Towards guidelines to validate and calibrate genetic evaluations for enteric methane emissions

Global Methane Genetics initiative

Led by WAGENINGEN UNIVERSITY & RESEARCH

In Partnership with BEZOS EARTH FUND Global Methane Hub

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Phenotypes and genetic evaluations for CH_4

- Dairy cattle, beef cattle and small ruminants
    - Rapid global development
    - Different methods across species, breeds, regions, and production systems
- Harmonized protocols are needed
    - ➔ Standardize phenotypes and genetic evaluations
    - ➔ Improve comparability

➔ Maximize the global impact of genetic selection for reduced CH_4 emissions

Aims

1. Survey on the current international status of genetic evaluations for enteric CH_4 emissions

2. Review of state-of-the-art validation techniques with a focus on CH_4-related genetic evaluations

3. Development of calibration approaches for CH_4 breeding values to demonstrate
    - ➔ the potential impact of genomic selection for reduced CH_4 emissions
    - ➔ that selection of animals with favorable EBVs will result in measurably lower enteric CH_4 emissions

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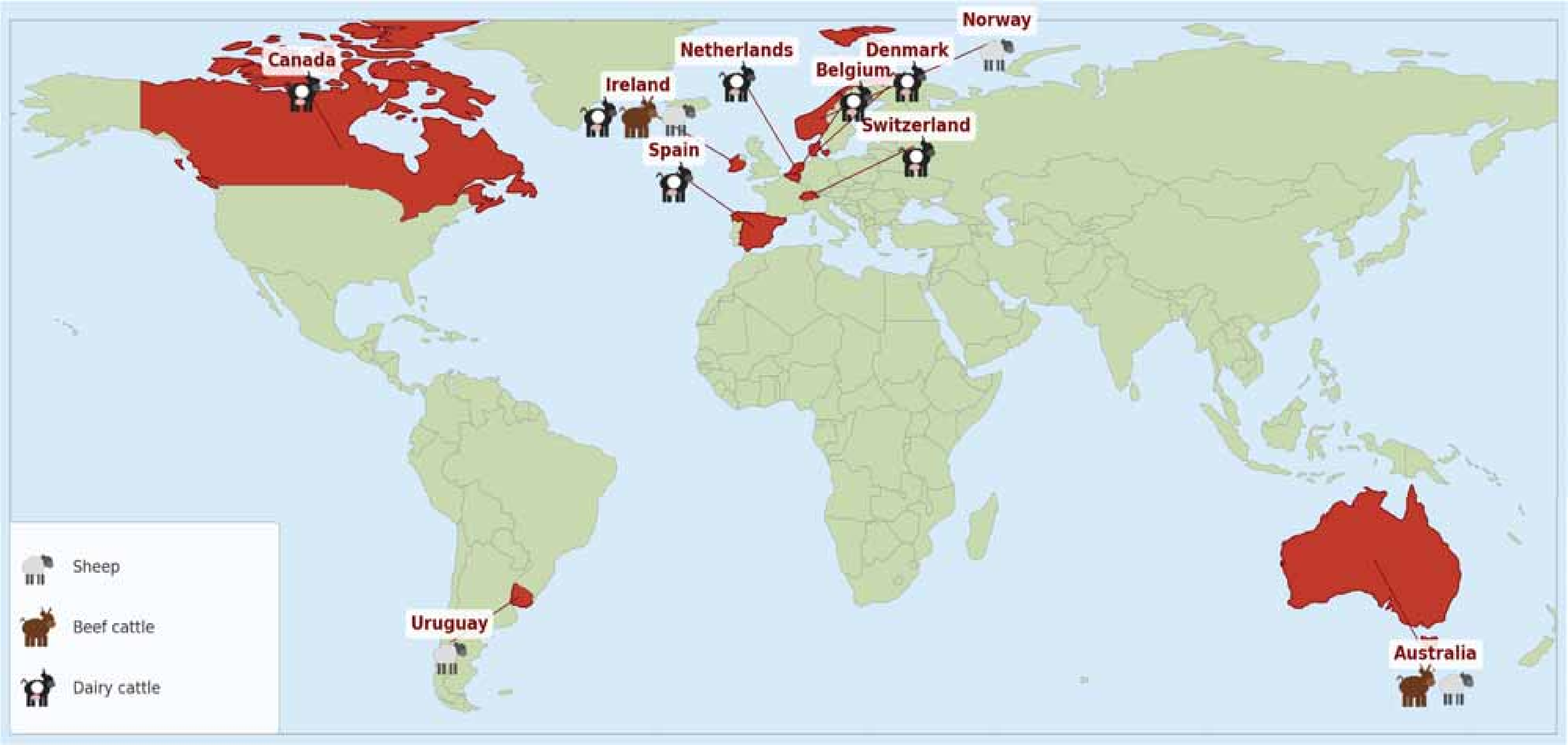
1. Survey – participating countries



