

Detection of QTL affecting Milk Fatty Acid composition in three French dairy Cattle Breeds

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Combining Mid Infra Red (MIR) prediction of fatty acid concentration in milk with high throughput SNP genotyping provides a strong opportunity to identify the main genomic regions responsible for genetic variation in bovine milk fat composition. Milk fatty acid composition was estimated from MIR spectrometry for more than 450,000 test-day from 86,458 cows in first or second parity in the three French Montbeliarde (MO), Normande (NO) and Holstein (HO) cattle breeds, within the national PhénoFinlait project funded by ANR and ApisGene. Among these cows, 8,000 cows (3,000 HO, 2,500 MO and 2500 NO) were genotyped either with the Illumina 50K Beadchip® (7,500) or with the Illumina LD Beadchip® (500) and then imputed. In a first step, analysis was relative to total saturated, unsaturated, mono- and polyunsaturated, C16:0, C14:1c9, C18:1c9, and C18:2c9t11 (CLA). Individual test-day records were first adjusted for environmental effects (herd x test-day, month of calving and days in milk within year and parity) after a polygenic evaluation and then averaged per cow. In a second step, after quality control, phasing and imputation, QTL detection was carried out within breed by Linkage and Linkage Disequilibrium Analysis (LDLA) within each breed. The most important regions were found on already described regions known to affect fat components, milk production, or fatty acid desaturation, e.g. on chromosomes 14, 19, or 26. Several dozens of additional QTL were found for each trait and overlapped only very partially across breeds. Most QTL were found to affect several traits simultaneously, in agreement with the genetic correlations and the metabolic pathways.