Gembloux Agro-Bio Tech
Université de Liège

Genomic evaluation of MIR predicted CH_4 exploiting correlations to MACE evaluated traits

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Steps Towards Genomic Evaluation for CH_4

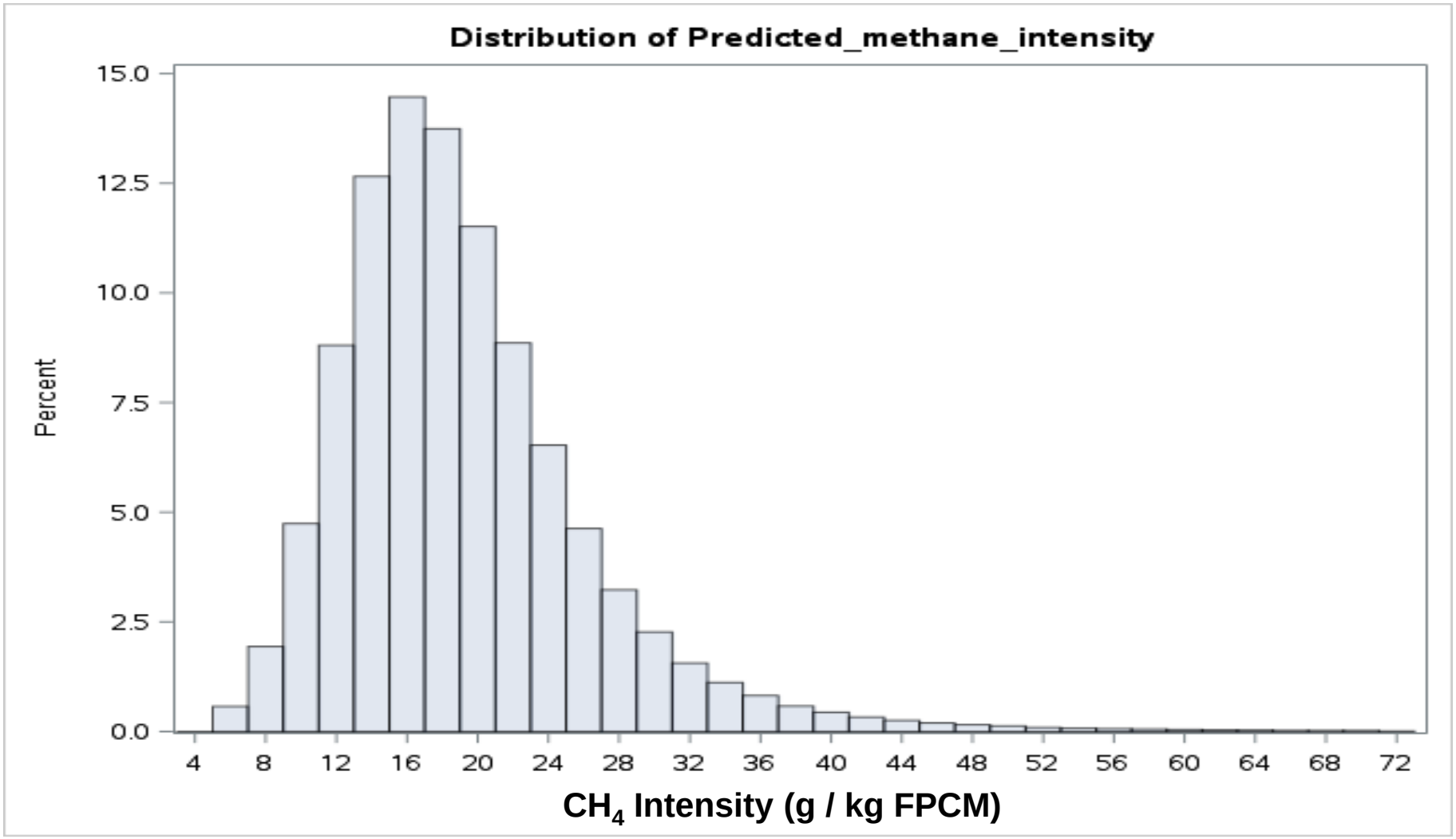
- **Breeding goal**
  - Trait definition
- **Phenotype**
  - Data recording
- **Genetic parameters**
- **Genetic and genomic evaluation system**

