

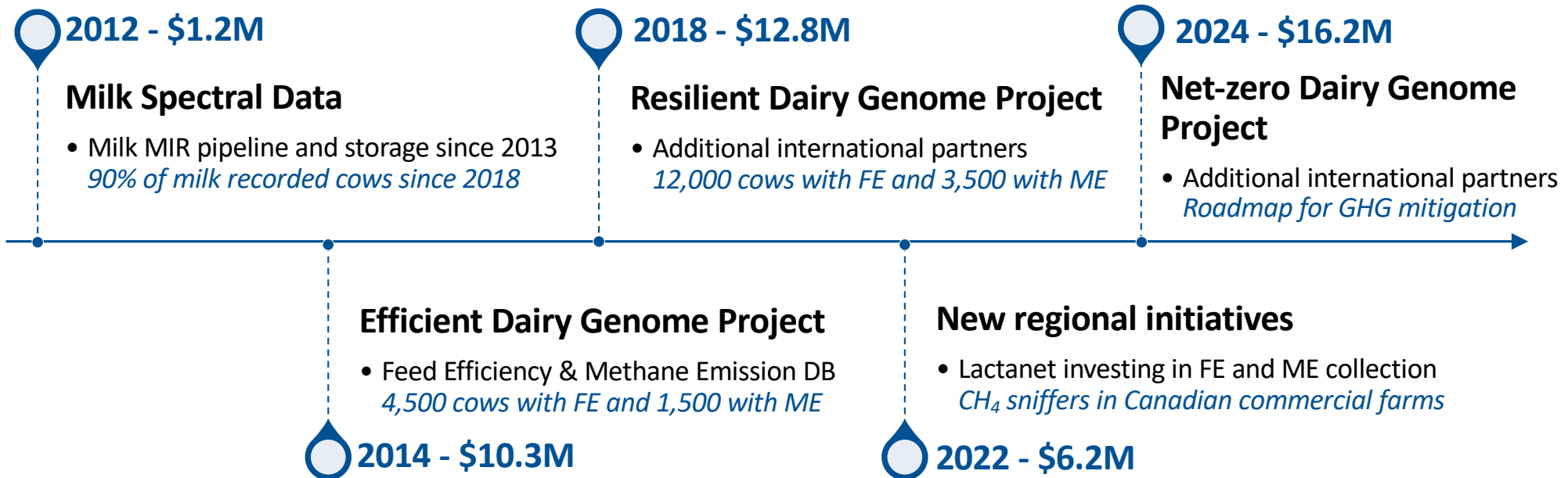


Canadian strategy to include methane trait in our breeding program

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Lactanet & University of Guelph
Guelph, Ontario, Canada**



Building Environmental Traits Capacity Over Time



Since 2013, multiple projects (\$4.2M) to genotype cows with medium-high density chips -> over 50,000 cows



Why we focused on MIR strategy

- Early investment in MIR storage and MIR analysis since 2013
- EDGP project built with main objective of consolidating DMI data across international partners
 - Genome reference population large enough to build genomic evaluations for FE (~5,000 cows phenotyped and genotyped)
- Additional EDGP objective was to consolidate methane data across partners (N~1,300)
 - Heterogeneous CH₄ recording across partners (GF, SF₆, sniffers)
 - Not enough cows to build reliable genomic evaluations for methane
 - Only pathway was to focus on rigid methane collection protocol and accurate milk MIR prediction development

Milk MIR Data – R&D and Pipeline

- NSERC & Dairy Cluster projects (2012-2018)
 - **Milk Fat Globule Size** (Fleming et al 2017a JDS)
 - **Milk Fatty Acids** (Fleming et al 2017b JDS)
 - **Lactoferrin & Casein Micelle Size** (Fleming et al 2019 CJAS)
 - MIR standardization (Bonfatti et al 2017a JDS)
 - Prediction calculation comparison (Bonfatti et al 2017b JDS)
 - Pipeline (Miglior et al 2016 ICAR)
- EDGP & RDGP projects and collaborations (2015-2024)
 - **DMI** (Shadpour et al 2022a JDS)
 - **Methane production** (Shadpour et al 2022b JDS; Liu et al 2022 Animal; Van Doormaal et al 2023 ITB Bulletin; Oliveira et al 2024 JDS Comm)
 - **BCS Change** (Frizzarin et al 2023, 2024; JDS)

How we recorded methane

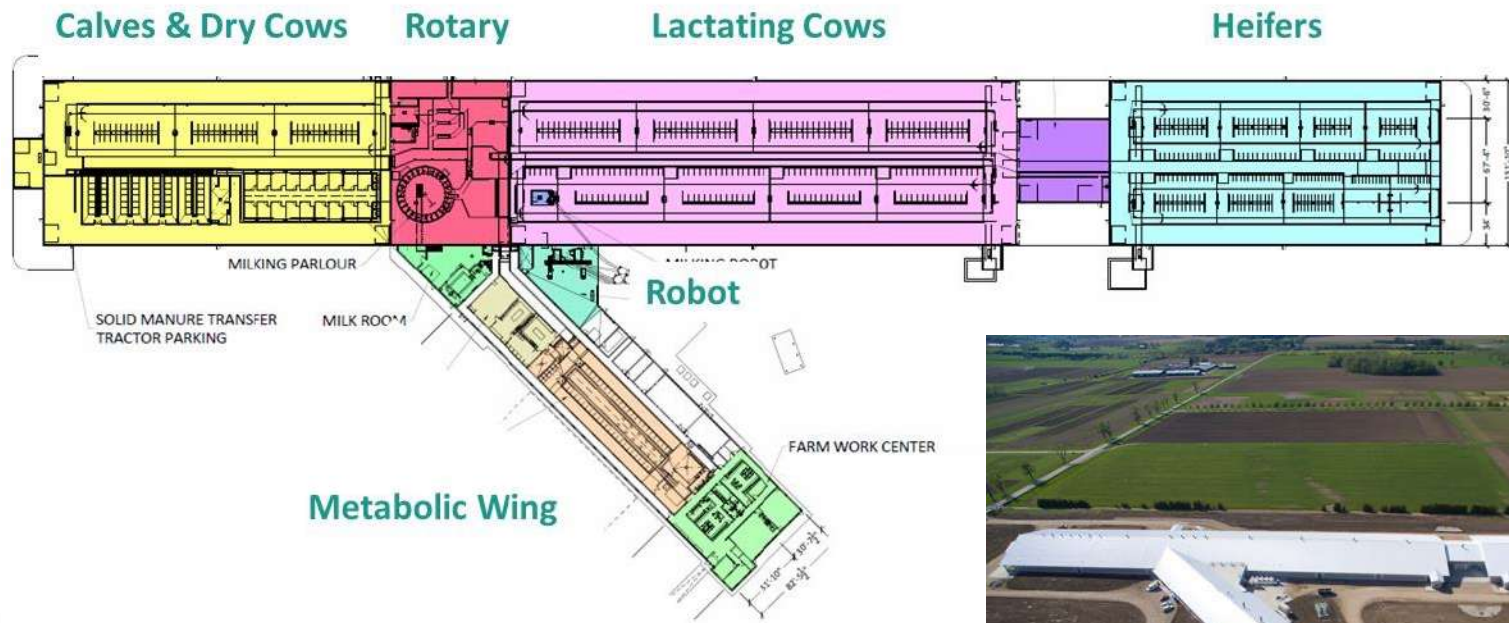
- Collected from the University of Guelph and University of Alberta under three international projects:



