



## 유전 및 육종



## Multi-algorithmic translation of genomic estimated breeding value (GEBV) into fattening types of Hanwoo cattle

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Hanwoo (Korean native cattle) production systems have increasingly adopted extended fattening periods and high-energy feeding programs to enhance carcass quality; however, these practices have concurrently driven up management costs and imposed substantial economic burdens on producers. Consequently, there is a growing demand for individualized feeding strategies that align nutritional management with the genetic potential of each animal. Although genomic estimated breeding values (GEBVs) enable early and accurate assessment of genetic merit, their practical application in on-farm feeding management remains largely limited. In this study, we present a framework that transforms GEBV data into biologically meaningful genetic growth categories to facilitate individual-specific precision feeding. Approximately 18,000 Hanwoo cattle with both GEBV and carcass trait records were used to derive four composite genetic types reflecting distinct growth patterns. To enable early-stage application, statistical and machine learning approaches were employed to predict these genetic types using only GEBV information during the initial fattening period. Among the tested models, CatBoost achieved the best overall predictive performance, with  $R^2$  values ranging from 0.58 for the least accurately predicted genetic type to 0.65 for the most accurately predicted type. Collectively, these findings demonstrate that translating genomic information into discrete genetic classifications can meaningfully support data-driven decision-making in Hanwoo production systems. However, the full predictive utility of such classifications is contingent upon the integration of additional covariates—including environmental conditions, herd management practices, and nutritional history—to enable more comprehensive and accurate phenotypic assessments. Nonetheless, this study establishes a foundational framework for advancing both economic viability and production sustainability in Hanwoo operations through the systematic implementation of precision feeding strategies.

**Key words :** genetic type, genomic estimated breeding value (GEBV), machine learning, smart livestock

## Comparative unsupervised clustering of Hanwoo cattle based on genomic estimated breeding values for carcass traits

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As a primary indicator for genetic progress and early-stage individual selection, GEBV (Genomic Estimated Breeding Value) offers significant potential for pre-emptively determining optimal feeding strategies. "However, its applicability as a criterion for clustering has not been sufficiently verified, particularly by using artificial intelligence; this study sought to classify GEBV-based clusters by using unsupervised AI-based clustering algorithms. GEBV data for four carcass traits—backfat thickness, carcass weight, eye muscle area, and marbling score—from 18,079 Hanwoo cattle were standardized and four different clustering algorithms were applied. To address limitations posed by the heteroscedasticity and unimodal distribution of the data, four clustering techniques with complementary mathematical foundations—K-means++ (distance-based), Gaussian Mixture Modeling (probability-based), HDBSCAN (density-based), and Spectral Clustering (graph-similarity-based)—were applied. The optimal number of clusters (K) was determined with reference to the results of the Gap statistic and NbClust, and cluster validity was assessed using the Silhouette Score and Davies-Bouldin Index. NbClust identified K = 2, 3, and 4 as the most supported cluster numbers (7, 6, and 5 votes, respectively) across 26 indices, with Davies-Bouldin Index values decreasing marginally from 1.437 at K = 2 to 1.349 at K = 4. This study presents a methodological framework for GEBV-based clustering in Hanwoo breeding programs with application of AI algorithms, and by comparing results across four distinct clustering algorithms, it is expected to provide practical guidelines for selecting clustering methods suitable for high-dimensional GEBV data.

**Key words:** clustering algorithm, genomic selection, Hanwoo, carcass traits, statistics

# Individual-level structural equation-based genome-wide association studies of direct and mediated genetic effects on carcass traits in Korean Jeju black cattle

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Carcass weight (CWT), eye muscle area (EMA), backfat thickness (BF), and marbling score (MS) are major economic traits in beef cattle. However, the genetic relationships among these traits and the biological pathways through which genomic variants influence them are still not fully understood. Conventional genome-wide association studies (GWAS) generally analyze each trait separately and therefore cannot distinguish direct genetic effects from mediated or opposing structural effects. In this study, we applied individual-level structural equation model GWAS (SEM-GWAS) to 1,826 genotyped Jeju Black Cattle (JBC) to investigate the structural genetic relationships underlying carcass trait variation. Among four competing SEM structures, a biologically informed model (Model D: CWT → EMA, BF; EMA + BF → MS) showed the best fit to the data (CFI = 0.977, RMSEA = 0.137, ΔBIC = −5,196 compared with the one-factor baseline model). Analysis of 150K autosomal SNPs detects 12 suggestive loci at the Bonferroni-adjusted threshold ( $p < 1.60 \times 10^{-6}$ ; corrected based on 31,266 independent SNPs) and 197 additional loci at a secondary exploratory threshold ( $p < 5 \times 10^{-5}$ ). Most loci showed direct trait-specific effects (91.5%), whereas 5.0% displayed both direct and mediated effects, and 2.5% showed antagonistic effects across structural pathways. Mediation analysis indicated that the CWT → EMA → MS pathway explained 19.5% of the total genetic effect on MS, while the CWT → BF → MS pathway explained an additional 5.3%, resulting in 24.8% of the total effect being indirectly mediated. Notably, SEM-GWAS identified 204 of 209 suggestive SNPs (97.1%) that were not detected by conventional single-trait GWAS, highlighting its substantially greater interpretive capacity. Candidate gene annotation highlighted *KIAA0586*, *ZNF385B*, *FSTL5*, *LPIN1*, *DROSHA*, and *UQCRCF1* as promising genes associated with adipogenesis, lipid metabolism, muscle energy metabolism, and marbling development. These findings define the structural genomic architecture of carcass traits in JBC and show that SEM-GWAS can uncover biologically meaningful pleiotropic effects that remain hidden in conventional univariate analyses with practical relevance for genomic selection and conservation breeding programs.

**Key words :** carcass traits, mediation analysis, direct effects, antagonistic pleiotropy