Trait Definition

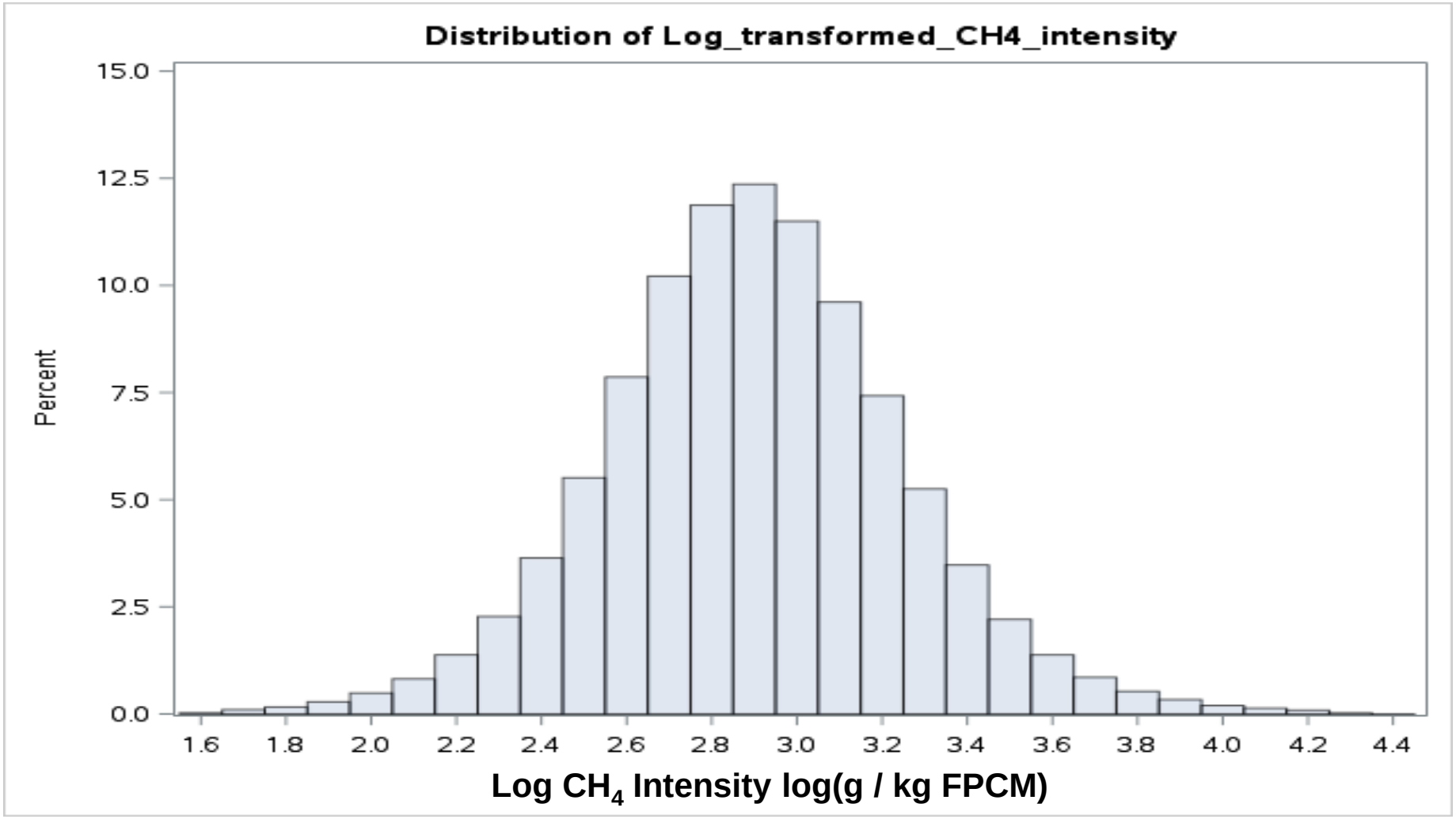
- **Highly difficult ongoing discussion:**
  - CH_4 emission vs. intensity (/output) vs. yield (/input)
- **Many aspects:**
  - "Economic"
  - Type of use
  - Potentially: breeding goal trait ≠ evaluated trait
- **Here we add another aspect:**
  - Optimizing computational setting to exploit correlations to MACE evaluated traits

