

Summary

Recent research showed the usefulness of using estimated breeding values (EBV) for mid-infrared (MIR) based biomarkers in genetic improvement. Similarly, research has also shown that genetic variation is contained in the absorbance traits along the MIR band of wavelengths. Targeted extraction of the useful genetic variance can be achieved by the combination of EBV. Direct estimation of EBV for absorbance traits was demonstrated. Our first objective was to show that the reduction of the rank of the (co)variance structure among spectral traits is possible by imposing linear functions, even if these functions represent lower accuracy MIR biomarkers. MIR based biomarkers traits were derived from ongoing research in the FP7 GplusE project. In this study, the pathway from MIR spectra to the use in genetic improvement will be described. First, blood reference phenotypic data was collected on Holstein cows, at early lactation for IGF1, glucose, urea, cholesterol, fructosamine, β -Hydroxybutyric (BHB) acid and non-esterified fatty acids (NEFA). These traits were calibrated against corresponding MIR spectral data. Calibration R_{CV}^2 ranged from 0.21 to 0.51, very low from a chemometrical point of view, but potentially sufficient to extract useful spectral variation. This was validated, using EBV that were based on these MIR predictions for 59,303 records (closest to days in milk 25), from 33,968 cows, in the Walloon region of Belgium. Single-trait, but multi-lactation (1, 2, 3+) models yielded h^2 estimates ranging from 0.15 to 0.30. At least 20 daughters with novel traits and official EBV for udder health, fertility and longevity were required; a total of 171 bulls met this criteria. Standard selection index theory would usually rely on prediction error variance minimisation and estimated population (co)variances. Alternatively in this study, Partial Least Squares were applied to EBV for the MIR based biomarkers to develop novel genetic predictors, for udder health, fertility and longevity, by extracting genetic variation along the wave band after rank reduction. Using all bulls, correlations between best predictors and EBV for udder health, fertility and longevity were at least 0.62, 0.59 and 0.52. Using selection index theory and based on significant increases of prediction abilities of longevity (0.68 compared to 0.64 from udder health or fertility alone) using also MIR based biomarkers, their potential contribution to genetic improvement of udder health, fertility and longevity will be demonstrated.

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Keywords: milk MIR spectra, blood biomarkers, genetic improvement, udder health, fertility, longevity