AARHUS
UNIVERSITY

CENTER FOR QUANTITATIVE
GENETICS AND GENOMICS

Milk as new phenotypes

Bart Buitenhuis



AARHUS UNIVERSITY

CENTER FOR QUANTITATIVE GENETICS AND GENOMICS

DK-SE Milk Genomics Innitiative

Fatty Acid profile

Protein profile

Coagulation properties

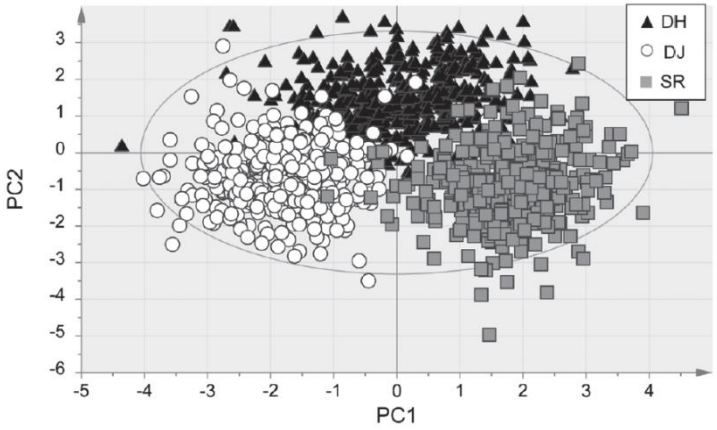
Micro- Macro elements

Vitamins

Metabolite profile

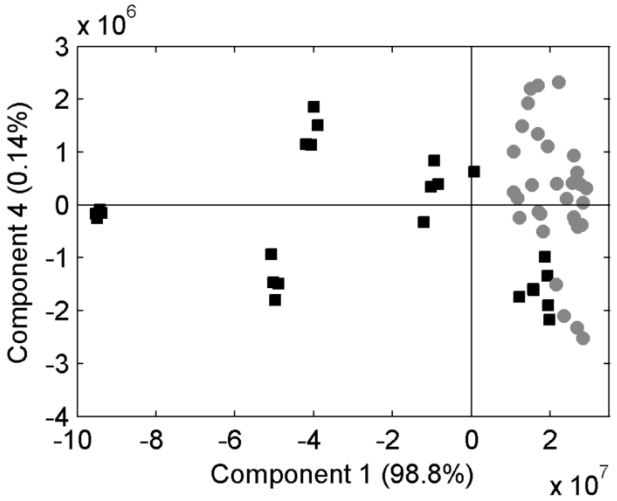
Image Credit: violetkaipa / Shutterstock

