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DETECTION OF SELECTION SIGNATURES FOR GASTROINTESTINAL HELMINTHS RESISTANCE IN MERINO AND CORRIEDALE SHEEP

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Sheep flocks in Uruguay experience production and reproduction losses due to gastrointestinal parasites (GIP). Genetic selection to enhance the natural resistance require phenotypic records of fecal worm egg count (FEC), though its records are difficult to measure. An alternative is to select parents through genetic markers. This study aimed to identify potential genome regions accounting for frequency differences of haplotypes, associated with GIP resistance. We analyzed contrasting individuals for GIP (resistant or susceptible), 98 Merino (Mer) a fine wool breed, 90 Corriedale (Cor) a dual purpose breed which has been bred selectively for resistance/susceptible to GIP since 1998, 10 sires of each, and 10 Creole (Cr) a breed with no selection. Cor were chosen to have contrasting individuals, resistant or susceptible. The analysis was performed using de hapFLK statistic. Significant regions were obtained, distributed in chromosomes 6, 7, 8 and 14. Within the detected regions, we found the genes MMP2 (chr:14) and TICAM2 (chr:7) which are related to the immune response. Being involved in pathways related to NF-kappa B signaling, Toll-like receptor signaling, Leukocyte transendothelial migration, Cytokine-cytokine receptor interaction, etc. In the regions of chromosomes 6 and 8 we did not find any gene related with immune response, but the selected genes in these regions could be related to other selected traits of agronomical interest, as wool quality or weight gain. Further research has to be done in order to validate MMP2 and TICAM2 as responsible for low GIP.

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GENETIC PARAMETERS OF DAYS OPEN, MILK, FAT AND PROTEIN YIELD OF URUGUAYAN HOLSTEIN ON PASTURE SYSTEMS

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Failures in reproductive performance represent the first culling factor in many dairy systems. The main cause is the antagonistic genetic correlation with production. Given this, many countries have added reproduction traits into selection indexes with successful results. In Uruguay, the inclusion of a reproduction trait with a significant economic value in a breeding objective and corresponding selection index requires the estimation of additive genetic correlations with other traits. The aims of this study were to estimate heritabilities and additive genetic correlations between days open (DO), milk yield (MY), fat yield (FY) and protein yield (PY). The database used contained information of 634, 161 and 127 thousand observations of 1st, 2nd and 3rd lactation, respectively. We run a tetra-variated repeatability model with fixed (herd-year-season and lactation-age) and random (animal and permanent) effects. The software Gibbs2f90 was run as a single chain of 200,000 samples, discarding the first 100,000 samples with a sampling interval of 10. Convergence diagnostic and statistical analysis was done with CODA package of the R language/environment. Heritabilities found were 0.05, 0.23, 0.21 and 0.21 for DO, MY, FY and PY, respectively. Additive genetic correlations between DO and production traits were between 0.44 and 0.55. The values obtained were consistent with the literature revised, confirming an unfavorable association between production and reproduction. Thus, both fertility and yield traits should be considered in genetic selection programs.