



## 유전 및 육종



## Comparison of genomic prediction methods for carcass traits in Hanwoo (Korean Brown Cattle) using genomic best linear unbiased prediction and machine learning approaches

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Genomic selection has become an essential tool for accelerating genetic improvement in livestock breeding. This study aimed to compare the predictive ability of single-trait GBLUP (ST-GBLUP), multi-trait GBLUP (MT-GBLUP), Random Forest (RF), Extreme Gradient Boosting (XGBoost), and Support Vector Regression (SVR) for four carcass traits in Hanwoo cattle: carcass weight (CWT), eye muscle area (EMA), backfat thickness (BFT), and marbling score (MS). A total of 10,170 Hanwoo steers were used, partitioned into a reference population ( $n = 9,170$ ) and a validation population ( $n = 1,000$ ). Genotyping was performed using the Illumina Bovine SNP50K BeadChip. ST-GBLUP and MT-GBLUP were implemented using the BLUPF90 software package, while RF, XGBoost, and SVR were applied as machine learning alternatives. Predictive ability was assessed as the Pearson correlation between predicted and observed values in the validation population. ST-GBLUP yielded predictive abilities of 0.487, 0.451, 0.429, and 0.453 for CWT, EMA, BFT, and MS, respectively, while MT-GBLUP produced comparable results at 0.487, 0.449, 0.431, and 0.451. Among machine learning models, SVR achieved the highest predictive ability at 0.411, 0.429, 0.414, and 0.447, followed by XGBoost at 0.425, 0.387, 0.316, and 0.384, and RF at 0.386, 0.359, 0.299, and 0.346. Although GBLUP-based methods generally outperformed ML models, SVR demonstrated competitive predictive ability, particularly for BFT and MS, suggesting that kernel-based approaches may partially capture nonlinear genomic effects in Hanwoo carcass traits.

**Key words :** Hanwoo, single nucleotide polymorphism (SNP), genomic best linear unbiased prediction (GBLUP), machine learning (ML), predictive ability

## Genomic characterization of Korean native chickens compared with Kyrgyz populations using genome-wide SNPs

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Indigenous chicken breeds represent important genetic resources due to their adaptability and unique genetic characteristics. However, intensive selection and commercialization have raised concerns about the loss of genetic diversity in native populations. This study aimed to investigate the population structure, genetic diversity, and effective population size ( $N_e$ ) of Korean native chickens (KNC) in comparison with Kyrgyz chicken populations using genome-wide SNP data. Whole-genome sequencing data were obtained from five Korean native chicken lines (GWR, GWY, CNW, GWB, and GWL) and two Kyrgyz populations (18\_KYG and 21\_KYG). Population structure was analyzed using principal component analysis (PCA), phylogenetic tree construction, and admixture analysis. Linkage disequilibrium (LD) decay patterns were used to estimate the effective population size. The results showed clear genetic differentiation between the Korean and Kyrgyz populations. Within the Korean native chickens, four distinct genetic clusters were identified, indicating lineage differentiation. Admixture analysis ( $K=6$ ) revealed well-defined ancestry components with limited gene flow among lines. LD decay analysis indicated that Kyrgyz populations exhibited faster decay rates, suggesting higher genetic diversity compared to that of Korean native chickens. Estimated  $N_e$  values varied among populations, with some Korean lines showing relatively low effective population sizes. These findings suggest that while Korean native chickens possess distinct genetic characteristics, they may face reduced genetic diversity in certain lines. Therefore, genomic-based conservation and management strategies are required to maintain genetic diversity and ensure the sustainable utilization of these valuable genetic resources.

**Key words :** Korean native chicken, genomic analysis, SNP, population structure, genetic diversity, effective population size

## Genetic evaluation of milk yield and heat tolerance in Korean Holstein cattle using a random regression model

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This study aimed to evaluate genetic parameters of milk yield and heat stress responses in Korean Holstein dairy cattle using a random regression model (RRM). A total of 5,620,888 test-day records from 380,940 animals across 3,326 herds were analyzed, incorporating temperature-humidity index (THI) as an environmental indicator of heat stress.

Heritability of milk yield varied across lactation stages, showing the lowest values in early lactation and gradually increasing toward mid- and late lactation. Among parities, second-parity cows exhibited the highest heritability and estimated breeding value (EBV) reliability, indicating optimal conditions for genetic evaluation.

Reaction norm analysis revealed clear genetic variation in heat tolerance. Heat-tolerant individuals maintained or increased EBVs under high THI conditions, whereas heat-sensitive individuals showed declining trends. Additionally, incorporating THI into the model resulted in substantial re-ranking of individuals, suggesting that genetic evaluation without environmental factors may misrepresent true performance.

These findings highlight the importance of integrating environmental factors such as THI into genetic evaluation systems and provide a foundation for improving heat tolerance in dairy cattle breeding programs.

**Key words :** random regression model, temperature-humidity index, days in milk, heterogeneous residual variance

## Comparison of growth curve models for Hanwoo cattle: a simulation analysis of sample size and measurement interval

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This study evaluated the effects of sample size and measurement interval on the goodness of fit of growth curve models in Hanwoo steers using simulated body weight data. A simulated population of 2,000 animals was generated from the 2024 monthly reference body weights for Hanwoo steers, and sample sizes of 10, 30, 50, and 100 animals were tested under three measurement interval schemes: monthly, every 2 months, and every 3 months. Each sampling condition was repeated 10 times. The Gompertz, Logistic, and von Bertalanffy models were fitted under each condition, and model performance was assessed using the coefficient of determination ( $R^2$ ) and root mean square error (RMSE). The von Bertalanffy model consistently showed the best fit across all sample sizes and measurement intervals, followed by the Gompertz model, whereas the Logistic model showed the poorest fit. Model fit improved as sample size increased, but the improvement became limited beyond 50 animals. In contrast, differences among measurement intervals were relatively small. Under the monthly measurement condition with 100 animals, the von Bertalanffy model showed the highest fit ( $R^2 = 0.99995$ , RMSE = 1.935 kg), followed by the Gompertz model ( $R^2 = 0.99937$ , RMSE = 6.723 kg), whereas the Logistic model showed the lowest fit ( $R^2 = 0.99473$ , RMSE = 19.479 kg). These results suggest that the von Bertalanffy model is the most suitable for describing average growth patterns in Hanwoo steers and that practical growth curve analysis may be possible with moderate sample sizes and less frequent measurements.