Breed differences



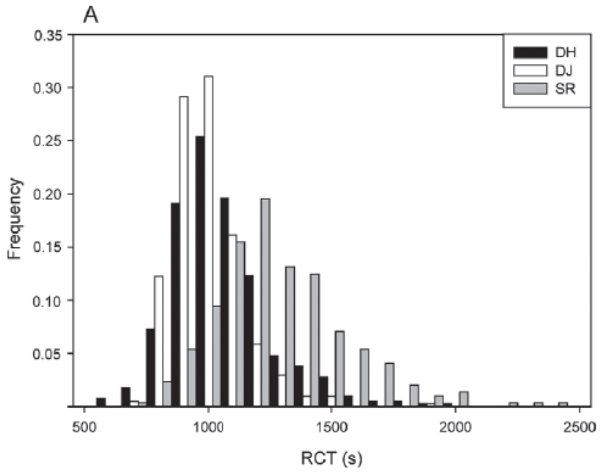
Poulsen et al. 2012. JDS 95: 6362-6371

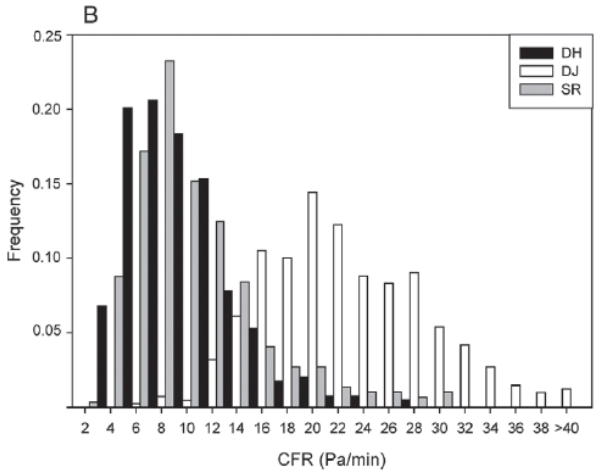
Fatty acid profile



Sundekilde et al. 2011. J. Agric. Food Chem 59:7360-7367

Metabolite profile





Poulsen et al. 2013. JDS 69:4830-4842

Co-agulation properties

Genetics or Environment?

h^2 for the Metabolites

< 0.15

- Metabolites
  - Lactic acid
  - Acetic acid
  - Fumaric acid
  - Galactose

0.15 - 0.40

- Metabolites
  - Alanine
  - Butyrate
  - Lactose
  - Valine
  - Ornithine
  - Isoleucine
  - Fucose

> 0.40

- Metabolites
  - Creatinine
  - Choline
  - Citric Acid
  - Glucose
  - Orotic acid
  - BHBA

Genetics or Environment?

h^2 for Fat and Protein

< 0.15

- Fatty acids
  - C15:0
  - C16:0
  - C17:0
  - C18:1c9
  - C18:1t11
- Proteins
  - A-s1-CN
  - A-s2-CN
  - B-CN

0.15 - 0.40

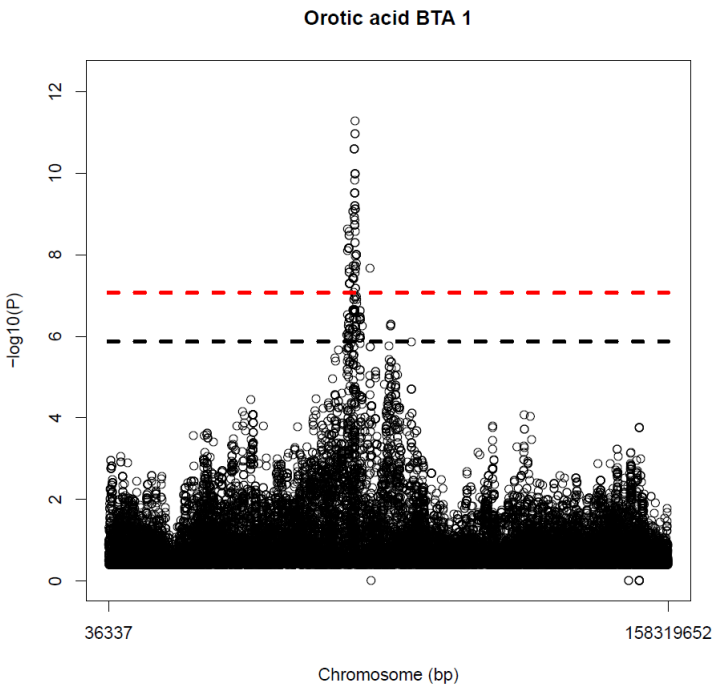
- Fatty acids
  - C6:0 to C12:0
  - C13:0
  - C14:0/C14:1
  - C18:0
  - C16:1
  - C18:2n6
  - C18:3n3
  - CLA

