ICAR 2026 VERONA ITALY

INTERBULL

LIÈGE université Gembloux Agro-Bio Tech

# Walloon strategies targeting new traits for efficiency, mitigation, adaptation and resilience in dairy cattle

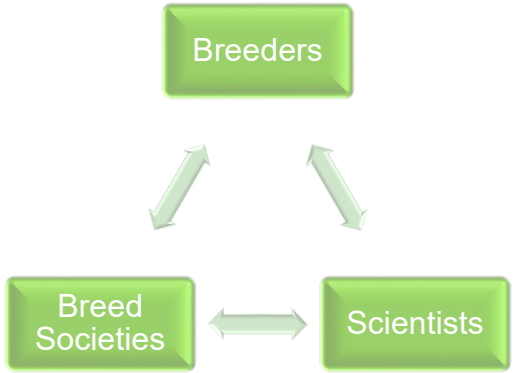
K. Wijnrocx, P. Lemal, H. Atashi, Y. Chen, H. Bérat, N. Gengler

Gembloux Agro-Bio Tech, University of Liège, Gembloux, Belgium.

# Introduction

- Achieving sustainable dairy production ← **coordinated efforts**
  - Define, record and improve novel traits
- **Walloon DEffi initiative** as defined by eleveo by avé, the Walloon Breed Society
  - Represents a substantial challenge, as multiple emerging traits must be simultaneously developed and implemented
- We report here our **current progress** on
  - Efficiency, mitigation, adaptation, welfare and resilience traits in dairy cattle

# Situation in Wallonia



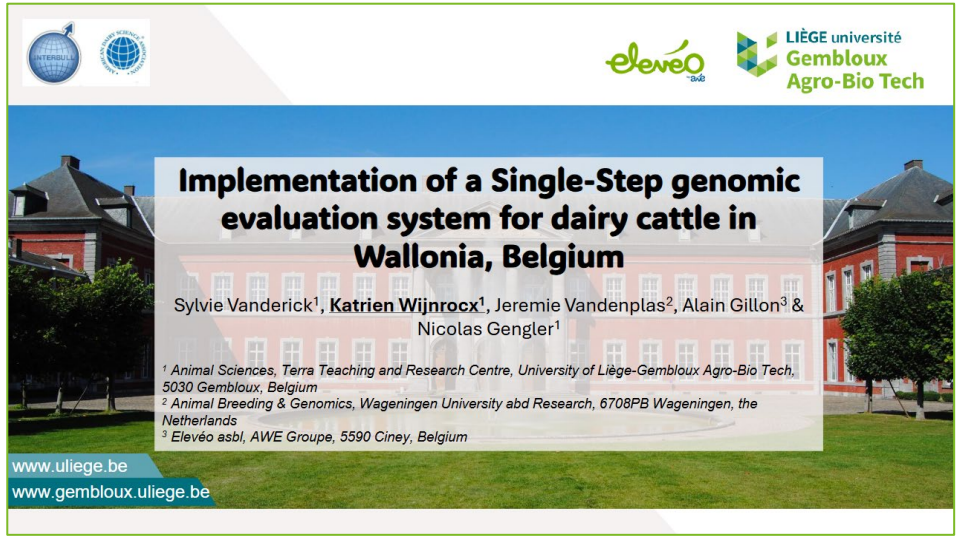

- Small region ➔ proximity ➔ easy exchanges

- Advances in **milk-based phenotyping**
  - Since 2008 **Futurospectre** R&D **Consortium** ➔
  - Access to MIR spectral data for all cows under **elevéo** DHIA + bulk milk for all herds through **CdL** since a long time….
  - All MIR spectra standardized through emr developed by **CRA-W**
  - Large number of **CRA-W** and **ULiège-GxABT** developed MIR prediction equations as those for **fatty acids**, **$CH_4$ prediction, heat-stress, …**

