Annual PhD Report 2012-2013

Genetic relationship between environmental impact traits and milk composition in dairy cows

Purna B. Kandel

Animal Science Unit, Gembloux Agro-Bio Tech,
University of Liège, Belgium

22 May 2013

Outline of Presentation

- Part I – Genetic parameters for methane indicators obtained from Mid-infrared spectroscopy (MIR) of milk fatty acids (Year 2011-2012 ~ short)
- Part II – Development of calibration equation from direct MIR spectra of milk samples (Belgium + Ireland)
- Part III – Genetic parameters for methane indicator traits (predicted from part II)

Introduction

- Methane (CH_4) is the largest contributor to total greenhouse gas emitted by the dairy sector.
- CH_4 is 21 times more potent than CO_2 in greenhouse effect.
- Respiration chamber or Sulphur hexafluoride (SF_6) method are commonly used to measure CH4.
- Phenotype gap for direct methane measurement leads to indirect indicators to estimate genetic parameters:
    - Milk fatty acids (FA) in milk
    - Direct MIR prediction from milk
    - Other proxies

IPCC (2007), FAO (2010), EU (1998), Johnson (1994), Chilliard et al. (2009), Dijkstra et al. (2011), Dehareng et al. (2012)

Why genetics ?

- Genetic selection of animal having low CH_4 emissions
  - ✓Additive
  - ✓Permanent

Objectives

- Predictions of CH_4 emissions (indicators)
- Estimation of genetic parameters
- Correlations with other economic traits

gembloux agro bio tech

Université de Liège

Part I

Genetic parameters for CH_4 indicators obtained from MIR of milk fatty acids in dairy cows (2011-12)

Kandel, P. B.[1], N. Gengler[1], and H. Soyeurt[1,2]

[1] Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium

[2] National Fund for Scientific Research, Brussels, Belgium

Article has been submitted with revision

Journal of Applied Animal Research

Taylor & Francis

Genetic parameters for mid-infrared methane indicators based on milk fatty acids in dairy cows

Journal:	*Journal of Applied Animal Research*
Manuscript ID:	JAAR-2012-0349.R1
Manuscript Type:	Original Research Paper
Keywords:	Mid Infra-Red, milk fatty acids, heritability, methane emissions, dairy

SCHOLARONE™ Manuscripts

Highlights of this study

- Previously published 5 CH_4 prediction equations developed from gas chromatographic analysis of milk fatty acids were selected
- These equations were calibrated with MIR spectroscopy to predict methane emissions from Walloon dairy cows
- The predicted methane was in general in range of published measurements
- Heritabilities for these five CH_4 indicator traits were estimated from 0.19 to 0.35

Chiliard et al. 2009; Dijkstra et al. 2011

Part II

Prediction of individual enteric methane emission of dairy cows from milk mid-infrared spectra

A. Vanlierde[1], F. Dehareng[1], E. Froidmont[1], P. Dardenne[1], **P. B. Kandel**[2], N. Gengler[2], E. Lewis[3], F. Buckley[3], M. Deighton[3], S. McParland[3], D. Berry[3] and H. Soyeurt[1]

[1] Walloon Agricultural Research Center, Gembloux, Belgium
[2] Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium
[3] Animal & Grassland Research and Innovation Center, Teagasc, Moorepark, Co. Cork, Ireland

Introduction

- Previous studies have shown that mid-infrared spectrometry can be used to predict milk FA
- FA are related to methane emissions.
- Therefore, direct prediction of methane from mid-infrared is a logical step.

