Genetic and Environmental Info in goat milk FTIR spectra

B. Dagnachew and T. Ådnøy

Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences

EAAP 2011
29th August, Stavanger, Norway

The Research Council of Norway

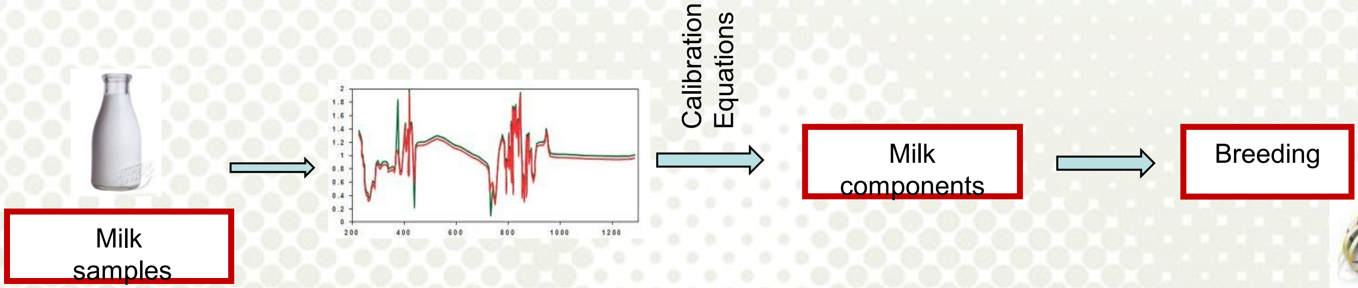
TINE

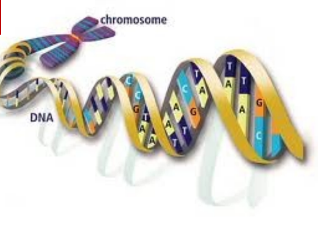
Outline

- Background
  - Milk composition
  - Infrared (IR) spectroscopy
  - Objectives
- Methods
- Results
- Conclusion

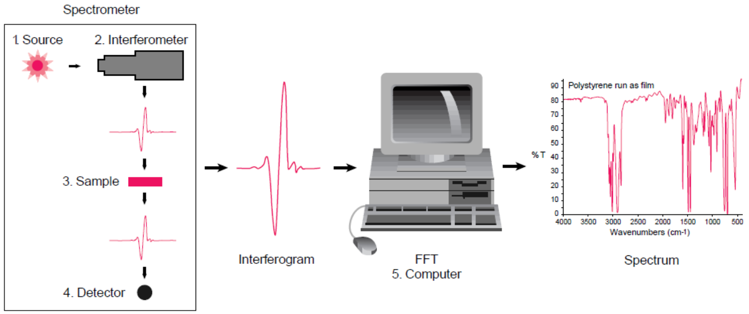
Background

- Milk is a complex mixture of several thousand kinds of bio-molecules
  - In the current animal breeding programs, only few major milk components are included
  - Fat %, protein %, lactose %, SCC, FFA, etc
- Infrared (IR) spectrometry is used
  - Rapid method (chemical analysis are time and labor intensive)





Infrared (IR) spectra



- Fourier Transform Infrared (FTIR)
  - ❖ Improve signal to noise ratio
  - ❖ Multiplexing capabilities
  - ❖ Higher energy throughput

- Genetic variability of cow milk based on MIR spectra (*Soyeurt et al., 2010*)
- Genetic variability of goat milk FTIR spectra have not been studied
  - – Some regions are indirectly known