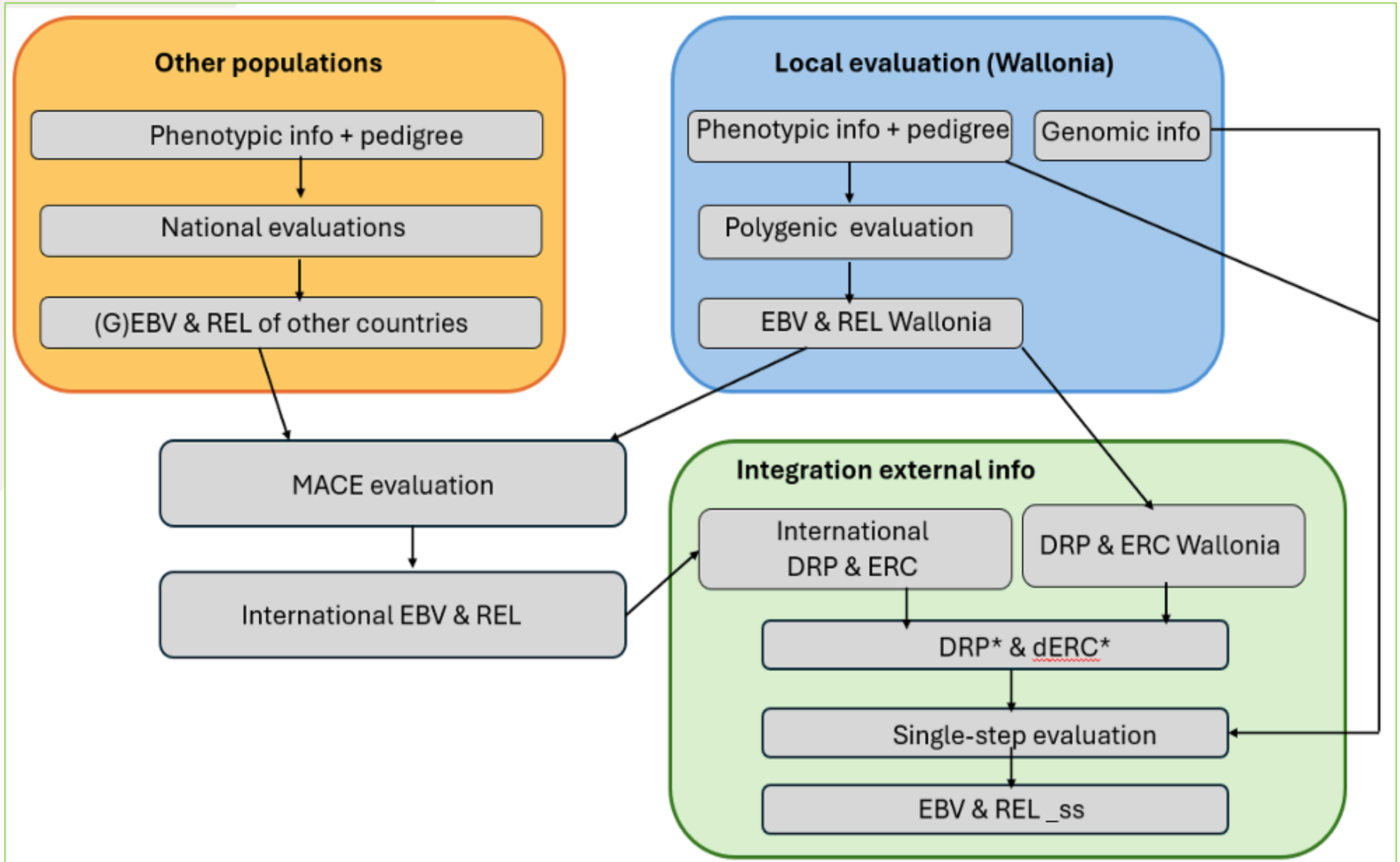
- WALLeSmart ➔ **digital facilitation platform** for farmers and breeders in Wallonia
  - Facilitates access to **(sensor) data** and direct **interaction with stakeholders**

# Generic ssGEBV Concept Used in Wallonia

- Last year Katrien Wijnrocx showed:



