A landscape of the heritability of single-band Fourier-Transform Infrared spectra data in Canadian Holstein

Introduction

- Fourier Transform mid-infrared spectrometry is worldwide used for composition and quality controls of milk samples.

- Main research efforts and industry applications using FT-MIR data has focused on developing *prediction equations* for economically important phenotypes.
  - Milk composition (Rutten et al., 2010; 2011);
  - Technological properties (Cecchinato et al., 2009);
  - Health and reproductive phenotypes (Heuer et al., 2001; Belay et al., 2017, Toledo-Alvarado et al., 2017);
  - Feed efficiency and methane emission (Shetty et al., 2017a; b).
Introduction

- Few authors have reported genetic parameters of FTIR data:
  - Soyeurt et al. 2010. ~1,600 Belgium Holstein, first parity;
  - Bittante & Cecchinato 2013, ~1,100 Italian Brown Swiss, multiparous;
  - Wang et al. 2016, ~1,750 Dutch Holstein-Friesians, first parity.

- These studies have shown that absorbance (and transmittance) at certain regions of the spectrum can be moderately heritable.
Objective

The aim of this study was to produce a landscape of the heritability ($h^2$) of FTIR spectra data across parities and different months of the lactation.
Data

- **Canadian DHI** milk recording from January 2013 to June 2016

- The individual milk spectra were obtained from the two laboratories, CanWest DHI (Guelph, ON) and Valacta (Sainte-Anne-de-Bellevue, QC), which used MilkoScan FT6000 spectrometers (FOSS, Hillerød, Denmark)

- **369,509 test-day**, 203,516 Holstein cows

- **19,164 herd-year-season**
Number of records in parity-months group
Model

\[ y_{ij} = \mu + hys_i + a_j + \varepsilon_{ij}, \]

\( y_i \) (\( i=1, \ldots, n \)) represents a phenotype
- **Milk yield, % Protein, % Fat, 1060 individual bands**

\( hys_i \) random effect of \( i^{th} \) herd-year-season level (33,119 hys levels),

\( a_j \) is the additive genetic effect of \( j^{th} \) cow

\( \varepsilon_{ij} \) is an error term.

\( hys \sim \text{MVN}(0, I\sigma^2_{hys}), a \sim \text{MVN}(0, A\sigma^2_a) \) and \( \varepsilon \sim \text{MVN}(0, I\sigma^2_\varepsilon) \)
Implementation

- 1063 trait * 18 groups of Parity (1 to 3) – Month of lactation (1 – 6) = 19,134 analyses

- BGLR software (Pérez and de los Campos, 2014).

Posterior means, posterior standard deviations and 95% credibility regions for each of the variance parameters and for the heritability ($h^2$) defined as: \[ \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{hys}^2 + \sigma_e^2} \].
RESULTS
Phenotypic mean and variation
Phenotypic mean and variation
Heritability for Milk yield, % protein and % fat
General landscape of bands’ heritability
Heritability by parity and month of lactation

- Lactose
- Acetone
- Urea
- Fat
- Protein
Conclusions

- We confirmed that there are regions of the spectra heritable, in the Canadian-Holstein population, using a significantly larger sample size.

- $h^2$ estimates for individual bands ranging from values near zero to values of about 0.55.

- There are multiple regions of the spectra showing higher $h^2$ than that of yield traits commonly used in genetic evaluations.

- Some regions of the spectra (e.g. MWIR 1) showed some differences in the landscape of $h^2$ estimates for first month of lactation.
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Thank you!
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