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Signatures of selection in the genome of Italian Holstein cattle for cheese production

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Dairy cattle breeds have been exposed to intense artificial selection for milk production traits over the last fifty years. In Italy, where over the 75% of milk is processed into cheese, selection has also focused on cheese-making traits. The most widely spread PDO Italian cheeses in the world are the Parmigiano Reggiano and the Grana Padano, which cover 16% and the 24% of the total Italian milk production. Intensive selection programs that aim at increasing production yield can cause loss of genetic variability and increased genomic homozygosity. To this end, recent advances in genome mapping have the potential both to improve our understanding of selection and to be used in the breeding program. The present study aims to detect potential selection signatures in the genome of Italian Holstein dairy cows bred for PDO cheese productions. High-density genotype information from SNP-chip was available for 400 cattle, reared in certified farms for Parmigiano Reggiano (PR=200) and Grana Padano (GP=200). The quality control (QC) of the data was performed by excluding both animals and SNPs with a call rate <90% and by removing both unassigned and on-sex-chromosome SNP. We then performed a genomic scan for runs of homozygosity (ROH) which were detected in PLINK 1.9 by using a sliding window approach. ROH were defined based on at least 1Mb-long homozygous segments, and by allowing for a maximum of one missing and one heterozygous SNP.

All animals passed the QC and 311,501 SNP were used to estimate ROH. In total, 142,211 ROH were detected (355.5 segments per animal), with an average length of 1.59 Mb. The mean number of homozygous segments in the PR and GP cattle was similar (354 and 356, respectively). For 115 PR and 122 GP cows, at least one ROH longer than 16 Mb was found, probably indicating recent inbreeding. Six genomic regions with ROH shared among more than 70% of the 400 cattle were located on the following chromosomes: BTA 11, 14, 16, 18, 21 and 29. As a small amount of regions showed a different rate of homozygosity when comparing PR and GP cattle, further studies will investigate any potentially-different signs of selection among PDO dairy chains. Further research is ongoing to demonstrate the role of those homozygous segments on cheese-making traits.

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