# Generic ssGEBV Concept Used in Wallonia

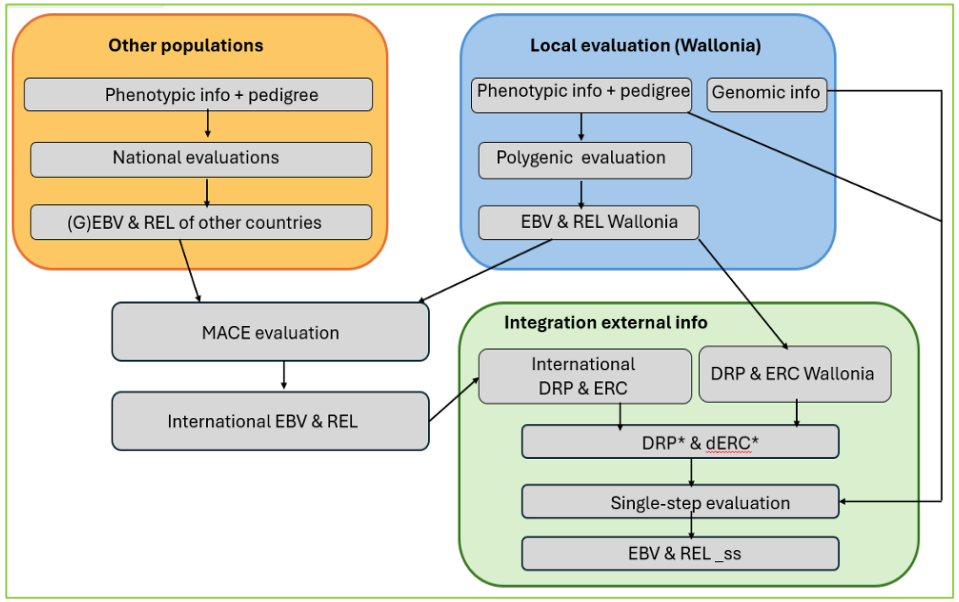


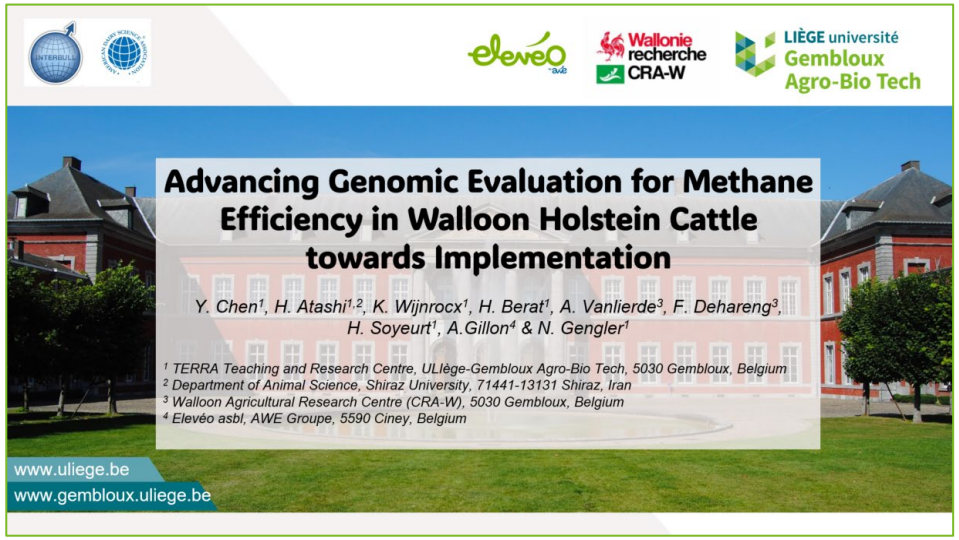
# Generic ssGEBV Concept ➔ MIR-Based Novel Traits

- Last year Katrien Wijnrocx showed:

- Also relevant here
  - M, F, P traits ⬅ TD records
  - Use of RR-ssGBLUP model

- As MIR-based traits ⇔ F, P traits
  - Example of **$CH_4$** shown last year:
  - Not explained:
    MIR-based traits ➔ replace M, F, P
  - Many different equations



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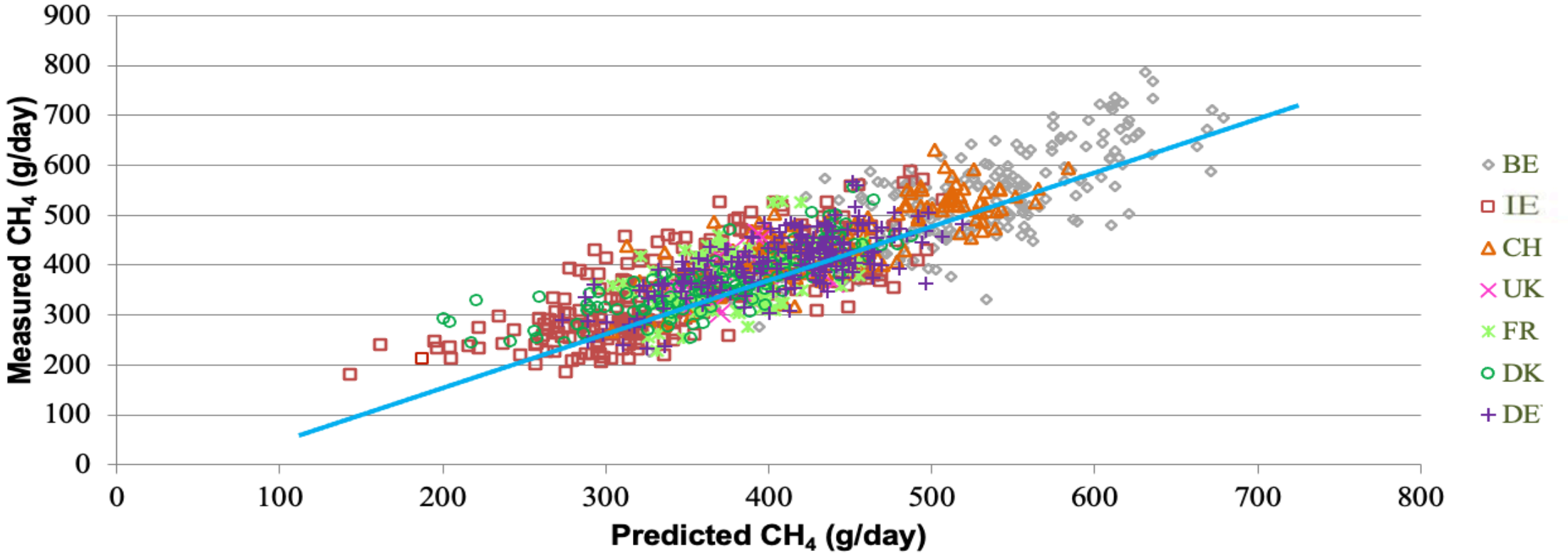
# MIR-Based $CH_4$ Emissions