➔ **Very important aspect in genomic evaluation**

Example of Trait Definition – CH_4 Intensity



Trait Definition – Log(CH_4 Intensity)



➔ Residual (Genetic) Methane

- **But we know also**
  - Log(CH_4 /"milk") = Log(CH4) – Log("milk")
- **Logical next step:**
  - Residual CH_4 = CH_4 – expected CH_4 given prod. + maintenance
  - Use of milk + milk components + body type traits
- **Advantage: Allows use of widely available MACE-evaluated traits**
  - Allows to considered this as a different trait ($r_g < 1$)
  - Leads to definition of **Residual (genetic) methane (RCH_4)**
- **Interesting set-up of genomic evaluation as bivariate model using:**

  Trait1: CH_4 EBV observed on Walloon cows from MIR data

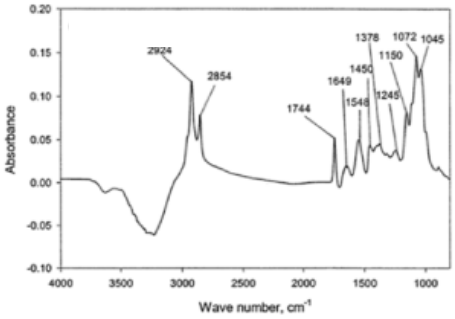
  Trait2: CH_4 EBV expected from MACE EBV for correlated traits
- **Reported RCH_4 EBV computed as difference between EBV above**

Reminder: Mid-Infrared (MIR) Predictions

Routine milk recording samples

(Foss, 2008)

MIR Spectrometry



Routine Spectra

Calibration or prediction equations

Predictions:

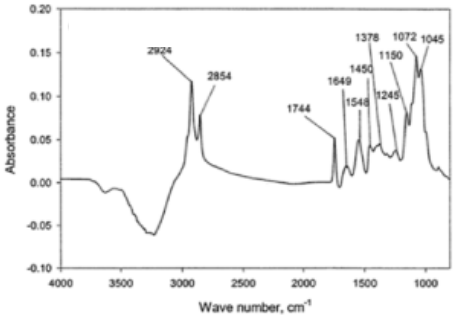
Fat, protein, urea, lactose ….

Large Scale Routine CH_4 Data Recording

Routine milk recording samples

(Foss, 2008)

MIR Spectrometry



Routine Spectra

CH_4 Prediction equation

Reference values (CH_4 ⇔ Spectra)

Predictions:

But also CH_4

…

MIR CH_4 Prediction Equation

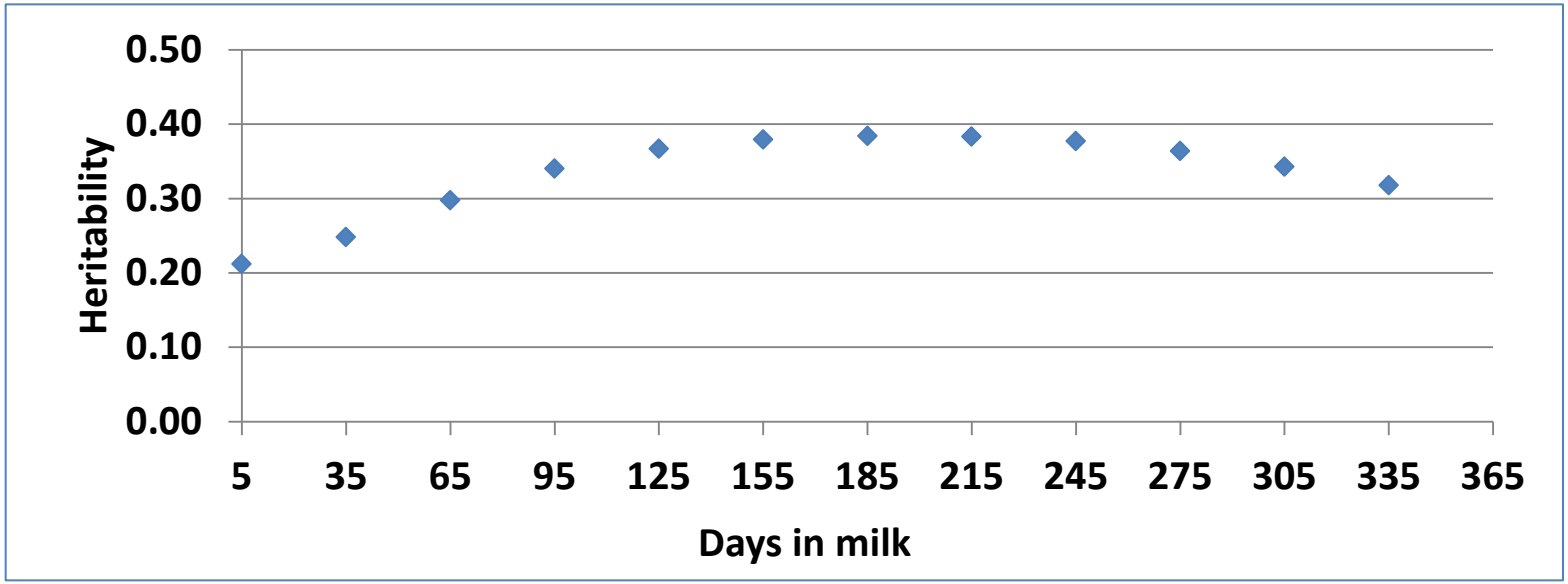
- **Developed by the MethaMilk consortium**
  - Started by BEL joint by IRL, CHE, DEU, LUX, FRA, AUS,…
  - Ongoing contributions by all groups recognized !
- **Ongoing calibration work since 2009 ← CRA-W lead partner**
  - Dehareng et al., 2012
  - Vanlierde et al., 2015 and 2016
- **Most robust current equation adapted to data used**
  - SF_6 based reference values from Hol and Hol x Jer
  - Data from BEL and IRL
  - 532 reference records
  - $R^2_c = 0.74$ and $R^2_{cv} = 0.70$

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

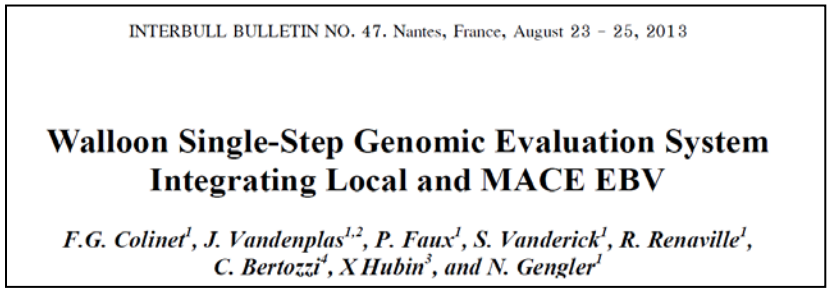
Genetic Parameters

- Based on 1.3 M records from 64 K cows in 1st, 2nd and 3rd lact.
  - Only a part of the database, can be extended for EBV estimation
- Intra-lactation RR test-day model
- Trait average lactation 305 day CH_4 emission EBV expressed in kg / lactation: 3 lactation average lactation $h^2 = 0.33$