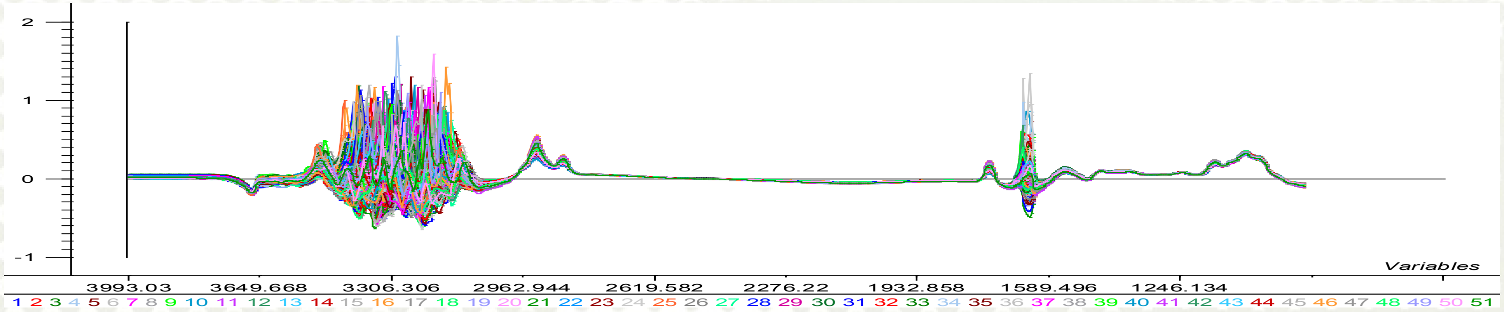
Objective:

Direct estimation of genetic and environmental variability of goat milk FTIR spectra

Materials and Methods

- Raw FTIR Spectra data
  - TINE (Norwegian dairies) has four D-labs performing routine FTIR analysis on milk samples
  - Raw FTIR spectra are stored since 2007 in a database
- For this study: :
  - Two years (2007 and 2008)
  - Total of 73,858 observations
    - 28,269 goats
    - 271 farms