**Key words :** Hanwoo, growth curve, Gompertz, Logistic, von Bertalanffy,  $R^2$ , RMSE

## Meta-GWAS reveals hidden shared genetic signals for meat quality traits across the Korean chicken populations

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Meat quality traits in chicken are genetically complex and often difficult to resolve within individual populations due to limited sample sizes and population-specific signals. This study applied a meta-genome-wide association study (meta-GWAS) framework to detect shared genetic variants associated with meat quality traits across three Korean chicken populations. Population-specific GWAS results were generated for multiple phenotypes and integrated through meta-analysis. Because of the limited sample size in each population, most traits did not reach significance in either single-population GWAS or meta-GWAS. Nevertheless, meta-GWAS identified a significant shared locus for inosine monophosphate (IMP), a representative nucleotide contributing to umami taste, on chromosome 5. Two significant SNPs showed consistent effect directions across populations with low heterogeneity, indicating a stable common association signal. Functional enrichment analysis of genes within the  $\pm 1$  Mb windows of these SNPs highlighted muscle structure-related components: troponin complex, striated muscle thin filament, myofilament, and insulin receptor recycling pathway. These findings suggest that the identified region may influence flavor-related variation through its effects on muscle structure and metabolic regulation. Overall, this study demonstrates the utility of meta-GWAS for identifying shared loci underlying complex meat quality traits in chickens under limited statistical power.

**Key words :** meta-GWAS, meat quality, flavor-related traits, Korean chicken populations

## Microsatellite markers for parentage testing in Korean native black goats: a review

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The domestic goat meat industry in South Korea has grown rapidly in recent years, raising concerns about mislabeled imported meat and the loss of purebred genetic characteristics through indiscriminate crossbreeding. To preserve the genetic integrity of Korean Native Black Goats (KNBG) and support traceability, a reliable microsatellite marker (MS) set is needed for parentage testing. This study reviewed articles on MS marker sets for parentage testing in goat. Literature screening was conducted using the databases PubMed, Web of Science, Scopus, and KCI with the terms “goat,” “microsatellite,” and “parentage,” along with their corresponding Korean keywords. As a result, 10 relevant articles were identified, collectively evaluating 430 candidate MS markers and ultimately recommending 125 final markers for goat parentage testing. The analysis showed that marker effectiveness varied across goat breeds, likely due to differences in genetic diversity, allele frequency distributions, and breed-specific mutations. Furthermore, only three of the 10 MS marker sets were validated in KNBG. Of these, the two earlier studies employed dinucleotide markers, which demonstrated high discriminatory power. A more recent study developed tri- and tetranucleotide markers, which reduced genotyping errors. However, these markers showed lower polymorphism than dinucleotide loci. Overall, the variable performance of existing marker sets highlights the need for a robust MS marker set with reliable performance across goat breeds in South Korea.

**Key words :** Korean native black goat, parentage testing, MS marker

## First haplotype-resolved assembly of Korean Jeju Black cattle using a trio-binning approach with nanopore sequencing

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Korean Jeju Black cattle are an important native genetic resource in Korea, yet a high-quality reference assembly is still needed to support future conservation and breed-specific genomic studies. In this study, we generated haplotype-resolved genome assemblies for both Hanwoo and Jeju Black cattle using a parent-offspring trio composed of a Hanwoo sire, a Jeju Black cattle dam, and their F1 hybrid fetus. Illumina short-read data from the parental individuals were generated at approximately 22.7× and 23.3× coverage, respectively, whereas the F1 offspring was sequenced using Oxford Nanopore Technologies (ONT) long-read sequencing at 75.8× coverage. To improve read accuracy prior to assembly, raw ONT reads were error-corrected using HERRO, and the corrected reads were assembled with Verkko using parental haplotype-specific k-mers. The Jeju Black cattle-derived haplotype assembly had a total length of 3,004,838,613 bp, which was close to the expected Hanwoo genome size (3.1 Gb). The longest haplotype-resolved scaffold length was 107.61 Mb and a scaffold N50 was 34.38 Mb. However, the assembly comprises 11,313 contigs, indicating limited contiguity and a fragmented state. The assembly achieved a BUSCO completeness of 95.36%, with 87.12% single-copy and 8.24% duplicated orthologs. Phasing accuracy showed switch and hamming error rates of 1.36% and 1.00%, respectively. This is the first *de novo* genome assembly of Korean Jeju Black cattle and provides a valuable resource for investigating breed-specific genomic research.

**Key words :** *de novo* assembly, Jeju Black cattle, long-read sequencing, phasing, trio-binning

## Genomic characterization of Holstein-Jersey crossbred cattle in Korea using genome-wide SNP data

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This study was conducted to establish a genomic reference for the Jersey population in Korea and to evaluate changes in breed composition across F1–F6 crossbred generations produced by repeated backcrossing of Jersey to Holstein. Genotype data were obtained using the Illumina BovineSNP50 V3 chip, and after quality control, 26,931 common SNPs from 742 Holstein, 494 Jersey, and 98 crossbred animals were used for analysis. Genetic structure was assessed using principal component analysis (PCA), and breed composition was estimated using supervised ADMIXTURE analysis. PCA clearly separated Holstein and Jersey into distinct genetic clusters, indicating strong genetic differentiation between the two breeds. ADMIXTURE analysis showed a progressive increase in Jersey ancestry across generations, with mean Jersey proportions of 55.2% in F1, 74.1% in F2, 87.0% in F3, and 99.7% in F4. The F5 and F6 generations also maintained more than 99% Jersey ancestry, and PCA showed that individuals from F4 onward nearly overlapped with the Jersey reference population. These results indicate that crossbred animals from the F4 generation onward are genetically almost indistinguishable from pure Jersey cattle. This study provides fundamental genomic information for establishing Jersey reference populations, determining breed composition in crossbred cattle, and developing registration criteria for Holstein–Jersey backcross progeny in Korea.

