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Genomic Approaches for the Conservation and Improvement of Korean Native Chickens – A Review

Minjun Kim[1], Eunjin Cho[2], Jaewon Kim[1], Roshani Fernando[1], Jinhyeong Kim[1] & Jun Heon Lee[1, 2*]

[1]Department of Animal Science and Biotechnology, Chungnam National University, Daejeon 34134, Korea
[2]Department of Bio-AI Convergence, Chungnam National University, Daejeon 34134, Korea

Abstract

Understanding the genomic basis of indigenous livestock is essential for both conservation and sustainable improvement. Korean native chickens (KNCs), although representing a small fraction of the poultry industry in Korea, are distinguished by their unique meat quality, robustness, and adaptability. Recent genomic studies have investigated their genetic diversity, evolutionary history, and economically important traits. High-density SNP arrays and population structure analyses have clarified the distinct identity of KNC lines, while runs of homozygosity have provided insights into inbreeding, conservation progress, and functional loci. Selection signature analyses have identified candidate genes related to growth, metabolism, reproduction, and immune function, reflecting line-specific adaptation. Genome-wide association studies have further identified variants associated with taste-active compounds, fatty acid composition, and growth traits, offering a foundation for genomic selection. Moreover, research on disease-related genes, such as the major histocompatibility complex B genes, has documented substantial genetic variability in KNCs, establishing important genomic resources for subsequent studies on avian immunity and pathogen response. Together, these findings highlight KNCs as valuable reservoirs of genetic variation with implications for both conservation and breeding. More broadly, the genomic insights obtained from KNCs provide a cautious yet informative model for indigenous livestock worldwide, demonstrating how genomic tools can support sustainable breeding programs that balance biodiversity preservation with productivity.

Keywords

Korean native chickens, genetic diversity, selection signatures, genomic selection, association study, diseas-resistance genes

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Correspondence to
Jun Heon Lee
junheon@vnua.edu.vn

ORCID
Jun Heon Lee
https://orcid.org/0000-0003-3996-9209

Introduction

With the improvement of individual income levels and changes in dietary habits, meat consumption in Korea has steadily increased. Among the various types of meat, chicken is particularly preferred due to its cost efficiency compared to other livestock and its lower cholesterol content relative to beef and pork. As a result, consumer preference for chicken has led to a continuous rise in annual chicken consumption in Korea (Jang *et al*., 2024).

In Korea, chickens raised for meat are classified into conventional broilers and Korean domestic chickens (KDCs). Conventional broilers account for the majority of chicken meat production and are the most common type of chicken raised on farms due to their short rearing period and rapid growth. In contrast, KDCs represent only about 3% of total meat production, reflecting their slower growth rate and lower productivity compared to conventional broilers (Park *et al*., 2020). As domestic chicken meat production relies heavily on foreign breeds, the industry remains vulnerable to fluctuations in international markets. Therefore, it is essential to preserve and improve domestic breeds by investigating their genetic characteristics and enhancing their competitiveness through selective breeding programs.

KDCs are traditionally divided into native and commercial breeds. The native group can be further subdivided into two categories. Indigenous breeds have preserved pure bloodlines without crossbreeding with foreign breeds for more than seven generations. Adapted breeds originate from foreign breeds introduced as inbred lines and have been maintained and selectively bred for at least seven generations in Korea, thereby adapting to the local climate (Choi *et al*., 2014).

Korean native chickens (KNCs), a subgroup of native breeds, consists of five breeds and 12 lines, with purebreds preserved by the National Institute of Animal Science (NIAS). Six lines from two breeds represent indigenous populations, namely Gray-brown (KNC-G), Black (KNC-B), Red-brown (KNC-R), White (KNC-W), Yellow-brown (KNC-Y), and Yeonsan Ogye. The remaining six lines from the other three breeds represent adapted populations, including the Rhode Island Red, Cornish, and Leghorn lines. In addition, the local breeds Hyunin KDC and Jeju KDC are maintained in small numbers at private institutions. Korean poultry breeding companies have developed commercial KDCs to meet local consumer preferences. Hanhyup, a representative breeding company, manages lines such as Rhode Island Red, Cornish, Plymouth Rock, and New Hampshire (Cho *et al*., 2023). These breeds and lines are registered in the Domestic Animal Diversity Information Service (DAD-IS) of the FAO (FAO, 2025).

