Genetic diversity of tyrosine hydroxylase (TH) and dopamine _-hydroxylase (DBH) genes in cattle breeds

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Abstract

DNA from four cattle breeds was used to re-sequence all of the exons and 56% of the introns of the bovine tyrosine hydroxylase (TH) gene and 97% and 13% of the bovine dopamine _-hydroxylase (DBH) coding and non-coding sequences, respectively. Two novel single nucleotide polymorphisms (SNPs) and a microsatellite motif were found in the TH sequences. The DBH sequences contained 62 nucleotide changes, including eight non-synonymous SNPs (nsSNPs) that are of particular interest because they may alter protein function and therefore affect the phenotype. These DBH nsSNPs resulted in amino acid substitutions that were predicted to destabilize the protein structure. Six SNPs (one from TH and five from DBH non-synonymous SNPs) were genotyped in 140 animals; all of them were polymorphic and had a minor allele frequency of > 9%. There were significant differences in the intra- and inter-population haplotype distributions. The haplotype differences between Brahman cattle and the three B. t. Taurus breeds (Charolais, Holstein and Lidia) were interesting from a behavioural point of view because of the differences in temperament between these breeds.