GENOME-WIDE ASSOCIATION STUDY FOR STAYABILITY MEASURED AT CONSECUTIVE CALVINGS IN NELORE CATTLE

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Stayability (STAY) is the probability of a cow remaining in the herd, being productive, up to certain age. In the present study, we carried out genome-wide scans for STAY measured at consecutive calvings in Nellore cattle in order to investigate the existence of genomic regions, with major effects on this trait, in common among earlier and later ages. The dataset included pedigree and phenotypic data of about 250,000 cows from 523 farms and three breeding programs (DeltaGen, PAINT and CIA de Melhoramento). A total of 3,869 animals (2,740 cows and 1,129 sires) had genotypic information for 472,640 SNP markers after quality control. There were considered seven measures of STAY (from the second to the eighth calving). At each calving, the value 2 (success) or 1 (failure) was attributed to the cows that, respectively, calved or not. There were 235,917; 208,755; 180,981; 155,132; 133,262; 111,240 e 93,994 phenotypes for the second, third, fourth, fifth, sixth, seventh and eighth calving, respectively. The single-step genomic BLUP approach was used to obtain variance components and genomic estimated breeding values (GEBVs), considering a single-trait threshold animal model. Fixed effects of contemporary groups (herd, year and season of birth) and age of cow at the first calving (7 classes) plus the random effect of animal were considered in the model. The GEBVs were back-solved into SNP effects and the proportion of the variance explained by windows of 150 consecutive SNPs was used to identify the genomic regions with major effects on STAY. Heritability estimates for the second, third, fourth, fifth, sixth, seventh and eighth calving were 0.11, 0.12, 0.17, 0.19, 0.19, 0.17 and 0.17, respectively. In general, the genes found are related with reproductive functions (LEO1, FAM160B1, PROKR1, PPP2R2A) and immune systems (CLEC3A, GEMIN4). There were identified regions, in common adjacent calvings, associated to STAY, as the region from 47,069,837 to 47,921,750 on chromosome 5 identified for the fifth, sixth, seventh and eighth calving. This genomic region has already been associated with STAY at 65 months of age and longevity in previous studies. Our results indicate a great region with possible candidate genes for STAY in Nellore cattle, affecting this trait at different ages, and open the possibility of selecting for STAY measured at earlier ages.

Keywords: longevity, reproductive traits, single-step GBLUP