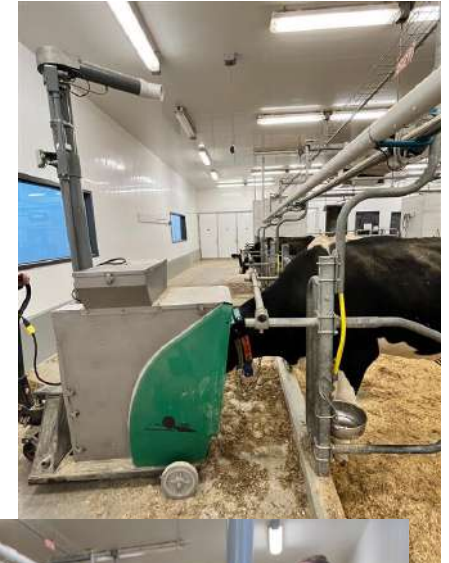
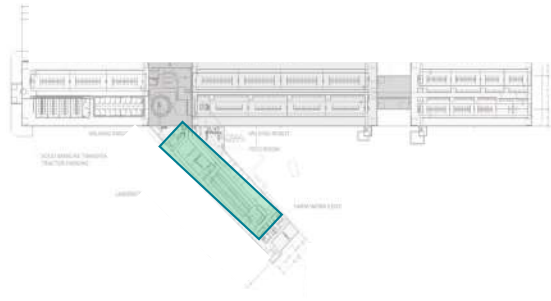
- Using GreenFeed system (C-Lock Inc., Rapid City, SD)



University of Guelph – Elora dairy herd (ODRC)



Elora dairy herd (ODRC) - Metabolic Wing



Methane Recording Protocol

- First parity Holstein cows 120-150 days DIM moved in groups of 2 to 4 into a tie-stall area (Metabolic Wing)
- Cows habituated to the barn and testing protocol for 3 days before test
- Late Friday they enter metabolic wing, adaptation on the weekend, first test day on Monday, last test day on Friday
- 3 times a day (8am, 12pm, 4pm), 10' each for 5 consecutive days
- GreenFeed moved away from animal and allowed to recalibrate for 3 min before testing the next animal
- DHI Test day on Wednesday (milk, fat, protein yield, lactose, BHB, MUN, SCC, MIR)
- Average daily g/d CH₄ production calculated for each animal (weekly average)