In recent years, the identification of quantitative trait loci (QTLs) has become a crucial approach in understanding the genetic basis of economically important traits in chickens, such as growth rate, carcass composition, meat quality, and disease resistance. QTL mapping integrates genetic marker information with phenotypic data to identify genomic regions associated with specific traits (Abasht *et al*., 2006). In the context of KNCs, QTL studies have helped identify loci associated with traits such as muscle fiber composition, fat deposition, and immune responses, providing valuable insights for marker-assisted selection. These findings have significantly contributed to the design of genomic selection strategies aimed at improving productivity and maintaining the unique characteristics of KNCs.

Although KNCs account for a small proportion of the domestic poultry industry, their unique flavor, texture, and robustness have recently led to an increase in demand. Consequently, research has focused on identifying genetic loci and candidate genes associated with the taste and texture of KNCs, as well as investigating their physiological advantages, including robustness and immune traits.

This review aimed to provide a comprehensive understanding and future directions for research on indigenous chickens, with a particular focus on KNC populations. By summarizing their genetic diversity and emphasizing the advantages of KNCs, such as their unique flavor and robustness, this review aimed to demonstrate their value and potential in both conservation and breeding programs.

Recent findings in genomic research on Korean native chickens

Genetic diversity analysis

KNCs have long been recognized as valuable livestock resources as they possess unique genetic characteristics and superior meat quality and have adapted to local environments. However, industrialization, crossbreeding with commercial breeds, and intensive breeding processes pose the risk of weakening the unique genetic characteristics of these populations. Genetic diversity analysis is crucial for assessing the conservation value of these resources and providing fundamental data for developing future breeding strategies. In particular, elucidating the genetic structure and variation within and across native chicken populations is essential for understanding their genetic uniqueness, exploring commercial viability, and developing long-term, sustainable genetic resource management strategies.

To elucidate the genetic structure of KNCs, comparisons with commercial and native chickens from other countries are required. To this end, the global data collected through the SYNBREED project in Germany consists of individuals selected from 174 breeds worldwide, including African, American, Asian, European, and commercial breeds (Malomane *et al*., 2019). These data can be useful for assessing the genetic structure of KNCs. Based on this data, Cho *et al*. (unpublished data) elucidated the genetic relationships between KNCs and global populations. Principal component analysis (PCA) based on high-density SNP array data (approximately 460,000 SNPs) revealed that the KNC population clustered with some European and commercial breeds. Furthermore, genetic distance (Reynold's distance) analysis and ADMIXTURE analysis clearly distinguished the indigenous KNCs from other global populations, while the adapted KNCs showed high similarity to commercial breeds of the same origin. Notably, the indigenous KNCs were found to be closely related to some European populations, including Hungarian Yellow, Rhode Island Red, and New Hampshire. This suggests that while maintaining regional uniqueness, KNCs may have partially shared genetic information through historical crosses or common ancestry with some exotic breeds. At the same time, KNCs exhibit high genetic homogeneity through long-term selection and population fixation, and possess value as unique genetic resources. These results serve as crucial baseline data for developing future trait-improvement and conservation strategies for KNCs.

In addition to global comparisons, a genetic analysis of 21 domestic chicken breed populations revealed clear population structure and genetic differentiation (Cho *et al*., 2023). PCA results revealed that indigenous KNCs were separated into distinct genetic clusters reflecting differences in breeding history and selection pressures, while some populations, such as the Hyunin and Jeju populations, exhibited partial admixture. Genetic distance and Fst estimates suggested close relationships among populations with similar origins, while highlighting differentiation among lineages that had been managed independently, such as the indigenous KNCs. ADMIXTURE results further support these populations, reflecting both common ancestry and subsequent divergence. While the indigenous KNCs generally maintained a distinct genetic identity, some local chicken populations exhibited stronger genetic drift and signs of inbreeding. These results highlight the heterogeneous genetic architecture within the KNC populations, suggesting that, despite sharing a common origin, these populations have differentiated through long-term breeding, local adaptation, and management practices. These results emphasize the importance of considering intra-breed variation when establishing conservation strategies and breeding programs for KNCs.