**Key words :** Jersey, Holstein, crossbred cattle, SNP, ADMIXTURE

## Blood transcriptome-based cell deconvolution for dissecting intrinsic gene expression changes in pigs

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Blood transcriptomes reflect both intrinsic gene expression and the composition of cell populations. Cell heterogeneity can substantially influence observed gene expression, potentially confounding conventional differential expression analyses. Therefore, this study aimed to integratively investigate the effects of cell composition and intrinsic gene expression changes in pigs. Blood transcriptome data were obtained from weaning (n = 3) and growing pigs (n = 3), and cell composition enrichment was estimated using the xCell method. Principal component analysis (PCA) was applied to cell enrichment profiles to capture the major variation in cellular composition, revealing that pigs were clearly separated by developmental stage. This indicated that the cell composition differed substantially between groups. Differentially expressed genes (DEGs) were identified using edgeR under two models: a baseline model without adjustment (WO) and an adjusted model account for cell type enrichment (WI). In the WO model, multiple DEGs were identified between groups; however, after adjusting for cell composition (WI), the number of significant DEGs was reduced. These results demonstrate that most gene expression differences in porcine blood are strongly influenced by cell composition. Our findings highlight the importance of accounting for cellular heterogeneity in blood transcriptome studies and provide a framework for disentangling cell composition effects from intrinsic gene expression changes.

**Key words :** pig, blood, transcriptome, cell deconvolution, intrinsic gene expression

## Glycobiology-based engineering of O-linked glycans in monkey FSH

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Follicle-stimulating hormone (FSH) is a glycoprotein hormone composed of  $\alpha$ - and  $\beta$ -subunits and plays essential roles in reproductive physiology. Because glycosylation is closely associated with hormone stability and biological activity, this study aimed to develop recombinant monkey FSH analogs with prolonged biological activity by introducing non-native O-linked glycosylation sites into single-chain monkey FSH. Two C-terminal peptide motifs, a 35-amino-acid equine CTP and a 31-amino-acid human CTP, were inserted between the  $\beta$ - and  $\alpha$ -subunits to generate O-linked glycan-enriched recombinant constructs. Recombinant proteins expressed in mammalian cells exhibited an increased molecular weight of approximately 50 kDa compared with native single-chain monkey FSH, which is generally 35–40 kDa. Enzymatic deglycosylation analysis using N-linked, O-linked, and sialic acid-cleaving enzymes partially confirmed that O-linked glycosylation contributed approximately 10–15 kDa to the observed molecular weight increase. These findings indicate that CTP-mediated O-linked glycosylation was efficiently incorporated into recombinant monkey single-chain FSH. In addition, receptor-mediated intracellular signaling, including pERK1/2 activation, is currently being investigated using FSH receptor-expressing cells and  $\beta$ -arrestin/GRK knockout systems. These results suggest that O-linked glycan engineering may provide a useful strategy for improving the molecular stability and sustained bioactivity of recombinant FSH.

**Key words :** recombinant monkey single-chain FSH, O-linked glycosylation, C-terminal peptide, pERK1/2 signaling

## Validation of an in-house SNP quality control pipeline using pedigree- and genomic-based relationship matrices

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This study validated an in-house SNP quality control (QC) pipeline for genomic estimated breeding value (GEBV) prediction in livestock using a pedigree of 7,498 individuals derived from 4,628 genotyped animals and genomic data from 4,032 individuals that passed batch- and population-level QC. Pipeline performance was evaluated by comparing the pedigree-based relationship matrix ( $A$ ) with the genomic relationship matrix ( $G$ ). Among the total 8,126,496 pairwise comparisons generated from 4,032 QC-passed individuals, 7,959,032 pairs with non-zero coefficients in  $A$  showed high concordance between  $A$  and  $G$  ( $r = 0.82$ ,  $RMSE = 0.068$ ). Linear regression analysis showed that the relationship between the two matrices was expressed as  $G = 0.9650A - 0.0569$ , indicating slight underestimation of  $G$  relative to  $A$ . The mean inbreeding coefficient was  $3.55 \pm 1.74\%$  in  $A$  and  $0.50 \pm 4.94\%$  in  $G$ , suggesting that genomic information more effectively captured Mendelian sampling variation. In addition, genomic relationship analysis identified 30,986 highly related pairs ( $G \geq 0.25$ ) among 4,028 pedigree-unrelated individuals. The number of related pairs per individual showed a median of 12 (IQR, 7–19), indicating that related pairs were concentrated within a subset of individuals. These findings suggest potential cryptic relatedness or undocumented pedigree relationships.

**Key words :** SNP quality control; in-house pipeline; validation; genomic relationship matrix; pedigree based relationship matrix

## Evaluation of single-step genomic best linear unbiased prediction integrating transformer embeddings in a closed nucleus herd

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To leverage complex genomic interactions in livestock evaluation, we incorporated deep feature representations from a Transformer architecture into single-step genomic best linear unbiased prediction (ssGBLUP). The simulated population, modeled as a closed nucleus herd to reflect the high levels of relatedness and linkage disequilibrium characteristic of intensive breeding programs, consisted of 20,000 individuals: 16,000 for training, 2,000 for validation, and 2,000 for testing. Transformer embeddings were utilized as a feature matrix to define an additional random effect, which was jointly predicted alongside the additive genetic effect in the single-step mixed model equations. Compared with baseline ssGBLUP, the integration of transformer embeddings improved the correlation between true breeding values and estimated breeding values from 0.3215 to 0.3418 for the validation set and from 0.2616 to 0.2994 for the test set. Similarly, the root mean square error (RMSE) decreased from 0.1604 to 0.1573 and from 0.1629 to 0.1586, respectively. These results indicate that Transformer embeddings can provide complementary information to standalone ssGBLUP. Further experiments using additional simulation replicates, hyperparameter tuning, and large observed datasets are required to assess robustness and practical utility.

**Key words :** genomic prediction, transformer, ssGBLUP, closed nucleus herd, stochastic simulation

## Single-cell transcriptomic atlas of Hanwoo *longissimus dorsi* muscle reveals marbling-associated cellular and molecular features

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Marbling is an important meat quality trait in Hanwoo cattle, but the cellular and molecular characteristics of skeletal muscle according to marbling grade remain unclear at single-cell resolution. In this study, we performed pilot single-cell RNA sequencing of Hanwoo *longissimus dorsi* muscle from high- and low-marbling samples to investigate marbling-associated cellular and transcriptional features. Single-cell transcriptomic data were processed and analyzed using standard bioinformatic pipelines, including quality control, doublet removal, integration, clustering, and marker-based cell type annotation. After filtering, 5,997 singlets from the high-marbling sample and 3,691 singlets from the low-marbling sample were analyzed. Integrated clustering identified 17 cell populations, including fibroblasts, myofibers, endothelial cells, pericytes, immune cells, satellite cells, and stromal populations. Marker gene analysis confirmed cell type-specific expression patterns related to muscle fibers, extracellular matrix, angiogenesis, immune cells, satellite cells, and metabolism. Differential expression analysis between high- and low-marbling samples revealed distinct transcriptional differences, including enrichment of muscle structural and contractile genes in the high-marbling sample. These findings provide a preliminary single-cell transcriptomic atlas of Hanwoo loin muscle and suggest potential cellular and molecular features associated with marbling grade. Further validation with additional biological replicates is required.