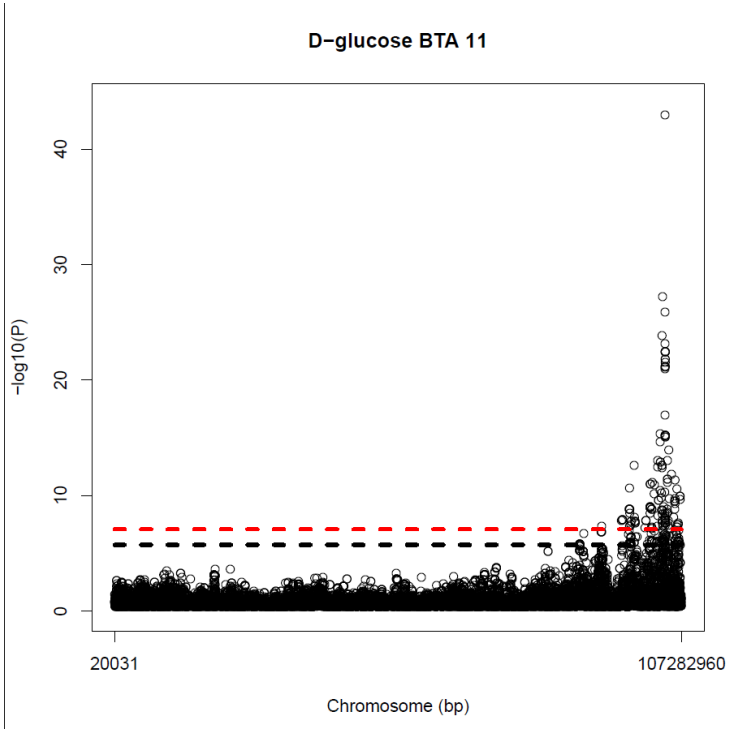
> 0.40

- Proteins
  - Caseine
  - K-CN

Association study

Metabolites: 8 QTL (Bonferoni P<0.05)





