

Consortium building allowing
the creation of common models
for MIR based prediction of CH₄

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Context

- ▶ CH₄ ← large scale phenotyping
 - Difficult, time consuming, expensive
 - Proxies ?
- ▶ Use of a milk mid-infrared (MIR) spectra based proxy
 - Was illustrated as being a real opportunity

Animal, page 1 of 8 © The Animal Consortium 2012
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Potential use of milk mid-infrared spectra to predict methane emission of dairy cows

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Hot topic: Innovative lactation-stage-dependent prediction of methane emissions from milk mid-infrared spectra

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Short communication: Development of an equation for estimating methane emissions of dairy cows from milk Fourier transform mid-infrared spectra by using reference data obtained exclusively from respiration chambers

A. Vanlierde,^{*} H. Soyeurt,[†] N. Gengler,[†] F. G. Colinet,[‡] E. Froidmont,[‡] M. Kreuzer,[§] F. Grandl,[#] M. Bell,^{||} P. Lund,[¶] D. W. Olijhoek,[¶] M. Eugène,^{**} C. Martin,^{**} B. Kuhla,^{††} and F. Dehareng^{††}
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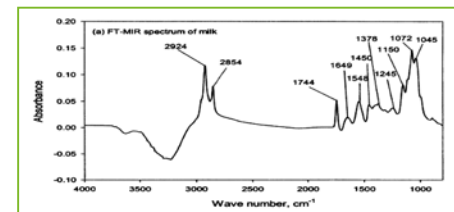
How Do MIR Based Predictions Work ?



Milk samples
(milk payment, milk recording)



MIR spectrometry analysis



Raw data = MIR spectra



Quantification:
Existing: fat, protein, urea,....

Calibration equations



Calibration (Spectra → Prediction)

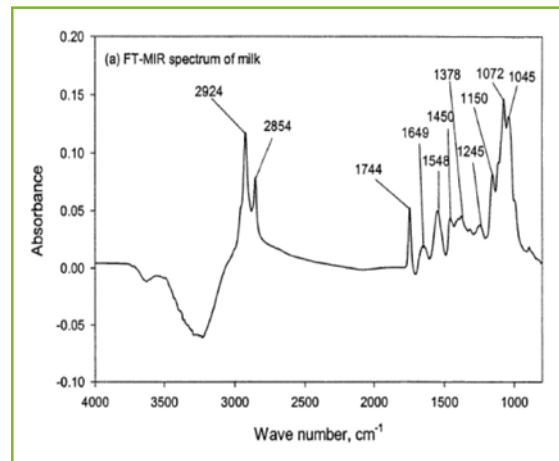
► Between 850 – 1060 absorbance values (abs)



► “Calibration”

- → Obtaining **b** coefficients

$$\text{e.g., } CH_4 = b_0 + \sum b_i (\text{abs})_i$$



TimeStamp	Lab	SampleID	Wavenumber	A1	A2	A3	A4	A5	A6	A7	A8	A9	A10	A11	A12	A13	A14	A15	A16	A17	A18	A19	A20	A21	A22	A23	A24	A25	A26	A27	A28	A29	A30	A31	A32	A33	A34	A35	A36	A37	A38	A39	A40	A41								
4/12/13 10:01	Normal	1	8647	594474	1	1	1060	1.174347	1.169028	1.161095	1.151462	1.144439	1.136975	1.130587	1.124671	1.118177	1.109347	1.099055	1.076414	1.050721	1.020011	0.987758	0.957773	0.93279	0.913417	0.897826	0.882442	0.867322	0.853996	0.802448	0.760545	0.714041	0.667507	0.621198	0.576286	0.532917	0.491621	0.451427	0.412271	0.374182	0.337181	0.301201	0.266177	0.232144	0.199041	0.166807	0.135481	0.105001	0.075414	0.046751	0.019071	0.000001

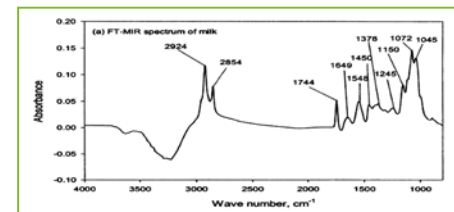
New MIR Predicted Phenotypes



Milk samples
(milk payment, milk recording)



