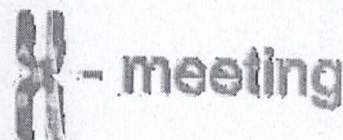


Genomics

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

Sequence Analysis

Evolution and Phylogeny



ID 100

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

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A genome scan was conducted in the Gyr bulls population in progeny test in Brazil to identify QTL affecting production traits as milk, protein, fat, lactose, and total solids, which are important for the genetic improvement of dairy herds in Brazil. Data used at this study were results from traditional genetic evaluations of the Brazilian Dairy Genetic Improvement Program for the Gyr breed computed by Embrapa Dairy Cattle, Brazil. DNA samples have been acquired for 236 bulls from Gyr breed, and their Predicted Transmitting Abilities (PTAs) for these traits were used for whole-genome association studies. Genotyping was performed using Illumina's BovineSNP50 BeadChip (Illumina Inc., San Diego, CA) with approximately 54,000 SNPs. 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 (20,735 markers retained). Bonferroni corrected level of 0.05 was used. ITSNBN software was used in order to detect association. This software uses a linear model and takes the pedigree information into account. For all traits, significant SNPs were found on many chromosomes, especially on BTAs 6, 8, 11, 12, 13, 15, 20, 21, and 22. Most part of the significant SNPs was located in similar positions on the chromosomes for all traits. Further analyses, regarding fat, protein and lactose milk contents, together milk yield, could be useful to infer about genes possibly affecting these different traits simultaneously. Results suggest that marker solutions may be useful for identifying chromosomal regions for production traits in zebu cattle.