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Characterization of single-nucleotide polymorphisms in 20 genes affecting milk quality in cattle, sheep, goat and buffalo

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ABSTRACT

Milk products are important dietary sources of nutrients, providing energy, high quality proteins, and a variety of vitamins and minerals. Recent researches have focused on altering fat and protein contents of milk, in order to improve its nutrient content to more suitably reflect current dietary recommendations and trends. We characterized single nucleotide polymorphisms (SNPs) in 20 candidate genes expected to have an influence on fat composition of milk in four ruminant species (cattle, sheep, goat and buffalo). Genes belonged to different families, including transporters, fatty acid biosynthesis, receptors and enzymes for saturation/desaturation. For each gene, PCR primers were designed using bovine sequence to amplify 3 gene fragments, that covered coding and non coding regions. For each gene, we found polymorphisms in at least one species, but none that was present in homologous fragments of all four species. As expected, different SNPs were found across species, but for a very few genes. We identified 61 SNP, 21 in exons, 19 in introns, 19 in 3'UTRs and 2 in 5'UTRs. We found all single bases substitution, 25 of which were C/T, 21 A/G, 6 A/C, 3 A/T, 2 G/C, 1 G/T. All SNPs were genotyped in 459 animals belonging to the 4 breeds. Major allele frequencies ranged from 0.509 (GHR) to 0.996 (PRLR). SNPs altering the amino acid sequence of the encoded protein are found at lower rate than silent substitutions. This probably reflects the effect of selection against deleterious alleles during evolution. Preliminary statistical analysis suggests association of some polymorphisms and milk quality.