MIR spectrometry analysis



Raw data = MIR spectra

New calibration equations

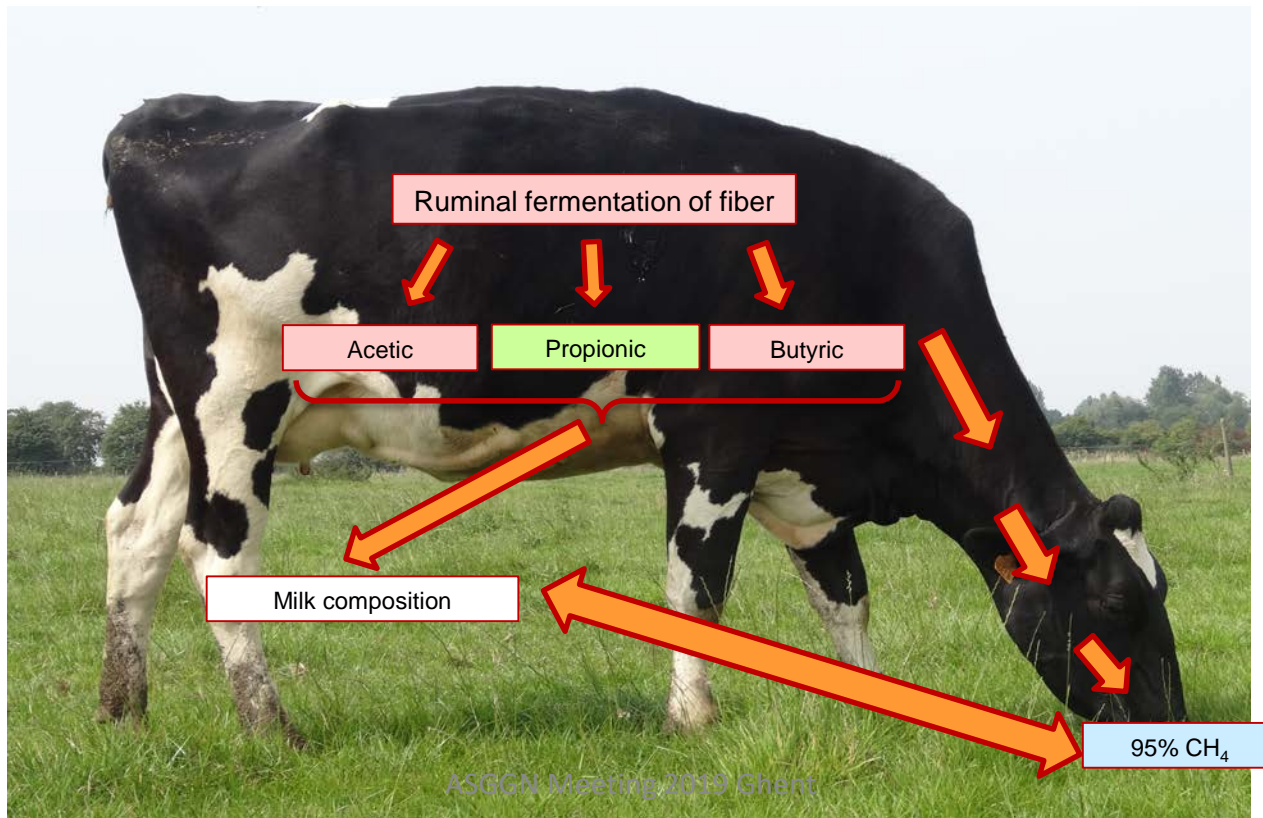


Quantification:

New: fatty acids, CH₄,



CH₄ ↔ Milk Composition

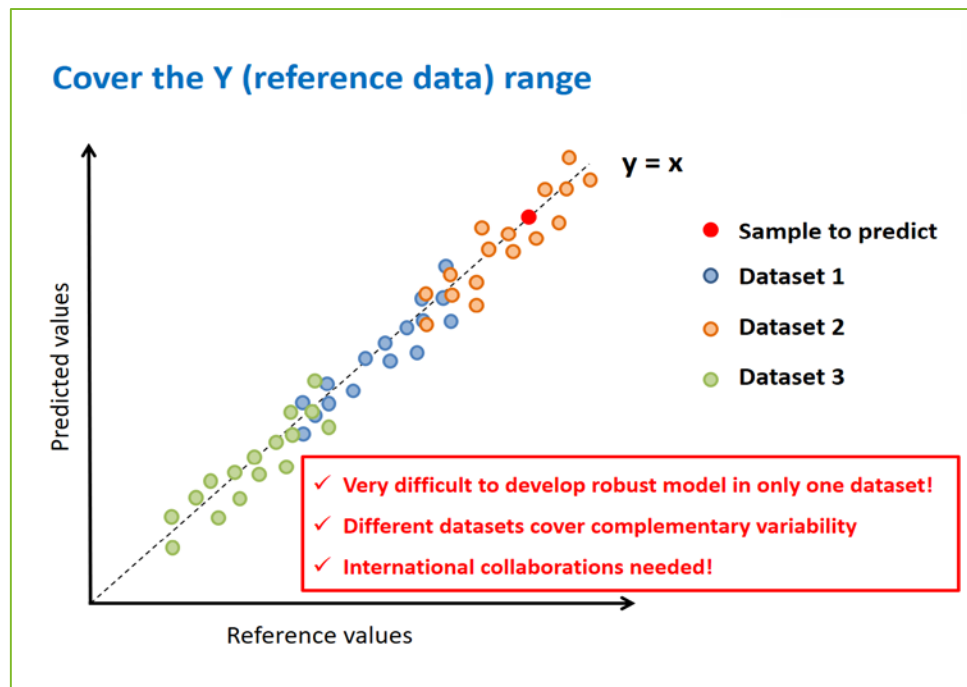


Calibration Needs....