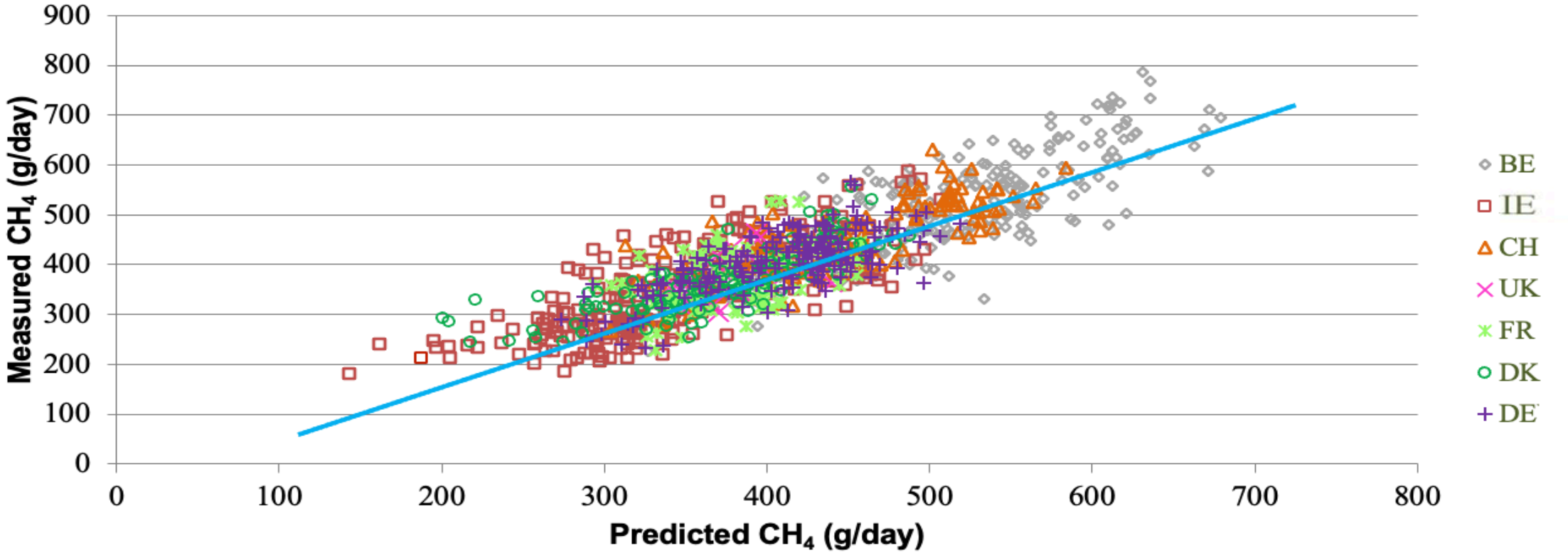
# Status: Routine Evaluations

# Used MIR Equation




| $CH_4$ Ref. method | n data | n cows | Origin | $R^2c$ | SEC (g/d) | $R^2cv$ | SECV (g/d) |
|---|---|---|---|---|---|---|---|
| $SF_6$ & RC | 1,089 | 299 | BE, IE, CH, UK, FR, DK, DE | 0.73 | 53 | 0.68 | 57 |

# Used MIR Equation ➔ Improvement cf H. Soyeurt's talk

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# Available MIR-$CH_4$ ( = PCH4) Genomic Evaluation Dataset

