

Whole genome scan to detect QTL for major milk proteins in three French dairy cattle breeds

Sanchez, M.P., Govignon-Gion, A., Ferrand, M., Gelé, M., Pourchet, D., Rossignol, M.N., Fritz, S., Miranda, G., Martin, P., Brochard, M., Boichard, D.

A whole genome scan was performed to detect QTL for milk protein composition in the three main French dairy cattle breeds i.e. Montbéliarde (MO), Normande (NO) and Holstein (HO). Protein composition was estimated from Mid-Infrared (MIR) spectrometry on almost 600,000 test-day milk samples from 116,495 cows in the first three lactations (PhénoFinlait programme). Among these cows, 8,080 (2,967 MO, 2,737 NO and 2,306 HO) were genotyped mainly with the Illumina 50k Beadchip. Individual test-day records were adjusted for environmental effects and then averaged per cow. After quality control, phasing, and missing genotypes imputation, QTL detection was carried out within breed by an approach combining linkage and linkage disequilibrium on clusters of 6 consecutive SNP. In each population, the most significant QTL regions were found on BTA6, 11 and 20 ($10^{-8} < P < 10^{-11}$). The BTA6 QTL region, spanning from 80 to 95 cM, affected α s1, α s2, β and κ -caseins in milk. The BTA11 QTL (100 cM), had an effect on β -lactoglobulin in milk as well as on β and κ -caseins in protein. The QTL on BTA20 (55 cM) affected α s1-caseins in protein. The proportion of genetic variance explained by the most significant QTL was around 10-30% and reached 54% for BTA11 and β -casein in protein. In these regions, caseins (BTA6), β -lactoglobulin (BTA11) and GHR (BTA20) genes are good candidates. Moreover, other significant QTL effects ($P < 10^{-5}$), partially overlapping across breeds, were highlighted on BTA1, 2, 14, 17 and 19. These first results pave the way to causal mutation identification.

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