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

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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**.
    - *Zaalberg et al. 2018*, (in WCGALP congress), **~3,300 Danish Holstein and ~3,400 Danish Jersey**.
- 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***

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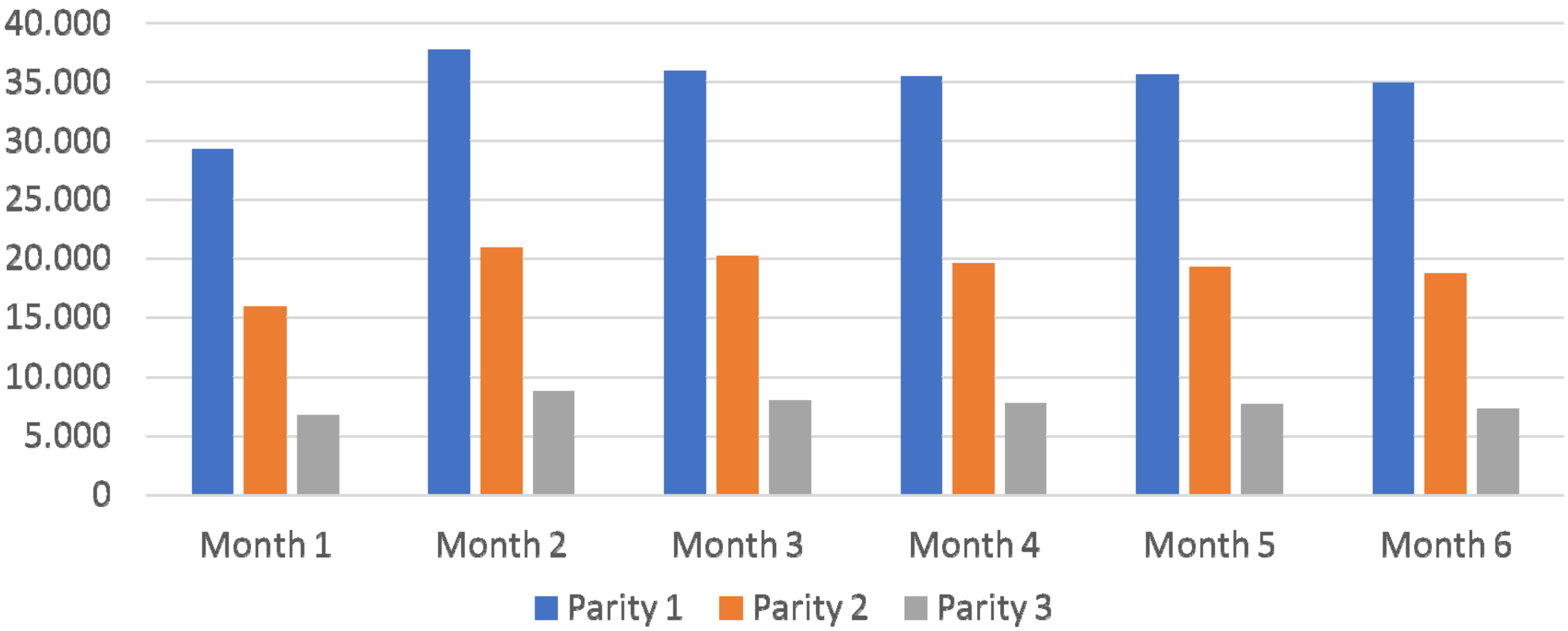
Number of records in parity-months group



Model

- $\boldsymbol{y_{ij} = \mu + hys_i + a_j + \varepsilon_{ij}}$,

$\boldsymbol{y_i}$ (*i*=1,…,*n*) represents a phenotype

- *Milk yield, % Protein, % Fat, 1060 individual bands*

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

$\boldsymbol{a_j}$ is the additive genetic effect of j^{th} cow

$\boldsymbol{\varepsilon_{ij}}$ is an error term.