- Plan is every year an evaluation before July
- Current results from 2025 ➔ 2026 only in preparation

| Parity | No. of records | No. of cows | Mean | SD |
|---|---|---|---|---|
| | | | | |
| 1 | 1,935,284 | 287,511 | 324 | 67.0 |
| 2 | 1,528,675 | 226,132 | 353 | 69.9 |
| 3 | 1,081,440 | 161,234 | 367 | 72.1 |
| All | 4,545,399 | 328,290 | 344 | 69.2 |

+ 9,631 genotypes for Holsteins

Walloon
MIR-$CH_4$ TD Records

Walloon (+ Other populations)
Milk, Fat, Protein, Other Traits

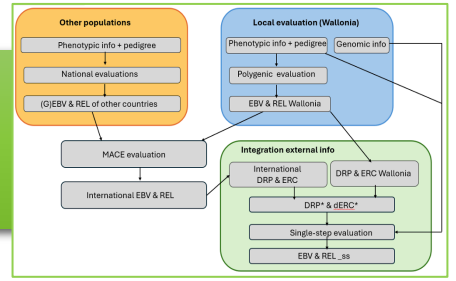
Local Genetic Evaluations
(1 / population x trait)

MACE Evaluations (1 / trait)

Walloon RR Genomic
$CH_4$ Evaluation*

https://www.flaticon.com/free-icons/correlation

Walloon Integrated Genomic
Evaluations (1 / trait)




MIR-$CH_4$
EBV (and REL)

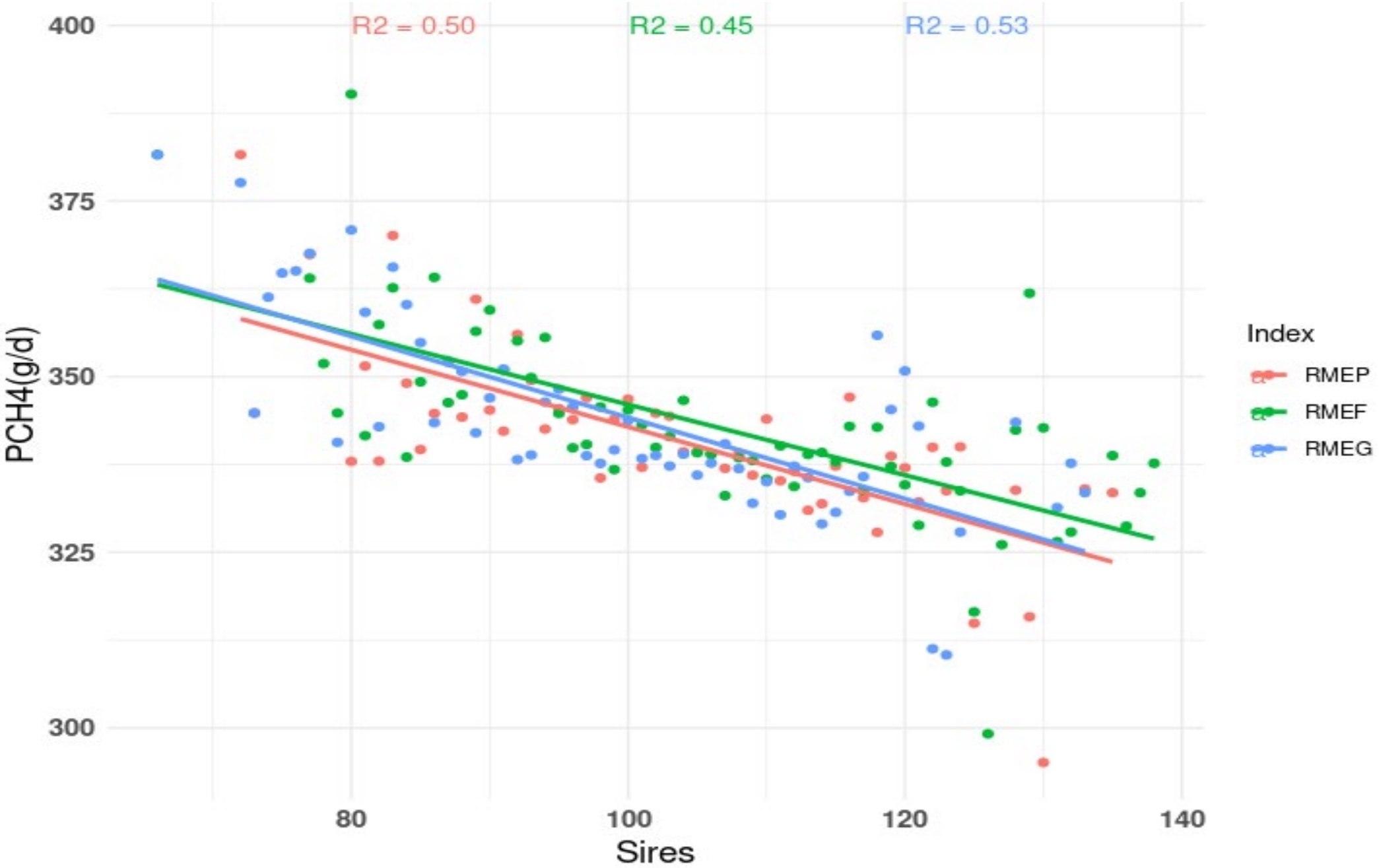
–

Expected $CH_4$
EBV (and REL)

