EAAP 2018

Methane estimated from milk MIR spectra: model on data from 7 countries and 2 measurement techniques

Vanlierde, A.[1], Dehareng, F.[1], Gengler, N.[2], Froidmont, E.[1], Kreuzer, M.[3], Grandl, F.[4], Kuhla, B.[5], Lund, P.[6], Olijhoek, D.W.[6], Eugene, M.[7], Martin, C.[7], Bell, M.[8], Mcparland, S.[9], Soyeurt, H.[2]

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Context

Reduction of CH_4 emitted by dairy cows

→ one of the most challenging aspect of dairy sector

Need of CH_4 measurements to study different factors influencing variation (nutrition, management, genetics, …)

Large scale studies

→ use of indirect proxies easily available in routine and at reasonable cost

CH_4 prediction from milk MIR

SF_6

N	SD	R^2c	R^2cv	SEC	SECV
532	129	0.74	0.70	66	70

N cows = 165

Teagasc
Agriculture and Food Development Authority

CSIRO PUBLISHING
Animal Production Science, 2016, **56**, 258–264
http://dx.doi.org/10.1071/AN15590

Milk mid-infrared spectra enable prediction of lactation-stage-dependent methane emissions of dairy cattle within routine population-scale milk recording schemes

Amélie Vanlierde[A,], Marie-Laure Vanrobays[B,G,*], Nicolas Gengler[B], Pierre Dardenne[A], Eric Froidmont[C], Hélène Soyeurt[B], Sinead McParland[D], Eva Lewis[D], Matthew H. Deighton[D,E], Michaël Mathot[F] and Frédéric Dehareng[A]*

J. Dairy Sci. 101:7618–7624
https://doi.org/10.3168/jds.2018-14472

***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**

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Respiration chambers

N	SD	R^2c	R^2cv	SEC	SECV
584	72	0.65	0.57	43	47

N cows = 148

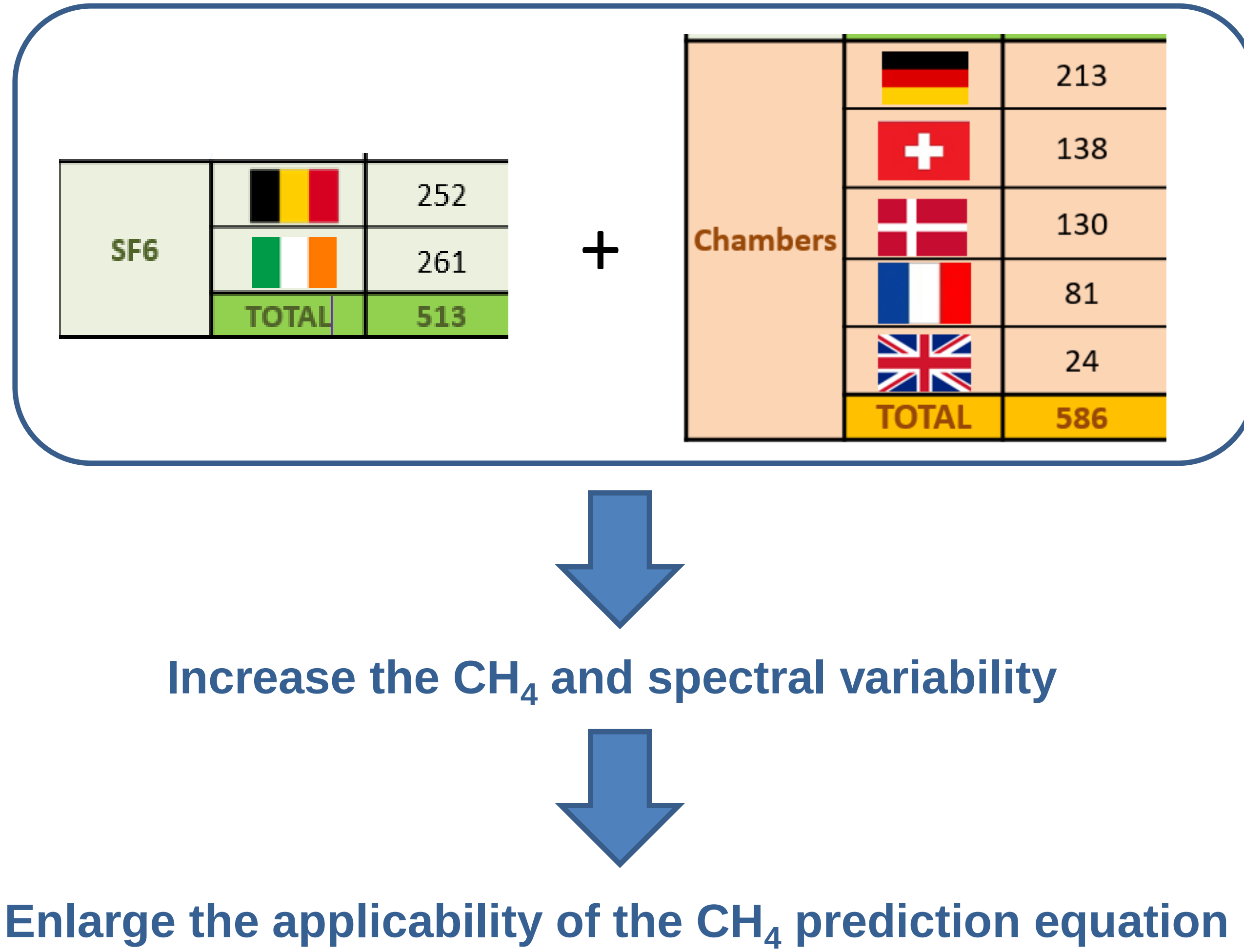
ETH Zürich
QUALITAS
AARHUS UNIVERSITY
FBN
INRA SCIENCE & IMPACT
afbi Agri-Food and Biosciences Institute