Chiliard et al., 2009; Dijkstra et al., 2011, Dehareng et al., 2012

Methodology

CH_4 was measured using SF_6 method and milk spectra was collected for same animal (some animals had multiple measurements)

	Ireland	Belgium
Number of SF_6 measurements Animals	285 119	196 27
CH_4/day (Mean ±SD)	356.99 ±101.64	466.13 ±101.87

Calibration for CH_4 equation

- After removing potential outliers in MIR spectra and CH_4
- Final calibration equation

N	452
Mean (Reference value)	394.58 g/day
SD	126.39 g/day
SEC (standard error of calibration)	61.97 g/day
SECV (standard error of cross validation)	68.68 g/day
R^2cv (cross validation coefficient of determination)	0.70
RPD (residual predictive deviation)	2.03

Part III

Genetic parameters for methane indicator traits obtained directly from MIR spectra in first lactation dairy cows

P. B. Kandel[1], M-L. Vanrobays[1], A. Vanlierde[2], F. Dehareng[2], E. Froidmont[2], P. Dardenne[2], S. McParland[3], N. Gengler[1] and H. Soyeurt[1]

[1] Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium

[2]Walloon Agricultural Research Center, Gembloux, Belgium

[3]Animal & Grassland Research and Innovation Center, TEAGASC, Moorepark, Co. Cork, Ireland

Equation applied to Walloon spectral database (Holstein)

Traits	Lactation 1 (N=412, 520)
CH_4 g/day	545.91±109.34
CH_4 g/kg of milk	25.01±8.88
Milk yield (kg/day)	23.44±5.97
Fat yield (kg/day)	0.92±0.23
Protein yield (kg/day)	0.78±0.19

Model : Two trait random regression test day

$y = X\beta + Q(Zp + Zu) + e$

y: MIR CH_4 indicators and milk traits (two traits-each pair)
β: herd x test day, 24 classes of days in milk, and 3 classes of age at calving → fixed effects
p: random permanent environmental effects
u: additive genetic effects
e: random residual effect
Q: coefficients of 2^{nd} order Legendre polynomials
Variance components: REML
Fixed effects: BLUP

Averaged daily heritability

Traits	heritability
CH_4 g/day	0.07±0.01
CH_4 intensity (g/kg of milk)	0.16±0.01

Model: Multi-trait random regression test-day model

$$y=X\beta+Q(Zp+Zu)+e$$

y: MIR CH_4 indicators and milk traits (total 5 traits)

β: herd x test day, 24 classes of days in milk, and 3 classes of age at calving → fixed effects