**Key words :** Hanwoo, biomarkers, marbling-associated cellular

## Wnt signaling pathway associated *cis*-lncRNA-mRNA crosstalk in Ogye breast muscle

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The Ogye, a unique Korean indigenous chicken breed with distinct black phenotypes, was compared to the Cornish breed to explore the molecular characteristics underlying the development of Ogye breast muscle. RNA-sequencing was performed on breast muscle tissues from 10-week-old Ogye and Cornish breeds to identify differentially expressed mRNAs and lncRNAs ( $|\log_2(\text{FC})| \geq 1$ ,  $P_{\text{adj}} < 0.05$ ). Functional enrichment was conducted through GSEA-based GO and KEGG analyses, and *cis*-acting targets of lncRNAs were predicted within a  $\pm 100$  kb window, followed by Spearman correlation and qRT-PCR validation. We identified 192 DEGs (61 up, 131 down). Down-regulated DEGs were primarily enriched in melanogenesis (e.g., *PMEL*, *TYRP1*, *MLANA*), while GSEA revealed that the Wnt signaling pathway and cell cycle regulation were significantly enriched in Ogye breast muscle tissues. Notably, the Wnt ligands *WNT16* and *WNT9A*, and the transcription factor *TCF7L2*, were up-regulated, alongside down-regulation of inhibitors such as *DKK2*. Furthermore, *cis*-acting analysis identified a strong positive correlation ( $|\rho| \geq 0.8$ ) between the DE lncRNA *MSTRG.4144* and its target *WNT9A* in both breeds, which was validated by qRT-PCR. These findings suggest that *MSTRG.4144*-mediated regulation of *WNT9A* may constitute a conserved mechanism, and its differential activation may contribute to the distinct developmental and functional characteristics of Ogye breast muscle. This research was supported by the Regional Innovation System & Education(RISE) program through the Jeonbuk RISE Center, funded by the Ministry of Education(MOE) and the Jeonbuk State, Republic of Korea.(2025-RISE-13-JBU)

**Key words :** Ogye, LncRNA, Wnt signaling pathway, *WNT9A*, *MSTRG.4144*

## Visualization of GEBV-phenotype relationships in Hanwoo steers for precision feeding

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This study aims to develop an AI-based precision feeding decision-making system that automatically recommends individualized feeding strategies for Hanwoo steers based on genomic information. The system is designed to maximize farm profit by applying enhanced feeding and extended rearing to top-GEBV (genomic estimated breeding value) animals and early slaughter to lower-GEBV ones. As a foundational module of this system, this study developed a visualization framework for the relationship between GEBV and carcass phenotypes using large-scale slaughter data. Phenotypic measurements and GEBV for carcass weight (CWT), eye muscle area (EMA), backfat thickness (BFT), and marbling score (MAR) were collected from 18,140 Hanwoo steers. CWT-GEBV and MAR-GEBV served as the X- and Y-axes of a  $3 \times 3$  matrix (top 30%, middle 40%, bottom 30%), on which phenotypic distributions (count, mean, variance) and individual-level patterns were overlaid. EMA phenotype responded positively to both axes, revealing genetic correlations among traits, while BFT phenotype responded only to CWT-GEBV. Within each GEBV region, phenotypic expression varied across individuals, enabling identification of animals that underperformed, matched, or exceeded their genetic potential. Future work will expand the matrix to  $6 \times 6$  or finer grids and integrate slaughter age, feeding stage, and ration data, advancing this framework into an AI-based decision-making system that automatically recommends differentiated feeding strategies by GEBV interval.

**Key words :** Hanwoo, genomic estimated breeding value (GEBV), carcass traits, visualization

## Genome-wide association study of coat color traits in Korean brindled cattle using genotype

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The Chikso is a Korean native cattle breed distinguished by its brindle coat color. This study aimed to elucidate the genetic signals affecting variation in brindle in Chikso cattle. The expression of brindle coat color was classified into four ordered scores, where higher scores indicate more extensive brindle expression (0 = non-brindle; 1 = sparse brindle; 2 = light whole-body brindle; 3 = clear whole-body brindle). A total of 9,370 phenotypic records and 4,100 genotyped animals were used in this study. A genome-wide association study (GWAS) was performed with sex and principal components included as covariates to account for potential false-positive associations. Estimated marginal mean brindle expression scores were lower in females than males (1.03 vs. 1.20). The heritability of brindle coat color was estimated at 0.52 using a Bayesian threshold animal model. In the GWAS, 18 SNPs reached genome-wide significance ( $p < 5 \times 10^{-8}$ ). Among these association signals, some were located near the previously reported ASIP and MC1R genes on BTA13 and BTA18, respectively. We also identified a novel locus on BTA6 harboring the CORIN gene, which is known to regulate ASIP signaling and therefore may act as a modifier of brindle expression in Chikso cattle. This study provides biologically plausible evidence for the variation in brindle expression and may contribute to breeding improvement of brindle expression in the Chikso population.

**Key words :** Korea Brindled Cattle (Chikso), coat color, GWAS, heritability, ASIP, CORIN, MC1R

## Evaluation of oleic acid and physicochemical meat quality in Hanwoo cattle

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This study investigated the potential of using oleic acid to enhance marbling score and tenderness in Hanwoo cattle. Using 2,852 progeny-test steers from the Korean Proven Bull program, genetic parameters for major fatty acid traits were estimated, and sires were classified into low-oleic, high-oleic, and intermediate groups based on estimated breeding values (EBVs) through clustering analysis. The progeny-test steers from the high-oleic sire group indicated a significantly higher ratio of monounsaturated to saturated fatty acids (MUFA/SFA) (mean = 1.290 vs. 1.184) than the low-oleic group, while maintaining comparable or slightly higher marbling scores (mean = 4.179 vs. 4.164). Multiple regression analysis showed that increased oleic acid proportion was significantly associated with reduced shear force, an indicator of meat tenderness (standardized coefficient = -0.435), and increased marbling score (standardized coefficient = 0.249). In particular, the genetic correlation between oleic acid and marbling score EBVs was estimated to be low (-0.028), indicating that oleic acid and marbling score may be regulated by relatively independent genetic mechanisms. Logistic regression analysis showed that progeny-test steers from the high-oleic sire group were significantly more likely than those from the low-oleic sire group to simultaneously rank within the top 25% for MUFA/SFA ratio and the bottom 25% for shear force (odds ratio = 3.04). Overall, incorporating oleic acid EBVs into breeding programs may provide an effective strategy for improving beef palatability and nutritional quality in Hanwoo cattle without adversely affecting current marbling levels.