► Largest possible (and expected) variability

- In **reference phenotypes**

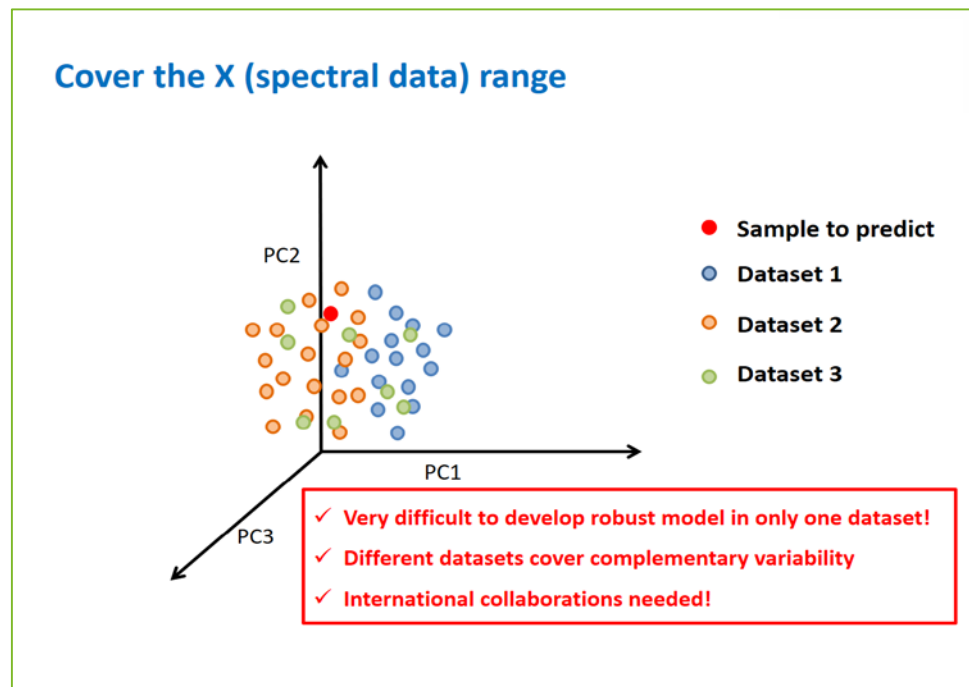
- › E.g., if values between 1 and 10 are expected, reference data from 1 to 10 are needed for calibration, potentially 1/10 of each



Calibration Needs....

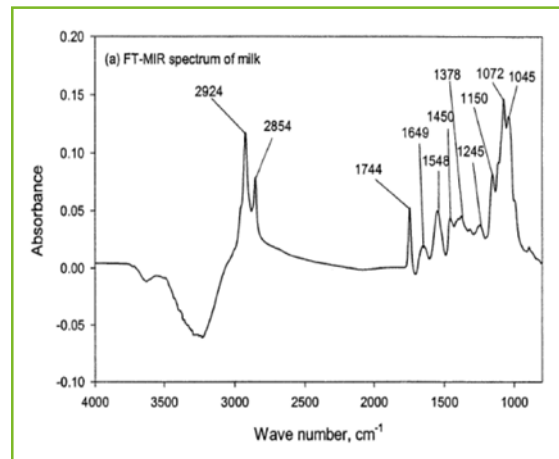
► Largest possible (and expected) variability

- In reference phenotypes
- But also **in spectral data**
 - › I.e., spectra used during calibration process should cover expected range of spectra used when predicting

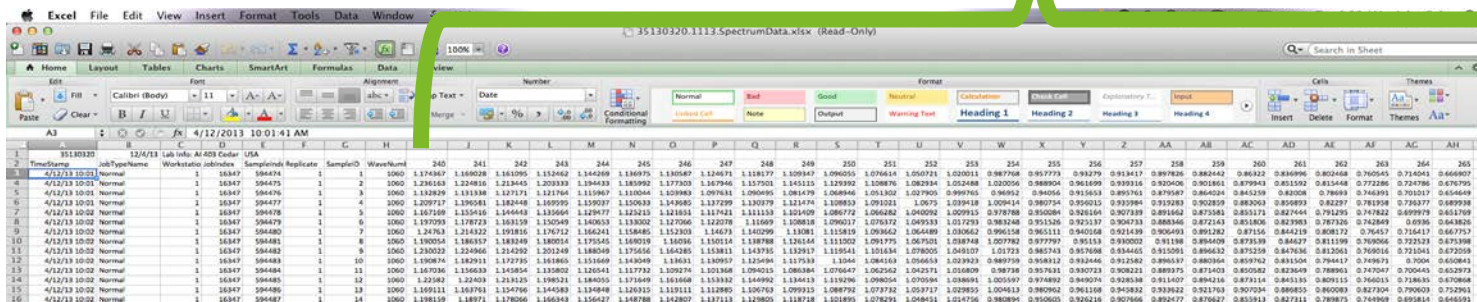


Calibration (Spectra → Prediction)

- ▶ Between 850 – 1060 absorbance values (abs)