Genomic Evaluation Setup

- **Combining**



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Walloon Single-Step Genomic Evaluation System Integrating Local and MACE EBV

F.G. Colinet[1], J. Vandenplas[1,2], P. Faux[1], S. Vanderick[1], R. Renaville[1], C. Bertozzi[4], X Hubin[3], and N. Gengler[1]

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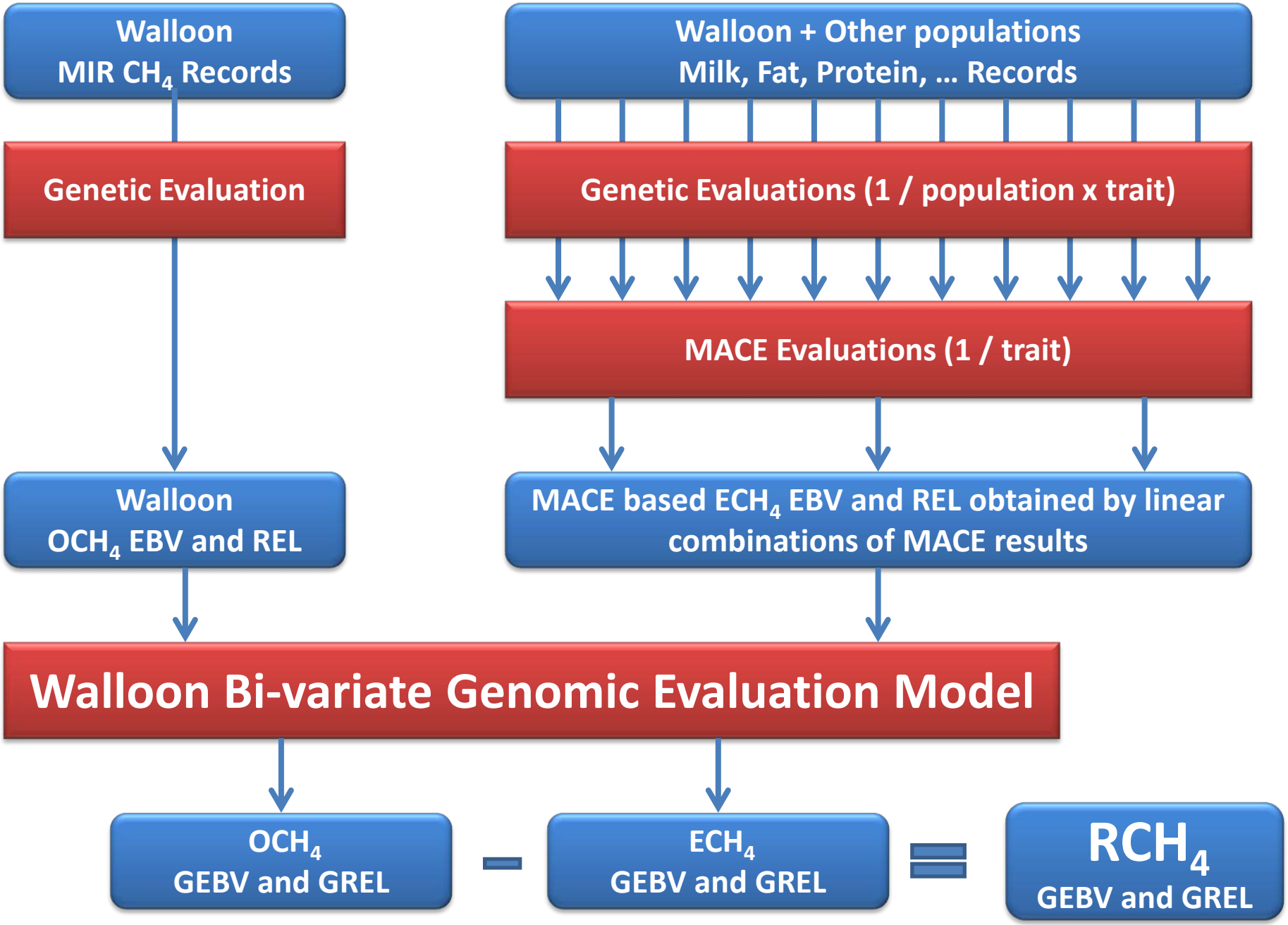
Integration of external estimated breeding values and associated reliabilities using correlations among traits and effects