**Key words :** Hanwoo, oleic acid, MUFA/SFA ratio, EBV, meat quality

## 젖소 산유능력 평가를 위한 신규 305일 보정계수 개발 및 정확도 검증

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젖소의 산유능력 평가를 위해 전 세계적으로 305일 보정유량을 개량 형질로 유전능력평가에 활용하고 있다. 우리나라는 2009년 개발된 보정계수(adjustment factor, AF)를 현재까지 사용하고 있으나, 개량 및 사육환경 변화로 기존 보정계수의 개선 필요성이 제기되고 있다. 본 연구는 유량, 유지방량, 유단백량 및 무지고형분량에 대한 신규 305일 보정계수(AF25)를 개발하고, 기존 보정계수(AF09)와 예측 정확도를 평가하였다. 분석에는 2019~2024년 유우군능력검정자료를 활용하였으며, 산차별로 이상치 제거와 검정일 범위, 군-분만년도, 검정횟수 및 비유기간 조건을 적용하여 자료를 정제하였다. 정제된 자료(1,728,258건)를 이용하여 최소자승평가를 추정하였으며, 이를 통해 형질·산차·그룹별 305일 보정계수를 산출하고, 보정계수 비선형 모델을 개발하였다. 정확도 검증은 두 단계로 수행하였다. 첫째, 검정 완료 개체 자료(46,080건)의 305일 누적 생산량을 실측값으로 설정하고, 305일부터 이전 검정기록을 단계적으로 삭제하여 AF09·AF25의 검증값과 실측값 간 RMSE(Root Mean Square Error)를 비교하였다. 그 결과, 유량, 유지방량, 유단백량 및 무지고형분량 모두에서 AF25의 RMSE가 AF09 대비 약 10%~20% 감소하였다. 둘째, 전자 유량계 자료(18,573건)의 실제 누적 유량을 실측값으로 설정하고, 10개의 가상 검정일 집단을 설정하여 검증값과 실측값 간 상관계수 및 RMSE를 비교하였다. AF25는 모든 집단에서 AF09 대비 높은 상관계수와 낮은 RMSE를 나타냈다. 결론적으로, AF25는 AF09보다 국내 젖소 산유능력 예측 정확도를 개선할 수 있으며, 향후 산유능력 평가에 활용할 수 있을 것으로 판단된다.

**Key words :** 젖소, 산유능력, 305일 유량, 보정계수

## Comparison of genetic evaluation models for meat quality pH traits in a Korean Duroc pigs

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This study was conducted to identify the optimal genetic evaluation model for the 24-h field pH trait in pigs, which is a critical indicator of pork meat quality. A total of 1,272 Duroc pigs, slaughtered between 2012 and 2025, were recorded for the phenotype. The herd-year-season (HYS) effect was fitted as fixed and random in two models, and termed as model-F and model-R, respectively. Slaughter year-season and slaughter age group were included as additional fixed effects in both models. Variance components were estimated using an animal model through REML in BLUPF90+ software. The estimated heritability ( $h^2$ ) was lower using model-R (0.087) than the  $h^2$  value using model-F (0.117). This difference in  $h^2$  could be attributable to the fit of HYS as a random effect. The AIC and  $-2\log L$  values from the model-R were  $-922.91$  and  $-928.91$ , respectively, which were lower than those of model-F ( $-912.76$  and  $-916.76$ ). The mean accuracy of estimated breeding values was 1.5%p higher in model-R ( $0.45 \pm 0.04$ ) than in model-F ( $0.44 \pm 0.04$ ). Despite the model-R yielded a lower  $h^2$  than the model-F, the former demonstrated higher breeding value accuracy and lower model fit indices (AIC and  $-2\log L$ ), suggesting that model-R could be more appropriate genetic evaluation model for 24-h field pH in Korean Duroc pigs.

**Key words :** Duroc, pH, genetic evaluation, model comparison, accuracy

## Engineering of O-linked glycan modification in recombinant bovine FSH

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Follicle-stimulating hormone (FSH) and luteinizing hormone (LH) are essential glycoproteins that regulate mammalian gonadal function via GPCR-mediated signaling. In this study, we engineered long-acting bovine FSH (bFSH) analogues by designing single-chain constructs that link the  $\alpha$ -subunit to the C-terminus of the  $\beta$ -subunit using overlapping PCR. To enhance biological activity and metabolic half-life, we incorporated O-glycosylated peptide sequences: the human CG  $\beta$ -subunit carboxyl-terminal peptide (hCTP) and the equine CTP (eCTP), featuring four and twelve O-linked glycosylation sites, respectively. These recombinant proteins (rec-bFSH), containing C-terminal Strep tags, were expressed in CHO-K1 and CHO-S cells. Western blot analysis identified broad bands at 44–52 kDa, which shifted to approximately 35 kDa upon deglycosylation, confirming the successful attachment of N- and O-linked oligosaccharides. Functional characterization is currently evaluating signal transduction through the FSH receptor, specifically examining  $\beta$ -arrestin and GRK pathways using knockout cell models. Our results suggest that strategic glyco-structure manipulation provides a powerful framework for developing next-generation, long-acting FSH analogues with enhanced therapeutic potential.

**Key words :** rec-bovine FSH, CHO cells, O-linked modification, knock out cell

## Genomic selection and metabolite profiling for quality differentiation of Goheung Hanwoo

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This study established a precision breeding system and brand strategy for Goheung Hanwoo by integrating genomic selection with scientific quality characterization. Based on a pedigree analysis of 41,616 cattle and MS marker-based paternity testing of 809 samples, a core foundation group was established by selecting superior individuals from 128 genomically analyzed cows. This selection maximized genetic reliability, securing vital resources for independent proven bull production. Simultaneously, quality assessments revealed superior water-holding capacity and juiciness, while metabolite profiling identified unique amino acid and fatty acid patterns contributing to the flavor profile of Goheung Hanwoo. By linking genomically verified resources with metabolic data, this study provides a scientific foundation for a self-reliant breeding model and premium branding. This paper was supported by Suncheon National University Glocal University Project Fund in 2025.