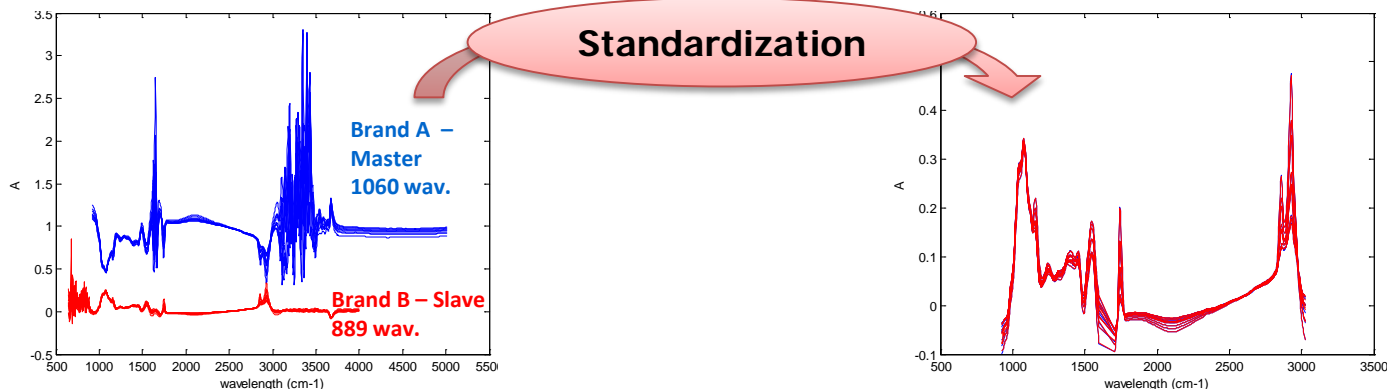


different between brands and models
 ⇒ **additional steps** necessary before
 calibration using different datasets



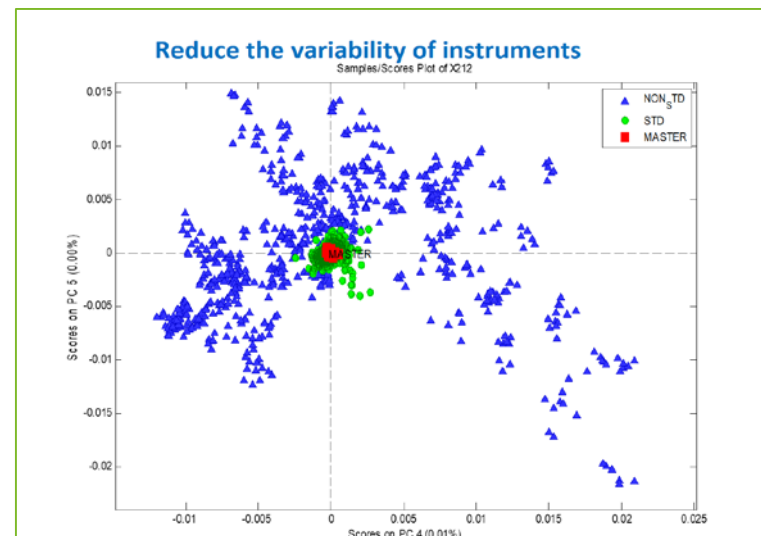
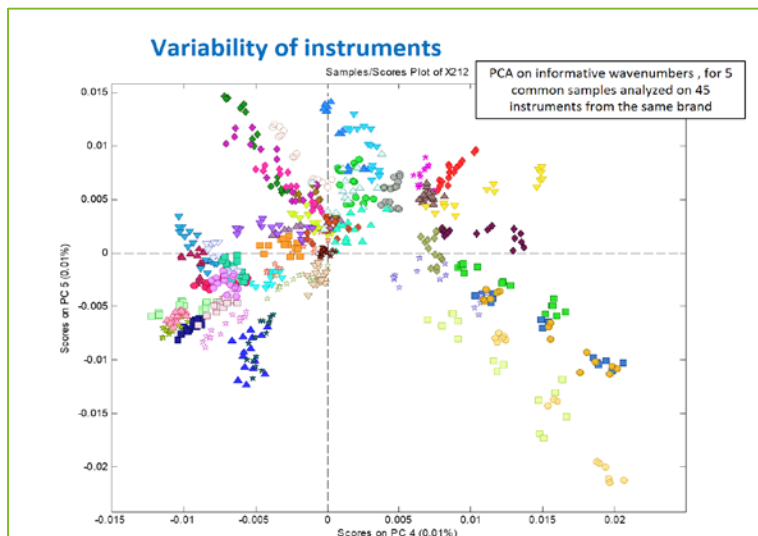
SampleID	Lab info: AI ADI Cedar	USA	WaveNum	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265										
1	16047	1.86028	1.161095	1.112462	1.144269	1.116975	1.130587	1.124671	1.118177	1.109547	1.090053	1.076414	1.050221	1.020011	0.987758	0.957773	0.93279	0.913417	0.897826	0.882442	0.86822	0.839696	0.802448	0.760545	0.714041	0.666007	0.617296	0.567995	0.518148	0.467726	0.416308	0.363908	0.310541	0.257241	0.203021	0.147891	0.091861	0.035931	0.000000

Standardization of MIR Spectra....



- ▶ Two steps to generate “standardized” (harmonized) spectral data
 1. Transforming from different ranges of wavelength to a common one
 2. Applying “bias” and “slope” corrections for each wavelength

Standardization of MIR Spectra....



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Standardization of milk mid-infrared spectra from a European dairy network