CombiFoss™ FT



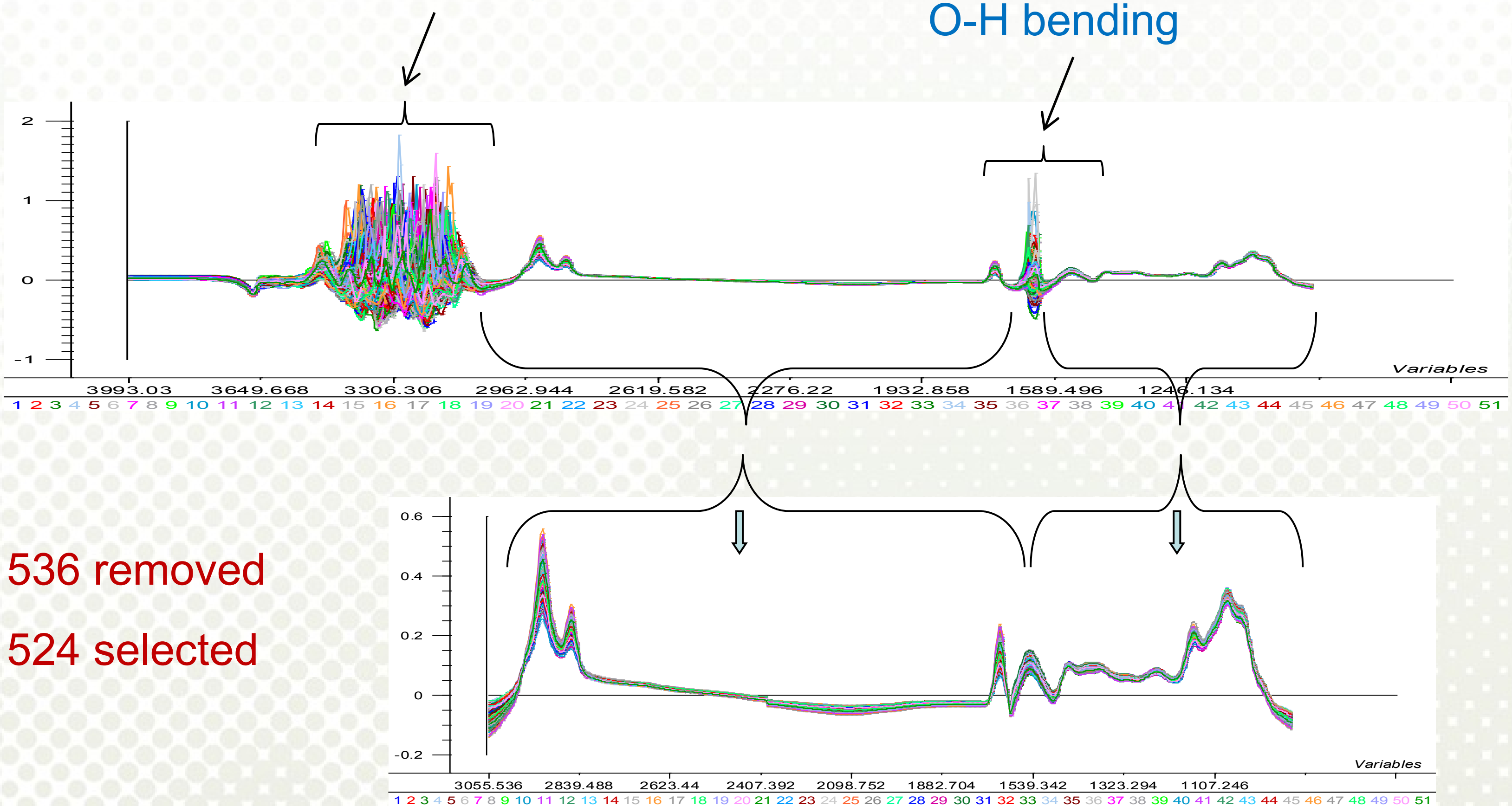
Cont…

- Selection of FTIR spectra
  - O-H bending region (between 1600cm^{-1} and 1700 cm^{-1})
  - O-H stretching region (between 3025 cm^{-1} and 3500 cm^{-1})

Low signal to noise ratio

O-H stretching

O-H bending



536 removed

524 selected

Cont …

- Limitations …
  - Simultaneous genetic analysis of selected spectra data points is not possible with the current methods available for genetic analysis

    e.g. DMU 31, WOMBAT 42, ASReml 21 traits, …

  - Two step analysis performed
    - Dimension (trait) reduction
      - Principal component analysis (PCA)
    - Genetic analysis
      - Mixed model

Cont …

- Principal component analysis (PCA)

Goal: to extract a set of fewer components that explain as much variation as possible of the original variation

$$Y = TP' + F$$

- **Y** are the FTIR spectral data
- **T** is score matrix
- **P** is loading matrix
- **F** is error term

- PROC PRINCOMP in SAS (SAS Institute, 1994)
  - On correlation matrix of Y
  - Scores, T, are considered as new traits → PC traits

- Pre-correction
  - PC traits T corrected for:
    - farm region (12 levels)
    - kidding season (3 levels)
    - lactation stage (4 co-variables)
    - age at kidding (5 levels)
    - lactation number (3 levels)

Methods Cont…

Model

- Multi-trait linear mixed model on pre-corrected PC traits

$$t_c = Xb + Za + Qp + Wh + e$$

- **t_c** is the vector of pre-corrected PC traits
- **b** is the vector of fixed effect (HTY and HTM)
- **a** is the vector of additive genetic effect
- **p** is the vector of permanent environment effect
- **h** is the vector of random herd-test-day (HTDr) effect
- **e** is the vector of random residual effect