**Key words :** Hanwoo, genomic selection, foundation cow, metabolite profiling, quality differentiation

## Genetic analysis of stage-specific survivability traits in Korean Holstein cattle

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Survivability is critical to dairy farm efficiency, reducing involuntary culling and replacement costs. This study evaluated the genetic potential of stage-specific survivability across the first three lactations in Korean Holsteins. Data from 92,591 cows calving between 2002 and 2024 were analyzed. Survivability was defined across three lactation stages (0–90, 91–299, and 300 days to next parity) within each lactation for three consecutive parities, and each stage was treated as a separate trait (T1–T9). Phenotypes were coded as binary (1 = survived, 0 = culled/dead). Both censored and uncensored records were included. Variance components were estimated with a 9-trait animal model in REMLF90, with calving herd-year, calving season, and age at first calving as fixed effects. Heritability estimates ranged from 0.012–0.013 (parity 1), 0.009–0.016 (parity 2), and 0.017–0.031 (parity 3), with slightly higher values in late lactation. Genetic correlations were generally low within parity, though T3, T6, and T9 showed the strongest associations. Early (0.22–0.38) and late (0.31–0.50) stage traits were more strongly correlated than intermediate stages. These results suggest that survivability is lowly heritable but genetically structured, supporting stage-specific selection to improve longevity and herd profitability in Korean Holstein.

**Key words :** survivability, lactation stage, multiple-trait, animal model, Korean Holstein

## Microsatellite Marker 기반 국내 소형견 품종의 개체식별 및 유전적 다양성 분석

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국내 가구 구조의 변화(1인 가구, 고령 가구 등)에 따라 반려동물 양육 가구 수는 지속적으로 증가하는 추세이다. 이에 따라 국가에서는 반려동물의 유실과 유기 방지 및 보호자 책임 강화를 위해 반려견 등록제를 시행하고 있으나, 기존 등록 방식은 장치의 분실·훼손 및 삽입 시술에 대한 부담 등의 한계를 가지고 있다. 이러한 문제를 보완하기 위한 방안으로 개체별 유전정보를 활용한 유전자 등록제가 주목받고 있다. 따라서 본 연구에서는 국내 반려견 양육 환경을 고려하여 소형견을 대상으로 Microsatellite Marker를 활용한 개체식별 및 유전적 다양성 분석을 수행하였다. 분석에는 국내에서 양육된 소형견 5품종, 총 189두의 샘플을 이용하였다. 분석에 활용된 17개 MS marker의 전체 대립유전자 수는 167개로 확인되었고, 푸들에서 132개로 가장 많은 대립유전자가 확인되었다. MS marker별 PIC값은 PEZ6에서 0.880으로 가장 높게 나타났고, REN197E16에서 0.458로 가장 낮게 나타났다. 집단의 유전적 균일도를 분석한 결과 K=2에서 시츄가 다른 품종과 차이를 보였고, K=5에서 품종별로 구분이 되었다. PCoA 및 유전거리 분석 결과 몰티즈와 시츄가 가장 먼 유전적 거리(0.244)를 나타냈으며, 비송프리제와 푸들이 가장 가까운 유전적 거리(0.124)를 나타냈다. 본 연구 결과 품종 간 유전적 차이가 뚜렷하게 확인되었으며, 이를 활용한 개체식별 가능성을 확인할 수 있었다. 또한 본 연구 결과는 향후 반려견 유전자 등록제 구축 및 품종 관리 체계를 마련하기 위한 기초자료로 활용될 수 있을 것으로 사료된다.

**Key words :** 반려견, 유전적 거리, 유전적 다양성, Microsatellite, 개체식별

## Estimation of genetic parameters for carbon emission intensity in dairy cattle based on milk production performance in Korea

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In September 2021, the Korean government enacted the ‘Framework Act on Carbon Neutrality and Green Growth’ to transition toward a carbon-neutral society. Furthermore, the ‘2030 Nationally Determined Contributions (NDC)’ target was established, aiming for a 40% reduction in total greenhouse gas (GHG) emissions compared to 2018 levels. The agricultural, livestock, and fisheries sectors are required to reduce emissions by 27.1% (targeting 18 million tons of CO<sub>2</sub>eq by 2030). As of 2020, the agricultural sector accounted for 3.2% (21.1 million tons CO<sub>2</sub>eq) of the national total, with the livestock sub-sector—specifically enteric fermentation (4.7 million tons CO<sub>2</sub>eq) and manure management (5.0 million tons CO<sub>2</sub>eq)—representing approximately 46% of agricultural emissions. This study calculated GHG emission intensity per 1 kg of milk produced by participating farms. The calculation formula for carbon emission intensity was derived by estimating the annual milk yield per cow, utilizing FAO data indices spanning from 1961 to 2020. Using herd examination and performance data provided by the Dairy Cattle Improvement Center, this study calculated the nationwide carbon emission intensity of milk. Furthermore, genetic parameters were estimated to evaluate the potential of using emission intensity as a selection trait.

**Key words :** carbon neutrality, greenhouse gas (GHG), dairy cattle, milk carbon intensity, genetic parameter estimation

# Genome-wide association analysis of insulin function phenotypes reveals distinct genetic architecture in Koreans

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Insulin regulates glucose homeostasis and broader metabolic processes, and its dysfunction is implicated in type 2 diabetes, cardiometabolic and hepatic diseases. Because insulin dysfunction in Koreans involve different contributions of secretion defects, insulin resistance, and  $\beta$ -cell compensation failure, these components should be analyzed separately. Therefore, this study aimed to dissect the genetic architecture of insulin secretion, insulin sensitivity, and  $\beta$ -cell compensation and identify related genetic signals in Koreans. Using oral glucose tolerance test data from 6,736 KoGES Ansan-Anseong participants, we calculated insulin indices and performed genome-wide association analyses. Independent signals were identified by LD clumping of variants using a suggestive significance threshold ( $p < 1 \times 10^{-5}$ ). We identified 15, 14, and 17 independent variants associated with insulin secretion, insulin sensitivity, and  $\beta$ -cell compensation, respectively. Candidate genes included *CDKAL1*, *KCNQ1*, and *HNF4A* for insulin secretion and  $\beta$ -cell compensation, and *RYR1*, *PTPRG*, and *SCARB2* for insulin sensitivity, suggesting involvement of  $\beta$ -cell function, insulin signaling, calcium regulation, and lipid metabolism. These findings suggest that insulin function associated genetic architecture in Koreans can be characterized according to distinct insulin phenotypes and provide insight into the pathophysiological basis of insulin-related diseases.

