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New tools to face lipolysis in dairy farms

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Abstract:

Mid infrared (MIR) spectra have been used since the late 2000s to phenotype new traits at large scale through prediction equations, primarily with regard to milk production traits. However, lipolysis (breakdown of milk fat) threatens the milk quality since by-products generated by the hydrolysis of milk lipids (i.e. free fatty acids and partial glycerides) severely impairs both technological and organoleptic quality of milk. Lipolysis is thus an ongoing issue for the dairy industry. In this context, we developed new equations based on MIR spectra to predict lipolysis within the framework of the LIPOMEC project funded by the French Research Agency and APIS-GENE (https://www.apis-gene.com/).

In dairy cows, a MIR equation has been used since 2012 to quantify free fatty acids in the framework of the french quality-based milk payment system. As the equation initially developed on herd milk was not fully appropriate for individual milks, a new prediction equation was constructed based on a joint analysis of lipolysis according ISO/TS 22113 standard (BDI method) and recording of MIR spectra of individual milk samples. The equation was developed by Partial Least Square regression. Its coefficient of determination R^2 reached 0.72, with a residual standard deviation Sy,x of 0.19 mmol/100 g of fat.

Regarding the goat species, to date, the only way to evaluate lipolysis in samples is by means of a chemical method, which is relatively expensive and time-consuming. We therefore aimed to develop a prediction equation for milk lipolysis that is specific to goat milk. Our new equation has a coefficient of determination R^2=0.91, with a residual standard deviation (Sy,x) of 0.20 mmol/100 g fat.

The accuracy of these new prediction equations constitute new tools to improve the control of lipolysis in dairy farms and opens new roads to explore the genetic determinism of milk lipolysis in goats and cattle.