

CONSTRUINDO SABERES, FORMANDO PESSOAS E TRANSFORMANDO A PRODUÇÃO ANIMAL

SINGLE-STEP GENOMIC BLUP FOR GENOMIC EVALUATION OF GENETIC RESISTANCE TO NEMATODE INFECTION IN MEAT SHEEP

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The improvement of genetic resistance of small ruminant to nematode infection is an important strategy of gastrointestinal nematode control. The purpose of this study was to predict genomic breeding values (GEBVs) for genetic resistance to nematode infection (GRNI), faecal egg count (FEC) and degree of anaemia (FAMACHA) using single-step genomic BLUP (ssGBLUP) and compare to breeding values predicted using traditional BLUP (EBVs). Therefore, data from 1,478 Santa Inês adult sheep raised in the states of Piauí and Maranhão and registered by the Brazilian Association of Sheep Breeders (ARCO) were used. A total of 271 animals among those mentioned above were genotyped using the Illumina Ovine SNP 50K BeadChip. Single-step GBLUP and traditional BLUP using animal models in single-trait analysis were adopted to predict breeding values. In the model, the random effects were animal and residual. The fixed effects were contemporary group (birth year, state, birth type, and farm), sex, and age of animal at the time of data collection. Gains in accuracy were observed for GRNI (45%), FEC (80%) and FAMACHA (99%) using ssGBLUP. The average gain in accuracy using ssGBLUP was 57.52%, due to the increase in the availability of information by using genomic data and correction of pedigree errors. Differences were observed in predictions, because Spearman rank correlations between EBVs and GEBVs were mostly low and close to zero. These results indicate that animals which were better ranked based on breeding values predicted using the traditional BLUP were not considered the best when the ranking was performed based on genomic breeding values predicted using ssGBLUP. Pearson correlation coefficients between breeding values predicted by using both methods were 0.20 for GRNI, 0.06 for FEC and 0.13 for FAMACHA. These results are evidence that the use of BLUP and ssGBLUP for prediction of breeding values for the traits evaluated in this study results in different predicted breeding values and ranking of animals. The ssGBLUP method is recommended, because it resulted in the prediction of more accurate breeding values.

Keywords: accuracy, genomic selection, Santa Inês sheep, ssGBLUP

Promoção e Realização:



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