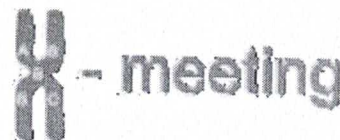


Genomics

X-meeting 2011 - 12-15 October, Florianópolis, Brazil

Sequence Analysis

Evolution and Phylogeny



ID 114

GENOME-WIDE ASSOCIATION ANALYSIS TO IDENTIFY LOCI FOR LINEAR TRAITS IN GYR BREED

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GENOME-WIDE ASSOCIATION ANALYSIS TO IDENTIFY LOCI FOR LINEAR TRAITS IN GYR BREED LG Andrade1, E Guedes1, WA Arbex1, MF Martins2, MA Machado2, RS Verneque2, JCC Panetto2, GG Santos2, MVGB Silva1 1Laboratory of Bioinformatics and Animal Genomics - EMBRAPA Dairy Cattle - MG - Brazil 2EMBRAPA Dairy Cattle - MG - Brazil Genome-wide association study using single nucleotide polymorphism (SNP) markers is a powerful tool for annotating phenotypic effects or quantitative trait loci (QTL) of important dairy traits along the genome. For this study five linear traits related to the productive life of the dairy cows were analyzed, i.e. rear udder, fore udder attachment, teat length, teat diameter, and udder depth. DNA samples from 196 bulls participating in the Brazilian Dairy Genetic Improvement Program for the Gyr breed were used for whole-genome association studies. A total of about 54,000 SNPs genotyped with the Illumina BovineSNP50 Bead Chip (Illumina Inc., San Diego, CA) were investigated to determine the usefulness of the associated SNPs for linear traits. For GWAS, any SNP with low call rate (<99%), departure from Hardy-Weinberg equilibrium (exact test $p < 0.01$), and minor allele frequency below 5%, were excluded from the final analysis (20,782 markers retained). Bonferroni corrected level of 0.05 was used. ITSNBN software was used in order to detect association. No significant SNPs for fore udder attachment was found. On BTAs 6 and 9 were found significant SNPs for all others traits. For teat length and teat diameter traits were found significant SNPs on BTAs 4, 5, 16, 17, 19, 20, 26 and 27. For teat length and udder depth traits were found significant SNPs on BTAs 8, 20, 26 and 27. The analysis of the results indicate that traits within a same phenotype group have a greater tendency to shared genes or gene regions with significant SNPs. Financial support: CAPES, EMBRAPA, CNPq, FAPEMIG