

Detection of QTL controlling cheese processing properties in a Holstein x Normande crossbred population

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Genome-wide association of fatty acids from summer milk of Dutch dairy cattle

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Bovine milk fat composition influences the nutritional and technological properties of milk and dairy products. Milk fat composition varies between cows and seasons. This variation can be due to several factors, e.g. factors related to nutrition and genetics or possibly an interaction between them. Previously we identified genomic regions responsible for variation in fatty acids from winter milk samples. The aim of present study is to perform a genome-wide association of fatty acids from summer milk samples. Two milk samples from 2,000 first lactation dairy cows were collected. The first milk sample was taken in winter, when Dutch cows are mainly kept indoors. The second milk sample, from the same set of cows, was taken in summer, when Dutch cows are often grazing outdoors for a part of the day. Milk fat composition was measured by gas chromatography. The most abundant fatty acids, i.e. C4:0-C18:0, C10:1-C18:1 and CLA, were analyzed. Summer milk contained more unsaturated fat and less saturated fat than winter milk, e.g. fat contained on average 29.2% C16:0 and 20.6% C18:1 in summer, and 32.6% C16:0 and 18.2% C18:1 in winter. Phenotypic correlations between winter and summer samples were low: 0.40-0.57 for short and medium chain fatty acids, and 0.36-0.40 for long chain fatty acids. The cows were genotyped for 50,000 markers. For each individual marker we determined whether there was a significant association with the milk fatty acids. Results showed that major regions detected on chromosome (BTA) 14, 19, and 26 in winter samples could be confirmed in summer samples. On BTA 14, DGAT1 showed association with several fatty acids. On BTA 26, SCD1 showed association with unsaturated fatty acids. Some additional regions could also be confirmed in the summer sample, such as the associations on BTA 13 and 17. However, not all associations could be confirmed in the summer samples, such as the associations on BTA 2 and 27. Novel regions were also detected in the summer sample.

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A QTL detection experiment has been carried out in 'Le Pin' INRA experimental farm by crossing Holstein and Normande dairy cattle. To study cheese processing ability, 'Camembert' type cheese was produced from 25 litres milk from 649 individual F2 primiparous cows. We present results on gelification time (RS) and time for firming (K20S) at formagraph test, gel firmness 30 min after adding rennet (A30S), time between between rennet addition and milk curdling in the cheese vat(RCT), fat/dry matter ratio (FDR) and cheese yield (CY). Milk was standardized for fat to protein ratio before processing. These stringent conditions were defined to avoid confounding effects with fat and protein contents and, as a consequence, direct effects of fat or protein content on cheese making properties should not be detected. Accordingly, a much smaller number of QTL are expected. Animals were genotyped with the Illumina 54k Beadchip, as well as for caseins, beta-lactoglobulin and DGAT1 genes. Combined linkage and linkage disequilibrium analysis was used, including the effects of the known genes. The most unexpected result was the strong effect of DGAT1 (BTA14) on nearly all traits, including cheese yield, with a favourable effect of the K allele, showing the likely influence of the fat globules size on cheese processing and water retention. Not surprisingly, formagraph traits and RCT were mostly determined by the casein loci, particularly the kappaand beta-caseins, but no effect of these loci was found on cheese yield. Additional strong QTLs were found on chromosomes 3 (42-45 cM), 23 (43 cM), 28 ((3 cM), and 29 (35 cM) for firmness and times for firming but no QTL other than DGAT1 was found on cheese yield. No clear QTL was found for FDR, in agreement with the standardization procedure.



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