J. Vandenplas,*†[1,2] F. G. Colinet,* G. Glorieux,‡ C. Bertozzi,‡ and N. Gengler*

- **Bivariate model using EBV and associated reliabilities:**
  - "Observed" CH_4 EBV (OCH_4 EBV) predicted locally using MIR data from Walloon cows
  - "Expected" CH_4 EBV (ECH_4 EBV) predicted from MACE EBV for correlated traits


Walloon
MIR CH_4 Records
Walloon + Other populations
Milk, Fat, Protein, … Records
Genetic Evaluation
Genetic Evaluations (1 / population x trait)
MACE Evaluations (1 / trait)
Walloon
OCH_4 EBV and REL
MACE based ECH_4 EBV and REL obtained by linear combinations of MACE results
Walloon Bi-variate Genomic Evaluation Model
OCH_4
GEBV and GREL
–
ECH_4
GEBV and GREL
=
RCH_4
GEBV and GREL

Expected CH_4 EBV Predicted from MACE EBV

- Group of 519 bulls with at least 30 daughters with CH_4 from MIR and MACE results (and having a genotype)
- Results showed problems using type EBV
- However predicting from milk, fat and protein successful
- Best predictor correlation of 0.55 (Calo corrected to $r_g = 0.64$)
  - Based on milk (-) and fat (+) yields, fat (-) and protein (+) %