**Key words :** glucose homeostasis, insulin secretion, insulin sensitivity,  $\beta$ -cell compensation, genome-wide association study

## Integrative network propagation analysis of GWAS candidate genes for carcass traits in Hanwoo

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Carcass weight, eye muscle area, backfat thickness, and marbling score are economically important carcass traits in Hanwoo cattle. Although previous GWAS studies have identified multiple candidate genes associated with these traits, their biological interpretation remains challenging due to polygenic architecture and linkage disequilibrium. This study aimed to reinterpret GWAS-derived candidate genes for Hanwoo carcass traits at the functional network level. Candidate genes reported in three Hanwoo GWAS studies were used as seed genes, and protein–protein interaction networks were constructed using the STRING database in Cytoscape with *Bos taurus* as the reference species. Network propagation analysis was performed using Cytoscape Diffusion, and genes were prioritized based on diffusion heat scores. The *PLAG1*–*CHCHD7* axis was repeatedly prioritized for carcass weight and eye muscle area, suggesting shared mechanisms related to growth and muscle development. For backfat thickness, *BECN1* and *ENPP1* were identified as candidates related to autophagy, insulin signaling, and metabolic homeostasis. For marbling score, *GPAT4* and lipid-related genes such as *ACACA*, *BMP4*, *TWIST2*, and *MITF* were highlighted. These results provide a network-based interpretation of GWAS findings and useful candidates for functional validation and genomic improvement of Hanwoo carcass traits.

**Key words :** Hanwoo, carcass traits, GWAS, network propagation

## Accuracy of genomic estimated breeding values for carcass traits in Hanwoo cattle

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Carcass weight (CWT), eye muscle area (EMA), backfat thickness (BF), and marbling score (MS) are major economically important carcass traits in Korean Hanwoo cattle. This study evaluated the accuracy of genomic estimated breeding values (GEBVs) for these traits using the GBLUP and Bayes B methods. Genotype and phenotype data from 9,303 Hanwoo cattle were analyzed using the Illumina 50K bovine SNP chip. Prediction accuracy was evaluated using genomic estimated breeding values (GEBV) and deregressed genomic estimated breeding value (DGE BV) by applying five-fold cross-validation. In each validation round, 80% of animals were used as the reference population, while the remaining 20% were treated as the validation group with masked phenotypes. Heritability estimates under the GBLUP model were 0.42, 0.36, 0.36, and 0.47 for CWT, EMA, BF, and MS, respectively. Corresponding estimates under the Bayes B model were 0.47, 0.37, 0.36, and 0.42. The accuracies under the GBLUP model for the four traits ranged from 0.69–0.74 using complete data set. GBLUP model accuracies for CWT, EMA, BF and MS were 0.72, 0.70, 0.69 and 0.74 respectively while Bayes B model accuracies were 0.80, 0.72, 0.73 and 0.72 respectively. On the other hand, the realized accuracy estimates using cross validation data set were 0.66, 0.60, 0.55 and 0.54 respectively for the CWT, EMA, BF and MS traits whereas model accuracy were 0.62, 0.59, 0.59 and 0.63 respectively under GBLUP method. The difference between model and realized accuracy under GBLUP method was ~3%. Whereas Bayesian B method demonstrated ~30% difference between model and realized accuracy. The accuracies of model versus realized under Bayes B model was estimated in CWT (0.53 vs 0.66), EMA (0.40 vs 0.61), BF (0.41 vs 0.57) and MS (0.37 vs 0.58) respectively using cross validation procedure. Therefore, both GBLUP and Bayes B method could be used to estimate the GEBV in Hanwoo genomic selection.

**Key words :** genomic selection, GEBV accuracies, GBLUP, carcass traits, Hanwoo

## 제주마의 혈통 분석 및 유효집단크기 추정

장찬우, 고유진, 송지연, 박연희, 이상훈, 박종은

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제주마는 제주의 고유의 품종으로서 제주도의 거친 자연환경에 적응하며 살아온 체구가 작고 강인한 체력을 가진 대한민국 천연기념물 제347호 고유 품종이다. 본 연구는 지속 가능한 번식 및 개량 전략을 개발하고 제주마 집단의 유전적 편향 문제를 진단하기 위해 수행되었다. 이를 위해 1968년부터 2025년 사이에 태어난 9,684마리의 혈통 데이터를 사용하여 집단의 유전적 구조를 분석하였다. 제주마의 혈통 구성 및 유효집단 크기( $N_e$ )를 추정하기 위해 POPREP 소프트웨어를 사용하였으며, Gutierrez 등(2009)이 제안한 계산 방법을 활용하였다. 제주마의 평균 근친교배 계수는 세대가 거듭됨에 따라 2004년 이후 증가 추세를 보였다. 또한, 세대 당 근친교배율을 기반으로 계산한 유효집단 크기는 40으로 추정되었다. 이러한 결과는 보전유전학적 임계치인 50을 하회하는 수준으로, 제주마 집단의 유전적 다양성 소실 위험이 높음을 시사한다. 이에 따라 특정 가계 중심의 번식이 경주성능에 미치는 영향을 규명하기 위한 후속 연구의 필요성 제기된다. 향후 이러한 분석 결과를 토대로 유전적 편향을 방지하고 다양성을 유지할 수 있는 체계적인 개량 전략 수립이 병행되어야 할 것이다.

**Key words :** 제주마, 혈통정보, 근교계수, 혈연계수, 유효집단크기

## Assessment of genetic structure, diversity, and inbreeding in a conserved line-breeding Hanwoo population

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This study evaluated the genetic structure, genetic diversity, and inbreeding level of a line-breeding Hanwoo population (LB), which has been conserved without the introduction of Korean proven bulls, and compared it with a general Hanwoo population (GH). A total of 2,599 animals, including LB and GH, with Bovine 50K SNP data and pedigree records were analyzed. Principal component analysis (PCA) and ADMIXTURE analysis were performed using quality-controlled SNP data to assess population structure. Genomic inbreeding was evaluated using runs of homozygosity (ROH) analysis in PLINK, and individual ROH-based inbreeding coefficients (FROH) were calculated from ROH segments  $\geq 5$  Mb. ROH segments were classified into four length categories to characterize genomic inbreeding patterns. Observed and expected heterozygosity were calculated using PLINK, and pedigree-based inbreeding coefficients and pedigree depth were also examined in relation to FROH. All results were visualized using R. These analyses provided an integrated assessment of the genetic structure and inbreeding status of the Hanwoo line-breeding population and may provide useful baseline information for maintaining genetic diversity and establishing sustainable conservation and breeding strategies in small and closed populations.

