Use of MIR to predict milk fat composition
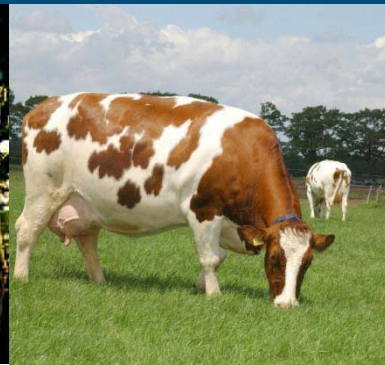
An across breed and country validation

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Acknowledgements

Ministry of Economic Affairs, Agriculture and Innovation (code: KB-04-002-021 and KB-05-003-041)

supported by the European Commission (Grand Agreement KBBE-211708)

The farmers

Milk quality

- **Milk quality related to human health**
  - Fat
  - Protein
  - Minerals

- **Fat → milk contains a wide range of different saturated and unsaturated fatty acids (FA)**
  - Favorable FA (like Conjugated Linoleic acid (CLA) and Omega 3)
  - Unfavorable FA (like Myristic acid and Palmitic acid)

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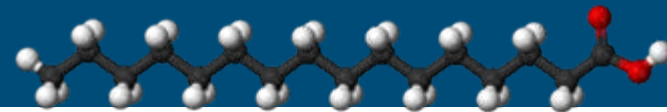
Methods to measure

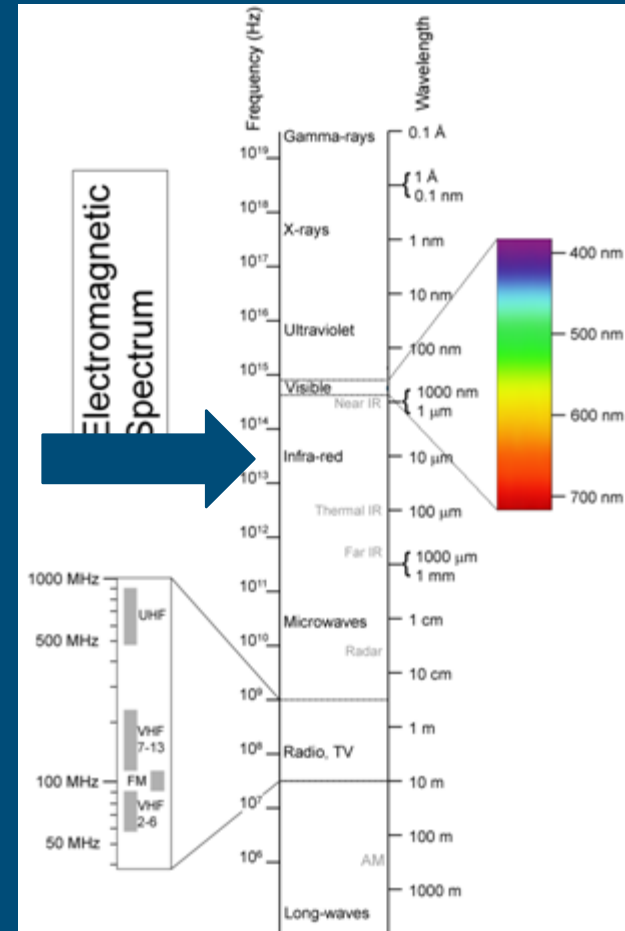- **Gas Chromatography (GC)**
  - Expensive ☹
  - Time consuming ☹
  - Accurate ☺

- **Mid-Infrared spectrometry (MIR)**
  - Cheap ☺
  - Fast ☺
  - Less accurate ..

MIR

- Measure absorption of different infrared frequencies

- Infrared range 900 cm^{-1} to 5,000 cm^{-1}; 1,060 data points

- Calibration equations to predict FA composition
  - GC as golden standard

Aim

- Validation of calibration equations to predict detailed fatty acid composition using MIR-spectra

  → Across breed and country

Calibration equations

- Developed in the EU FP 7 project RobustMilk

- Calibration data set contained <u>1236 milk</u> samples
  - from herds in Ireland, Scotland, and the Walloon Region of Belgium
  - with purebred and crossbred cows from different breeds like Holstein Friesian, Jersey, Red and White, and dual purpose Belgium Blue.

- Calibration data samples were selected based on maximizing variability of MIR spectra

Validation data set

■ 190 milk samples from 12 herds in the Netherlands

■ Cows from different breeds:
  - 47 samples from Dutch Friesians (DF)
  - 52 samples from Meuse-Rhine-Yssel (MRY)
  - 45 samples from Groningen White Headed (G)
  - 46 samples from Jersey (JER)

■ Each milk sample was analyzed using both MIR and GC

DF   MRY   G

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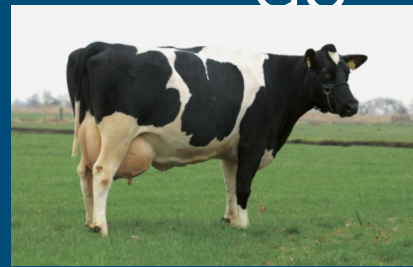
Results: R^2 of prediction – individual FA

Trait	Breed[1]			
	G	MRY	DF	JER
C14:0	**0.93**	**0.97**	**0.93**	**0.92**
C16:0	0.86	**0.90**	**0.93**	0.86
C18:0	0.80	0.64	0.65	0.58
C18:2 cis 9,12 (omega 6)	**0.17**	0.63	0.26	0.32
C18:3 cis 9,12,15 (omega 3)	0.29	**0.10**	**0.02**	**0.10**
C18:2 cis9 trans11	0.36	0.30	0.49	**0.00**

[1]G = Groningen White Headed, DF = Dutch Friesian, MRY = Meuse-Rhine-Yssel, JER = Jersey, and HF = Holstein Friesian.
[2] Breeds total is R^2 across all predictions for G, DF, MRY, and JER.