- **X**, **Z,** **Q**, and **W** are the corresponding design matrices

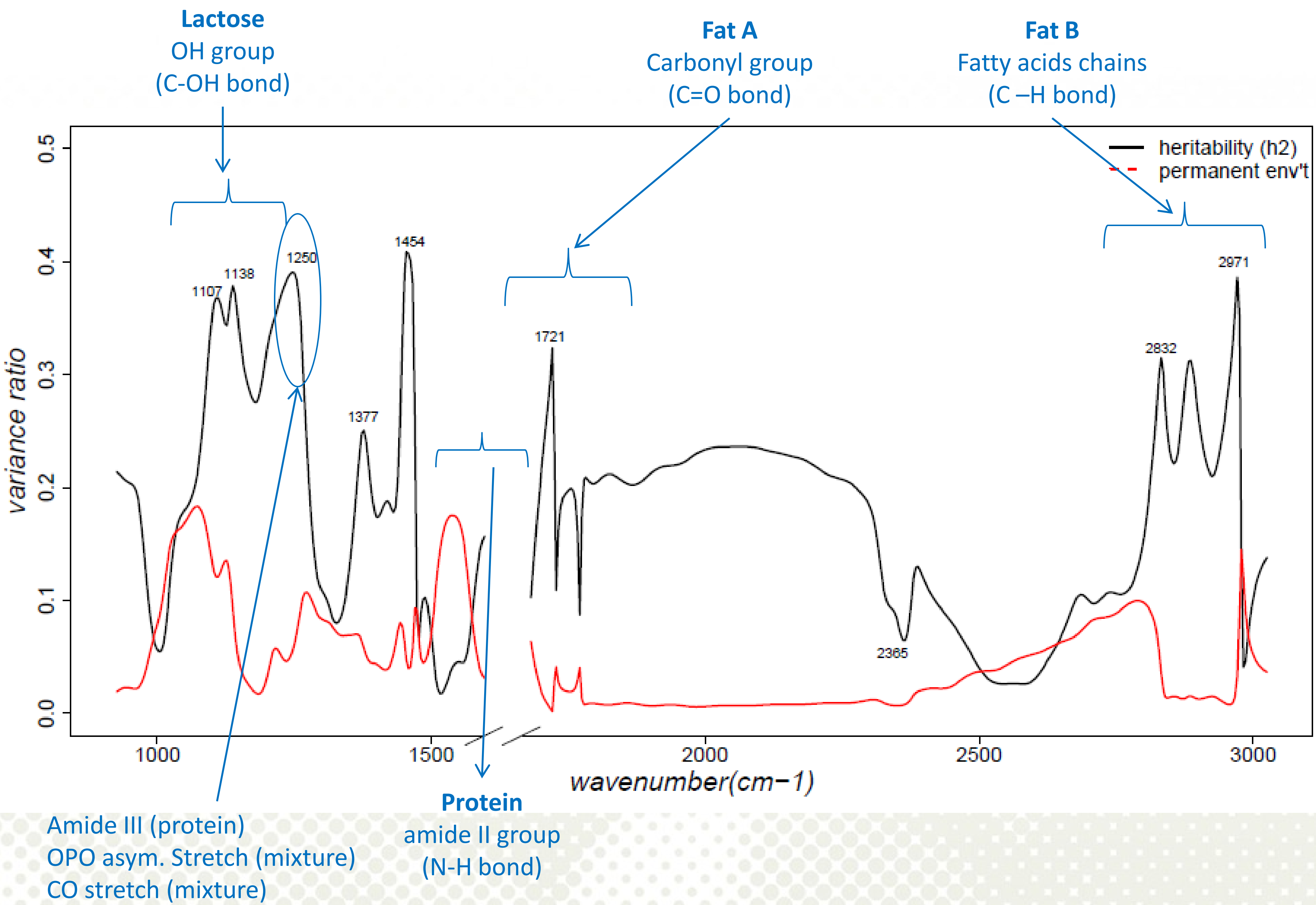
- AI-REML of WOMBAT (*Meyer, 2007*)

Results and Discussion

- PCA
  - Resulted in 8 PCs which explain ~99% of the total spectral variation
  - The dramatic reduction of the number of components suggests there is high correlation among spectral variables

Table 1: Variance ratios for genetic, permanent environment, HTDr and residual random effects

PCs	Relative eigenvalues	Genetic (heritability)	Permanent environment	Herd test-day (HTDr)	Residual
1	58.96	0.154	0.020	0.105	0.721
2	25.62	0.264	0.091	0.298	0.347
3	7.74	0.146	0.015	0.388	0.451
4	3.24	0.057	0.270	0.020	0.653
5	1.66	0.011	0.013	0.941	0.035
6	1.07	0.229	0.135	0.277	0.359
7	0.41	0.211	0.058	0.298	0.432
8	0.28	0.285	0.033	0.140	0.542