=

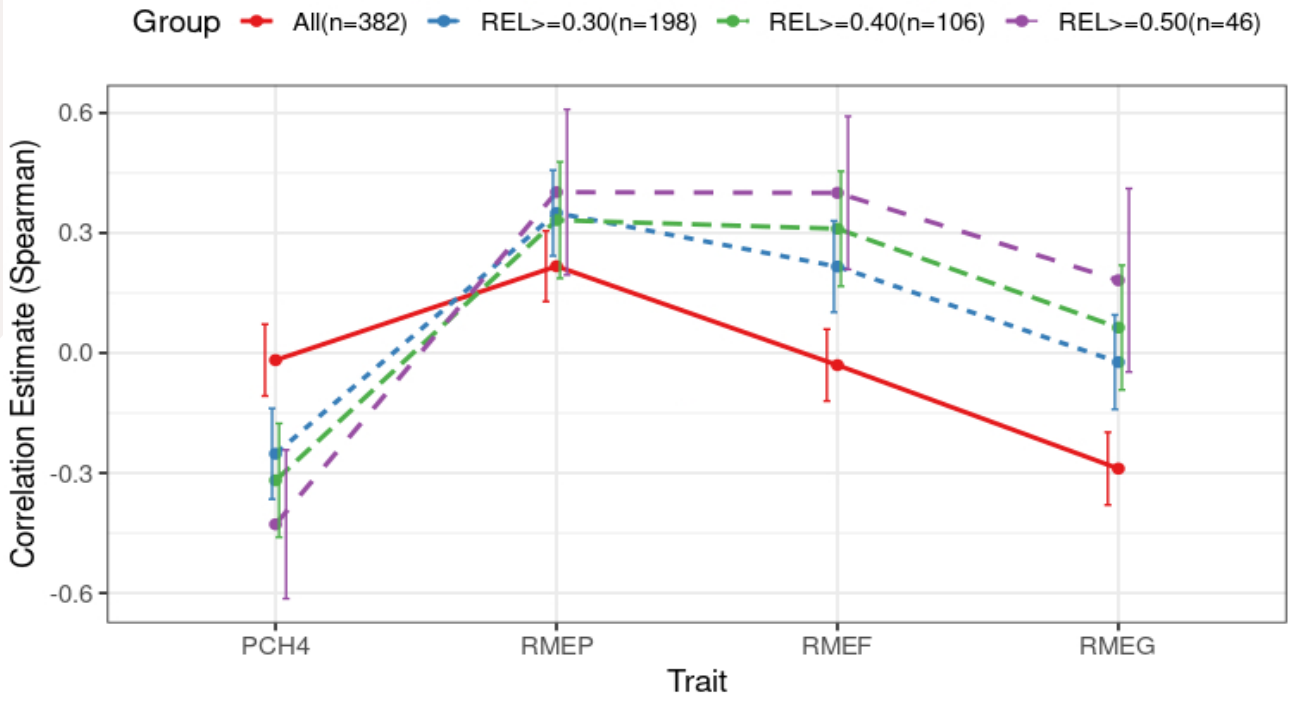
$CH_4$ Efficiency
EBV (and REL)