Methane Strategy Over Time

2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026

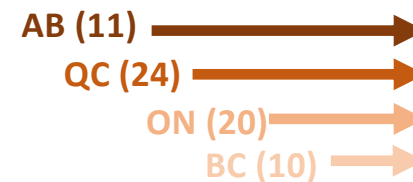
Milk MIR



GreenFeed



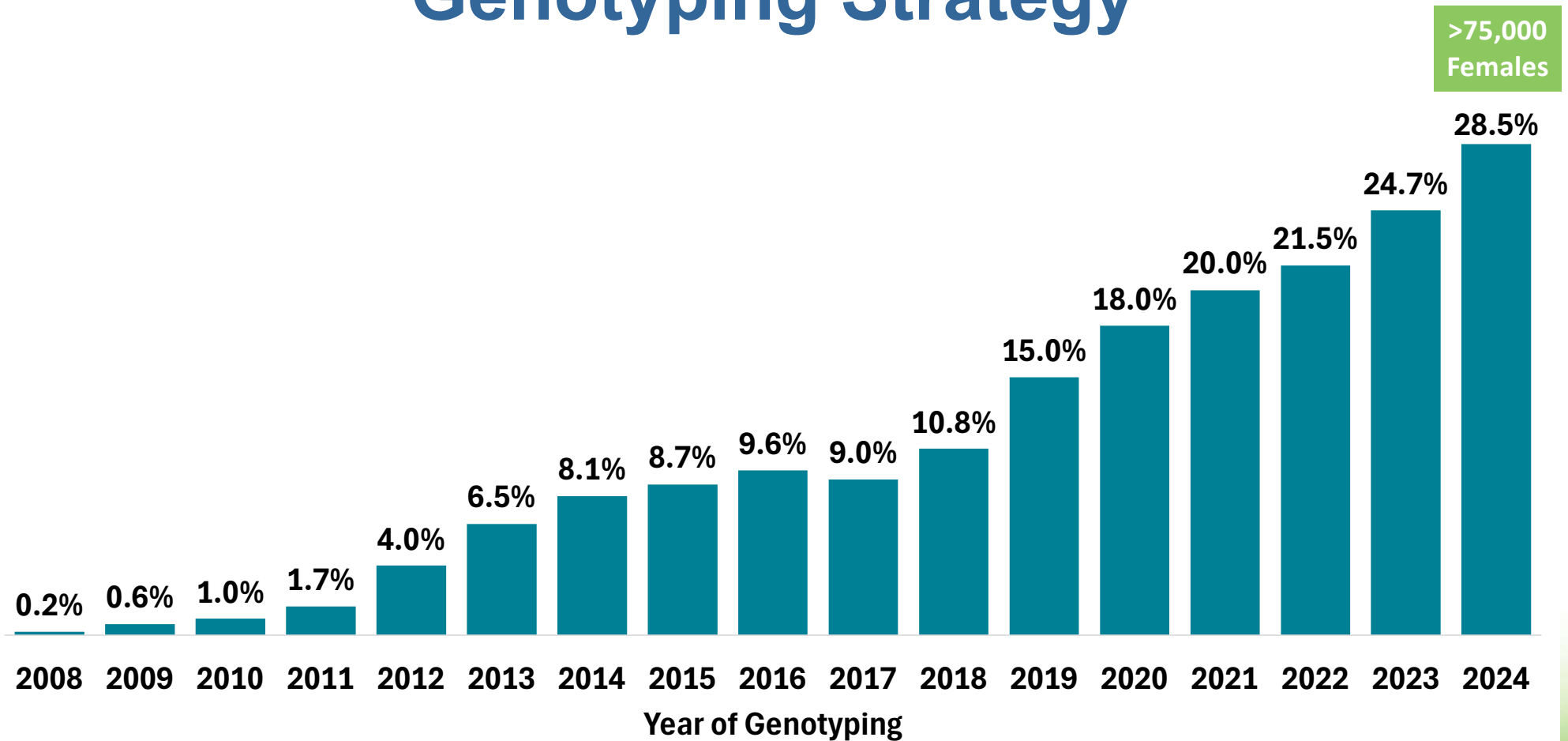
Sniffers



Bulk Tank
Milk MIR



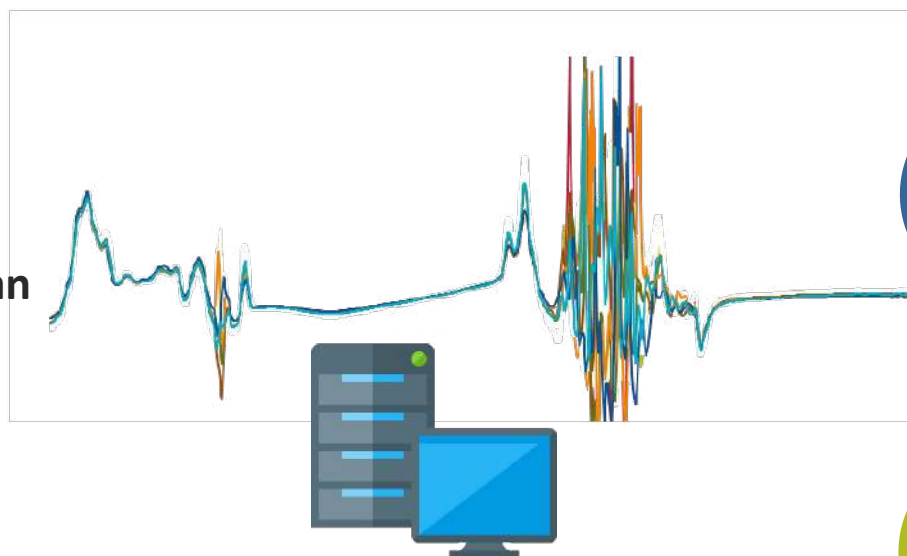
Genotyping Strategy



MIR Data Processing



Individual milk samples
processed by FOSS Milkoscan
FTIR spectrophotometers



Predicting Methane

- MultiLayer Perceptron Artificial Neural Network based on Bayesian regularization model
- 241 MIR spectral datapoints used as input predictors
- Collected average daily methane from 496 cows from two herds between 5-305 DIM

Prediction accuracy of 0.70

Genetic Correlation 0.92 (0.22)



**JDS
Communications®**
TBC; TBC

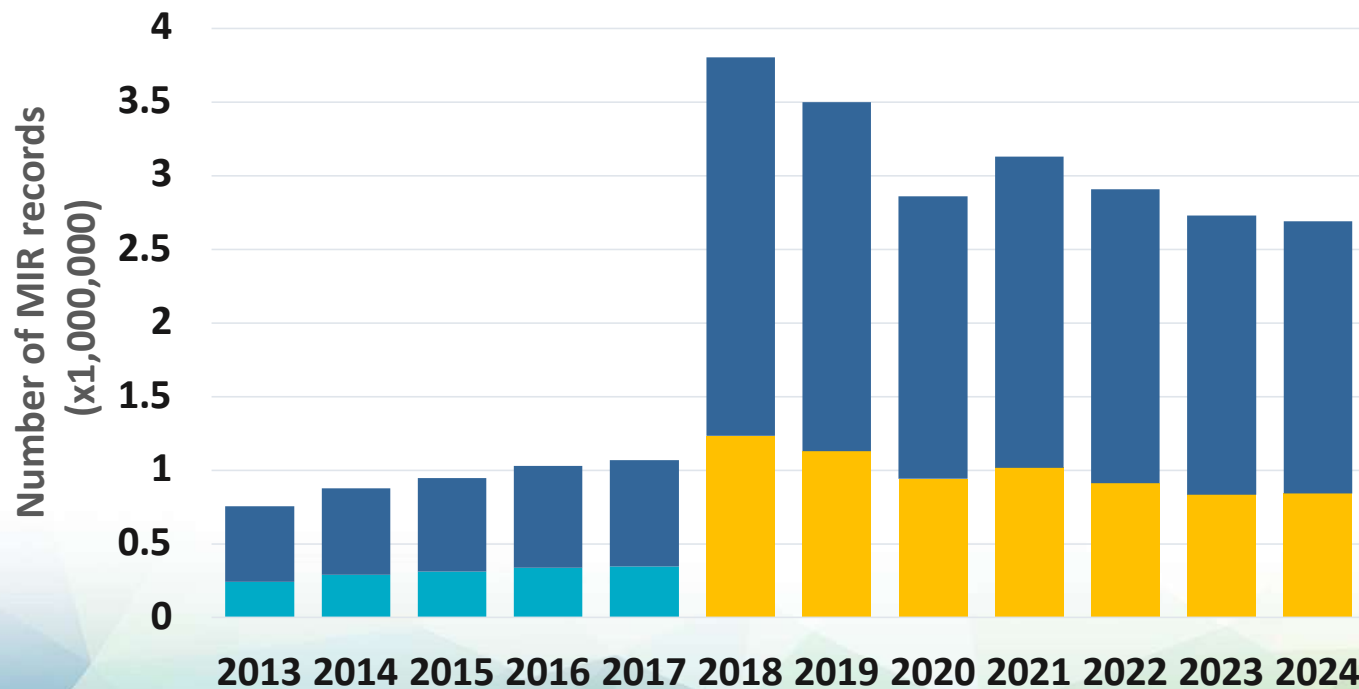
<https://doi.org/10.3168/jdsc.2023-0431>
Symposium Review
Genetics