$\boldsymbol{hys} \sim MVN\left(\boldsymbol{0}, \boldsymbol{I}\sigma^2_{hys}\right)$, $\boldsymbol{a} \sim MVN(\boldsymbol{0}, \boldsymbol{A}\sigma^2_a)$ and $\boldsymbol{\varepsilon} \sim MVN(\boldsymbol{0}, \boldsymbol{I}\sigma^2_{\varepsilon})$

Implementation

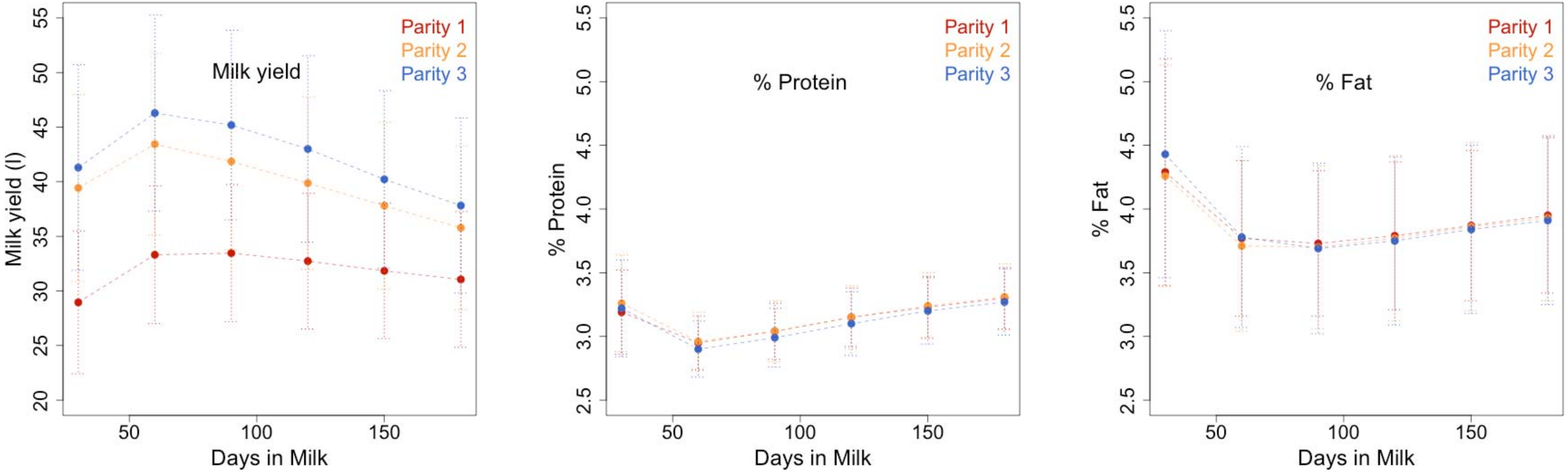
- 1063 trait * 18 groups of Parity (1 to 3) – Month of lactation (1 – 6)

  19,134 analyses

- pedigreeR R-package (Vazquez & Bates, 2017).
- 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: $\frac{\sigma_a^2}{\sigma_a^2 + \sigma_{hys}^2 + \sigma_\varepsilon^2}$.

