Harmonisation of milk analysers for fatty acid determination by FTMIR - An essential step prior to collective data use

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Abstract:

General objectives of PhénoFinlait programme were to establish effective relations between the fatty acid (FA) milk composition of individual cow, goat and sheep and usual factors influencing milk production (breed, feeding, genealogy) and to relate individual fatty acid phenotypes so-measured to genotypes, so as to establish appropriate levers applicable by farmers to orient milk fatty acid production.

Throughout more than a one-year period on 2009-2011, FTMIR analysis were periodically performed using 13 milk analysers located in 9 different laboratories on 1500 selected farms (1152 for cattle, 215 for goat and 160 for sheep) of various regions of France, in order to acquire MIR spectra and build up a national spectrum data base. Fatty acid compositions were then to be predicted from the central data base through specific sets of calibration equations, i.e. one set per species and type of analyser.

Since a unique calibration set could be applied to the spectra produced by several Milkoscan FT6000 need was to evaluate how far milk analysers could be comparable in predicting fatty acid composition. Therefore repeatability and reproducibility were measured through an inter-laboratory study for a selection of 18 fatty acids and fatty acid families, putting in light high reproducibility figures and significant differences between Milkoscan FT6000 milk analysers.

To improve the precision performances, the possibility of a central calibration for FTMIR analysers for the future use of individual laboratories was successfully evaluated and a centralised system based on deep-frozen and liquid control milk samples was implemented to monitor and align FTMIR analysers for fatty acid results during the whole period of the programme.

Whereas, for the whole period, raw predictions showed rather large and often multimodal distributions depending on the fatty acid (or fatty acid family), the applied corrections resulted in end in significant squeezes of fatty acid data populations characterized by single dominant modes.