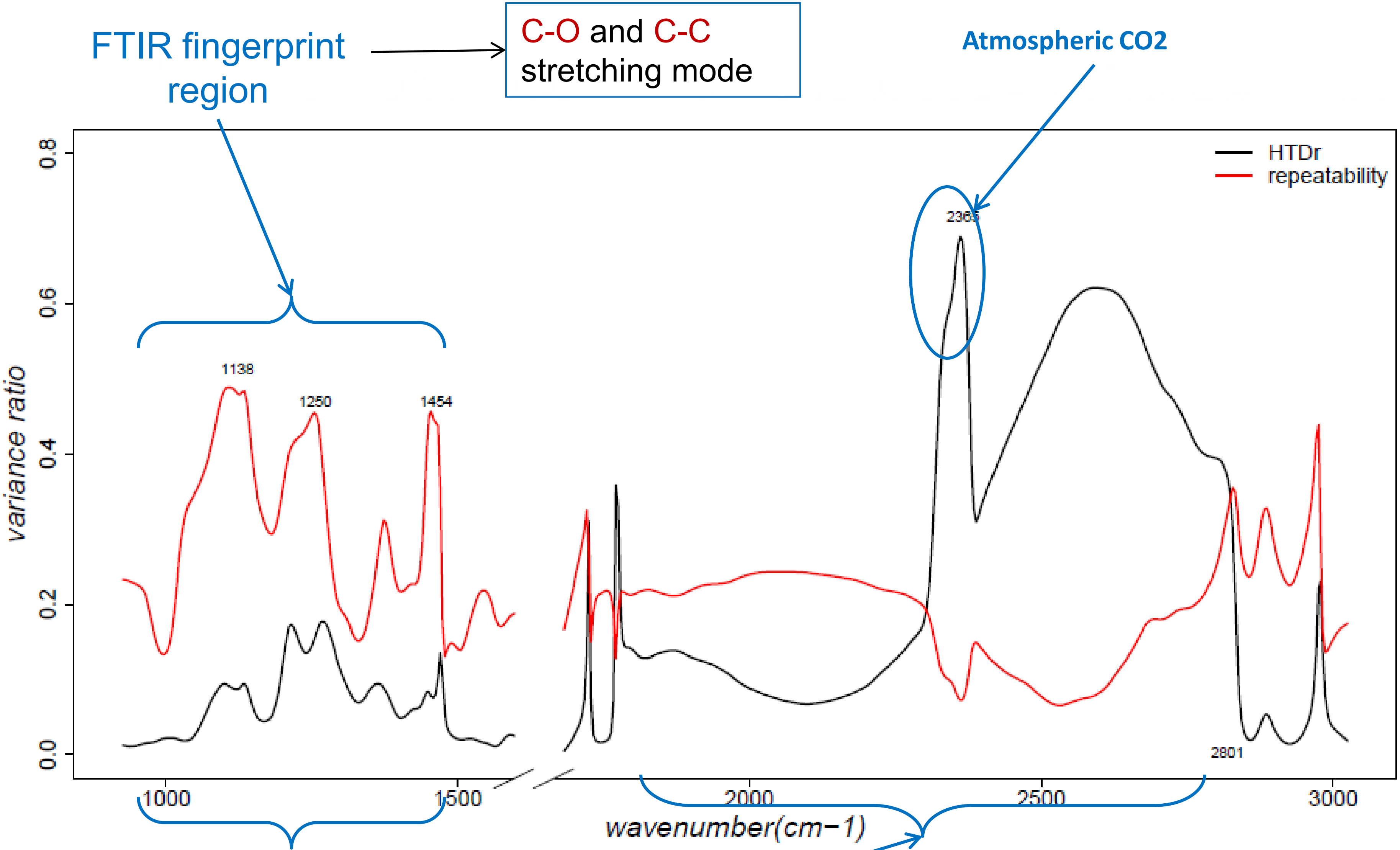
Lactose
OH group
(C-OH bond)

Fat A
Carbonyl group
(C=O bond)

Fat B
Fatty acids chains
(C –H bond)