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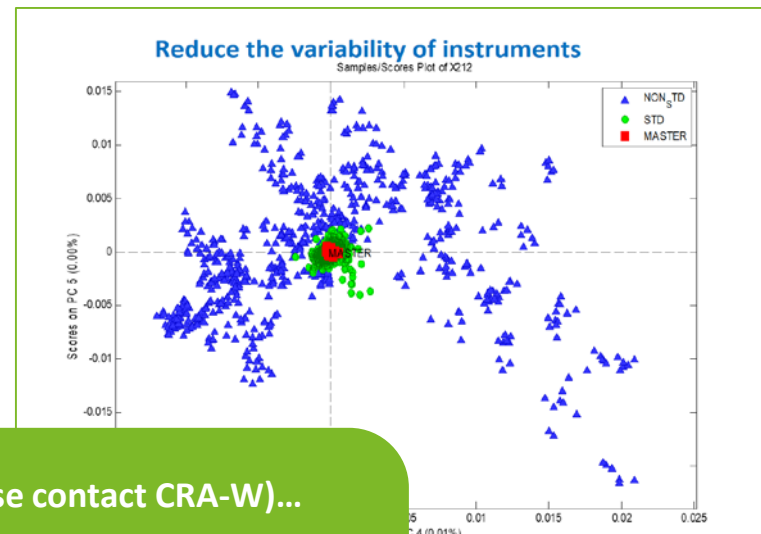
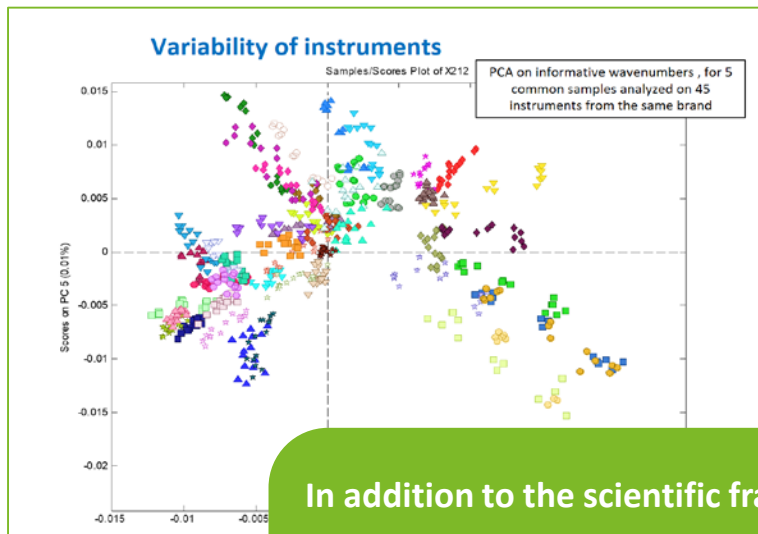


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Standardization of milk mid-infrared spectrometers for the transfer and use of multiple models

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Standardization of MIR Spectra....



In addition to the scientific framework (please contact CRA-W)...

Commercial services were started by EMR (European Milk Recording)
please visit: www.milkrecording.eu



Calibration Needs....

- ▶ Largest possible (and expected) variability
 - In reference phenotypes
 - But also in spectral data

➔ Importance of **international collaborations** obvious

Needed: Consortium building allowing the creation of common models for MIR based prediction of CH₄

Innovative Consortium Building

- ▶ Why → last slides!
- ▶ **How** → building an efficient consortium ?
 - In the **MIR world tradition of machine-builder equations** 😞
- ▶ But **inspiration** from Near-Infrared Spectrometry (NIRS) world 😊
 - Existence of NIRS forage and feed testing consortia
 - › A well documented example: NIRSC in the USA ([see: http://www.nirsconsortium.org](http://www.nirsconsortium.org))

→ **“Open” consortium building**

“Open” Consortium Building: Principles

- ▶ Defining **calibration building organizations**
 - Can be different for each equation, here CH₄: CRA-W and ULiège-GxABT
- ▶ Consortium members retain **full ownership and control of their data**
 - Providing their data only to equation builders
 - Data can only be used to improve equations under development
- ▶ By **helping improving equations**, consortium members get:
 - **Access** to calibrated equations
 - Access to all future **updates** when additional data from new members is included
- ▶ **“Open”** as everybody can join same conditions



As Scientists → Why Joining?

- ▶ First interest in “Open” calibration process
→ users of equations → industry!
- ▶ But from a scientific point of view?
→ interest for scientists?

**Creation and use of MIR based prediction (of CH₄ or other traits)
→ additional contributions and research efforts needed**

Additional Contributions and Research Efforts

- ▶ **Many aspects** as development of CH₄ MIR based proxies
large research needs as:
 - Different types of CH₄ reference traits → alternative equations
 - Novel calibration strategies, e.g. machine learning
 - Important questions outside the direct scope of calibration (e.g. of usefulness of equations): genetic vs. phenotypic correlations → breeding
- ▶ Leading to interesting publications during process
→ **Some examples next slides**