Selection signature analysis

Indigenous livestock breeds have been shaped by long-term environmental pressures, resulting in distinct genetic characteristics. KNCs, which underwent severe bottlenecks and subsequent restoration programs, exhibit genomic patterns reflecting both historical adaptation and artificial selection (Jin *et al.*, 2017). Selection leaves characteristic footprints such as extended linkage disequilibrium, reduced genetic diversity, and increased homozygosity, which can be used to trace evolutionary history and identify loci for economically important traits, including egg production, growth, immunity, and resilience (Saravanan *et al.*, 2020). Furthermore, runs of homozygosity (ROH) further provide insights into inbreeding levels where pedigree information is limited (Purfield *et al*., 2012). Recent studies employing selection signature analyses in KNCs have revealed line-specific adaptation, inbreeding patterns, and candidate genes, contributing to the genetic characterization and improvement of these indigenous populations.

To investigate genomic regions under selection in KNCs, recent studies have utilized high-density SNP chip data and homozygosity-based analyses (integrated haplotype score (iHS) and the ratio of integrated extended haplotype homozygosity between populations (Rsb)) across different lines. Using a 600K SNP array, five lines (KNC-G, KNC-B, KNC-R, KNC-W, and KNC-Y) were analyzed with iHS and Rsb to detect selection signals within and between populations (Cho *et al*., 2021). While selective sweep regions showed limited overlap among the lines, each exhibited distinct genomic targets shaped by unique selection histories. Several candidate genes, including *IGF11*, *ERBB4*, *MEF2D*, *APOO*, and *CNTN1*, were located within these regions. These genes are associated with muscle development, immune function, neurogenesis, and metabolic regulation, highlighting their potential contributions to growth, reproduction, and environmental adaptability. Notably, the NL and NW lines displayed selection patterns resembling those of commercial layers and broilers, respectively, underscoring their relevance for trait-specific breeding.

Analyses of ROH have provided important insights into the genomic architecture and inbreeding history of KNCs. In KNC-R, SNP data from 651 samples across four generations revealed an average of 49 ROH segments per individual, the majority of which were shorter than 4Mb, indicating low levels of recent inbreeding (Macharia *et al*., 2024a). The ROH-based inbreeding coefficient (FROH) ranged from 0.039 to 0.327, with no marked differences observed among the four generations analyzed. These results demonstrate substantial progress in conserving KNC-R and the effective maintenance of genetic diversity through breeding programs. Five ROH islands were detected, overlapping with quantitative trait loci (QTL) associated with carcass traits and production performance. Functional annotation of these regions highlighted notable genes, including *NELL1* and *BBOX1*, linked to bone development and feed efficiency, and *LGR4*, involved in metabolic regulation and growth performance. Additional candidates, including *BDNF*, *COL6A1*, and *AMYA1* were also identified, suggesting roles in environmental stress response, intramuscular fat deposition, and glucose metabolism. Collectively, these findings underscore the effectiveness of conservation programs in preserving genetic diversity while demonstrating the utility of ROH analysis for uncovering functional genes and selection hotspots associated with production traits.

In KNC-Y, an analysis of 675 samples identified 29,958 ROH segments with an average length of 2.71 Mb and a FROH of 0.13 (Kim *et al*., 2024). ROH islands enriched on chromosomes 1, 2, 4, 5, 7, 8, and 11 contained genes such as *ANO5*, *LSS*, *PLA2G4A*, and *PTGS2*, many of which are involved in metabolic and reproductive processes. Notably, *PTGS2*, which may play a pivotal role in follicular maturation and development, suggests promising opportunities for the genetic improvement of egg production traits in KNC-Y through future breeding programs.