Amide III (protein)
OPO asym. Stretch (mixture)
CO stretch (mixture)

Protein
amide II group
(N-H bond)



FTIR fingerprint region

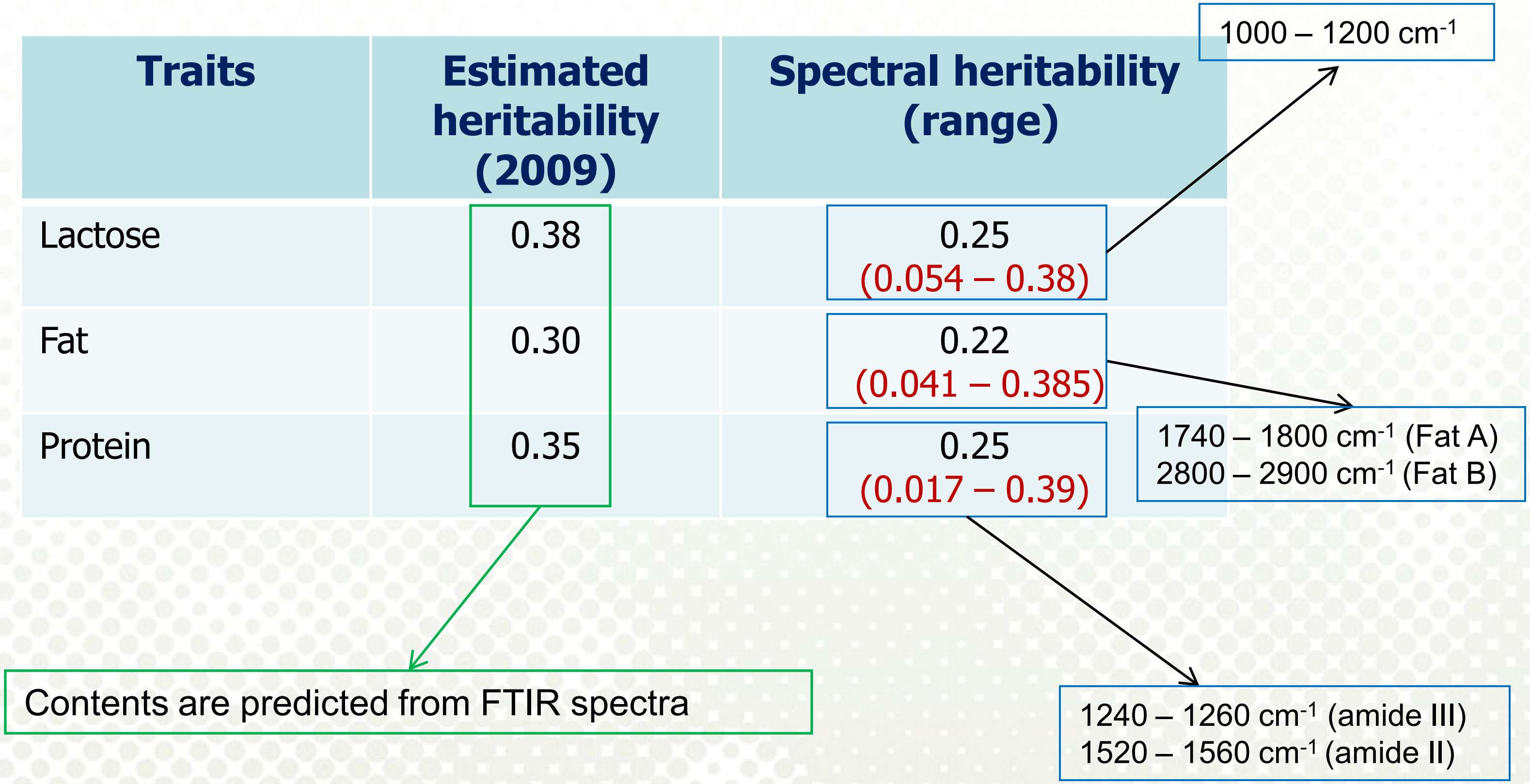
C-O and C-C stretching mode

Atmospheric CO2

No specific chemical information

Cont …

- Average spectral heritabilities



Traits	Estimated heritability (2009)	Spectral heritability (range)
Lactose	0.38	0.25 (0.054 – 0.38)
Fat	0.30	0.22 (0.041 – 0.385)
Protein	0.35	0.25 (0.017 – 0.39)