CH₄ Equation

CH₄

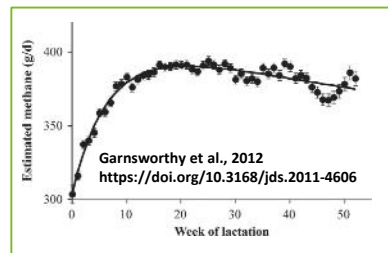


Equation



MIR milk
spectra

CH₄ Equation → Lactation Stage Dependent

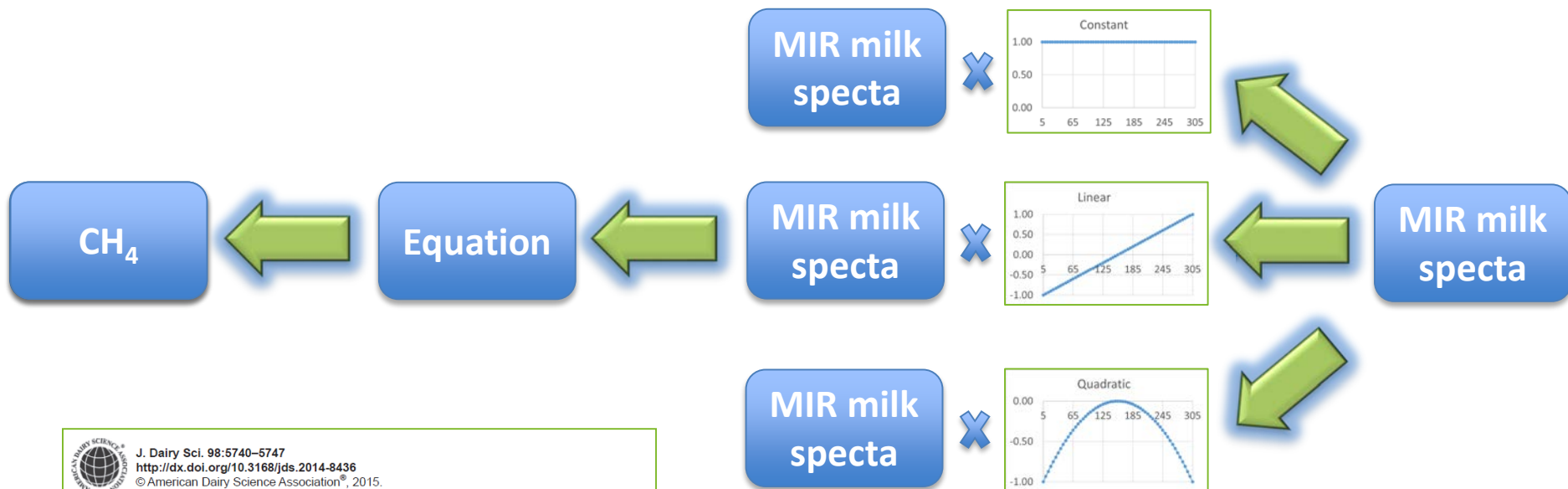


CH₄

Equation

MIR milk
spectra

CH₄ Equation → Lactation Stage Dependent




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First Test of Chamber Data

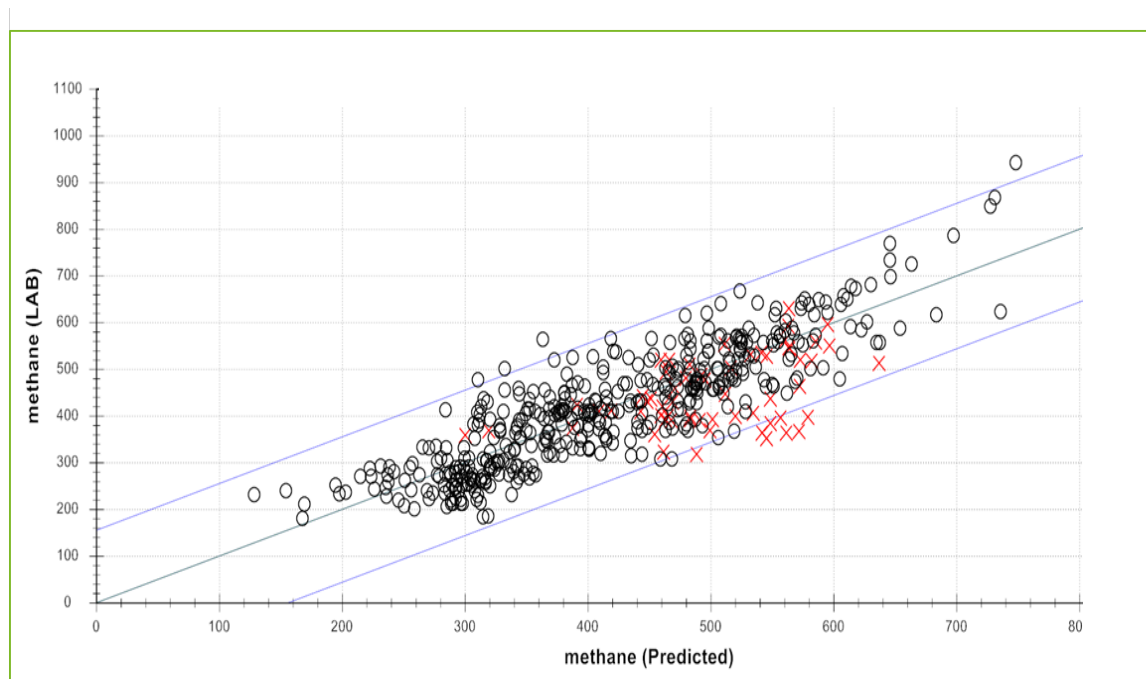
- ▶ X chamber CH₄
- ▶ O reference SF₆
- ▶ Reported in




