GENETIC AND GENOMIC PARAMETERS FOR RESISTANCE TO NEMATODE INFECTION IN SANTA INÊS SHEEP

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The improvement of genetic resistance of small ruminants to nematode infection is an important strategy of gastrointestinal nematode control. The purpose of this study was to estimate (co)variance components and genetic parameters for genetic resistance to nematode infection (GRNI), faecal egg count (FEC) and degree of anemia (FAMACHA) in Santa Inês sheep. Therefore, pedigree data from 1,478 animals raised in the states of Piauí and Maranhão, Brazil, were used. A high-density panel (Illumina Ovine SNP50K BeadChip) was used for genotyping 271 animals which had phenotypic information for the traits in study. The (co)variance components and genetic parameters were estimated using a conventional multitrait BLUP model with pedigree-based relationship matrix and a multitrait single-step genomic BLUP (ssGBLUP) model with joint relationship matrix combining pedigree and genomic information, under Bayesian inference. Direct additive genetic and residual effects were included as random effects. The fixed effects were contemporary group (birth year, state, birth type, and farm), sex, and age of animal at the time of data collection. The accuracy of prediction was used to compare the methods and models in study. When the genomic information was included in the model, different values of (co)variance components were estimated. This is an indicative that the partition of the (co)variance components is more efficient when genomic models are used, as these models allow calculating the realized kinship between individuals. Heritability estimates for GRNI, FEC, and FAMACHA were 0.49, 0.33, and 0.32, respectively, using multitrait ssGBLUP. When the multitrait traditional BLUP was used, the heritability estimates were 0.54, 0.36, and 0.37, for GRNI, FEC, and FAMACHA, respectively. The genetic correlations estimated using both models were positive and ranged from 0.22 to 0.69. The highest gains in accuracy were obtained using the genomic model. The differences in accuracy that were verified with inclusion of genomic information may be due to a reduction in the prediction error. Correlated selection may not be efficient for the traits in study. The heritability estimates indicate that the traits in study presented an adequate genetic variability to respond to direct selection in Santa Inês breed. The inclusion of genomic information using the ssGBLUP model provided more accurate estimates of genetic parameters for the evaluated traits, in comparison to traditional BLUP.

Keywords: accuracy, meat sheep, parasites resistance, ssGBLUP