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Integrating methane breeding values into carbon accounting frameworks

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AGRISCIENCE CONSULTANTS

Lactanet

SEMEX

Motivation

Why should we include methane genetics in carbon calculators?

- Genetic selection can permanently **reduce enteric methane emissions**
- Carbon calculators do not currently **include animal-level or farm-level genetic variation**
- Consequently, carbon footprints are less precise, and farmer **progress** is not **measured, recognised, or incentivised**

Current barriers

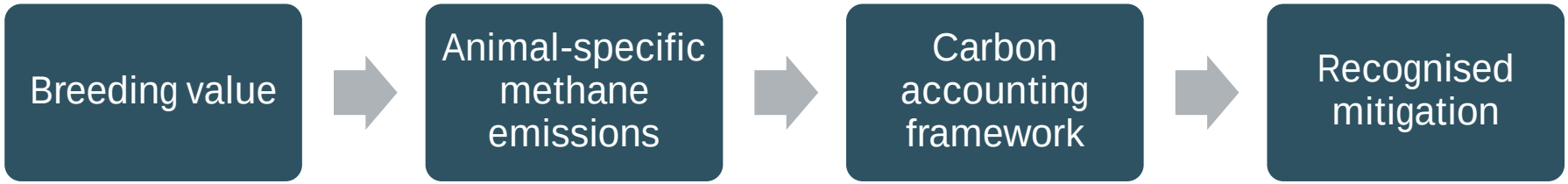
Communication	• Communication and coordination between genetic evaluation centres is essential
Trait definitions	• Methane production, yield, intensity and residual
Attribution	• Separate genetic variation from management effects
Validation	• Demonstrate predicted reduction is realized in research and commercial herds
Recognition	• No incentivization until we can prove impact. • No impact until there is incentivization.

Method

Building a bridge between genetic evaluation outputs and carbon accounting inputs

Approach

- Outline how carbon accounting frameworks can **integrate methane breeding values**
- Demonstrate with a **practical case study** based on the Canadian dairy industry
- Understand how accounting for **genetic variation** would **change carbon footprints**



Breeding values

We outlined how all methane breeding values could be integrated:

Trait Definition		Units	Corrected for production or feed?
Residual methane	RMe	g/day	Yes
Methane production	MeP	g/day	No
Methane yield	MeY	g/kg DMI	Yes
Methane intensity	MeI	g/kg product	Yes
Methane concentration	MeC	ppm	No

Carbon accounting frameworks

- We **targeted the IPCC Tier 2 model,** since this is what most carbon calculators use for calculating GHG emissions from livestock enteric fermentations (DEFRA, 2024; Bourassa and Vinco, 2022).

Carbon accounting frameworks

Adapt IPCC Tier 2 model to include genetics:

$$GHG_{t,\ \text{enteric } CH_4} = \sum_{k} EF_{t,k} \times n_{t,k}$$

Carbon accounting frameworks

Adapt IPCC Tier 2 model to include genetics:

$$GHG_{t,\ enteric\ CH_4} = \sum_k EF_{t,k} \times n_{t,k}$$

$$EF_{t,k} = DMI_{t,k} \times EC_{t,k} \times Y_m \times 365 \times 0.01796 \times GWP$$

$$\frac{kg\ CO_{2eq}}{\frac{head}{year}} = \frac{kg\ DMI}{\frac{head}{day}} \times \frac{MJ}{kg\ DMI} \times [proportion\ MJ] \times \frac{days}{year} \times \frac{kg\ CH_4}{MJ} \times \frac{kg\ CO_{2eq}}{kg\ CH_4}$$

Carbon accounting frameworks

Adapt IPCC Tier 2 model to include genetics:

RMe → $\widehat{\mathrm{EF}}_{t,k} = \mathrm{EF}_{t,k} + \left(\mathrm{RMe}_{t,k} \times 0.001 \times 365 \times \mathrm{GWP}\right)$

MeP → Covert to residual → Apply residual equation

MeY → $\widehat{\mathrm{EF}}_{t,k} = \mathrm{DMI}_{t,k} \times \left[\mathrm{EC}_{t,k} \times \mathrm{Y}_m \times 0.01796 + \mathrm{MeY}_{t,k} \times 0.001\right] \times 365 \times \mathrm{GWP}$

MeI → Covert using product units → Apply residual equation

MeI → Covert using feed units → Apply yield equations

MeC → Not directly compatible and must be converted into standardized units → Apply respective equation