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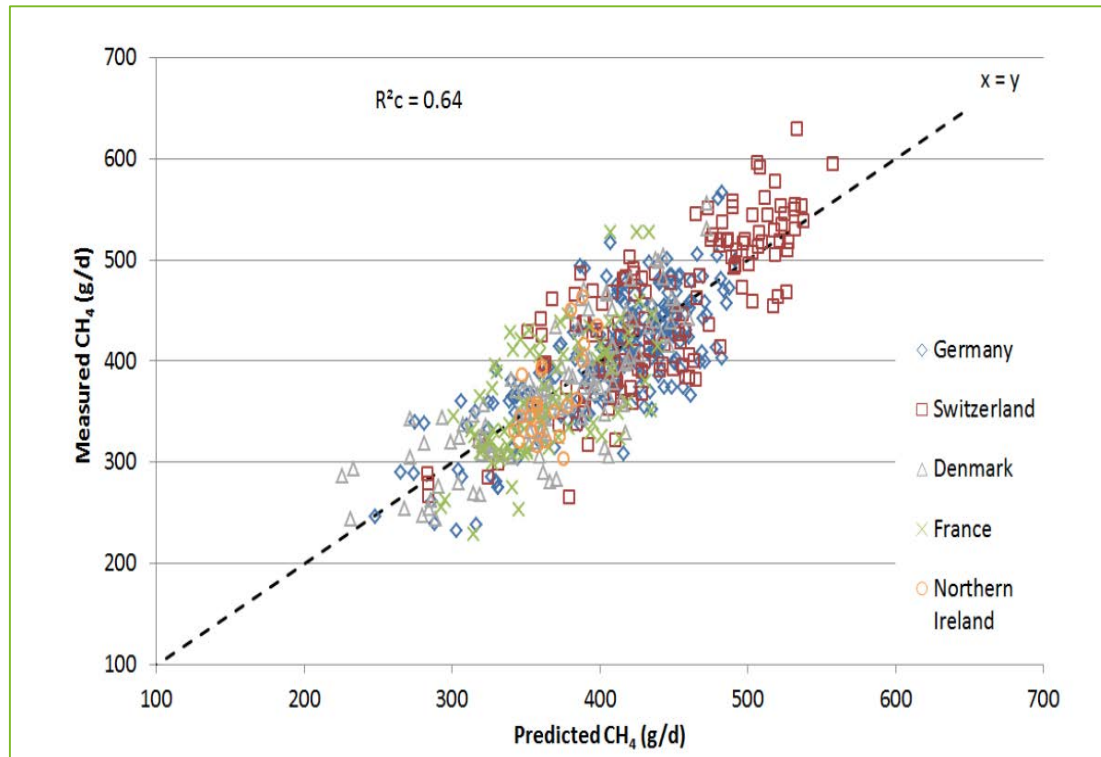
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Use of Chamber Data

- ▶ Collaboration throughout  and beyond (Switzerland and France)
- ▶ Created opportunity to generate first chamber equation
- ▶ Please see in:



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⁴ETH Zurich, Institute of Agricultural Sciences, 8092 Zurich, Switzerland

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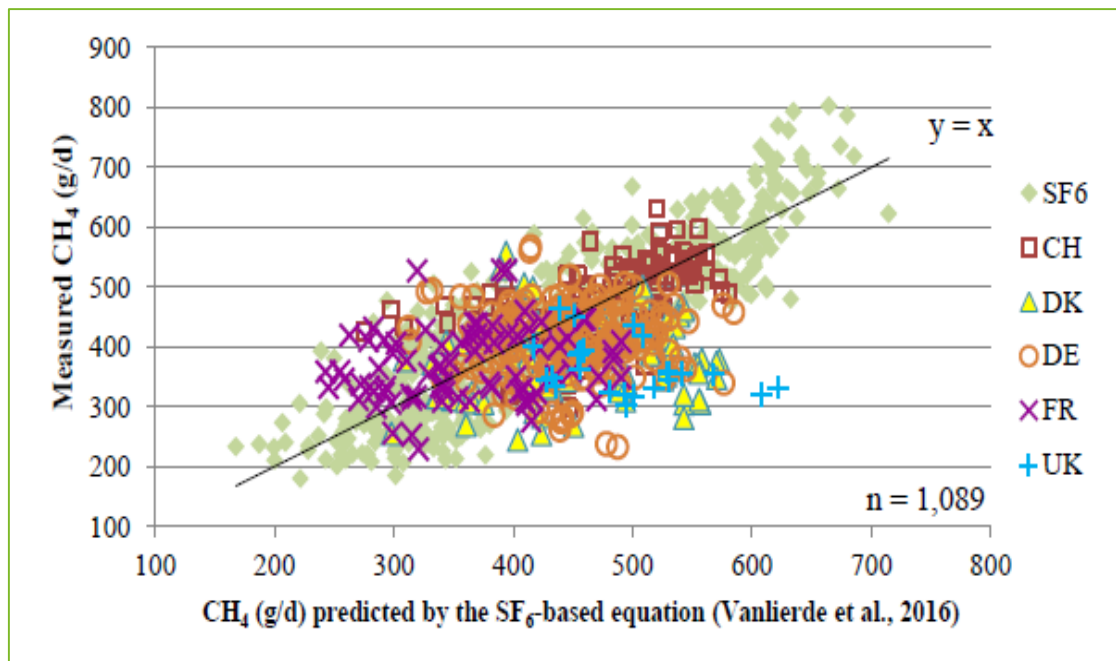
⁷Department of Animal Science, AU Foulum, Aarhus University, 8830 Tjele, Denmark

⁸UMR Herbivores, INRA, VetAgro Sup, Université Clermont Auvergne, 63122 Saint-Genès-Champagnelle, France

⁹Leibniz Institute for Farm Animal Biology (FBN), Institute of Nutritional Physiology, 18166 Dummerstorf, Germany

