Targeted combination of estimated breeding values for lower accuracy mid-infrared biomarkers increases their usefulness in genetic evaluation of dairy cattle

***N. Gengler*[1]** *& GplusE Consortium*[2]

[1]*ULg-GxABT, Passage des Déportés 2, 5030, Gembloux, Belgium*
[2]*http://www.gpluse.eu, Lead partner: UCD School of Veterinary Medicine, Belfield, Dublin 4, Ireland*

Abstract

Recent research has shown the possibilities to predict different biomarkers for health and fertility from milk mid-infrared (MIR) spectra. However MIR predictors do not always show high R^2 of cross-validation (R^2_{CV}). We investigated strategies to use also lower accuracy predicted phenotypes in genetic evaluations as MIR predictors of blood based biomarkers (IGF1, glucose, urea, cholesterol, fructosamine, BOHB; NEFA) calibrated inside the GplusE project (on-going research currently R^2_{CV} ranging from 0.21 to 0.51). A total of 59,303 records from 33,968 cows in the Walloon region of Belgium in early lactation (before 50 DIM) were available. Using a single-trait, multi-lactation model (1, 2, 3+), variance components were estimated (h^2 ranging from 0.15 to 0.31). Estimated breeding values (EBV) were computed and used when based on at least 20 daughters. A total of 171 bulls met these criteria. First, EBV for each individual biomarker were compared with official EBV for somatic cell score (udder health), fertility and longevity. Observed correlations (i.e. lower bound estimates of genetic correlations), were diverse (in absolute values) ranging from 0.00 to 0.31. The highest value was found between fertility and fructosamine in third lactation. We postulated that by combining the different MIR based biomarker EBV, weighting them according to their contribution to the estimation of udder health, fertility and longevity EBV, the observed correlations between combinations of MIR based biomarkers and observed EBV would be significantly larger than the individual correlations. Results confirmed this with values of 0.62, 0.59, and 0.52 for udder health, fertility and longevity, respectively. Udder health (somatic cell score) is available early in lactation, fertility later and direct longevity much later in life. Therefore, udder health and fertility are often used as predictors of longevity. Based on our data, correlations of longevity with udder health and fertility were 0.52 and 0.57, respectively. These values were similar to 0.52 found for our predictor of longevity based on combined MIR biomarkers. Combining udder health and fertility put this correlation to 0.64, adding MIR biomarkers increased it to 0.68. Results showed that combining even lower accuracy MIR based biomarker EBV increased their usefulness for genetic evaluation. The presented strategy can be complemented by several others as alternative phenotype definition directly targeting desired phenotypes (e.g. metabolic status), better calibration models, multi-trait evaluations and optimized selection index procedures to combine individual information sources.

Keywords: prediction, longevity, health, fertility