Symposium Review: Development of genomic evaluation for methane efficiency in Canadian Holsteins

Hinayah R. Oliveira,¹² Hannah Sweett,¹ Saranya Narayana,¹ Allison Fleming,¹ Saeed Shadpour,³ Francesca Malchiodi,³⁴ Janusz Jamrozik,¹³ Gerrit Kistemaker,¹ Peter Sullivan,¹ Flavio Schenkel,³ Dagnachew Hailemariam,² Paul Stothard,² Graham Plastow,² Brian Van Doormaal,¹ Michael Lohuis,⁴ Jay Shannon,⁴ Christine Baes,³⁶ and Filippo Miglior¹³

Apply prediction to MIR population

- Great potential and availability – over **26M** records since 2013
- Milk MIR data on **90% of milk recorded cows** since 2018



≈7.2M records from
1st parity Holsteins
in ~7,500 herds



≈1.7M cows

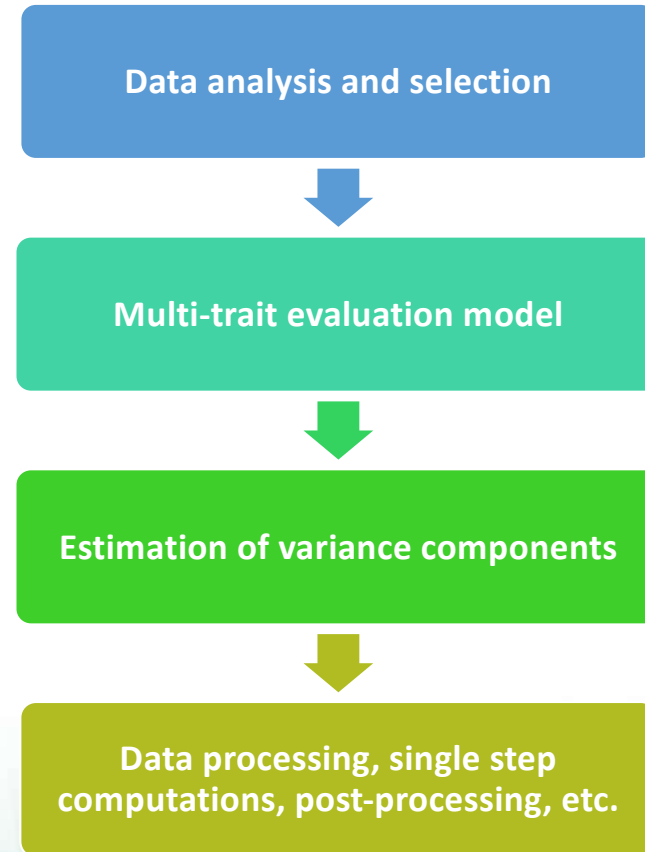


≈215,000
genotyped cows

From research to service mode



Lactanet and Semex collaborated on the development of the prediction and a new, single step genomic evaluation system



Data Used for Genetic Evaluation

- First parity Holsteins from 6,128 herds
- Between 120 and 185 DIM

Records	1,026,133	Genotyped Animals	311,751
Cows	706,775	Genotyped Cows	151,892
Sires	11,491	Genotyped Sires	8,932

*Numbers for December 2024 evaluations

Genomic Evaluation for Methane Efficiency

- **Single-step four-trait repeatability Animal Model (using MiX99)**
 - MIR Predicted Methane (CH_4 , g/d), Milk (kg/d), Fat (kg/d), Protein (kg/d)
 - Fixed: Age at calving, DIM, Year-Season of calving
 - Random: Herd-Test-Date, Permanent Environment, Animal
- **Post-evaluation, Methane Efficiency (ME) is calculated:**
 - Recursive re-parameterization, Jamrozik et al., 2017 JDS <https://doi.org/10.3168/jds.2016-12177>
 - Predicted CH_4 production genetically independent of Milk, Fat and Protein yields via linear regression

Methane Efficiency helps to reduce the methane production of the herd without impacting production levels

Genetic Parameters

	Predicted CH ₄	Milk Yield	Fat Yield	Protein Yield
Predicted CH ₄	0.23	-0.13	0.38	-0.11
Milk Yield	-0.06	0.38	0.48	0.83
Fat Yield	-0.18	0.66	0.27	0.71
Protein Yield	0.01	0.90	0.74	0.28

Heritabilities on diagonal, Genetic correlations above diagonal, Phenotypic correlations below diagonal

