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SELECTION OF SINGLE NUCLEOTIDE POLYMORPHISMS FOR USING IN PATERNITY ANALYSIS IN ZEBU BREEDS

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DNA marker technology represents a promising means for determining the genetic identity and kinship of livestock. Compared with other types of DNA markers, single nucleotide polymorphisms (SNPs) are appealing because they are abundant, genetically stable, and amenable to high-throughput automated analysis. Recent advances in DNA sequencing, computing tools and bioinformatics have facilitated and improved the identification of SNPs from amplified segments of genomic DNA. SNPs have been already employed in animal identification and paternity analysis in American and European beef and dairy breeds and in analysis on genetic distance. In cattle, the challenge has been to identify a minimal set of SNPs with sufficient power for using in a variety of popular breeds and crossbred populations. A total of about 58,000 SNPs genotyped with the Illumina BovineSNP50 Bead Chip (Illumina Inc., San Diego, CA) were investigated to determine usefulness of the associated SNPs for paternity analysis. The informativity of these SNPs was estimated from the distribution of minor allele and genotype frequencies in two zebu breeds: (a) Gyr (with 319 animals), and (b) Nellore (with 959 animals). SNPs with a minor allele frequency between 0.44 and 0.56, and genomics distance $\geq$ 3 cM were selected. Existence of Hardy-Weinberg equilibrium was investigated by probability test. Paternity tests were performed using CERVUS 3.0 for 53 offsprings and 39 candidate sires for each offspring. For paternity analysis, the proportion of loci typed was 0.9691 and the simulated genotyping error rate was set at 0.01. Critical values of LOD were determined for 90% and 99% confidence levels based on simulations of 100,000 offsprings. This report describes a set of 109 highly informative bovine SNPs markers distributed among 28 autosomes and both sex chromosomes for using in paternity analysis in zebu breeds.