Analysis of BTA6 in Bruna Italiana and Pezzata Rossa cattle assayed with 2,535 SNPs

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ABSTRACT

A high density SNP marker panel (54,000 SNPs) was used to investigate the genome of 775 Bruna Italiana and 493 Pezzata Rossa bulls. Observed and expected heterozygosities were calculated overall and per chromosome. In both breeds, values were not significantly different. *Bos taurus* Chromosome 6 (BTA6), carrying the casein loci, was analysed in higher detail. Overall, 2,535 markers were assayed on this chromosome. After discarding monomorphic markers, those having more than 10 missing values, and those having minor allele frequency below 2%, 1,814 and 2,061 SNPs were retained in Bruna Italiana and Pezzata Rossa, respectively. To detect signatures of ancient and recent selection, we calculated F_{IS} inbreeding coefficient values of all BTA6 polymorphic markers, within sliding windows of groups of 5 adjacent SNPs and within 122 adjacent regions spanning 1 Mb intervals. These preliminary analyses indicated that genotyping of several thousand SNPs potentially allows the detection of the footprint of selection dodging the confounding effects of the population demographic history (i.e., effective population size, genetic structure, and mating pattern). A wider understanding of how and where selection shaped patterns of genetic variation along the genome may provide important insights into the dynamics of evolutionary change, facilitating both the identification of functionally significant genomic regions and genotype-phenotype correlations. Outlining such regions could allow focusing the fine mapping strategy to identify candidate genes and causative mutations affecting important economic or adaptive traits.

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