2 data sets with different variability

		N	Cows	Mean	SD	Min.	Max.
SF6 g/d		252	42 HO	510	105	225	786
		261	98 HO, 6 HOX, 6 NR	347	89	180	588
	TOTAL	513	152	427	127	180	786
Chambers g/d		213	51 HO	405	60	233	566
		138	40 BS, 9HO, 8RH, 1HOxSI	451	75	267	630
		130	9HO, 10 JER	366	64	244	556
		81	9HO	366	61	229	527
		24	6HO, 6RX	365	44	304	464
	TOTAL	586	149	433	87	229	630

2 data sets with different parity distribution

		N cows	Parity (N cows)		
			First	Second	Third or +
SF6		42	16	11	15
		110	45	29	36
	TOTAL	**152**	**71**	**40**	**51**
Chambers		50	/	34	16
		57	8	16	33
		19	8	4	7
		9	/	7	2
		12	/	3	9
	TOTAL	**147**	**16**	**64**	**67**


SF6
252
261
TOTAL
513
+
Chambers
213
138
130
81
24
TOTAL
586
Increase the CH_4 and spectral variability
Enlarge the applicability of the CH_4 prediction equation

Descriptive statistics

g/d	N	Cows	Mean	SD	Min.	Max.
SF6	513	152	427	127	180	786

g/d	N	Cows	Mean	SD	Min.	Max.
Chambers	586	149	433	87	229	630

↑ mean
↓SD
for chambers

Take into account a potential method bias?

Method Bias Correction

J. Dairy Sci. 90:2755–2766
doi:10.3168/jds.2006-697

Methane Emissions from Dairy Cows Measured Using the Sulfur Hexafluoride (SF_6) Tracer and Chamber Techniques

C. Grainger,*[1] T. Clarke,* S. M. McGinn,† M. J. Auldist,* K. A. Beauchemin,† M. C. Hannah,* G. C. Waghorn,‡ H. Clark,§ and R. J. Eckard#
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§AgResearch, Grasslands Research Centre, Tennent Drive, Palmerston North, New Zealand
#Faculty of Land and Food Resources, University of Melbourne, Victoria, Australia

→ Respiration chambers **8%** higher than SF_6 technique (gases from rectum)

J. Dairy Sci. 95:3139–3148
http://dx.doi.org/10.3168/jds.2011-4298

Comparison of the sulfur hexafluoride tracer and respiration chamber techniques for estimating methane emissions and correction for rectum methane output from dairy cows

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‡AFBI Biometrics Department, Belfast, BT9 5PX, United Kingdom

Respiration chambers **3%** higher than SF_6 technique (gases from rectum) ←

Method Bias Correction

Development of different equations with

- Raw data
- Respiration chamber data reduced for 3% (Grainger et al., 2007)
- Respiration chamber data reduced for 8% (Munoz et al., 2012)

