Signatures of selection in Holstein Friesian dairy cattle

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The identification of genomic regions affected by past selection is of interest for understanding selection history and molecular pathways underlying breeding goal traits. The aim of the current study was to detect signatures of selection in the genome of Holstein-Friesian dairy cattle. Our data consisted of 2,029 cows from experimental herds in four European countries (Ireland, Netherlands, Scotland, and Sweden). These cows were genotyped with the Illumina Bovine SNP50 BeadChip as part of the RobustMilk project. To identify signatures of selection we applied the integrated haplotype score statistics averaged in 500 kb non-overlapping windows. We analyzed data from each country separately but also performed analyses based on a combined data set. In total 51 chromosomal regions were detected that showed evidence for selection in at least one of the four countries. Nine of these chromosomal regions showed evidence of selection in the combined Holstein-Friesian population. Of these regions, three – located on chromosome 10 (50-63 Mb), 13 (46-47.5 Mb) and 20 (24-38.5 Mb) – were independently detected in experimental herds from three countries. The large 14.5 Mb region on chromosome 20 includes the growth hormone receptor gene which has previously been associated with various production traits in cattle including milk yield.