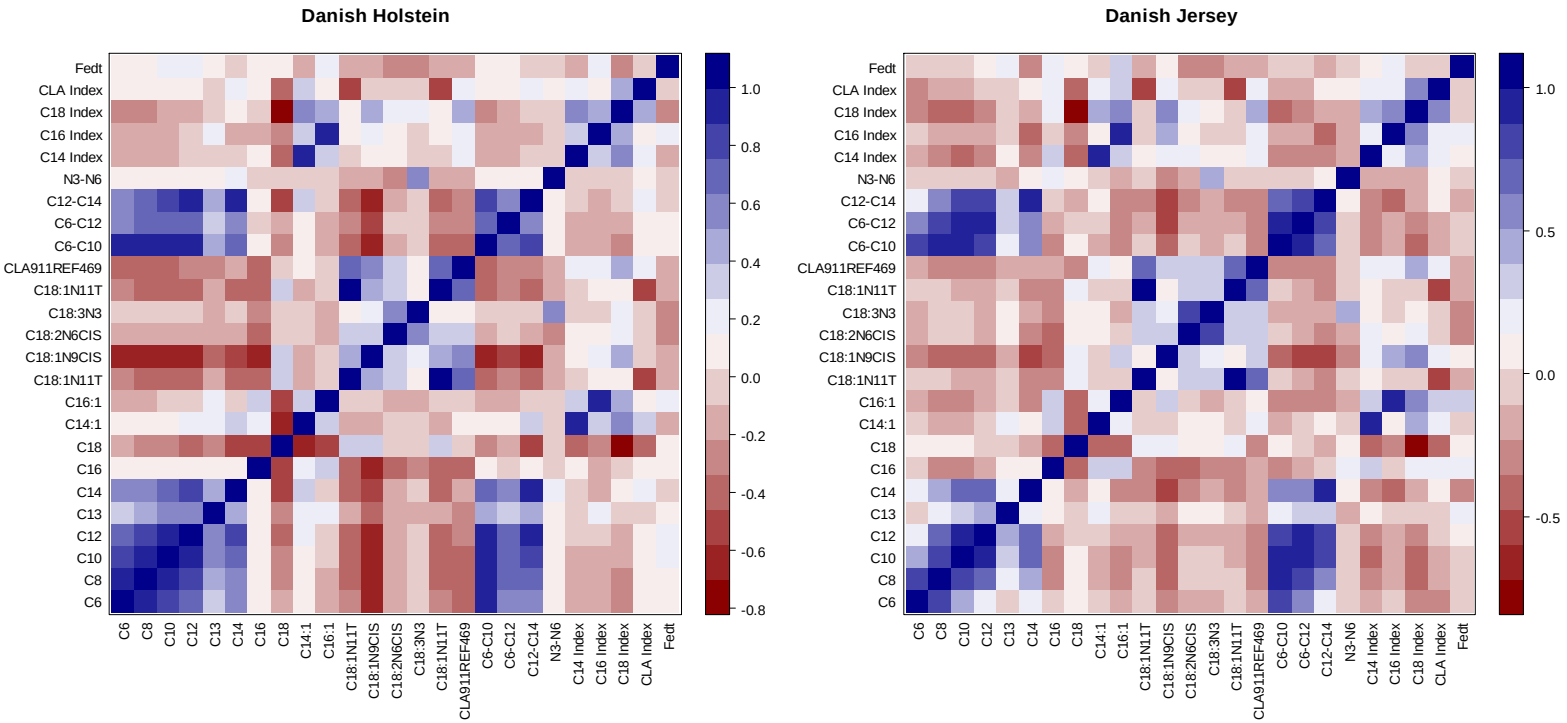
AARHUS UNIVERSITY

CENTER FOR QUANTITATIVE GENETICS AND GENOMICS

Association study

Fatty acid profile:

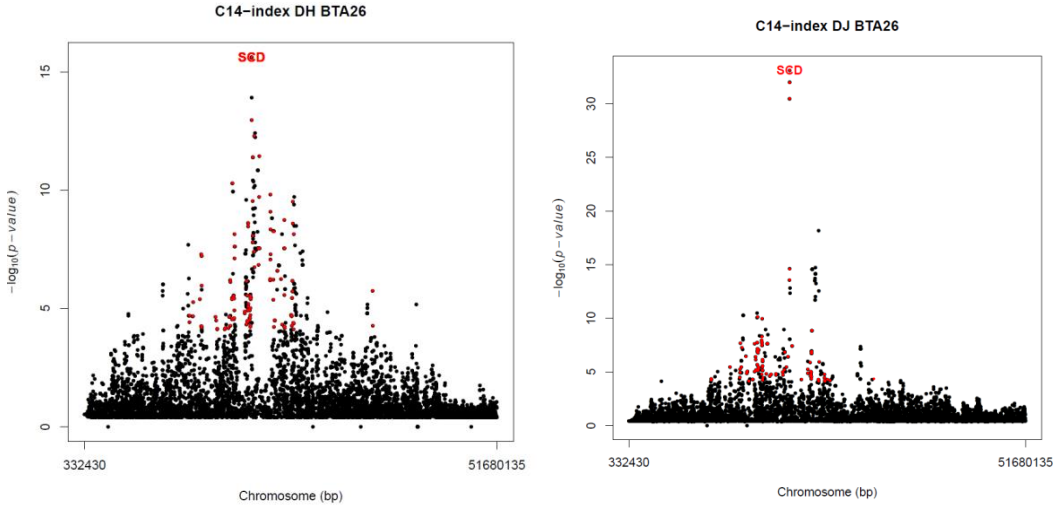
- Holstein vs Jersey: phenotypic level → different

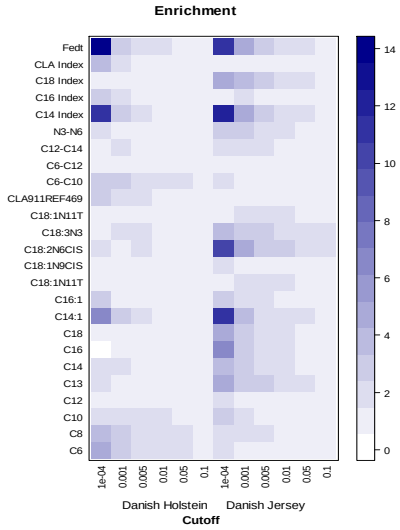


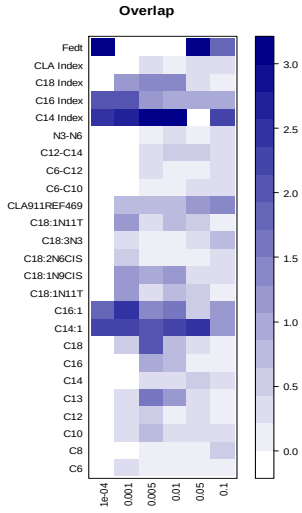
AARHUS UNIVERSITY

CENTER FOR QUANTITATIVE GENETICS AND GENOMICS

Association study







- QTLs found are already known from the literature.
- Significant overlap of SNP markers between HOL and JER for:
  - Fat%
  - C16 index
  - C14 index
  - C16:1
  - C14:1

What did we learn from the MG project?