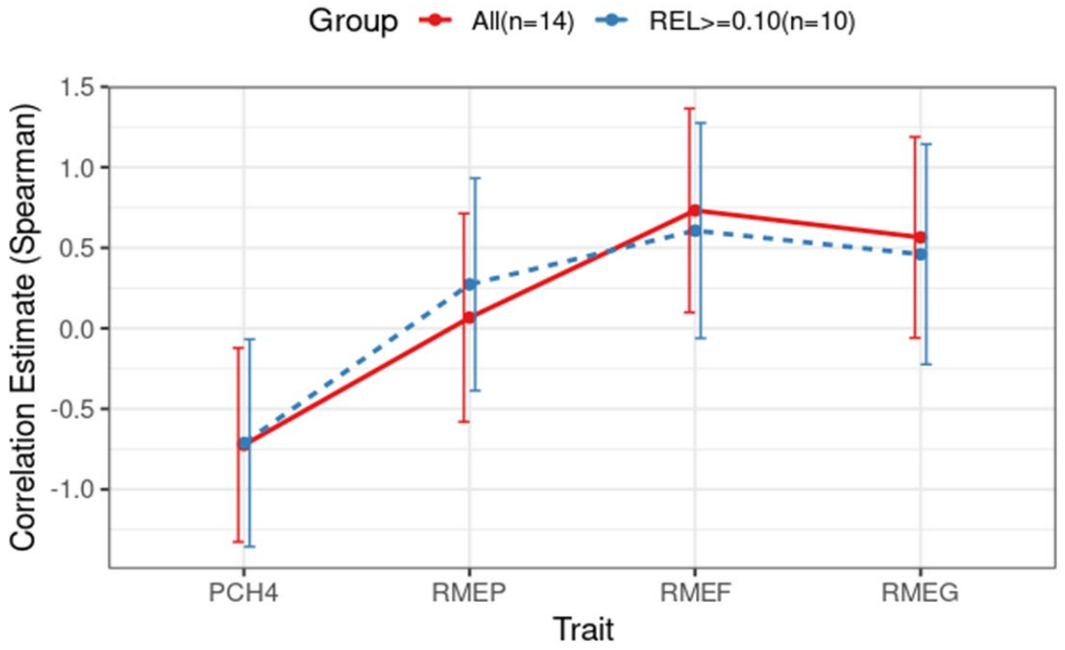
*We change the traits from M, F, P ➔ MIR-$CH_4$


R2 = 0.50
R2 = 0.45
R2 = 0.53
400
375
350
325
300
PCH4(g/d)
80
100
120
140
Sires
Index
RMEP
RMEF
RMEG

# Final Question: Do MIR-$CH_4$ represent correctly Breath-$CH_4$?

- Indirect comparision through internationally **available GEBV**
- Comparison with other countries
  - Country A based on sniffers and Greenfeed (382 bulls in common)
  - Country B based on sniffers (only 14 bulls in common)



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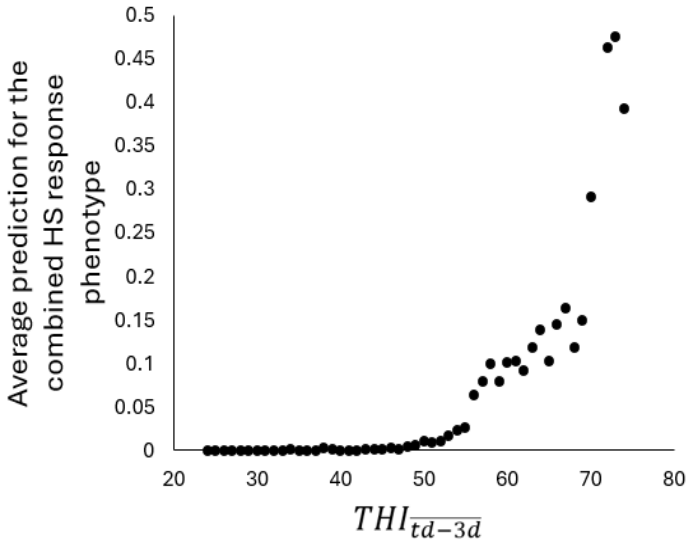
# MIR-Based Heat Stress Response

# Status: Advanced Prototype

# Heat Stress Response ➔ MIR Equation

- Developed on 399 Holstein cows recorded in 2024
  - THI-independent method
  - **MIR-based prediction of Heat Stress Response**




- Applied on 1,038,149 MIR spectra from Holstein cows recorded from 2020 to 2022

- More details in the **presentation of Pauline Lemal** @ ICAR 2026
  - Industria Room - Thursday – June 4, 2026
    Technical session 4: 9:15– 9:30

# Heat Stress Response ➔ Genomic Evaluation

- Phenotype “Heat Stress Response” (HSR) on a 0 to 1 scale
  - Heritability: 0.10
- However additional data selection
  - Only CG ( = HTD) with average of at least 0.1 ➔ detecting CG that are affected
  - Finally 64,035 cows with phenotypes (146,427 animals in pedigree) and 7,170 genotypes
- Generated 6,708 GEBVs with reliabilities ≥ 0.5
- Place of HSR in breeding
  - Approximate genetic correlations (based on GEBV):

| | Milk | Fat | Protein | SCS | Longevity | Fertility |
|---|---|---|---|---|---|---|
| HSR | 0.15 | 0.04 | -0.14 | 0.16 | -0.33 | -0.39 |