p: random permanent environmental effects

u: additive genetic effects, e: random residual effect

Q: coefficients of 2^{nd} order Legendre polynomials

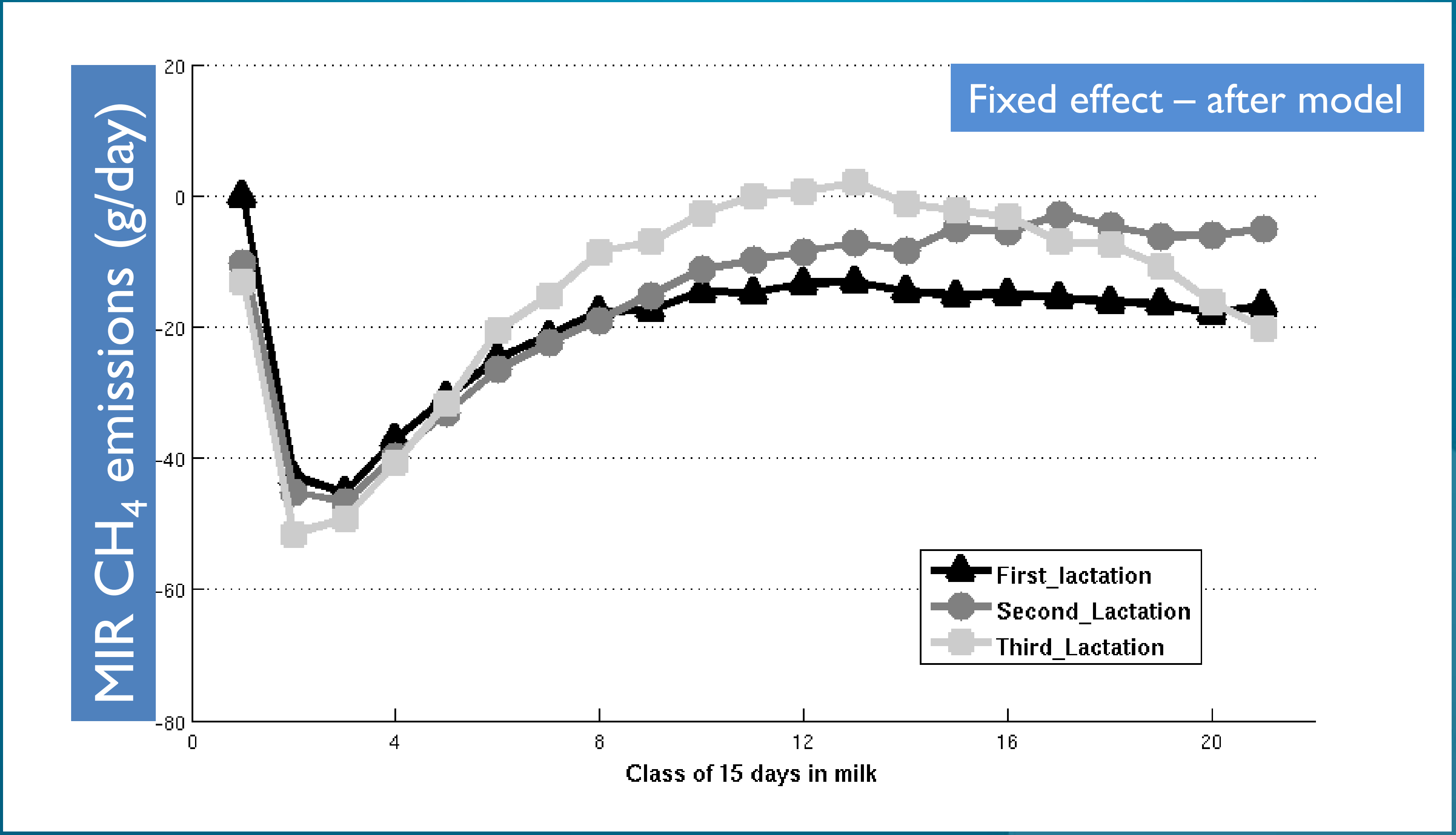
Prior variance components- REML

Variance components – Gibbs Sampling

Fixed effect- BLUP

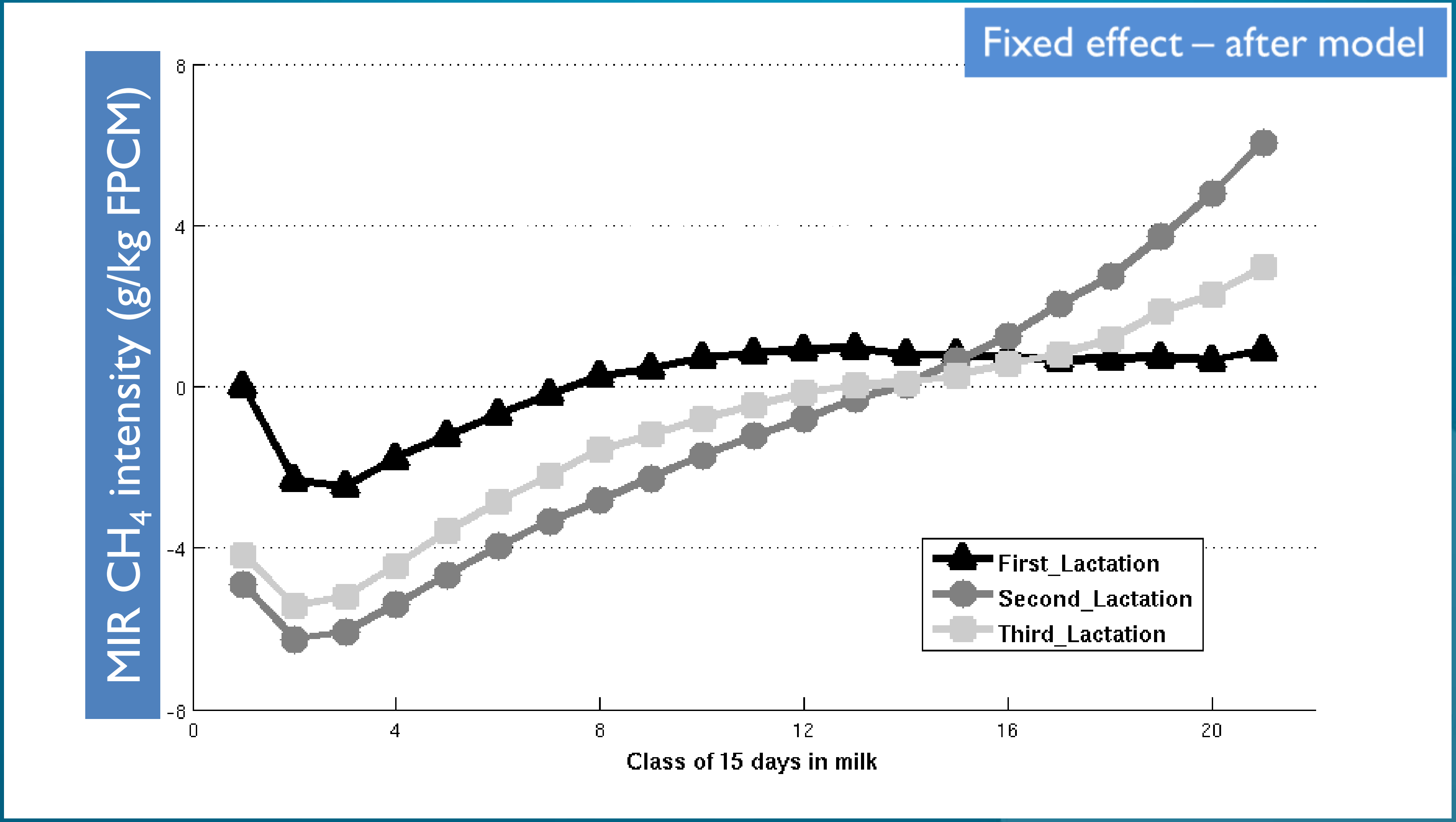