- Broad overview of:
  - Phenotypic differences between breeds
  - Which traits are heritable
  - Genetic and phenotypic correlations among traits measured in the project
  - QTLs within/across different breeds

Spinn-off projects:

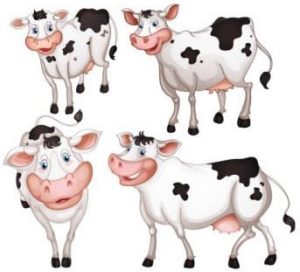
- Metagenome project (Dansk Kvæg)
- Coagene (HTF)

Can we get more out of milk?

Milk control system: Data

Breeds

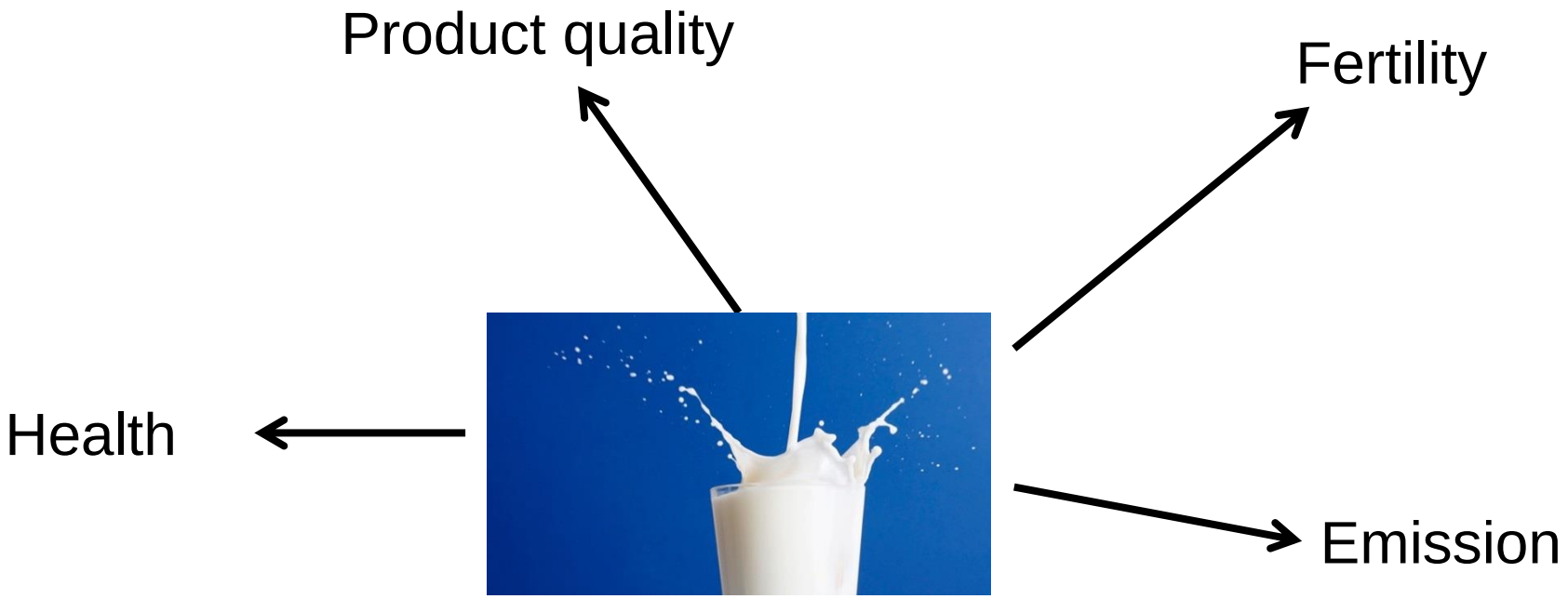
Individual level



Herd level

Once or twice a month

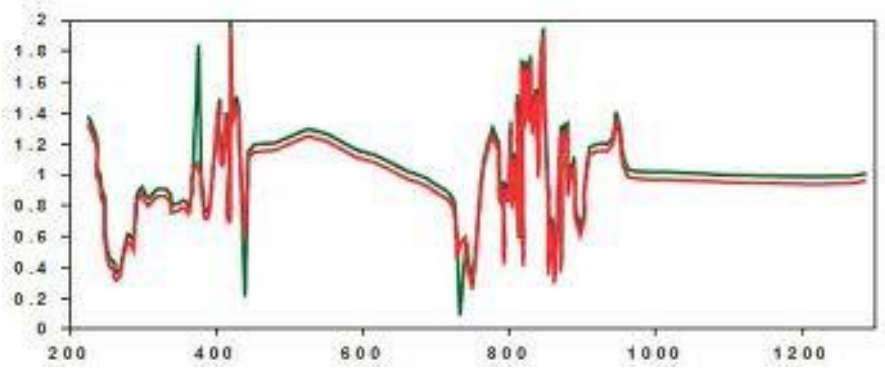
Can we get more out of milk?



How to measure this in the milk?

Technology is already implemented at RYK:

FT-IR



Lactose Fat Protein Urea

Saving full spectra is necessary!

AARHUS UNIVERSITY

CENTER FOR QUANTITATIVE GENETICS AND GENOMICS

Examples

Product quality

Fertility/ Energy balance

Health

Emission

J. Dairy Sci. 94:5683–5690
doi:10.3168/jds.2011-4520
© American Dairy Science Association®, 2011.

Predicting bovine milk protein composition based on Fourier transform infrared spectra

M. J. M. Rutten,*[1] H. Bovenhuis,* J. M. L. Heck,† and J. A. M. van Arendonk*
*Animal Breeding and Genomics Centre, Wageningen University, PO Box 338, 6700 AH, Wageningen, the Netherlands
†Friesland Campina Research, PO Box 87, 7400 AB, Deventer, the Netherlands

Acta Agriculturae Scand Section A, 2010; 60: 79–87

ORIGINAL ARTICLE

Predicting early lactation energy balance in primiparous Red Dairy Cattle using milk and body traits

P. MÄNTYSAARI[1] & E. A. MÄNTYSAARI[2]

[1]*Animal Production Research, MTT Agrifood Research Finland, Jokioinen, Finland, and* [2]*Biotechnology and Food Research, MTT Agrifood Research Finland, Jokioinen, Finland*