Together, these studies illustrate the diverse genomic signatures shaped by historical selection, inbreeding, and conservation in KNCs. By identifying line-specific selection signals and candidate genes, they provide valuable resources for understanding functional differentiation and for guiding sustainable breeding strategies that balance genetic improvement with the preservation of indigenous diversity.

Association study

Genomic selection has emerged as an effective approach to accelerate genetic improvement in indigenous livestock populations. For quantitative traits, the identification of QTL represents a prerequisite, as it provides the foundation for the application of genomic selection. As meat-type chickens, KNCs are primarily valued for two economic traits: meat quality and growth performance. KNC meat is known to contain higher levels of taste-active compounds than commercial broiler meat (Jin *et al.*, 2017). These compounds act as precursors of flavor development during cooking, and the elevated abundance of umami-related substances contributes to the favorable sensory properties of KNC meat.

In recent years, genome-wide association studies (GWAS) have been conducted in KNC-R to identify QTL associated with the levels of taste-active compounds. Nucleotide-related metabolites, such as inosine-5'-monophosphate (IMP) and the dipeptides carnosine and anserine, are recognized contributors to umami taste (You *et al.*, 2024), while fatty acids play a key role in meat flavor generation through lipid oxidation during cooking (Dinh *et al.*, 2021). A GWAS for nucleotide-related compounds in KNC breast meat revealed significant associations on chromosome 5, with *DUSP8* and *IGF2* identified as candidate genes linked to IMP and its metabolites (Kim *et al.*, 2023). Subsequent Sanger sequencing-based fine mapping detected variants within these genes that showed significant associations with the traits (Munyaneza *et al.*, 2023). For dipeptides, a GWAS identified *HNMT* on chromosome 7 as a candidate gene associated with carnosine and anserine content (Kim *et al.*, 2024), and fine mapping research further revealed variants within this gene associated with carnosine content (Munyaneza *et al.*, 2024). Regarding fatty acid composition, significant signals were identified on chromosomes 2, 10, and 22, and candidate genes such as *GPNMB* and *SFRP1* were implicated as regulators of fatty acid metabolism, underscoring their potential utility for simultaneously improving meat flavor and nutritional quality (Munyaneza *et al.*, 2025). GWAS targeting growth-related traits in KNCs have also yielded informative results. Significant associations for live body weight were identified on chromosome 11, while carcass weight was associated with loci on chromosomes 1, 3, and 10. These genomic regions harbored putative candidate genes involved in cell growth, muscle development, and energy metabolism (Macharia *et al.*, 2024b). These studies provide a foundation for genomic selection in KNCs. Expanding such efforts to traits beyond meat quality and growth, including immunity and reproduction, will enable broader genetic improvement of this indigenous breed.

Studies on immune-related genes

As the demand for poultry continues to rise, so does the spread of infectious diseases, which ultimately compromise the health of the animals and their growth and production. These challenges highlight the need to enhance the birds' immunity through genetics and breeding. The major histocompatibility complex (MHC) region is a set of genes that present antigens to the immune system, and it plays a key role in immune defense. The chicken MHC is smaller and simpler than its human counterpart, consisting of classical class I (*BF*) and II (*BL*) genes (Kaufman *et al.*, 1995). The LEI0258 marker, a variable number of tandem repeats (VNTR) located within the MHC-B region, has been widely used to assess genetic diversity due to its high level of polymorphism and correlation with specific serological haplotypes (Fulton *et al*., 2006; Chazara *et al*., 2008). More recently, a high-density 90-SNP panel was developed to characterize the MHC-B haplotype diversity (Fulton *et al*., 2016).

Native chicken breeds possess unique characteristics, such as the ability to thrive in harsh environmental conditions and disease resistance, in low-input, low-output systems (Mwacharo *et al*., 2006). The aforementioned six KNC lines have been extensively studied for growth-related traits, whereas fewer studies have focused on disease resistance. In this context, studies have investigated the MHC-B diversity

(Manjula *et al*., 2020a; Manjula *et al*., 2020b; Manjula *et al*., 2021), characterization of the MHC-B region genes (Ediriweera *et al*., 2022; Agulto *et al*., unpublished data), and the *ANP32A* gene, which has been associated with avian influenza virus (Kim *et al*., 2025) in KNC lines.