RESULTS

Phenotypic mean and variation



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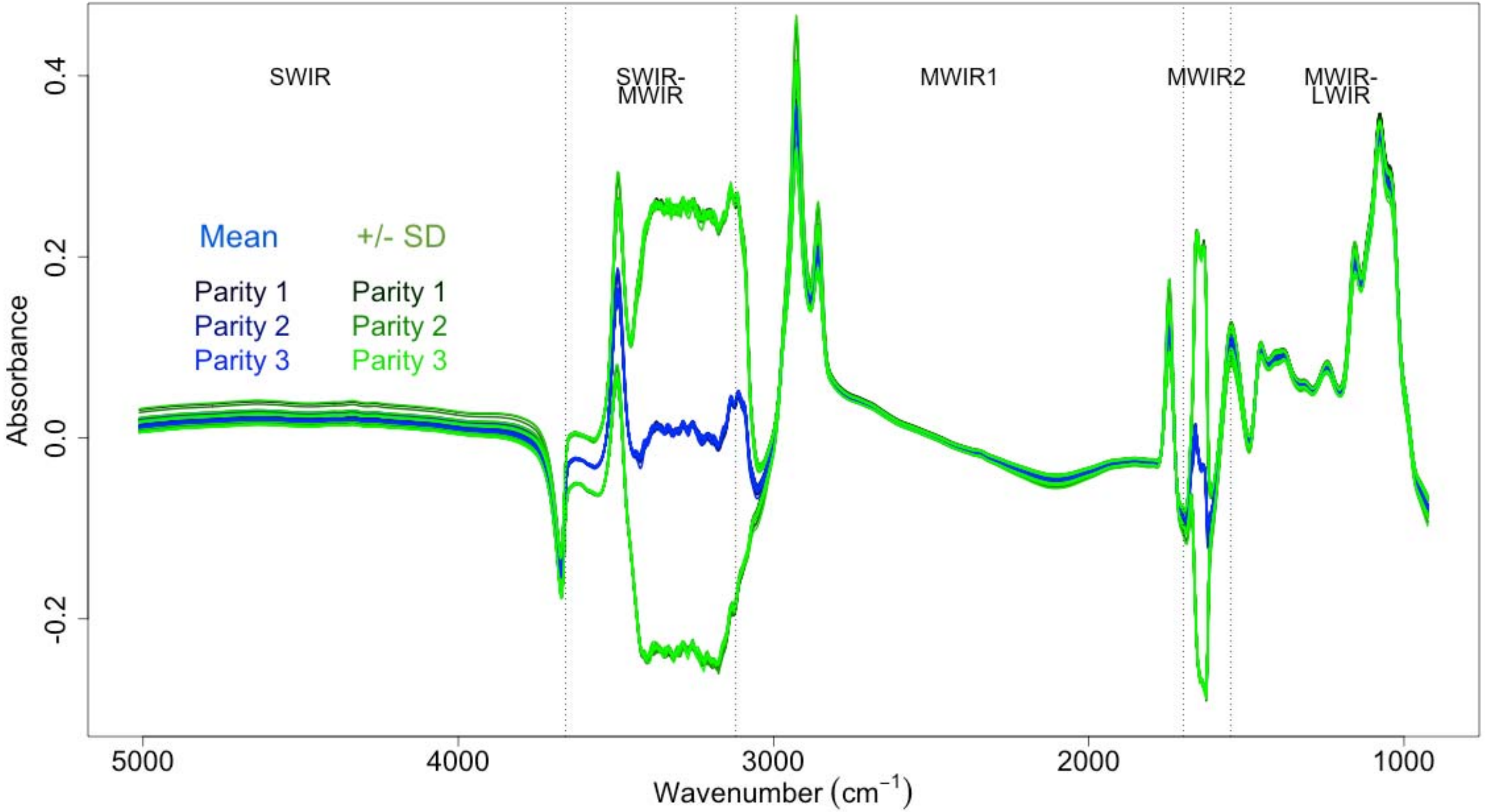
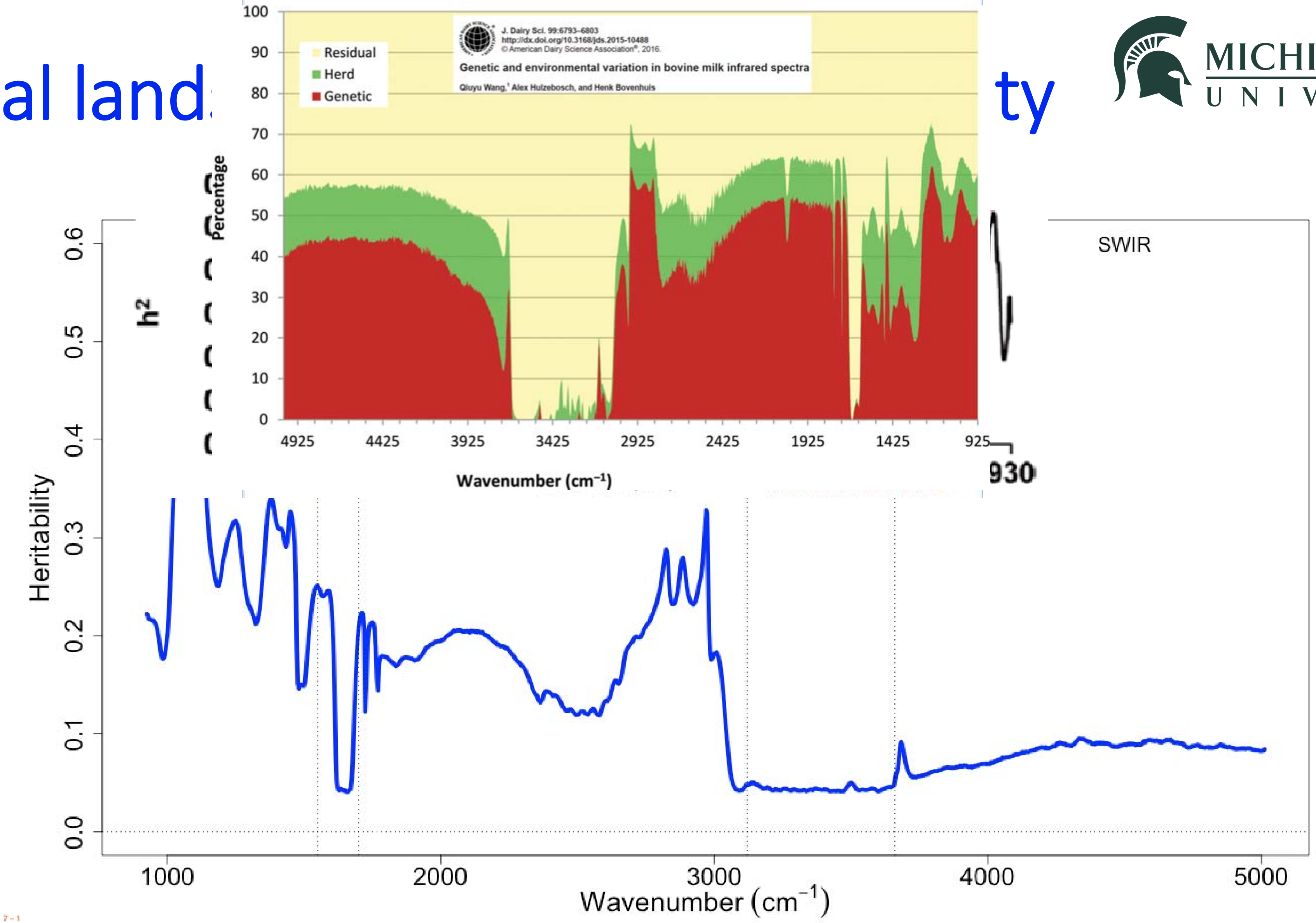


