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 EC FP7 funded '3SR' project (no. 245140). The project was based on a large daughter design of Alpine and Saanen bucks and data were gathered on 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 synthetized 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 with a major effect for PY and FY on CHI 6 (caseins region) and for FY and FAs on CHI 14 (DGAT1 region). Interestingly, a region of CHI 19 showed a QTL for SCC and also for milk and udder type traits. FA results seemed to be breed-specific as clusters of QTL were generally found on CHI 8, 11 and 14 in the Alpine but on CHI 18, 25 and 26 in the Saanen breed. This project receives financial support from Apis-Gène, UE 7th PCRDT, Ministry of Agriculture (CASDAR), FranceAgriMer and FGE.

Mapping a putative autosomal gene controlling ovulation rate and infertility in Cambridge sheep

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Lambing percentage is a major driver of profitability in a sheep enterprise. The identification of a major gene controlling ovulation rate and hence litter size is a viable option to increase lambing percentage via genetic testing and selection. Cambridge sheep are characterised by having a high ovulation rate with extreme variation between individuals, consistent with segregation of major genes controlling ovulation rate. Ovarian hypoplasia with resultant female sterility is also found in the Cambridge breed, and polymorphisms in both GDF9 and BMP15 have been shown to be associated with increased ovulation rate in heterozygous carriers and sterility in homozygous carriers within breed. Recent data has provided evidence of a third major gene controlling ovulation rate in the Cambridge breed. The inheritance pattern suggests that this gene is autosomal and unlinked to GDF9 or BMP15. Mapping this gene was one of the goals of the EU-funded project 3SR, Sustainable Solutions for Small Ruminants. Sterile ewes with ovarian hypoplasia, where sterility cannot be explained by GDF9 or BMP15 polymorphisms, were identified along with their parents, and 26 animals were genotyped using the Illumina ovine 50 Beadchip. Homozygosity mapping was then used to identify regions of homozygosity in the unexplained sterile animals that were heterozygous in their carrier parents. Two regions of homozygosity were mapped to OAR 2 and OAR 8. The coding region of 2 candidate genes in the region of interest on OAR2, namely ACVR1 and ACVR1C were sequenced but no polymorphisms associated with sterility were identified. Whole genome sequencing of 5 animals is currently being performed in help refine the region of interest, and to fine map the major gene regulating ovulation rate. These results were obtained through the EC-funded FP7 Project 3SR-245140.

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