

## Genomic evaluation for persistence of lactation in Girolando cattle

M. V. G. B. Silva<sup>1</sup>, J. C. C. Panetto<sup>1</sup>, R. Negri<sup>2</sup>, S. Kluska<sup>3</sup>, P. I. Otto<sup>4</sup>, M. A. Machado<sup>1</sup>, E. Ferreira Junior<sup>3</sup>, J. A. Cobuci<sup>5</sup>, D. S. Daltra<sup>3</sup>

<sup>1</sup> Embrapa, Dairy Cattle Research Center, Rua Eugenio do Nascimento, 610, 36038-330 Juiz de Fora - MG, Brazil, <sup>2</sup> Sao Paulo State University, Avenida Brasil, 56, 15.385-007 Ilha Solteira - SP, Brazil, <sup>3</sup> Brazilian Association of Girolando Breeders, Rua Orlando Vieira do Nascimento, 74, 38040-280 Uberaba - MG, Brazil, <sup>4</sup> Federal University of Santa Maria, Av. Roraima, 1000, 97105-900 Santa Maria - RS, Brazil, <sup>5</sup> Federal University of Rio Grande do Sul, Av. Paulo Gama, 110, 90040-060 Porto alegre - RS, Brazil

Genomic evaluations were carried out using 784,093 test day milk yield records from first lactation Girolando cows spanning from 1998 until 2021. The aim was to identify a suitable model for future lactation persistence genomic evaluations. Genomic breeding values were predicted using random regression models with different Legendre polynomial functions through the best genomic unbiased linear predictor in a single step (ssGBLUP) approach. Following this, ten different measures of lactation persistence were evaluated. The model employing fourth-order Legendre polynomials, along with fixed effects of contemporary groups and heterozygosity, was identified as the best fit to the data based on the goodness-of-fit criteria. Heritability estimates for persistence ranged from 0.08 to 0.69. Genetic correlations between persistence and 305-day milk yield records varied from low to high magnitude (-0.04 to 0.96). The average genomic estimated breeding values (GEBV) of sires for the different persistence measures ranged from -41.46 to 249.70 kg. In conclusion, the measure of persistence represented by the sum of GEBVs considering the period from 55 to 270 days of lactation, obtained as GEBVs deviations at 50 days of lactation, should be preferred in genomic genetic evaluations for this trait in the Girolando breed.

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## Genetic Characterization and Pathway Analysis of Carcass Weights in a Jeju Native Black×Hanwoo Crossbred Population

M. Won<sup>1</sup>, Y. K. Kim<sup>1</sup>, S. M. Sin<sup>1</sup>, T. H. Kim<sup>2</sup>, H. B. Park<sup>2,3</sup>

<sup>1</sup> National Institute of Animal Science, Subtropical Livestock Research Institute, 593-50, Sallokbuk-ro, 63242 Jeju, South Korea, <sup>2</sup> Kongju National University, Department of animal Resources Science, 54, Daehak-ro, Yesan-eup, 32439 Yesan-gun, South Korea, <sup>3</sup> Kongju National University, Resource Science Research Institute, 54, Daehak-ro, Yesan-eup, 32439 Yesan-gun, South Korea

Jeju Island, which boasts a unique environment due to its isolation, has historically seen the Jeju Native Black (JNB) cattle playing an indispensable role in the island's agrarian society. Despite facing endangerment during Japanese occupation and agricultural modernization, the JNB population surged from 31 in 1994 to 1,611 in 2016; however, the current population stands at 1,087. This study investigates genetic traits crucial for the preservation of JNB, utilizing a genome-wide association study and examining biological pathways in a Jeju-huekhanwoo (JHH, Jeju Native Black×Hanwoo) Cattle. The analysis, based on 39,055 SNP markers from 256 JHH cattle, identifies six quantitative trait loci (QTLs) associated with carcass weights on Bos taurus chromosomes 3, 5, 6, 10, and 13. The genes EIF2B3 and HECTD3 on BTA3, SOX5 on BTA5, ENSBTAG00000064813 on BTA6, ENSBTAG00000064392 on BTA10, and KLF6 and PHACTR3 on BTA13 were identified as positional candidate genes for these QTLs. Moreover, the identified positional candidate genes linked to carcass weights were enriched in pathways related to lysine degradation, axon guidance, tryptophan metabolism, glycerolipid metabolism, fatty acid metabolism. Future verification studies of these identified SNPs and positional candidate genes in other cattle populations hold the potential to provide valuable insights into the genetic architecture of carcass weights within Jeju Native Black cattle and Hanwoo-related populations.