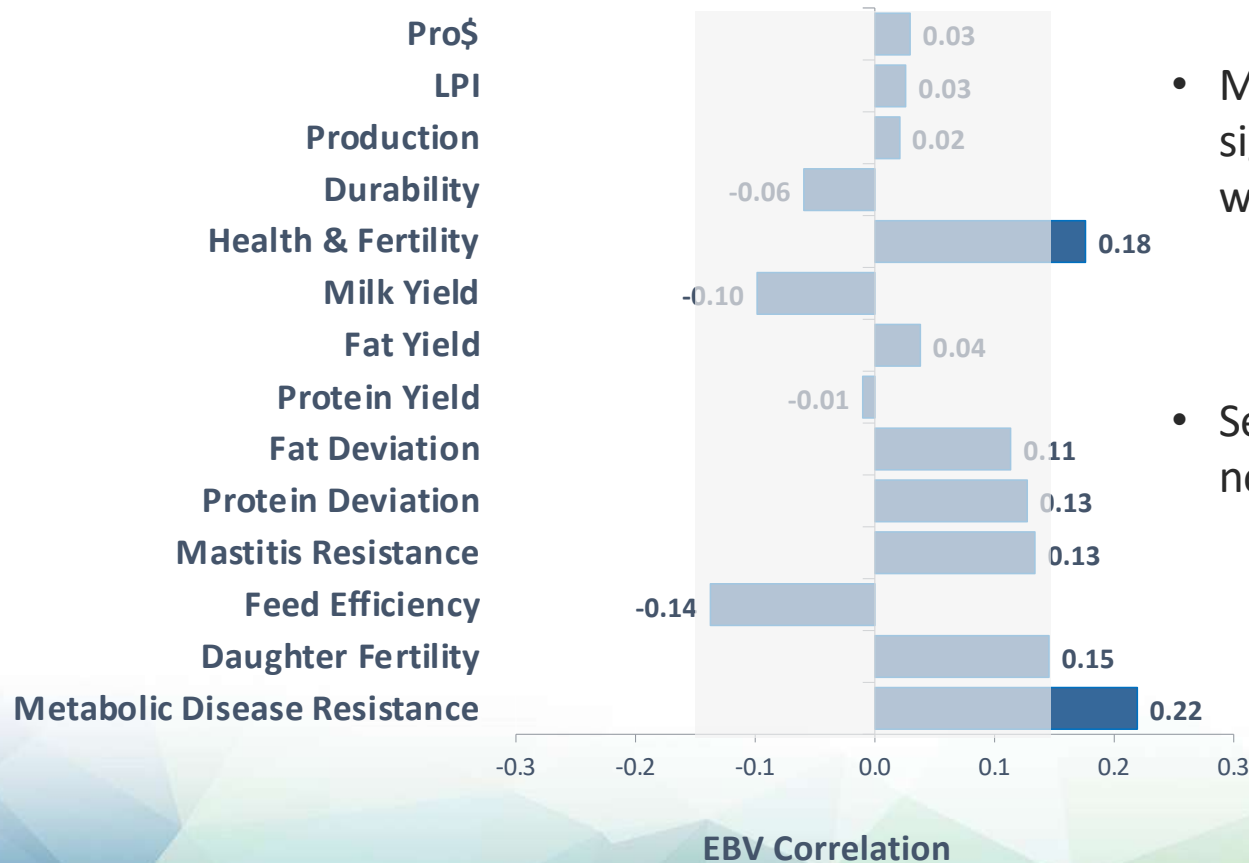
*all approximated SE are <0.033

Methane Efficiency vs Methane Production

- 75% genetic correlation between Methane Efficiency and Methane Production
- Methane Efficiency is not genetically correlated with any production traits

	Milk	Fat	Protein
Methane Production	-0.13	0.38	-0.11
Methane Efficiency	0.00	0.00	0.00

Methane Efficiency is a New Trait



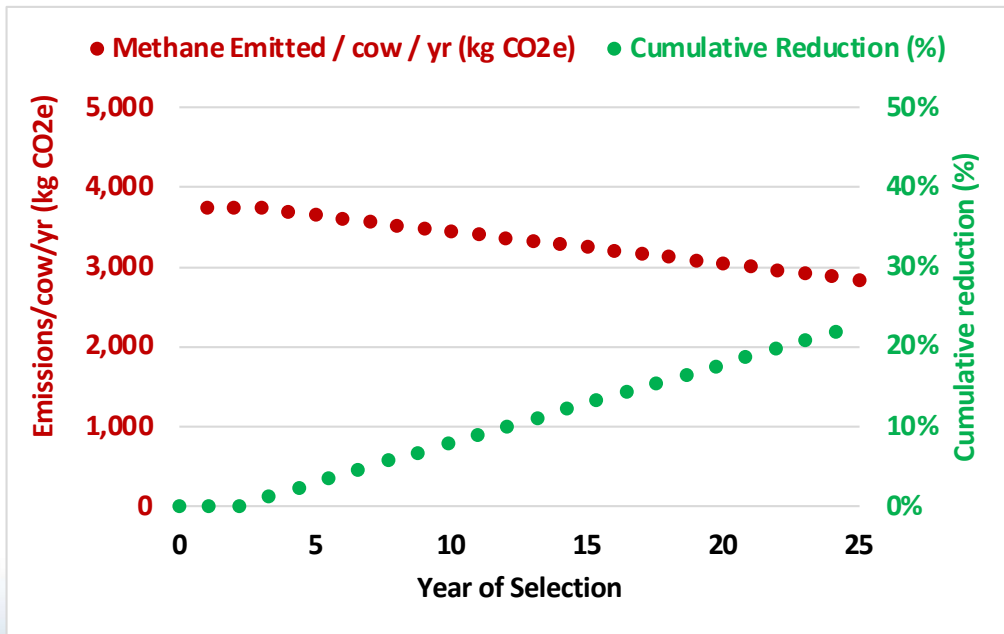
- Methane Efficiency does not have a significant unfavorable correlation with any other evaluated trait
- Selection for Feed Efficiency does not also improve Methane Efficiency
 - Both traits are independent of production yields

Reliability of Methane Efficiency RBV

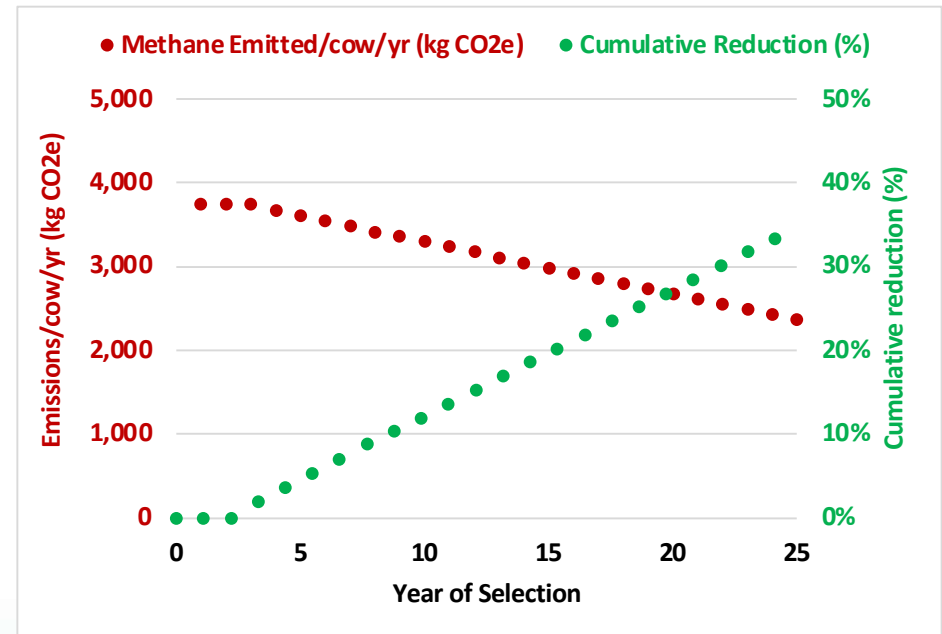
	Reliability
Genotyped cows with data	86.7%
Ungenotyped cows with data	56.3%
Proven bulls	95.9%
Genotyped young bulls	77.7%
Genotyped heifers	72.2%

