

F39 POSTER

TESTING A SOFTWARE FOR PATERNITY EXCLUSION USING A HIGH DENSITY SNP CHIP AND NELORE CATTLE SAMPLES

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Misinformation about paternity is a problem for beef and milk cattle breeding programs. High density genotyping platforms using SNPs have been used for GWAS (Genome Wide Association). Moreover these platforms generate a rich resource of genotyped SNPs that can be used as markers in paternity exclusion tests. In this work we developed a software that provides an exclusion paternity test for high throughput SNP genotyping. Samples from 32 Nelore sires chosen to represent the main genealogies marketed in Brazil and 136 nelore steers produced by artificial insemination were genotyped. The platform used was Illumina BovineHD Genotyping Beadchip that has ~770k SNPs. The algorithm developed first run a quality control filter that selected only markers that: i) were in Hardy Weinberg equilibrium, ii) had MAF>0.4 and iii) had Illumina's accuracy GC Score > 0.8. Around 450k markers were selected and pair wise comparisons of the 168 individuals were performed by counting mendelian inconsistencies between them. A statistic test was implemented to provide the probability of excluding relatives of the true father. Initially, around 600 markers for each pair of individuals compared were used and the power of exclusion of a true father was around 1e-15. The results showed 9 wrong father-son classifications that could be fixed using our methodology. The software was developed in the Perl language with use of a MySQL database and run in a 12-core local linux server machine.

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