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A Genome-Wide Association Study of Meat Tenderness in Nelore Beef Cattle

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Meat tenderness has been identified as one of the major concerns of the beef industry, especially in animals with indicine ancestry. Most important production traits in cattle are polygenic and are controlled by a large number of quantitative trait loci (QTLs). Genome-wide association studies utilizing Bayesian or GBLUP models used for genomic selection are increasingly being used to identify QTLs associated with complex traits. Six hundred and four Nelore steers out of 34 sires chosen to represent the main breeding lineages in Brazil, were used to identify QTLs for Warner-Bratzler shear force (WBSF) measured at 14 days post-slaughter. After filtering Kleinfelter individuals (N=1) and for call rate, allele frequency and Hardy-Weinberg equilibrium genotypes were available for 687,681 SNP loci from the Illumina BovineHD BeadChip on both the steers and their sires and 0.80% of missing values were imputed using BEAGLE. The genotypic and residual variances for WBSF were estimated using BayesC (h^2=0.095) and the parameter Π was estimated using BayesCΠ. Using these genetic and residual variance, and Π estimates as starting values, BayesB was used to estimate marker effects for WBSF. All analyses were performed using GenSel software. This analysis identified QTLs for meat tenderness in Nelore cattle.

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