Genetic progress over time

Bulls > 1 SD



Bulls > 1 SD & Cows > mean



Interpretation

Reduce CH₄ production by selecting for higher Methane Efficiency without impacting production traits

5-point ↑ in a sire's RBV for ME, daughters are expected to produce 3kg less CH₄ per year



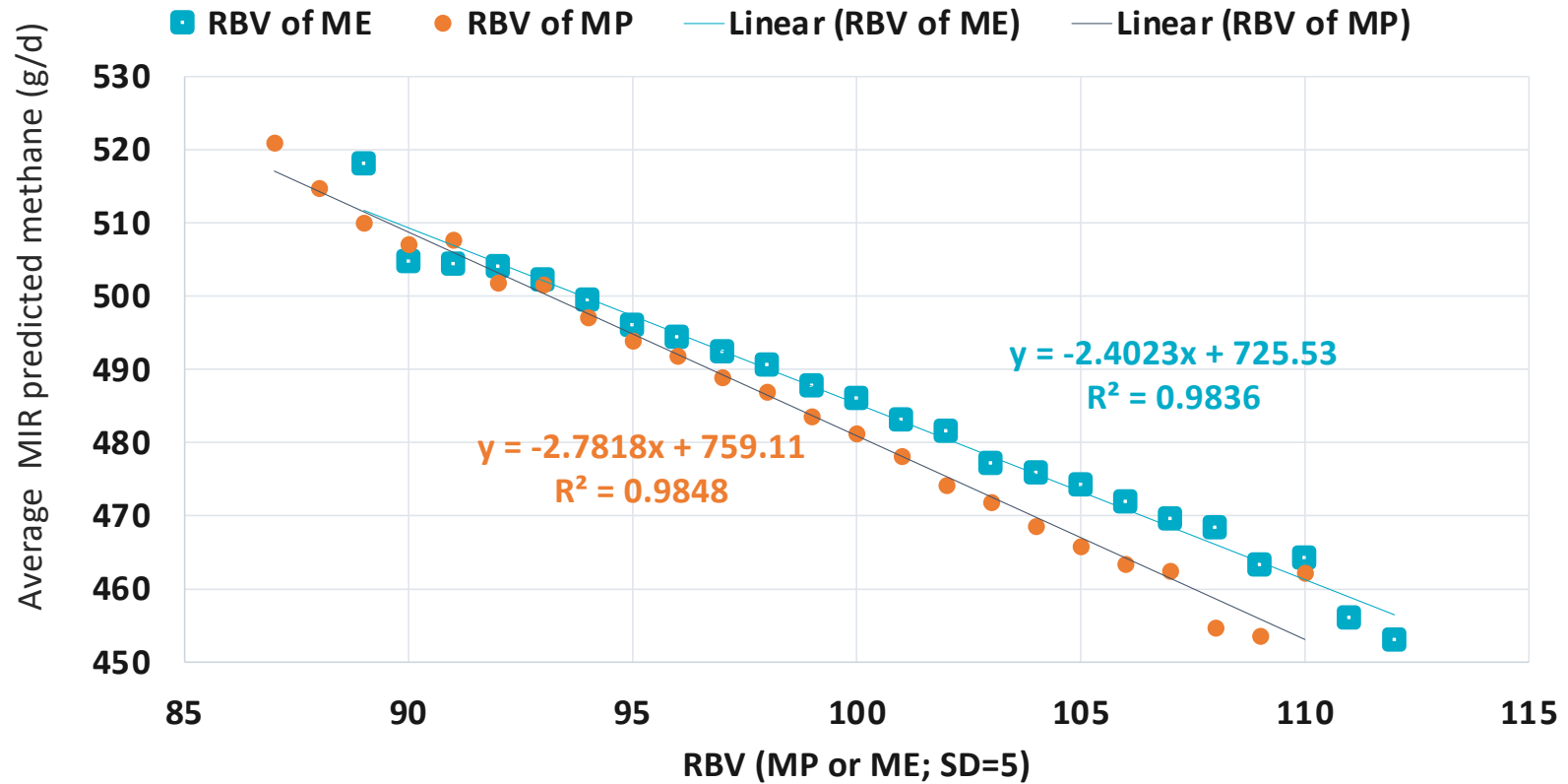
1.5% decrease in CH₄ emissions per cow per year



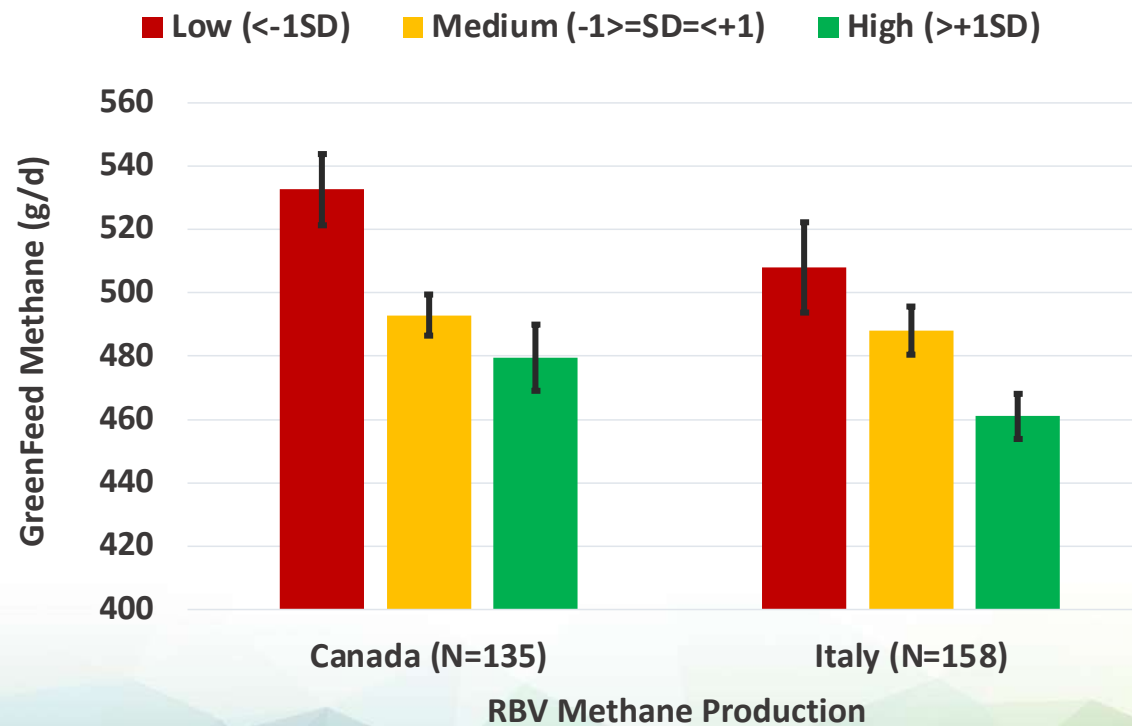
Herd owners selecting for ME can achieve 20-30% reduction in CH₄ emissions from their herd by 2050