# Heat Stress Response ← Role of Sensors

- Two points critical for HSR
  - Valida HSR when creating the reference phenotypes
  - Rapidity of detection of HSR when there is exposure to HS
    - MIR-based or in general DHIA recording based linked to milk sampling
- Role of sensors
  - Acquisition of behavior data was already shown to be useful →
  - Better reference data for calibration


- Limits:
  - Degree of equipment on farms and use on animals (all ?)
  - Very positive trend in Wallonia

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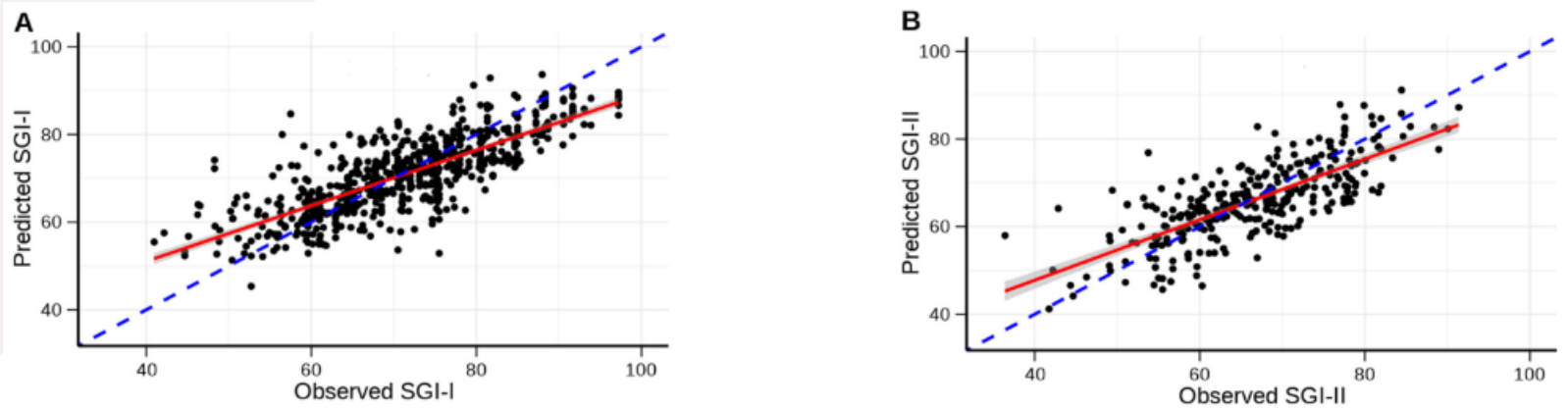
# Other MIR-Based and Novel Traits

# Status: Active Research

# Other Ongoing Developments

- All MIR-based traits → replacing M, F, P ← needed good MIR equations
- Examples (from the more advanced to the least advanced):
  - Welfare scores
    - Phenotype based on a pilot study using welfare quality scoring system (WQP©)
    - Here prediction from MIR no satisfactory but innovative MT approach
      i.e., not replacing but adding novel trait to M, F, P (here also SCS)

# Welfare Scores (With- or Without Behavior)




- Method can be incorporated into existing recording systems extending RR-ssGBLUP

J. Dairy Sci. 109:6376–6386
https://doi.org/10.3168/jds.2025-27722


**Prediction of welfare scores throughout lactation by random regression test-day models in Walloon Holstein dairy cows**

Y. Chen,[1]* H. Atashi,[1,2]*† P. Lemal,[1] K. Wijnrocx,[1] M. N. Tran,[3] J. Evrard,[4] B. Christiaens,[3] and N. Gengler[1]
[1]TERRA Teaching and Research Center, Gembloux Agro-Bio Tech, University of Liège, 5030 Gembloux, Belgium
[2]Department of Animal Science, Shiraz University, 71441-13131 Shiraz, Iran
[3]Elevéo asbl by AWE Groupe, 5590 Ciney, Belgium
[4]Regional Association for Animal Registration and Health (ARSIA) asbl, 5590 Ciney, Belgium

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    - Here prediction from MIR no satisfactory but innovative MT approach
      i.e., not replacing but adding novel trait to M, F, P (here also SCS)
  - "Feed" efficiency ➔ work on DMI and "Nitrogen Use Efficiency" ongoing
    - Basic equations exists with some limitations ➔ **CRA-W leading efforts**
    - Integration with ssGBLUP as easy as with $CH_4$
- Also: Use of AMS data
  - Traditional data + innovative data….
  - Integration with MIR-based traits, on-line recordings….

# GEBV → SNP effects → DGV

- Lauch in July 2025 → GEBV for group of bulls
- Estimation of SNP effects → Estimation of DGV
  - Allowing others to get access to our predictions
- In progress → fine tuning → alternative dissemination evaluation results

# Thank you for your attention

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HoliCow