

QTL detection for traits of interest for the dairy goat industry

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Since 2008, a program for mapping traits of interest in dairy goats has been carried out in France as part of the national “PhénoFinlait” program and the EU project ‘3SR’. This project was based on a large daughter design of Alpine and Saanen bucks and gathered production traits, mastitis resistance (SCC), type and fatty acid (FA) composition based on mid infrared spectra prediction. A total of 2 254 goats and 20 AI sires (11 Alpine, 9 Saanen) were genotyped with the 50K Illumina SNP goat beadchip. After classical quality control, a total of 49 647 out of 53 347 synthesized SNPs were validated for further analyses. Yield deviations were computed for 57 traits: milk, fat and protein contents and yields (FY, PY), SCC, 11 type traits and 38 FA-related traits. QTL detection based on linkage analyses (LA) and linkage disequilibrium (LD) was implemented using the QTLmap software. Bonferroni correction was applied to p-values in order to provide experience-wise significant thresholds. Fourteen regions controlling milk production traits, conformation and FAs were found with LA analyses on CHI 1, 6, 7, 8, 11, 14, 18, 19, 21, 29. LD analyses identified many more QTLs (480) and confirmed LA regions. There was evidence for QTLs of major effect for PY and FY on CHI6 (caseins region) and for FY and FAs on CHI14 (DGAT1 region). Interestingly, a region of CHI19 showed a QTL for SCC but also for milk and udder type traits. FA results seemed to be breed-specific as clusters of QTL were preferably found on CHI 8, 11 and 14 in Alpine but on CHI 18, 25 and 26 in Saanen breed.

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