GE Validation – MIR predicted methane



GE Validation – GreenFeed Methane



A Team Effort

Allison Fleming
Janusz Jamrozik
Gerrit Kistemaker
Filippo Miglior
Saranya Narayana
Hinayah Oliveira
Hannah Sweett
Brian Van Doormaal



Christine Baes
Flavio Schenkel
Saeed Shadpour
And over 100 grad students and post-docs that every day, three times a day have been collecting CH4 data since 2016



Francesca Malchiodi
Mike Lohuis
Jay Shannon



Dagnachew Hallemariam
Graham Plastow
Paul Stothard

2023 International Dairy Federation Innovation in Climate Action Award



2024 ADSA J.D. Lush Award in Animal Breeding



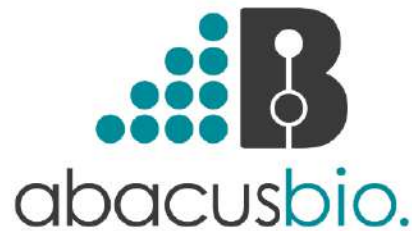
2023 University of Guelph Innovation of the Year Award awarded to team



2025 Genome Canada Genomics Impact Award for Industry Collaboration



Development of GHG index



Breeding for sustainability:
development of an index
to reduce GHG in dairy
cattle

Invited talk at EAAP 2024 – Florence, Italy

2024 Dairy Cattle Industry Forum - Toronto

Caeli Richardson, P. Amer, T. Oliveria, K. Grant J.
Crowley, C. Quinton, A. Fleming, F.M. Miglior
and F. Malchiodi



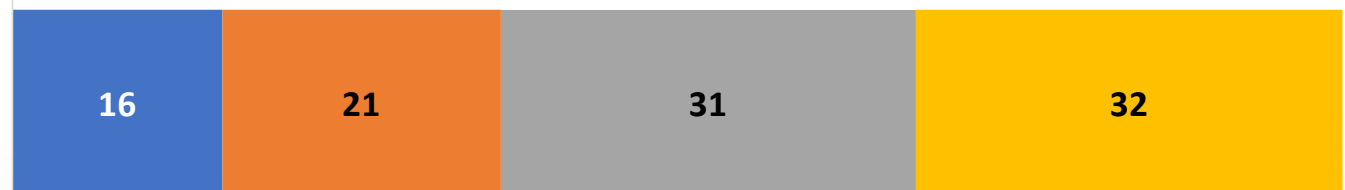
Trait Relative Emphasis in a GHG Index

■ Herd Life ■ Feed Efficiency ■ Methane Efficiency ■ Body Maintenance Requirement

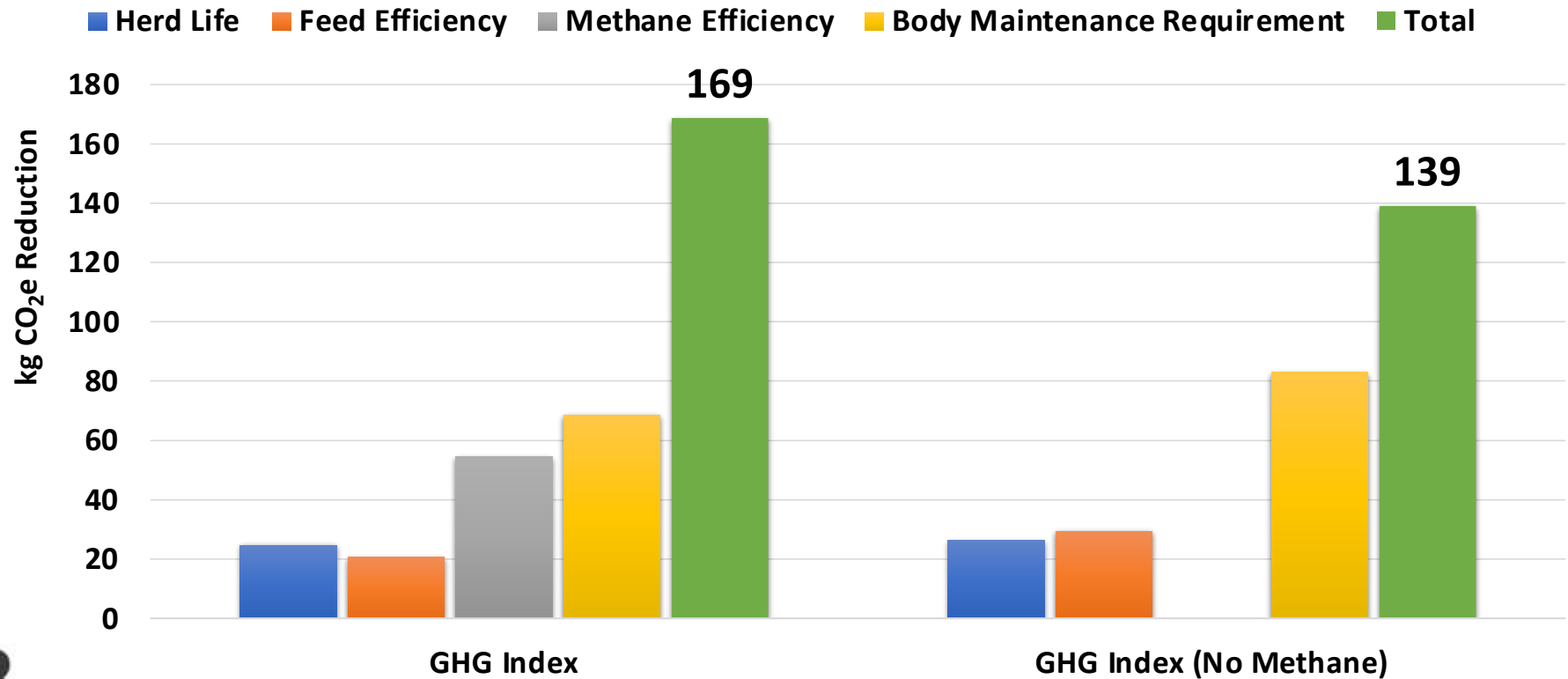
GHG INDEX (NO METHANE)



