

## Genetic analyses of principal components of milk mid-infrared spectra from Holstein cows

Y. Chen<sup>1\*</sup>, P. Delhez<sup>1</sup>, H. Atashi<sup>1,2</sup>, H. Soyeurt<sup>1</sup>, N. Gengler<sup>1</sup>

<sup>1</sup> ULiège-GxABT, 5030 Gembloux, Belgium; <sup>2</sup> Department of Animal Science, Shiraz

University, 71441-13131 Shiraz, Iran. \*: [yansen.chen@uliege.be](mailto:yansen.chen@uliege.be)

**Abstract:** Milk mid-infrared (MIR) spectra are widely used to predict milk composition and phenotypes linked to animal health, efficiency, emissions, resilience, and even milk processability. However, the milk phenome represented by the large number of individual MIR wavenumbers (hereafter called MIR spectral traits) could allow strategies to develop innovative and holistic monitoring and decision-making PLF tools by avoiding phenotypic calibrations. The objectives of this study were to start exploring the complete genetic architecture of MIR spectral traits by studying principal components of milk MIR traits from Holstein cows and their genetic correlations with milk fat percent. In total, 27,855 records for 311 MIR spectral traits and fat percent from 3,303 first-parity Holstein cows were used. All principal components (PCs) of 311 wavenumbers were extracted and single-traits and bivariate (PC and fat percentage) repeatability models were used. The first 75 PCs explained already 99.99% of the phenotypic variance across the 311 wavenumbers. However, the genetic variances of these 75 PCs explained only 85.54% of the total genetic variances of the 311 PCs. Their range of heritability was from 0.00 to 0.47. The mean and standard deviation of genetic correlations (absolute value) between 311 PCs and fat percent were 0.25 and 0.28, respectively. After first 75 PCs, some PCs (e.g., PC 86) still had genetic correlations (here 0.37) with fat percent. This preliminary study showed that phenotypic rank reduction using first 75 PCs might be dangerous, also as even some PCs (e.g., PC 145) with very low phenotypic variances (< 0.001%) showed heritability (here 0.05) over 0.01. By estimating heritability and in future studies genetic correlations among MIR spectral traits associated with

genomics, understanding the genetic architecture of MIR spectral traits will not only help us optimize their use for breeding, but also manage by avoiding phenotypic calibration steps.

**Key words:** mid-infrared, fat percent, heritability, genetic correlation