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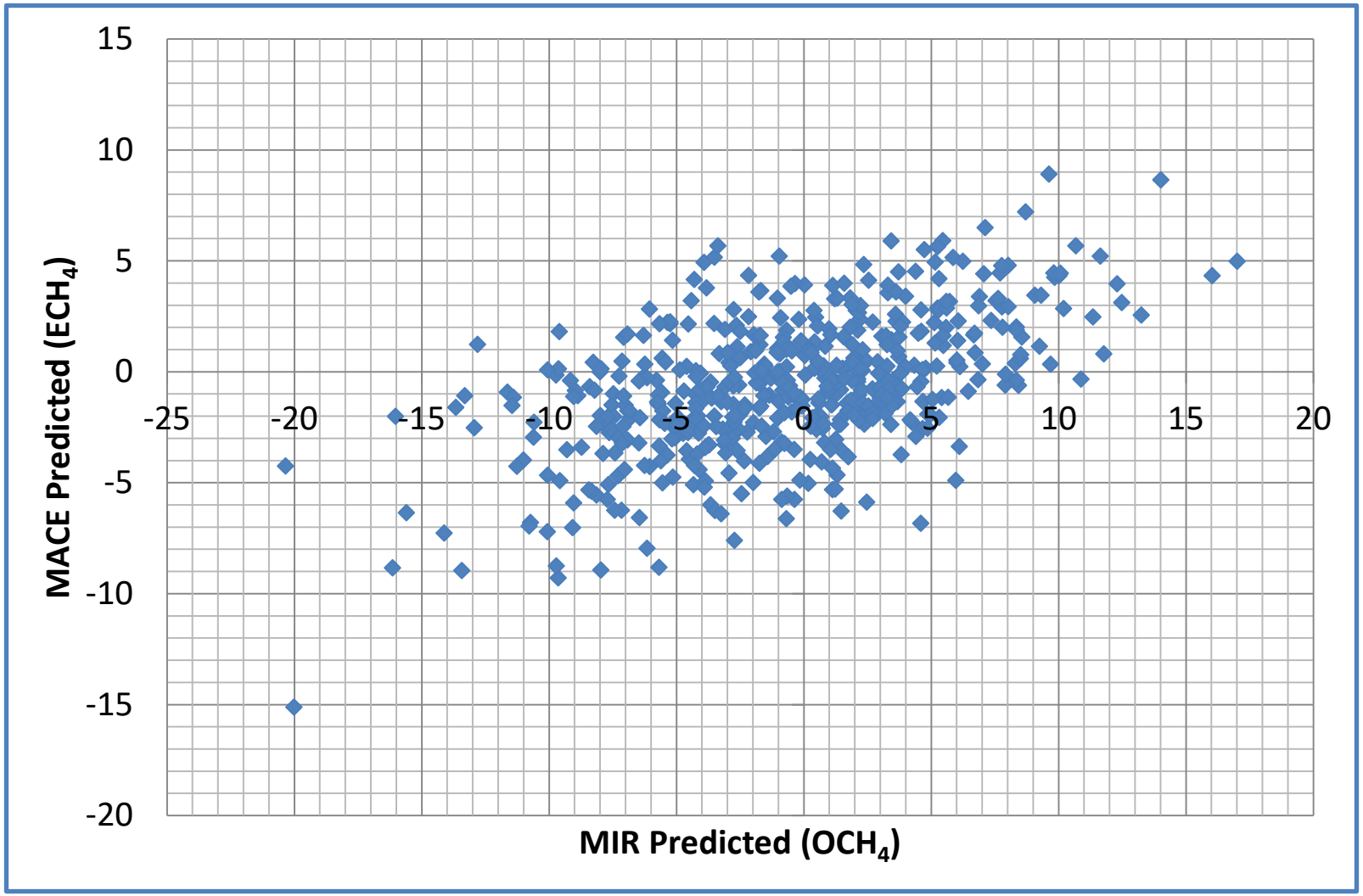

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- Best predictor correlation of 0.55 (Calo corrected to $r_g = 0.64$)
  - Based on milk (-) and fat (+) yields, fat (-) and protein (+) %
  - Indirect proof that CH_4 from MIR contains information not in milk yield and fat and protein components
- Hypothesis:
  - Predictor also based on link of CH_4 to energy in milk (e.g., expressed as ECM) and CH_4 emissions

Practical Issues

- **Bulls with MACE only information (no OCH_4 phenotypes and no genotypes) suboptimal**
  - **Obtaining genotypes for these bulls necessary to work correctly ➔ flow of information from correlated trait to OCH_4 GEBV**

- **All animals with genotypes will get RCH_4 GEBV**
  - **Older bulls and cows with records ➔ reference population**
  - **Younger animals and selection candidates**

- **If people are interested to nominate their animals, do not hesitate to contact me !**

Some Concerns and Perspectives

- **MIR predicted data limited ⇔ International collaboration**
  - Cf. expanding MethaMilk consortium
- **Failure to correlate to type traits**
  - Are we missing an element in observed CH_4 as prediction equation only MIR + DIM based ← BW – DMI (maintenance missing) ?
  - **Need for "real" CH_4** (what ever this could be) ???
- **"Breeding Goal Trait" (BGT) or "Index Trait" (IT)**
  - RCH_4 more IT then BGT as based on "indirect" predictor traits → **"real" CH_4 as BGT**
- **However basic strategy very flexible**
  - **Adding 3rd trait ("real" CH4)** with obviously little (no if pure BGT) data → replacing OCH_4 in RCH_4 or directly used as reported trait??
  - Also Vandenplas' systems of equations can be amended to include **external direct SNP / QTL effects ⇔ International collaboration** → SNP-based Single-Step methods

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GPLUSE – Genotype plus Environment – Integration for a more sustainable dairy production system

OptiWIR – WITH THE SUPPORT OF – Wallonie

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