PhenoFinLait (LactoScan): French national program for high scale phenotyping and genotyping to detect QTL linked with fine composition of ruminant milk.

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Milk is a very complex product with a large number of components such as proteins either included in micelles or in the serum, fat globules with phospholipids and triglycerides with a large variety of fatty acids, lactose, minerals, and many other molecules at low concentration. Fine milk content relies on environmental (feeding, breeding techniques) and genetic (species, breed and animal genotype) factors. Individual milk components could have positive or negative effects on human health. For the future, milk and dairy products must fulfil new human nutritional challenges. Therefore it is now of major interest to accurately measure elementary milk components at low cost and to identify the genetic and environmental factors affecting fine milk composition in order to define efficient tools to obtain desired milk composition.

The aim of PhenoFinLait program is to develop reliable, high throughput, cheap and easy-to-use methods for individual proteins and fatty acids content measurement and to use these methods to identify genetic, environmental factors and their interactions affecting these contents, to better understand milk synthesis in the mammary gland, to develop new opportunities in the definition of the breeding goals in selection, and to propose new tools in breeding and feeding management of animals.

To carry out such a large collaborative project, we gather all scientific (*INRA*, *Institut de l'Elevage, Actilait*) and economic stakeholders, from milk production (milk recording, DHI, analysis laboratories, cattle, goat and sheep breeding, extension services) to milk-processing (federation of dairy factories).

In 2008, the project aimed to develop equations to predict fatty acid content using Mid Infra-Red (MIR) spectra from milk samples of French experimental farm. Partial Least Square (PLS) regressions applied on MIR spectra gave rather good prediction for the main fatty acid content of cow milk and for ratios with techno functional (C18:1/C16:0) or nutritional (omega 6/ omega3) interests. In 2009, predictive equations will be straightened up to goat and sheep milk. We will also establish a reference method to quantify 12 milk proteins and try to determine from MIR spectra predictive equations for their milk content. Then, we will organize sample collection (milk, blood, MIR spectra) and register breeding strategy (especially feeding) for about 20 000 animals of French farms spread in several regions. Milk fat and protein contents will be estimated from MIR spectra using predictive equations. In the following years, animal genotyping using high density SNP chips will provide new genome regions with impact on milk content and new references for Genomic Selection.

Cross information of genotype and breeding strategy data will define new tools for genetic selection, breeding strategy and interactions between them to react quickly to human nutrition demand and competitiveness of the dairy industry.