

Genetic parameter estimation for major fatty acids in French dairy goats

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Fatty acids (**FA**) are well-known for their importance on human nutrition. In France, since 2008, an important research and development project on phenotyping and genotyping the milk composition (FA and proteins) of cattle, sheep and goat has been carried out ("PhénoFinlait"). The project was based on a large scale on-farm phenotyping scheme for milk components allowed by the use of mid infrared (**MIR**) spectra.

In the present study, genetic parameters for twenty fatty acids and milk production traits were estimated by restricted maximum likelihood with an animal model, using 45,259 test-day records from 13,677 first lactation of Alpine and Saanen goats. Heritability estimates ranged from 0.19 to 0.51 for fatty acids and were highest (0.21 to 0.37) for short and medium chain fatty acids which are beneficial to human health, i.e. C6:0 to C14:0. High positive correlations (>0.50) were found between fatty acids of the same origin: short and medium chain fatty acids, i.e. from C6:0 to C14:0, synthesised de novo in the mammary gland and long chain unsaturated fatty acids coming from the diet and biohydrogenate in the rumen. In both the Saanen and Alpine breeds, no significant genetic correlation was found between C16:0 and fat content, whereas positive correlations (0.17 to 0.87) were found between fat content and specific goat fatty acids, i.e. C6:0 to C10:0. This result suggests that selection on fat content will not be correlated with undesirable changes in FA profile for human health.

A sample of 2 254 goats was genotyped with the 50K goat SNP beadchip (Illumina) for QTL detection.

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