

Deciphering the genetic variability of milk composition and quality in French dairy goats

C. Maroteau* † ‡1 , I. Palhière†, H. Larroquet†, V. Clément§, G. Tosser-Klopp‡, R. Rupp†

*UNCEIA, Service Génétique, 149 rue de Bercy, F-75595 Paris, France

† INRA, UR631, SAGA, F-31326 Castanet-Tolosan, France

‡INRA, UMR444 Génétique Cellulaire, F-31326 Castanet-Tolosan, France

§ Institut de l'Elevage, F-31326 Castanet-Tolosan, France

Key-words: Genetic parameters, QTL detection, dairy goats, milk composition

Since 2008 in France, an important research and development program for mapping traits of interest in dairy goats has been carried out. This project is based on a large daughter design of 20 artificial insemination Alpine and Saanen bucks. The considered traits are milk production traits, udder morphology as well as new traits of interest such as mastitis resistance, through the milk somatic cell count (SCC), and the fatty acid (FA) composition of milk thanks to a large on farm phenotyping and genotyping project called PhenoFinlait based on mid infrared spectra estimations.

Prior to any genomic study, the first aim was to evaluate the feasibility of genetic selection for controlling the nutritional and hygienic quality of goat milk. Genetic parameters were therefore estimated by restricted maximum likelihood with an animal model, using 24,267 and 20,992 test-day records from 7,359 and 6,337 Alpine and Saanen first lactation goats respectively, for milk, fat and protein content, twenty fatty acids and SCC. Heritability estimates ranged from 0.19 to 0.51, for FA and were highest for short and medium chain fatty acids (C6:0 to C14:0) which are beneficial to human health, i.e. from 0.21 to 0.37. Heritability for SCC ranged from 0.09 to 0.15. In both the Saanen and Alpine breeds, no significant genetic correlation was found between C16:0 content in fat and total fat content, whereas strong positive correlations were found between fat content and specific goat FA in fat, i.e. C6:0 to C10:0. This result demonstrates that an increase in fat content by selection should not correlate to undesirable changes in FA profile for human health. Moreover, highly positive correlations between FA of the same origin were found: short and medium chain FA, i.e. from C6:0 to C14:0, synthesised de novo in the mammary gland and long chain unsaturated FA coming from the diet and biohydrogenate in the rumen.

A total of 2 254 goats (1,316 Alpine, 938 Saanen) and 20 IA sires (11 Alpine, 9 Saanen) were then genotyped with the 50K Illumina SNP goat beadchip, which was released in 2011 in the frame of the International Goat Genome Consortium. After classical quality control, a total of 49 647 out of 53 347 synthesized SNPs were validated for further analyses. Almost all animals had information for milk production traits (milk, fat and protein contents and yield), SCC and eleven udder type traits. Daughter yield deviations for ten individual FA plus 8 groups of FA as well as desaturation and elongation indexes were also available. Finally milking speed was recorded in a subset of goats, with an average of 40 daughters of the 20 Alpine and Saanen sires.

QTL detection based on linkage analyses (using the QTLmap software) are in progress for milk production, SCC and FA traits.

The project was funded by the French PhenoFinlait programme (ANR, Apis-Gène, CASDAR, CNIEL, FranceAgriMer, France Génétique Elevage and Ministry of Agriculture) and the European 3SR project