J. Dairy Sci. 93:3065–3069
doi:10.3168/jds.2009-2847
© American Dairy Science Association®, 2010.

Short communication: **Ketone body concentration in milk determined by Fourier transform infrared spectroscopy: Value for the detection of hyperketonemia in dairy cows**

A. T. M. van Knegsel,*[1] S. G. A. van der Drift,†[2] M. Horneman,‡ A. P. W. de Roos,‡ B. Kemp,* and E. A. M. Graat#
*Adaptation Physiology Group, Wageningen Institute of Animal Sciences, Wageningen University, PO Box 338, 6700 AH Wageningen, the Netherlands
†Schothorst Feed Research, PO Box 533, 8200 AM Lelystad, the Netherlands
‡CRV BV, PO Box 454, 6800 AL Arnhem, the Netherlands
#Quantitative Veterinary Epidemiology Group, Wageningen Institute of Animal Sciences, Wageningen University, PO Box 338, 6700 AH Wageningen, the Netherlands

Animal (2012), 6:10, pp 1694–1701 © The Animal Consortium 2012
doi:10.1017/S1751731112000456

animal

Potential use of milk mid-infrared spectra to predict individual methane emission of dairy cows

F. Dehareng[1*†], C. Delfosse[1*], E. Froidmont[2], H. Soyeurt[3,4], C. Martin[5], N. Gengler[3,4], A. Vanlierde[1] and P. Dardenne[1]

FTIR spectra and Genetics I

J. Dairy Sci. 93:1722–1728
doi:10.3168/jds.2009-2614
© American Dairy Science Association®, 2010.

Genetic variability of milk components based on mid-infrared spec

H. Soyeurt,*†[1] I. Misztal,‡ and N. Gengler*†
*Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, 5030 Gembloux, Belgium
†National Fund for Scientific Research, 1000 Brussels, Belgium
‡Department of Animal and Dairy Science, University of Georgia, Athens 30605

