Implementing a genetic evaluation for milk fat composition in the Walloon Region of Belgium

Gengler, N.[1], Troch, T.[1], Bastin, C.[1], Vanderick, S.[1], Vandenplas, J.[1,2] and Soyeurt, H.[1,2], [1]ULg – GxABT, Passage des Déportés, 2, 5030 Gembloux, Belgium, [2]FNRS, Rue d'Egmont, 5, 1000 Brussels, Belgium; nicolas.gengler@ulg.ac.be

A genetic evaluation system for milk fat composition is currently under development in the Walloon Region of Belgium. Based on the currently used genetic evaluation model for production traits a multi-trait (milk, fat and protein yields, saturated (SFA) and monounsaturated (MUFA) fatty acid contents in milk) and multi-lactation (first, second, third lactation) random regression test-day model was developed. (Co)variance components were developed from results obtained in previous research. Milk production test-day records are available since 1974 (currently 7,019,000 in first, 5,253,000 in second and 3 757 000 in third lactation) and, fatty acids predicted from MIR spectral data since 2007 (currently 499,000 in first, 392,000 in second and 277,000 in third lactation). Mixed model equations were solved as the current routine evaluations with a preconditioned conjugate gradient implementation with integrate outlier checking and correction. Reliabilities were computed using the procedures developed for production traits. By evaluating SFA and MUFA contents in milk together with correlated traits, milk, fat and protein yields were used as predictors in order to improve estimation of EBV for those novel traits. Therefore a total of 525,048 respectively 249,027 evaluated cows achieved reliabilities equal or greater than 0.35 for SFA and MONO compared to 640,072 for milk yield. Among the sires of cows with fatty acid records 876 respectively 613 had reliabilities equal or greater than 0.75 for SFA and MUFA compared to 1,074 for milk yield. Breeding values will be expressed using two indices that represent the desaturation (or mono-desaturation) of milk fat compared to the expected level. Additional research is ongoing to extend this genetic evaluation system to a genomic single-step GBLUP using INTERBULL breeding values as a priori information for correlated indicator traits.