Using the MHC-B 96-SNP panel, noticeable genetic diversity was observed among KNC populations compared with commercial breeds (Manjula *et al.*, 2020a). A total of 117 haplotypes were identified, with native populations contributing the majority of the unique variants. These findings highlight the importance of maintaining immune competence against a vast variety of pathogens. Following the above study, a total of 41 BSNP haplotypes were identified in six KNC lines using the updated MHC-B 90-SNP panel (Manjula *et al*., 2020b). This analysis showed a high level of genetic diversity in the MHC-B region. Interestingly, 33 haplotypes were novel while eight haplotypes were found in previously described standard haplotypes (Fulton *et al*., 2016), showing the specificity of the genetic background of the KNCs and evidence of shared ancestry with commercial breeds. Furthermore, the LEI0258 marker revealed only 14 alleles, showing the superiority of SNP-based analysis. The disparity highlights the limitations of relying solely on the LEI0258 marker for diversity studies, confirming the value of SNP-based approaches for assessing the extent of MHC-B variation. An analysis of 11 MHC-linked MS markers across 29 populations from Sri Lanka, Bangladesh, South Korea, and Nigeria revealed noticeable diversity among the indigenous chickens (Manjula *et al*., 2021). The widely used LEI0258 marker was the most polymorphic, with 38 alleles. Indigenous chicken populations from Sri Lanka, Bangladesh, and Nigeria exhibited higher allele richness and haplotype diversity than the Korean and commercial chicken breeds. In total, 409 haplotypes were identified, of which 89 were shared and 320 were unique. The findings highlight the high allelic richness and structural variability of the chicken MHC-B region in native chicken breeds compared to commercial lines, paving the path for future breeding strategies of native chickens, with a special focus on KNCs.

Completing these findings, a full consensus of 15 MHC genes (*BG1-BF2*) in six KNC lines was successfully generated using the long-range PCR method followed by next-generation sequencing (Ediriweera *et al*., 2022). The study showed a high level of genetic diversity, with each line carrying between 567 and 658 variants, of which 25% to 33% were unique. Importantly, the greater levels of polymorphisms observed, particularly in the *BF1*, *BF2*, *BLB2*, and *BG1* genes, suggests altered antigen presentation capacity in KNC, which is responsible for their unique disease resistance profile. More recently, six KNC lines were analyzed for *BF2* gene diversity using the individuals homozygous for both the MHC-B 90-SNP panel and LEI0258 marker (Agulto *et al*., unpublished data). Two standard BF2 haplotypes, B06 and B09, were found to be identical. In total, 30 novel variants were identified with more than half located within the peptide-binding region (exons 2 and 3). The majority of these variants overlapped with previously reported data (Ediriweera *et al*., 2022), providing a validation for the present study. Interestingly, four unique BF2 haplotypes were identified in the KNC populations, highlighting their role as a reservoir of genetic diversity. Collectively, these findings demonstrate that KNC populations are a rich reservoir of MHC diversity, emphasizing their implications for both conservation and the development of disease resistance in poultry. Apart from the genes in the MHC-B region, special focus was given to the *ANP32A* gene, which plays a pivotal role in avian influenza virus replication, as its 33-amino acid avian-specific insertion uniquely supports viral RNA polymerase activity (Domingues & Hale, 2017). Extensive genetic diversity has been reported within the *ANP32A* region, with 510 variants identified across 60 individuals in KNC chicken lines (Kim *et al*., 2025). Notably, two frame shift variants (rs733744684 C>CTCTGG and rs732131973 ACT>A) were detected, and both were predicted to disrupt protein function. Moreover, a synonymous variant (rs733980419 G>A) located within the avian-specific insertion was consistently observed in all the KNC lines. The genetic diversity observed in the *ANP32A* gene in KNCs is evidence of its potential role in avian influenza virus resistance, providing valuable resources for future breeding strategies.