**Key words :** genetic diversity, genomic inbreeding, Hanwoo, line-breeding, runs of homozygosity (ROH)

## Blood type diagnostic method using the GGTA1 gene structure differences in pigs

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Pigs are known to have two types of blood type, A and O. We developed a method to analyze precisely and rapidly pig blood types by utilizing gene structural differences in the causative gene, GGTA1. Pig blood type A has eight normal exons of the GGTA1 gene, whereas blood type O has an incomplete gene structure due to nucleotide large deletions after exon 7. Specifically, nucleotide deletions (731 bp, 260 bp, and 43 bp) were observed at three different locations within the intron 7 region of blood type O. In this study, we designed primers capable of distinguishing 43 bp sequence insertions/deletions (INDELs) within intron 7 region. As a result, we were able to detect the three genotypes of GGTA1 (AA, AO and OO) by electrophoresis after simple PCR amplification. PCR product sizes for each genotype were 272 bp (A-type) and 229 bp (O-type) on a 2% agarose gel. Using this method, it is possible to accurately identify the GGTA1 genotype and select pigs with specific blood types. When organs from pigs with blood type O are transplanted into humans, it may help alleviate immune responses caused by differences in ABO antigens.

**Key words :** AO blood types, gene structure, GGTA1, INDEL, pigs

## Evaluation of single-step genomic BLUP for milk production traits in Korean Holstein cattle

Jeyran Jabbari Tourchi<sup>1</sup>, Monira Akter Mou<sup>1</sup>, Yewon Shin<sup>1</sup>, Yurim Kim<sup>1</sup>, Hui-Eun Lee<sup>2</sup>, Jong-Joo Kim<sup>1</sup>

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Korean Holstein is the predominant dairy breed in South Korea and contributes most of the national milk production. This study aimed to estimate the accuracy of estimated breeding values (EBVs) for 305-day milk production traits, including milk yield (Milk305), fat yield (Fat305), and protein yield (Prot305), using pedigree-based best linear unbiased prediction (PBLUP) in Korean Holstein cows. A single-trait and multi-trait repeatability model was applied for five parities using the BLUPF90 software package. The phenotypic records were collected from a total of 11,036 Korean Holstein cows for the studied traits, while the pedigree information was covered up to the 5<sup>th</sup> generation, with a total of 21,553 individuals. In single-trait analysis, the estimated heritability across the five parities was 0.17, 0.16, and 0.16 for Milk305, Fat305, and Prot305, respectively. Similarly, in multi-trait analysis, the estimated heritability across the five parities was 0.17, 0.16, and 0.15 for Milk305, Fat305, and Prot305, respectively. The accuracies of EBVs for the single trait model were 0.47, 0.45, 0.45; while the accuracies of EBVs in the multi-trait was 0.48, 0.47, 0.46 for Milk305, Fat305, and Prot305, respectively. The repeatability value for both the single-trait and multi-trait models was similar such as 0.37, 0.35, and 0.37 for Milk305, Fat305, and Prot305, respectively. The results showed that multi-trait analysis slightly outperformed the single-trait model, providing higher EBV accuracies, while heritability and repeatability estimates were similar between the two approaches. Therefore, multi-trait pedigree-based BLUP may provide more reliable selection information than single-trait pedigree-based BLUP for improving milk production traits in Korean Holstein cattle.

**Key words :** Holstein, milk production traits, PBLUP, repeatability, accuracy

## Pedigree-based genetic evaluation of milk production traits in Korean Holstein cattle across different parities

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**Key words :** Holstein, PBLUP, milk production traits, prediction accuracy

# 유전체 통계 분석 툴킷(PLINK)과 새로운 SNP 품질관리 검증 프로그램(popQC)의 성능 비교 분석

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유전체 품질관리(QC)는 GWAS 및 가축의 유전체 선발 분석의 정확성을 높이기 위한 필수 전처리 과정이다. 현재 널리 사용되는 PLINK는 인간 유전체 데이터를 위해 개발되어 가축 집단에 적용 시 친자 확인, 정밀한 HWE 검정, 중복 개체 관리 등 한계를 보인다. 본 연구에서는 가축의 유전체 QC 파이프라인인 popQC를 개발하고, 4,628두의 요크셔 돼지 및 76,756개 SNP 데이터를 이용해 PLINK v1.9와의 성능을 비교하였다. popQC는 분석 전 단계에서 중복 SNP 142개를 자동 감지 및 제거하여 76,614개의 고유 마커를 확보하였다. QC 수행 결과, popQC는 53,208개, PLINK는 46,977개의 SNP를 최종 통과시켜, popQC가 13.3% 더 많은 유효 마커를 확보하였다. popQC는 Bonferroni 보정 HWE 정확 검정 (임계값:  $1.31 \times 10^{-7}$ )으로 10,033개의 SNP를 제거하였으며, 이는 PLINK의 일괄 제거 방식보다 정밀하다. 또한 popQC는 2-pass Mendelian 불일치 검증, 156두에 대한 자동 부모 재탐색, X염색체 기반 성별 불일치 탐지, 그리고 유전자 일치도를 통한 중복 개체 자동 병합 기능을 수행하였다. 이는 단순 필터링 위주인 PLINK의 기능을 넘어, 가축 집단의 계통 정보를 유기적으로 통합 관리하는 고도화된 처리 공정이다. 메모리 사용량 측면에서도 popQC는 해시테이블 기반 Architecture를 통해 경량 구동이 가능한 반면, PLINK는 동일 데이터셋에 대해 128,706 MB의 RAM을 차지하는 것으로 나타났다. 이상의 결과는 popQC가 돼지 유전체 QC에 있어 보다 포괄적이고 정확하며 효율적인 솔루션을 제공함을 입증하며, 타 가축 종에도 폭 넓게 적용 가능한 파이프라인임을 시사한다.

**Key words :** popQC, PLINK, hardy-weinberg, mendelian inconsistency