Heritability for Milk yield, % protein and % fat

General land ty



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Genetic and environmental variation in bovine milk infrared spectra

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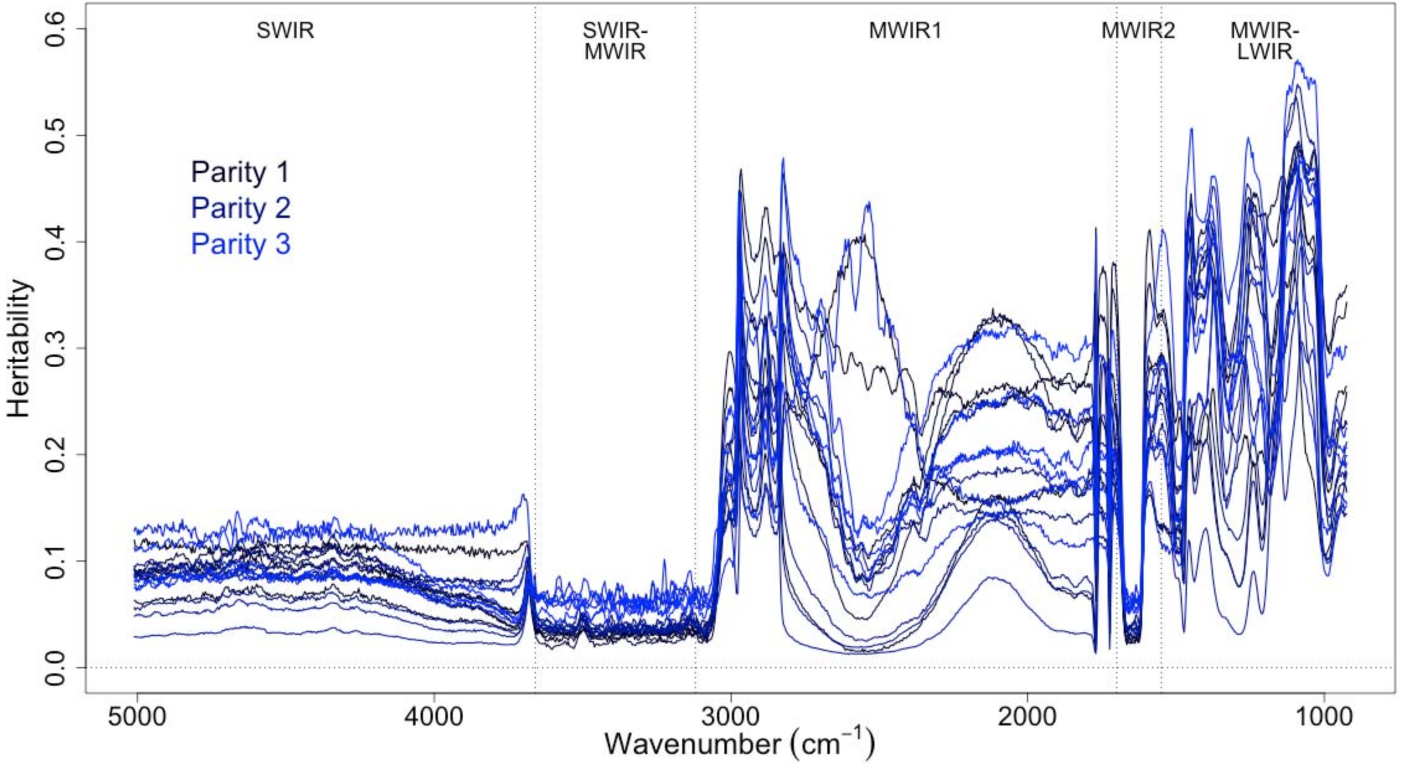
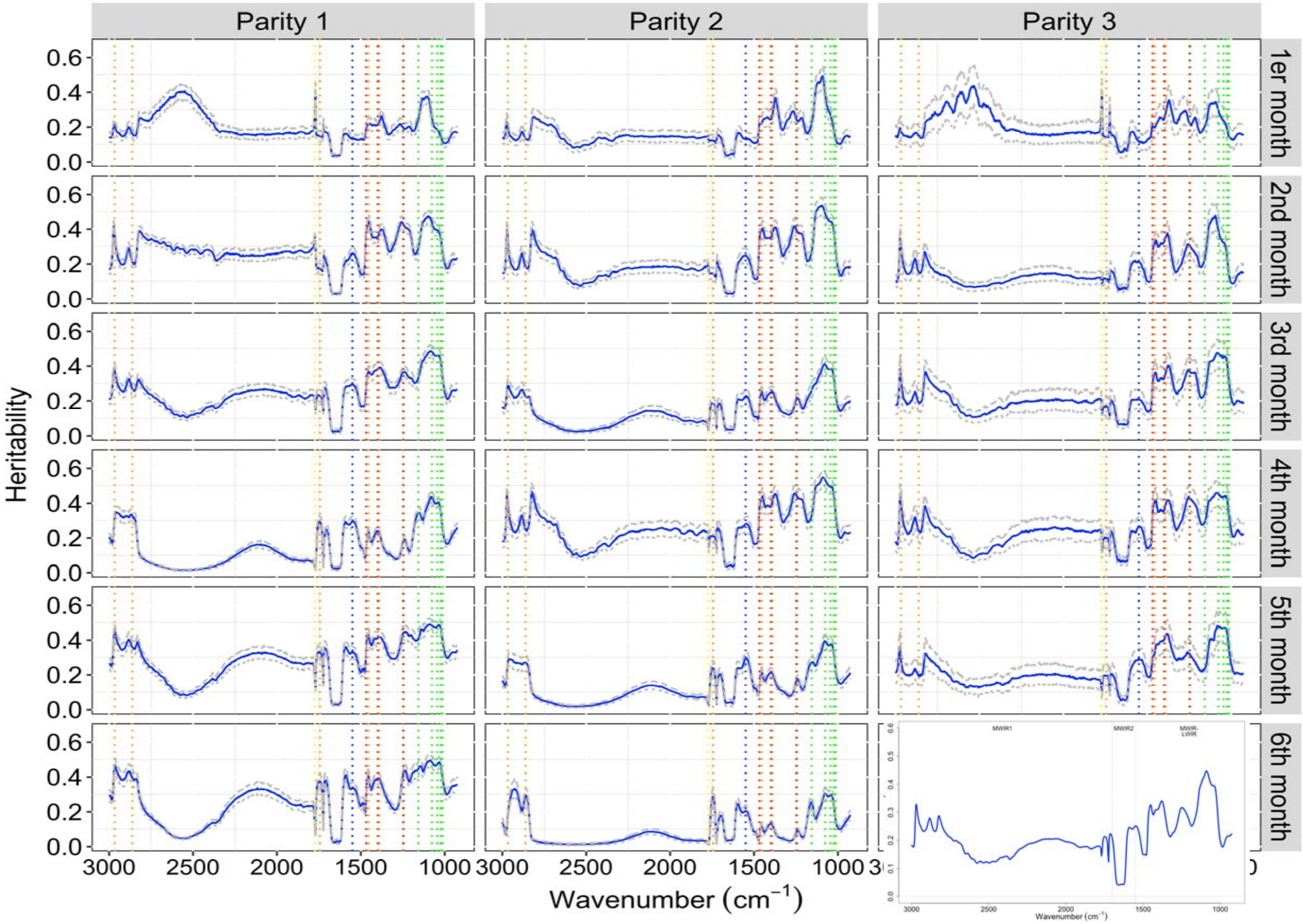
General landscape of bands' heritability



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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