1. Survey – Take-aways

- Majority of the participants: routine genomic evaluations

- Various phenotypes (Greenfeed, Portable Accumulation Chamber, SF6 tracer gas technique, Sniffers, Lasers, Milk MIR-based predictions)
- Various traits (CH_4 concentration, CH_4 production, CH_4 rate)
- Indicators traits (feed efficiency, milk production, growth)
- Published GEBVs (various reporting scales and publication criteria)

Survey – Take-aways

- Main challenges
    - Validation, standardization, phenotyping costs, economic incentives
- Most promising opportunities
    - International collaborations, common standards
- Survey report will be published on the ICAR wikipage (Section 20)

2. Validation procedures – current status

- Interbull validation methods, Linear Regression method
    - Typically: many years of data, large numbers of well-proven bulls, extensive progeny across many herds
    - ➔ Sufficient sample size for testing, reliable and robust validation results

➔ Not designed for CH_4 genetic evaluations

➔ Adaptation of Method II and method LR for beef genetic evaluations

- See "Towards standardised LR protocols for international beef cattle genetic evaluations", Gabriel Soares Campos (TS14)

- K-fold cross-validation
    - Easy to implement
    - Not realistic in an animal breeding setting

3. Validation vs Calibration

- Validation of genetic evaluations
  - process of assessing whether EBVs accurately predict the true genetic merit of animals for the evaluated trait

  ➔ does the genetic evaluation work?

- Calibration of genetic evaluations
  - process of quantifying and verifying the correspondence between EBVs and the phenotypes observed in animals for a target trait

  ➔ how much phenotypic change correspond to a given difference in EBVs?

3. Calibration procedures - proposition

- External calibration using an independent dataset with phenotypes for a target trait
  - Regression of phenotypes for the target trait on third-party EBVs
  - Quintile analysis using yield deviations of the target trait

- For a set of animals
  - Target trait: phenotypes (e.g., CH_4 production in g/day)
  - Third-party EBVs: predicted from an independent population (e.g., for CH_4 concentration in ppm)

3. Calibration procedures – regression analysis

- Regression analysis
    - Linear mixed model
        - Phenotypes of the target trait
        - Fixed covariate: third-party EBVs
        - Other fixed and random effects (but no additive genetic effects)
    - Key output: regression coefficient of phenotypes on EBVs

- Strengths
    - Straightforward to implement
    - Results directly interpretable

3. Calibration procedures – regression analysis

- Regression coefficient β_{ij}
  - Association between target trait (i) and third-party EBVS (j)
  - Quantifies the change in the target trait per breeding value unit

- Approximated accuracy of the third-party EBVs for the target trait

$$Acc_{ij} = \beta_{ij}\sqrt{\frac{Var(\hat{\mathbf{u}}_j)}{\sigma^2_{u_i}}}$$

- Approximated genetic correlation between evaluated trait and target trait

$$Corr\left(u_i, u_j\right) = \beta_{ij}\sqrt{\frac{\sigma^2_{u_j}}{\sigma^2_{u_i}}}$$

(assuming unbiased EBVs)

3. Calibration procedures – quintile analysis

- Approach
  - Animals ranked based on third-party EBVs and divided into 5 equal groups (quintiles)
  - Comparison of yield deviations for the target trait across groups
  - Tests whether genetic ranking reflects yield deviations
- Key idea
  - Higher-ranked animals should emit less CH_4 than lower-ranked animals
- Strengths
  - Simple and intuitive
  - Clear visual trend

3. Calibration procedures - illustration

- Evaluated trait = concentration
    - 27,472 weekly sniffer records (ppm)
    - 3,317 Holstein cows with records
    - 2,570 genotyped cows with records

- Single-step genetic evaluation
    - Heritability: 0.17
    - Relative EBVs
        - mean 100 and SD 4
        - higher EBVs ➔ less CH_4

3. Calibration procedures - illustration

- Target trait = production
    - 5,923 weekly GreenFeed records (g/day)
    - 921 cows with records
- Genetic correlation (g/day-ppm): 0.59

- Regression analysis of GreenFeed records
    - Covariate: relative EBV (ppm)
    - Fixed: herd, GreenFeed ID, Year-Month of trial
    - Random: permanent environment, residual
- Quintile analysis: yield deviations from GreenFeed records