To be on the SF_6 technique level

Methods

	N	Cows	Mean	SD	Min.	Max.
SF6	513	152	427	127	180	786

+

	N	Cows	Mean	SD	Min.	Max.
Chambers	586	149	433	87	229	630

RC -3%

between - 7 and - 19 g/d

RC -8%

between - 18 and - 50 g/d

CH$_4$ measurement

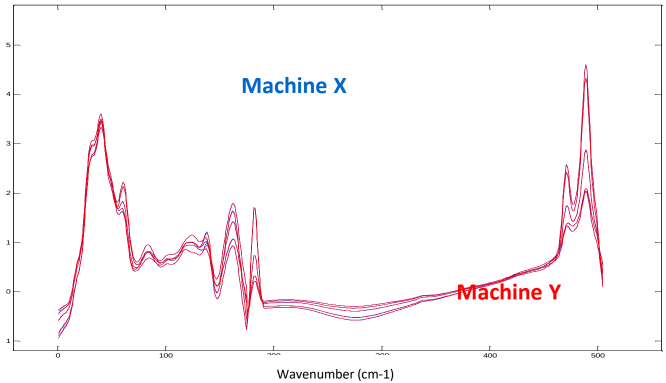
WinISI 4.6 (Foss)

PLS

5 groups cross-validation

Standardized Milk MIR spectra

(Grelet et al, 2017)



+ Days in Milk

RAW MIR CH$_4$

RC -3% MIR CH$_4$

RAC -8% MIR CH$_4$

Equation Statistical Parameters

RAW

N	SD	R^2c	R^2cv	SEC	SECV
1089	102	0.68	0.64	57	61

RC -3%

N	SD	R^2c	R^2cv	SEC	SECV
1089	102	0.70	0.64	57	61

RC -8%

N	SD	R^2c	R^2cv	SEC	SECV
1089	104	0.70	0.66	57	61

SD : standard deviation ; SEC *:* standard error of calibration ; SECV : standard error of cross validation

Equation Statistical Parameters

RAW

N	SD	R^2…	[illegible]	…C	SECV
1089	102	[illegible]	[illegible]	57	61

RC -3%

N	SD	R^{2}c	[illegible]	[illegible]	…SECV
1089	102	[illegible]	[illegible]	…57	61

RC -8%

N	SD	R^{2}c	R^{2}cv	SEC	SECV
1089	104	0.70	0.66	57	61

No significant method effect on residuals obtained for all 3 equations

…d deviation ; SEC : standard error of calibration ; SECV : standard error of cross validation