1000 – 1200 cm^{-1}

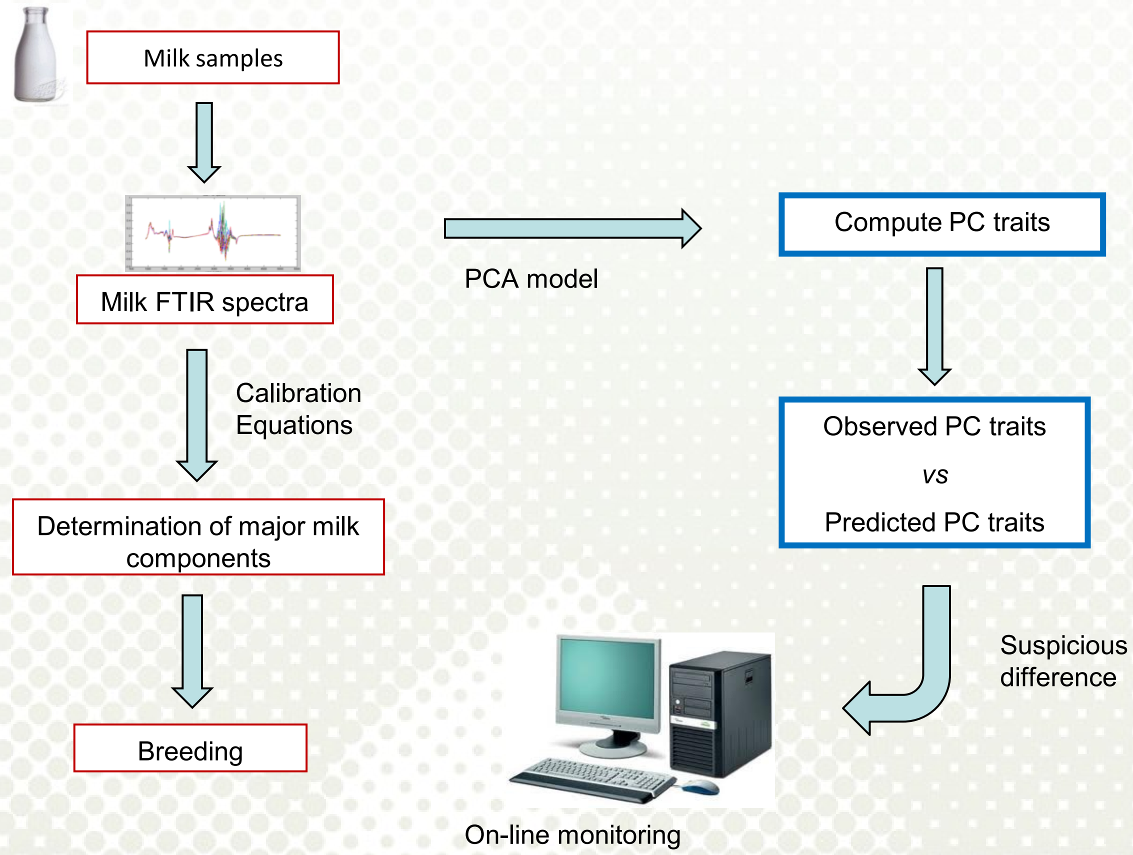
1740 – 1800 cm^{-1} (Fat A)
2800 – 2900 cm^{-1} (Fat B)

1240 – 1260 cm^{-1} (amide III)
1520 – 1560 cm^{-1} (amide II)

Contents are predicted from FTIR spectra

Conclusion

- There is a substantial amount of genetic variation in goat milk FTIR spectra
    - Not all FTIR regions are of breeding interest
    - But could be used in herd management



Thank you for your attention!

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