Table 1. Recent genomic research on Korean native chickens

Research category	Description of population	Method	Key gene	Reference
Diversity analysis	21 KDC breeds and 179 global chicken populations (n = 4,224)	PCA, Fst, GD and ADMIXTURE\ (600K SNP chip)	-	Cho *et al*. (unpublished data)
	21 KDC breeds (n = 935)	PCA, Fst, GD and ADMIXTURE (600K SNP chip)	-	Cho *et al*. (2023)
Selection signature analysis	5 KNC lines and 5 commercial breeds (n = 245)	iHS and Rsb (600K SNP chip)	*IGF11, ERBB4, MEF2D, APOO, CNTN1*	Cho *et al*. (2021)
	KNC-R line (n = 651)	ROH (60K SNP chip)	*NELL1, BBOX1, LGR4, BDNF, COL6A1, AMYA1*	Macharia *et al*. (2024a)
	KNC-Y line (n = 675)	ROH (60K SNP chip)	*ANO5, LSS, PLA2G4A, PTGS2*	Kim *et al*. (2024)
Association study	KNC-R line (n = 637)	GWAS (60K SNP chip) (IMP, Inosine, and Hypoxanthine)	*IGF2, DUSP8, C5NT1AL*	Kim *et al*. (2023)
	KNC-R line (n = 284)	PCR-RFLP and KASP (IMP, Inosine, and Hypoxanthine)	*IGF2, DUSP8*	Munyaneza *et al*. (2023)
	KNC-R line (n = 637)	GWAS (60K SNP chip) (Carnosine and Anserine)	*HNMT, HNMT-like*	Kim *et al*. (2024)
	KNC-R line (n = 384)	PCR-RFLP and PACE (Carnosine)	*HNMT, HNMT-like*	Munyaneza *et al*. (2024)
	KNC-R line (n = 382)	GWAS (60K SNP chip) (C18:2, C20:2, and C24:1)	*GPNMB, SFRP1*	Munyaneza *et al*. (2025)
	KNC-R line (n = 637)	GWAS (60K SNP chip) (Live body weight and Carcass weight)	*FHOD1, TBC1D2B*	Macharia *et al*. (2024b)
Studies on immune-related genes	6 KNC lines (n = 36)	Targeted gene sequencing, MS genotyping and 90-SNP panel	*BF2*	Agulto *et al*. (unpublished data)
	6 KNC lines (n = 60)	Next-generation sequencing and Sanger sequencing	*ANP32A*	Kim *et al*. (2025)
	6 KNC lines (n = 6)	Long-range PCR amplification followed by next-generation sequencing	*BG1* to *BF2*	Ediriweera *et al*. (2022)
	6 KNC lines, 2 adapted KNC lines, 5 Korean commercial lines, 9 global native chicken breeds, 6 commercial lines, and MHC-B standard line (n = 490)	MS genotyping	*TRIM/Blec* gene region*, DMB1*	Manjula *et al.* (2021)
	3 KNC lines, 4 adapted KNC lines, 2 Korean commercial lines, 1 global native chicken breed, and 2 commercial lines (n = 477)	MHC-B genotyping using 96-SNP panel	*BG* region to *CD1A2*	Manjula *et al*. (2020a)
	6 KNC lines (n = 379)	MHC-B genotyping using 90-SNP panel and MS genotyping	*BG2* to *CD1A1*	Manjula *et al.* (2020b)

Note: KDC: Korean domestic chicken; KNC: Korean native chicken

Conclusions

Recent genomic research on KNCs has generated valuable insights into their genetic diversity, selection signatures, functional QTLs, and immune-related genes. These findings confirm that, despite their relatively small contribution to the poultry industry, KNCs carry distinctive traits such as superior meat quality, robustness, and disease resistance. At the same time, the genomic insights obtained from KNCs illustrate how indigenous livestock can be studied in a way that balances the preservation of local biodiversity with genetic improvement. Future research should extend beyond meat quality and growth to encompass reproduction, adaptation to climate stress, and disease resilience, ideally through multiomics integration, functional validation, and genomic selection in breeding programs. Moreover, these findings provide a cautious yet valuable model for other indigenous breeds worldwide, particularly in low-input production systems.

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