- PC analysis
- 8 traits 99.18% of variation
- 3 regions of interest
  - 926-1,612 cm^{-1}
  - 1,682-3,064 cm^{-1}
  - 3,672-5,010 cm^{-1}

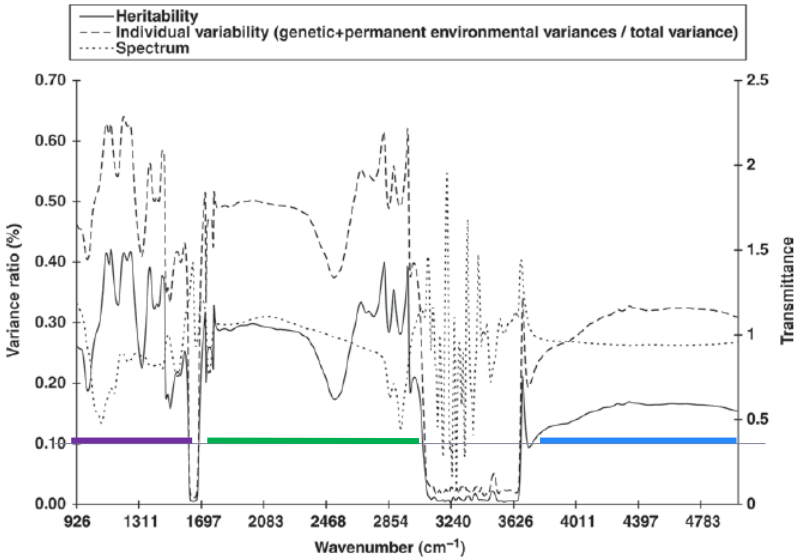


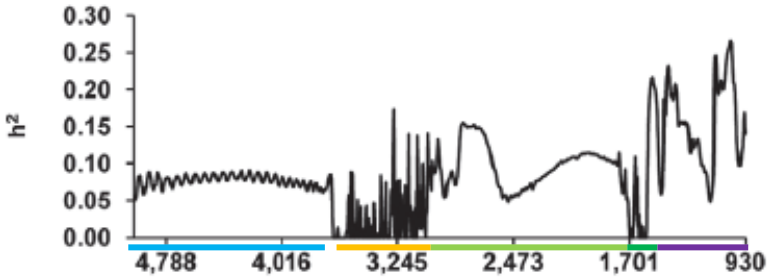
Figure 2. Repeatability estimated from the ratio of the sum of the genetic and permanent environmental variances to the total variance and heritability calculated for 1,060 spectral data points expressed in wavenumber (cm^{-1}) and illustration of mid-infrared milk spectrum.

FTIR spectra and Genetics II

J. Dairy Sci. 96:5991–6006
http://dx.doi.org/10.3168/jds.2013-6583
© American Dairy Science Association®, 2013.

Genetic analysis of the Fourier-transform infrared spectra of bovine milk with emphasis on individual wavelengths related to specific chemical bonds

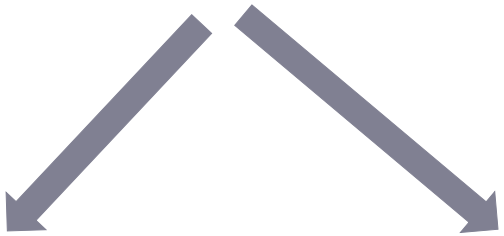
G. Bittante and A. Cecchinato[1]
Department of Agronomy, Food, Natural Resource, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy



- 1,056 analyses (Animal Model)
- 5 regions of interest
  - SWIR 5,000-3,673 cm^{-1}
  - SWIR-MWIR 3,669-3,052 cm^{-1}
  - MWIR-1 3,048-1,701 cm^{-1}
  - MWIR-2 1,698-1,586 cm^{-1}
  - MWIR-LWIR 1,582-930 cm^{-1}
- Wave lengths close to each other are more correlated than WL far apart

What do we need?

- Contract herds (pilot herds)
- Platform to save the full FT-IR spectra
- Data 1: full FT-IR spectra
- Data 2: ‘new’ phenotypes to be predicted from FT-IR



Genetics/Breeding

Herd management