Relative CH_4 emission across lactation

For comparison first lactation first day was made zero



Relative CH_4 intensity across lactation

For comparison first lactation first day was made zero

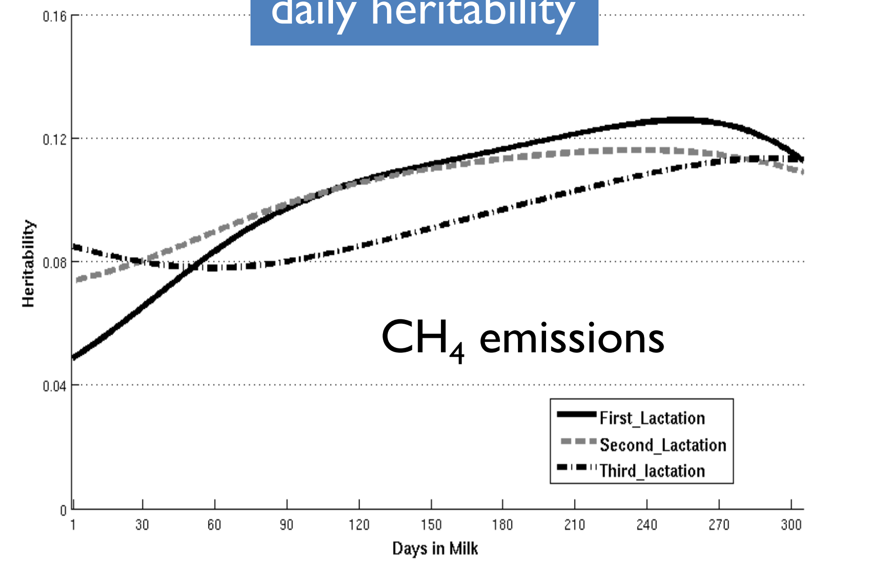


Heritability

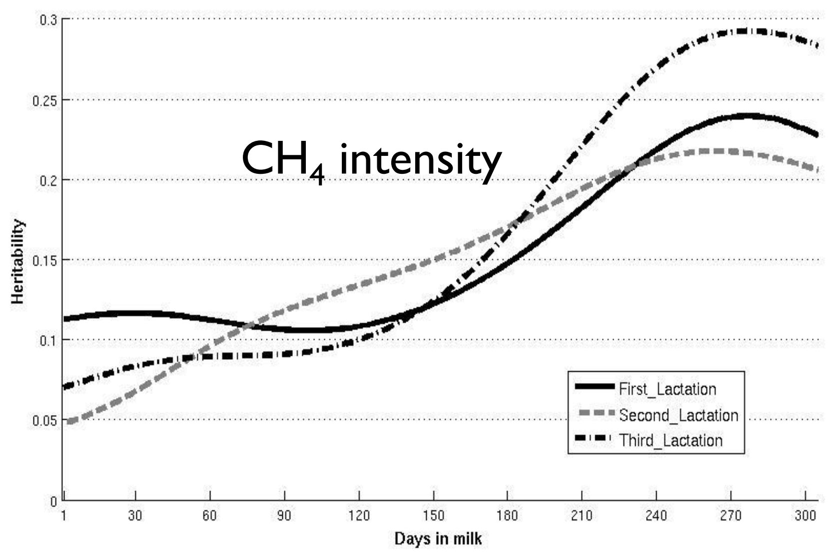