We prefer to keep initial CH_4 values

Equation Statistical Parameters

RC -3%

between - 7 and - 19 g/d

N	SD	R^2c	R^2cv	SEC	SECV
1089	102	0.70	0.64	57	61

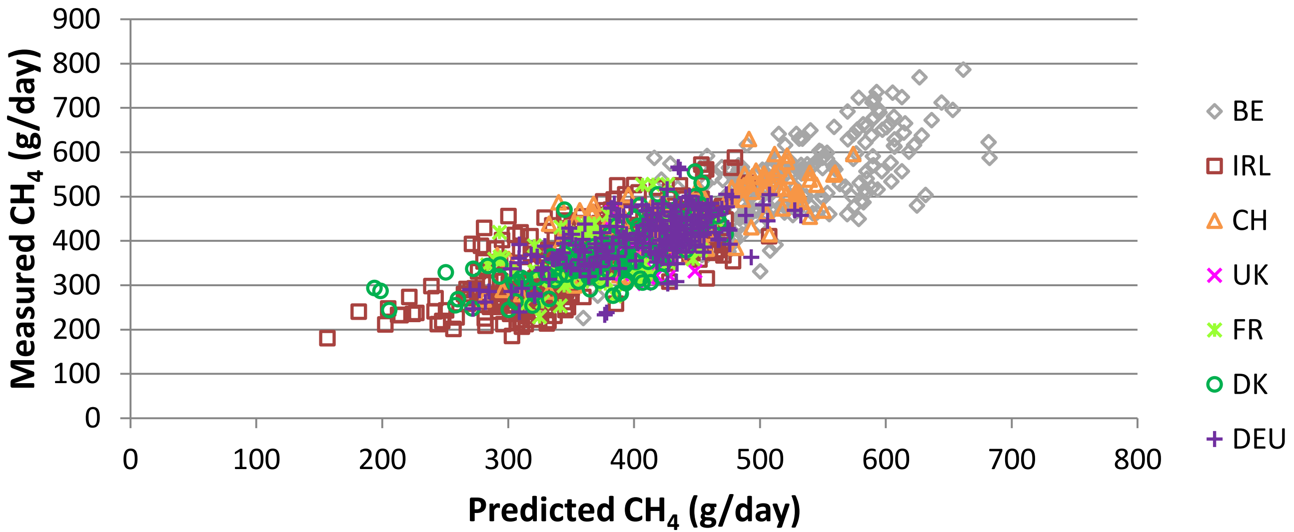
RC -8%

between - 18 and - 50 g/d

N	SD	R^2c	R^2cv	SEC	SECV
1089	104	0.70	0.66	57	61

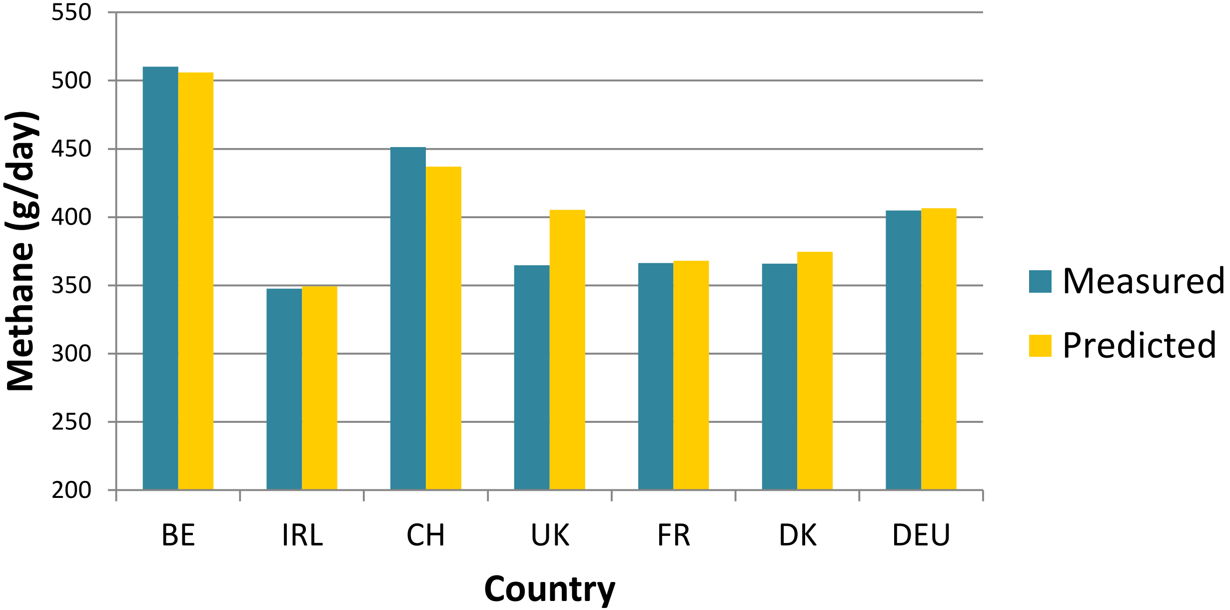
→The SECV is higher than the RC reference values modification

→It might « mask » the impact of the RC values modification on the residuals



RAW

N	SD	R^2c	R^2cv	SEC	SECV
1089	102	0.68	0.64	57	61



Methane (g/day)
550
500
450
400
350
300
250
200
BE
IRL
CH
UK
FR
DK
DEU
Country
Measured
Predicted

Conclusions

- Combination of both data sets available (SF_6 tracer and RC-based) permitted the development of a new model.

- The slight improvement due to adjustment of chamber measurement does not permit to conclude that this correction is needed.

- R^2cv of this new equation is lower than for the SF_6 based-version (0.64 vs. 0.70) but SECV is lower (61 vs. 70 g/day).

- 7 countries and 6 breeds are included in this model
  → increase of the covered variabilities and the applicability of the model.

Conclusions

→ Statistics confirm its potential as proxy especially for genetic evaluation

→ This model demonstrate the interest of collaborations to built robust models

→ Data of interest are still required to improve the model

Acknowledgments

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The views expressed in this publication are the sole responsibility of the author(s) and do not necessarily reflect the views of the European Commission.

Thank you

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