Case Study

Canadian dairy industry

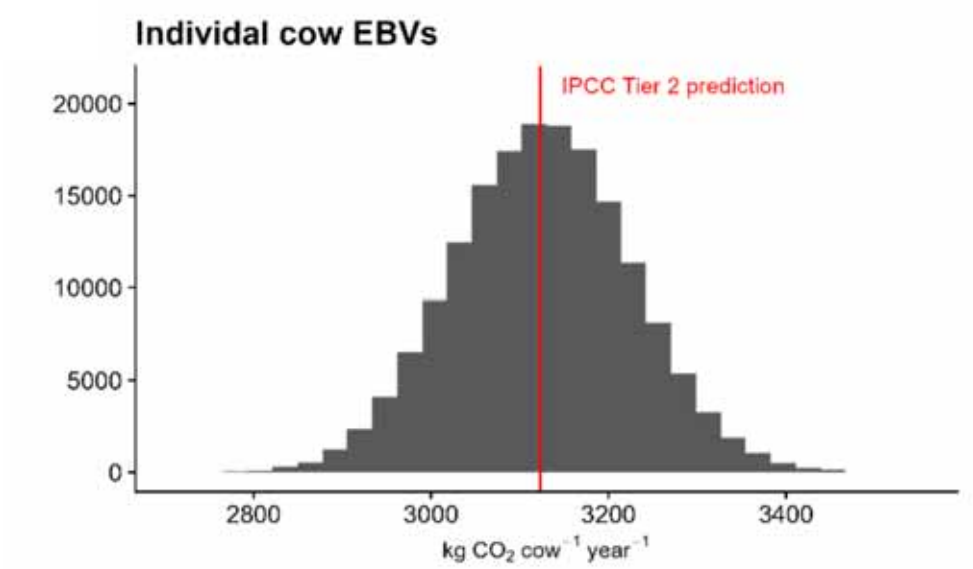
Breeding Values

Lactanet provided breeding values for **all genotyped Holstein females** in the Canadian Dairy Herd Improvement (DHI) inventory.

- Residual trait definition
- Filtered to remove reliabilities < 70%
- Filtered to only include cows born 2014–2024
- Resulted in 171,909 cows across 2986 herds

Results

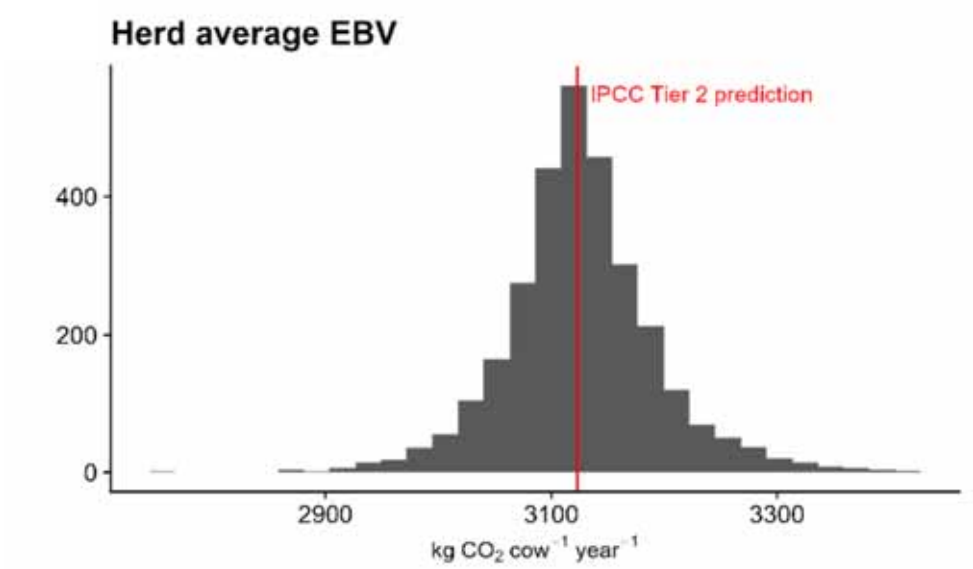
There is genetic variation in methane emissions at **the animal-level**...



	Group	Emissions (kg CO_{2eq} $year^{-1}$ $head^{-1}$)	% change relative to IPCC
IPCC Tier 2	NA	3,123.10	0.00%
IPCC Tier 2 + Genetics	Min 10%	2,950.72	−5.52%
	Average	3,125.41	0.07%
	Max 10%	3,300.76	5.69%

Results

...and **the herd-level.**



	Group	Emissions (kg CO_{2eq} year^{-1} head^{-1})	% change relative to IPCC
IPCC Tier 2	NA	3,123.10	0.00%
IPCC Tier 2 + Genetics	Min 10%	3,008.98	–3.65%
	Average	3,126.04	0.09%
	Max 10%	3,253.49	4.18%

Next steps

Recommendations

- **How should we define a trait?**
  - We consider residual methane, methane intensity, methane yield the most robust trait definitions.
- **Can this work for other industries?**
  - This approach can be applied to all ruminants
- **What about if we do not use IPCC equations?**
  - Can apply to various equations
- **How to streamline data between stakeholders?**
  - We need coordination to allow breeding values to be shared directly from GE provider to carbon calculators

Next steps

Manuscript submitted to Journal of Dairy Science

- Method will be **freely available**
- Method is **trait definition agnostic** and outlines how all methane breeding value definitions can be integrated into IPCC models
- Intended to be **accessible to non-genetic audience**

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THANK YOU

Questions?

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