Averaged daily heritability

	CH_4 (g/d)
Lactation 1	0.10±0.01
Lactation 2	0.10±0.01
Lactation 3	0.09±0.01

daily heritability



Daily heritability



Averaged daily heritability

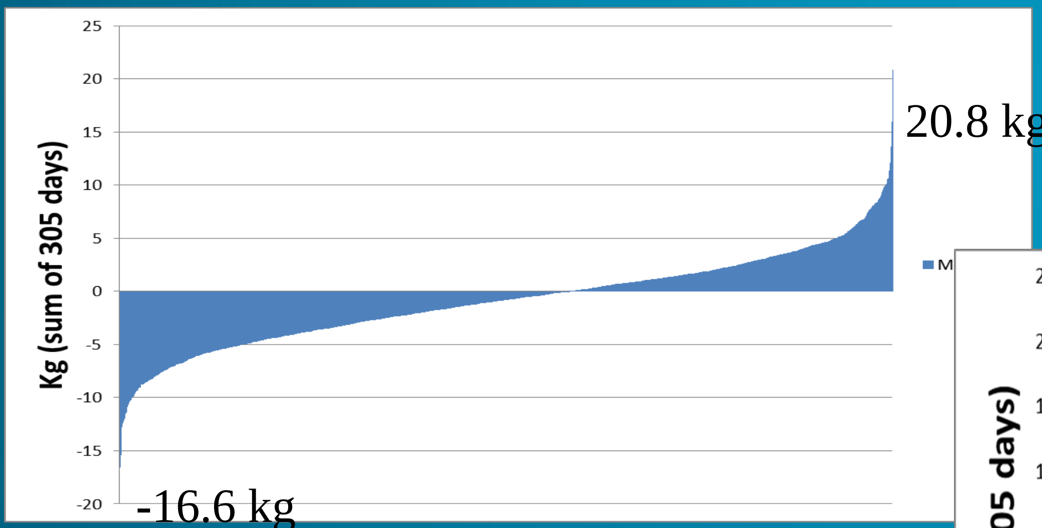
	CH_4 intensity (g/kg FPCM)
Lactation 1	0.15±0.01
Lactation 2	0.15±0.01
Lactation 3	0.16±0.02