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Results: R² of prediction – groups of FA

Trait	Breed[1]			
	G	**MRY**	**DF**	**JER**
Saturated FA	**0.99**	**1.00**	**1.00**	**0.98**
Mono unsaturated FA	**0.94**	**0.99**	**0.97**	0.79
Unsaturated FA	**0.97**	**0.99**	**0.98**	0.75
Short chain FA	**0.91**	**0.93**	**0.93**	**0.93**
Medium chain FA	**0.91**	**0.93**	**0.93**	**0.93**
Long chain FA	**0.94**	**0.93**	**0.91**	0.67
C18:1 cis (total)	**0.97**	**0.93**	0.69	**0.91**

[1]G = Groningen White Headed, DF = Dutch Friesian, MRY = Meuse-Rhine-Yssel, JER = Jersey, and HF = Holstein Friesian.

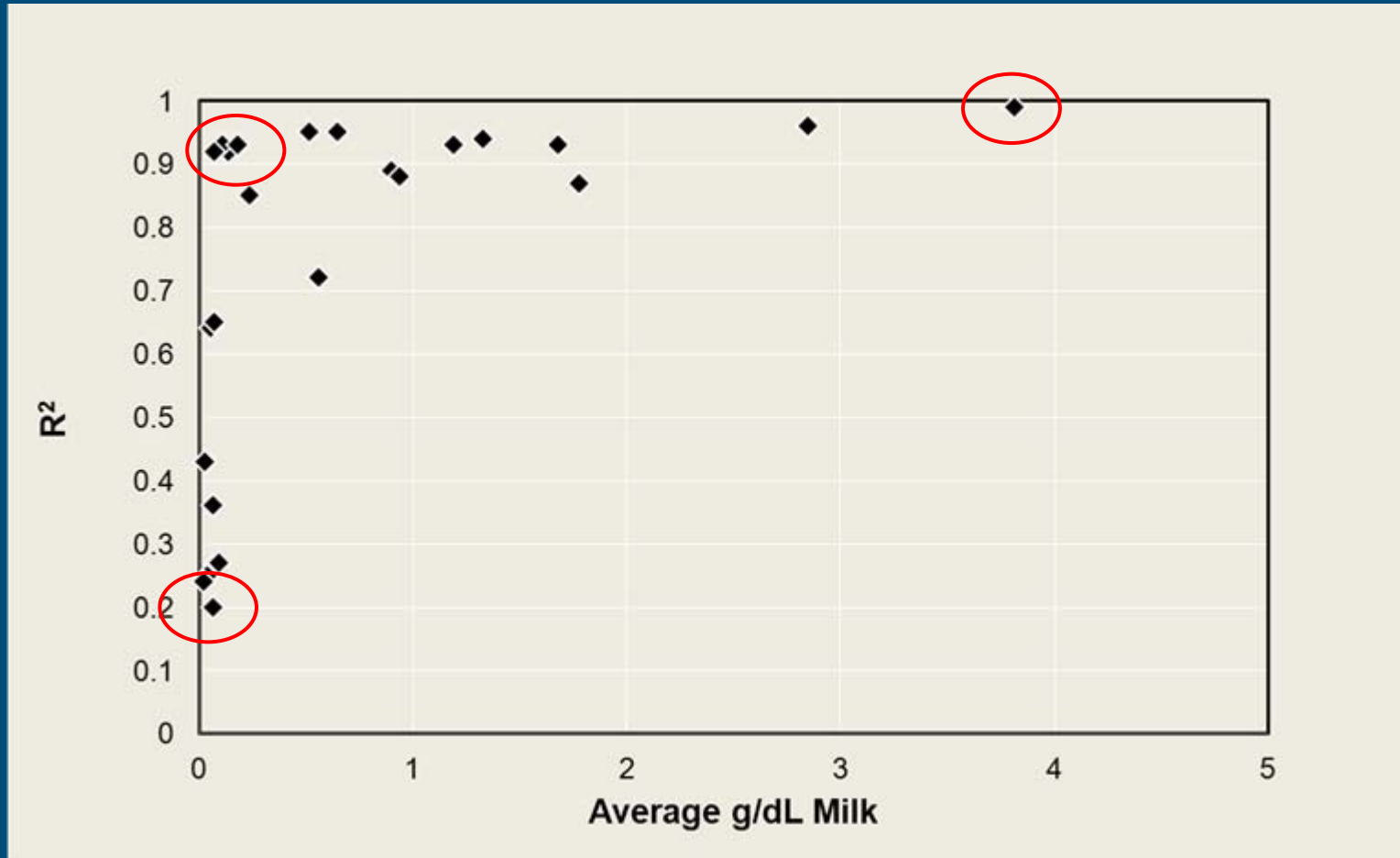[2] Breeds total is R² across all predictions for G, DF, MRY, and JER.

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Results: R^2 vs. concentration g/dL milk

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Conclusions

- RobustMilk calibration equations accurately predict FA content for G, DF, MRY, and JER cows in the Netherlands

  - Groups of FA and FA with higher content in milk are generally predicted with high accuracy

  - Predictions were highly accurate ($R^2 > 0.80$) over all breeds for:
    - C4:0, C6:0, C8:0, C10:0, C12:0, C14:0, C16:0, C18:1*cis*9
    - groups of FA

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Thank you for your attention!

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