Improving Robustness and Accuracy

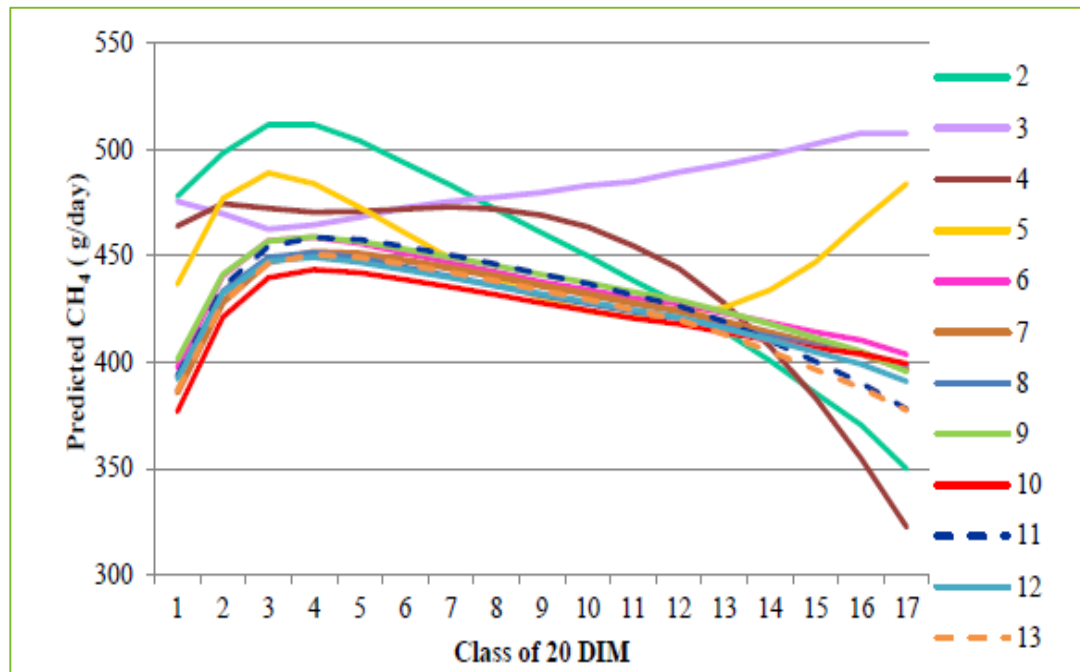
- ▶ Glimpse to ongoing research
- ▶ Here
 - How a SF₆-based equation predicts chamber data
 - › Not included in calibration



Evolution of Equations Applied to $\frac{1}{2} \times 10^6$ TDR

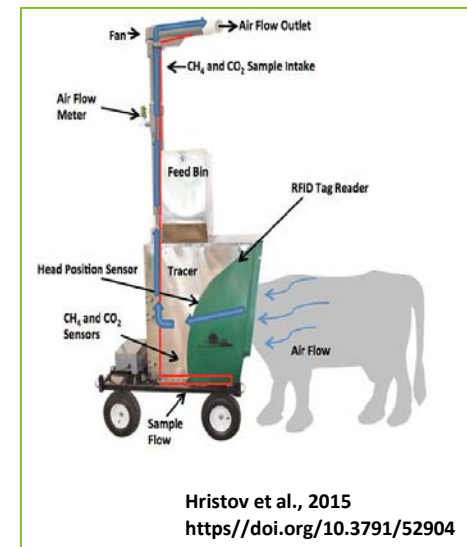
- ▶ Differences between equations:
 - Based on more data*
 - › 2 to 5 ← SF₆ →
 - Chamber and SF₆
 - › 6 to 13 ← RC + SF₆
 - Adding effects:
 - › 6 → 13

*equation 3 not lactation stage dependent



Research Focuses → Opportunities

- ▶ Equations with **more data**
- ▶ Equations with **novel variables**
 - Milk, live-weight, parity, breed,....
- ▶ **Other methods**....
 - Machine learning
 - Federated learning,...
- ▶ Opportunity widespread use of Greenfeed:
 - **Creating Open “Greenfeed – MIR” consortium**
- ▶ **Important:** adding genetic and genomic context
 - Phenotypic vs. genetic correlations → interest of proxies



Other Advantages (And Disadvantages) of Our “Open” Type of Consortia

- ▶ Compared to “joint” databases
 - Their partners contribute to, but also have (restricted) access
 - Mostly project linked where “few” partners \leftrightarrow different objectives
- ▶ Our approach has **one major advantage**
 - We can **accommodate many different data protection schemes**
 - From highly proprietary data (e.g. from industry projects) to publically available “open data”
- ▶ Should compensate **major disadvantage** as obviously
 - Use of this calibration database **only for equation building**
- ▶ But **objectives different!**
 - Situations where other type of consortia fit better

Belgian Motto

L'union fait la force – Eendracht maakt macht - Einigkeit macht stark



UNITY MAKES STRENGTH!

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- ▶ Support throughout the Futurospectre partnership

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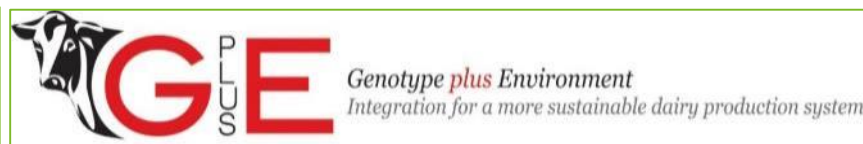
- ▶ Service Public de Wallonie (SPW – DGO3, Belgium)



- ▶ National Fund for Scientific Research



- ▶ Support by different European Projects:



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Thank you

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