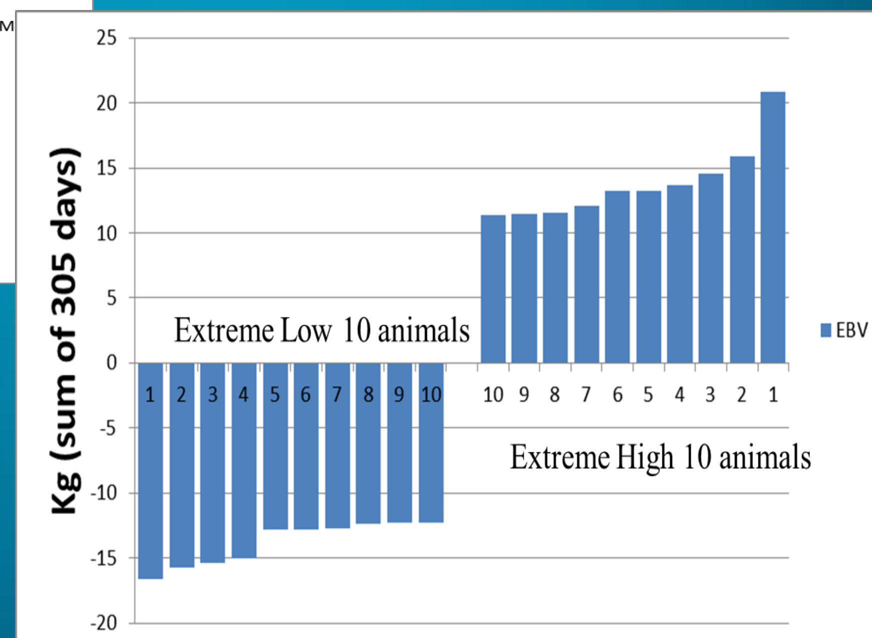
Phenotypic (below diagonal) and genetic (above diagonal) correlations

Traits	MIR CH_4 (g/d)	MIR CH_4 intensity	FPCM	Fat yield	Protein yield
MIR CH_4 (g/d)		0.52	-0.01	0.16	-0.02
CH_4 intensity (g/kg of FPCM)	0.21		-0.84	-0.68	-0.78
FPCM	-0.02	-0.65			
Fat yield	0.01	-0.58			
Protein yield	-0.01	-0.60			

Estimated Breeding Values

Sires which have daughters with MIR CH_4 records





Population mean =166 kg
EBV= -16.6 kg
Expected methane next gen=166-16.6=149.4 kg (if both selected sire and dam) 10%reduction
If only selected sire and average cow=166-(16.6/2) 8.3= 157.7 kg (5% reduction)

Conclusions

- Production on less CH_4 (g/day) during peak milk production
- First lactations and second lactation different genetically and within lactations
- Obtained heritability- selection for these traits possible
- Selection of methane intensity decreases yield of milk production traits
- Genetic variability seems to exist

Perspectives

- Extend to the Walloon genetic evaluation system to access the profitability (+ve/-ve) from inclusion of methane traits in the selection index
- Genome wide association study to detect potential region of chromosome for methane emissions (50k SNP data will be utilized from DairySNP project)

gembloux agro bio tech

Université de Liège

Acknowledgements

Supervisors/Collaborators

- Hélène Soyeurt
- Nicolas Gengler
- Marie-Laure Vanrobays
- Amélie Vanlierde
- Fréderic Dehareng
- Eric Froidmont
- Pierre Dardenne
- Eva Lewis
- Frank Buckley
- Mathew Deighton
- Sinead McParland
- Donagh Berry

GREENHOUSE MILK

PEOPLE

Teagasc Agriculture and Food Development Authority

Wallonie

DGO 3

cra-w

OptiMIR

fnrs LA LIBERTÉ DE CHERCHER

Contact: pbkandel@ulg.ac.be