3. Calibration procedures – regression analysis

- Regression coefficient: -4.55 (+/- 1.08) g/day / BV unit

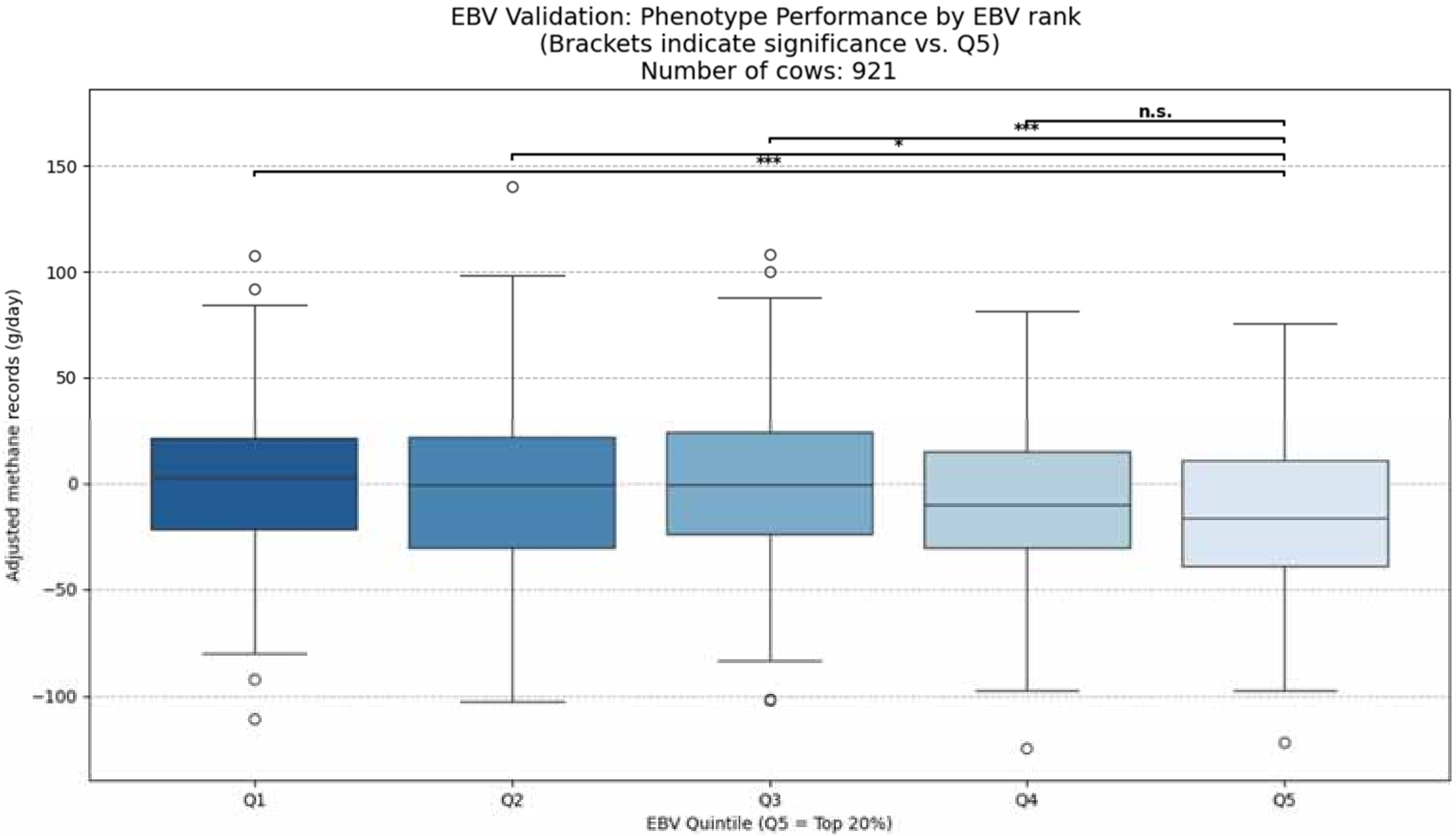
  ➔ **One breeding value unit** ➔ reduction of **4.55 CH_4 g/day**

  ➔ **Not significantly different than the expectation (-6.04 g/day /BV unit)**

- Approximated accuracy of genomic prediction for the target trait: 0.19

- Approximated genetic correlation (evaluated trait, target trait): 0.44

3. Calibration procedures – quintile analysis



Cows with favourable EBVs (ppm) ➔ cows producing less CH4 emissions (g/day)

Conclusions

- Survey
  - Majority of the participants: routine genomic evaluations
  - Main challenges: validation, standardization, phenotyping costs, economic incentives
  - Opportunities: international collaborations, common standards

- Current validation approaches not designed for CH_4

- Calibration approaches using an independent dataset for a target trait

Thank you!

- All participants in the survey
- WUR colleagues

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