 SNPs selected for the final chip including 62 breed-specific markers (IPSA, 2025).

5. Conclusion

Genome-Wide Association Studies have provided valuable insights into the genetic architecture of production, disease resistance and heat tolerance traits in indigenous chickens of tropical countries. Moderate to high heritabilities and numerous significant SNP-trait associations have been identified with plausible candidate genes implicated in growth (*PBX1*, *LDB2*, *NCAPG*), disease resistance (*MX1*, *CDC16*, *TOLLIP*, *ROBO2*) and heat tolerance (*ATP1A1*, *TSHR*, *HSF1*, *RYR2*). The polygenic nature of most traits suggests that genomic selection may be the most effective breeding strategy. The absence of adverse genetic correlations between production and disease resistance traits supports the feasibility of simultaneous improvement of productivity and resilience. However, challenges including small sample sizes, limited phenotyping infrastructure and genotype-by-environment interactions must be addressed. With appropriate investment in genomic infrastructure and breeding programs, GWAS can contribute to the sustainable improvement of indigenous chicken production in tropical countries enhancing food security and rural livelihoods while preserving valuable genetic resources.

References

[1] Banos, G., Lindsay, V., Desta, T. T., Bettridge, J., Sanchez-Molano, E., Vallejo-Trujillo, A., Matika, O., Dessie, T., Wigley, P., Christley, R. M., Kaiser, P., Hanotte, O., & Psifidi, A. (2020). Integrating genetic and genomic analyses of combined health data across ecotypes to improve disease resistance in indigenous African chickens. *Frontiers in Genetics, 11*, 543890.

[2] Berihulay, H., Luo, W., Lao, A., Chuxiao, L., Jebessa, E., Zou, X., Ji, J., Qu, H., Chen, P., Cai, M., Shu, D., & Luo, C. (2026). Genome-wide association study reveals putative genetic determinants of longitudinal immune responses to avian influenza and Newcastle disease in chickens. *Genetics Selection Evolution*. https://doi.org/10.1186/s12711-026-01077-2

[3] CTLGH. (2021). Tropical poultry production: Research towards sustainable systems. Centre for Tropical Livestock Genetics and Health.

[4] Dessie, T., et al. (2024). African Chicken Genetic Gains: Building the business case. ILRI.

[5] Dzomba, E. F., et al. (2024). South African indigenous chickens' genetic diversity, and the adoption of ecological niche modelling and landscape genomics as strategic conservation techniques. *Poultry Science, 104*(1), 104508.

[6] Elbeltagy, A. R., et al. (2019). Natural selection footprints among African chicken breeds and village ecotypes. *Frontiers in Genetics, 10*, 376.

[7] FAO. (2023). The State of Food and Agriculture 2023. Food and Agriculture Organization of the United Nations.

[8] Gheyas, A. A., Rachman, M. P., Bamidele, O., Dessie, T., Smith, J., & Hanotte, O. (2026). Genetic variants associated with reduced body size in indigenous chickens of Eritrea: A genome-wide association study. *Poultry Science, 105*(11), 107502.

[9] Guo, X., et al. (2022). Genome-wide scan for selection signatures and genes related to heat tolerance in domestic chickens in the tropical and temperate regions in Asia. *Poultry Science, 101*(7), 101917.

[10] Habimana, R., Ngeno, K., Okeno, T. O., Hirwa, C. D., Tiambo, C. K., & Yao, N. K. (2021). Genome-wide association study of growth performance and immune response to Newcastle disease virus of indigenous chicken in Rwanda. *Frontiers in Genetics, 12*, 723980.

[11] Hosseinzadeh, S., Rafat, S. A., Javanmard, A., Hasanpur, K., & Bardou, P. (2025). Whole genome analysis of selection associated with resistance to heat stress in chickens. *BMC Genomics, 26*, 145.

[12] Kanlisi, R. A., Amuzu-Aweh, E. N., Naazie, A., Otsyina, H. R., Kelly, T. R., Gallardo, R. A., Lamont, S. J., Zhou, H., Dekkers, J., & Kayang, B. B. (2024). Genetic architecture of body weight, carcass, and internal organs traits of Ghanaian local chickens. *Frontiers in Genetics, 15*, 1297034.

[13] Kebede, F. G., et al. (2024). Landscape genomics reveals regions associated with adaptive phenotypic and genetic variation in Ethiopian indigenous chickens. *BMC Genomics, 25*, 232.

[14] Morris, K. M., Sutton, K., Girma, M., Sánchez-Molano, E., Solomon, B., Esatu, W., Dessie, T., Vervelde, L., Psifidi, A., Hanotte, O. H., & Banos, G. (2024). Phenotypic and genomic characterisation of performance of tropically adapted chickens raised in smallholder farm conditions in Ethiopia. *Genetics Selection Evolution, 56*, 28.

[15] Mrode, R., et al. (2026). Optimization of response to selection using genomic selection in indigenous chicken breeding programmes. *Animal Breeding and Genetics*.

[16] Nawaz, A. H., et al. (2021). Climate change and poultry production: A review. *World's Poultry Science Journal, 77*(4), 869–882.

[17] Psifidi, A., Banos, G., Matika, O., Desta, T. T., Bettridge, J., Hume, D. A., Dessie, T., Christley, R., Wigley, P., Hanotte, O., & Kaiser, P. (2016). Genome-wide association studies of immune, disease and production traits in indigenous chicken ecotypes. *Genetics Selection Evolution, 48*, 74.

[18] Rachman, M. P., Bamidele, O., Dessie, T., Smith, J., Hanotte, O., & Gheyas, A. A. (2025). Genomic analysis of Nigerian indigenous chickens reveals their genetic diversity and adaptation to heat-stress. *Scientific Reports, 15*, 3421.

[19] Walugembe, M., Mushi, J. R., Amuzu-Aweh, E. N., Chiwanga, G. H., Msoffe, P. L., Wang, Y., Saelao, P., Kelly, T., Gallardo, R. A., Zhou, H., Lamont, S. J., Muhairwa, A. P., & Dekkers, J. C. M. (2019). Genetic analyses of Tanzanian local chicken ecotypes challenged with Newcastle disease virus. *Genes, 10*(7), 546.

[20] Wong, J. T., et al. (2017). Small-scale poultry production in Africa: A review. *World's Poultry Science Journal, 73*(4), 851–866.

[21] Xu, N. Y., Liu, Z. Y., Yang, Q. M., Bian, P. P., Li, M., & Zhao, X. (2022). Genomic analyses for selective signatures and genes involved in hot adaptation among indigenous chickens from different tropical climate regions. *Frontiers in Genetics, 13*, 906447.

[22] Xu, N. Y., et al. (2026). Integrative genomic analysis and gene expression patterns reveal a cardio-neuroendocrine signaling network for heat adaptation in geographically diverse chickens. *Poultry Science, 105*(6), 106744.

[23] Zhou, H., Baltenweck, I., Dekkers, J., Gallardo, R., Kayang, B. B., Kelly, T., Msoffe, P. L. M., Muhairwa, A., Mushi, J., Naaziee, A., Otsyina, H. R., Ouma, E., & Lamont, S. J. (2024). Feed the Future Innovation Lab for Genomics to Improve Poultry: A holistic approach to improve indigenous chicken production focusing on resilience to Newcastle disease. *World's Poultry Science Journal, 80*(2), 271–291.