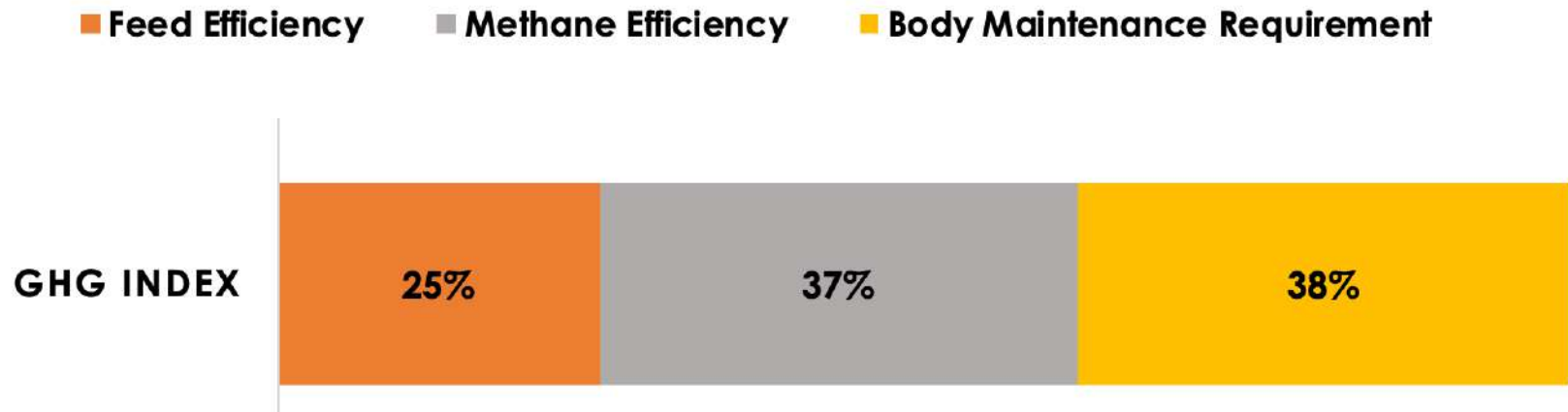
GHG INDEX



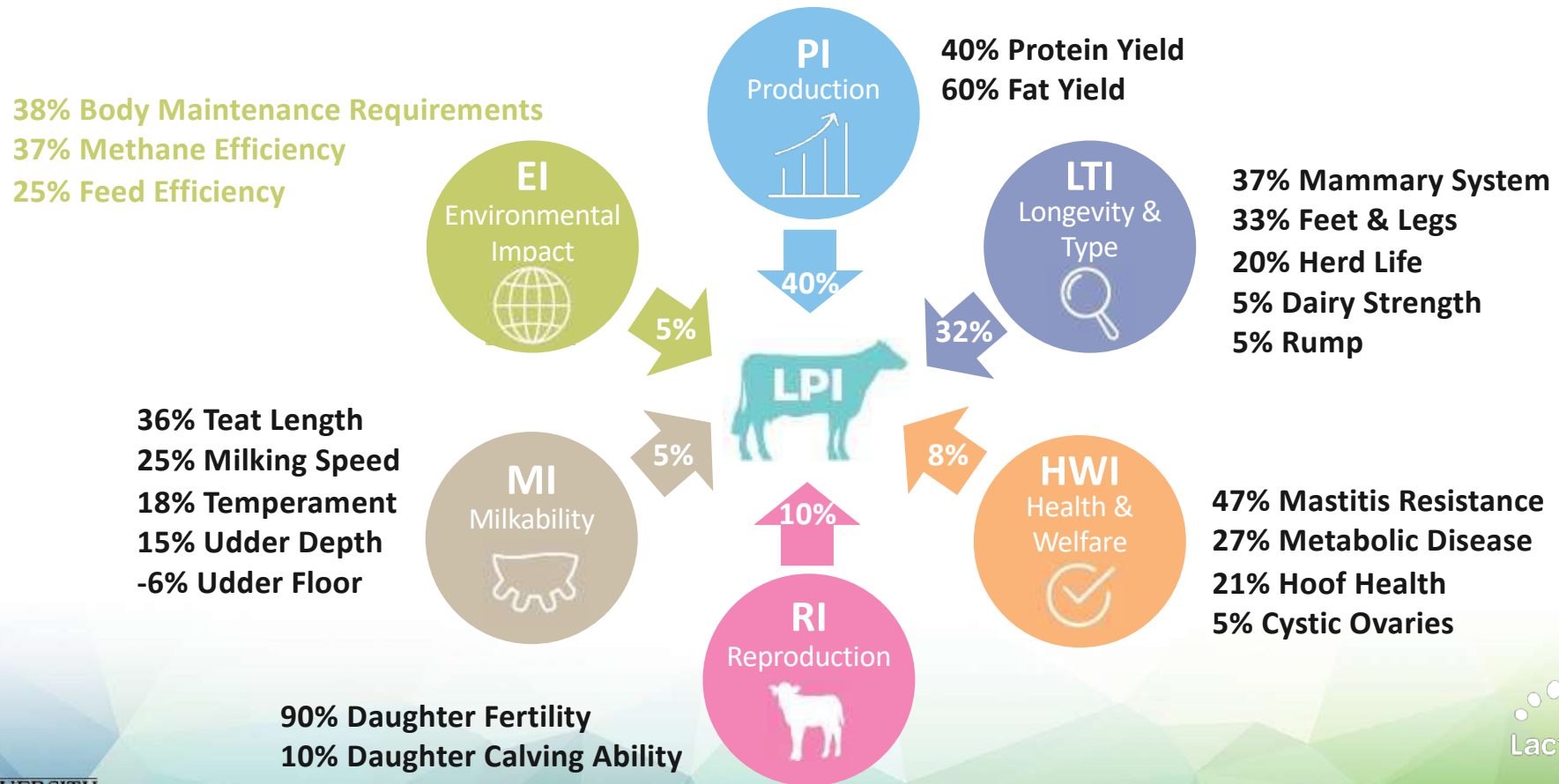
Genetic Gains in GHG Emission Reductions (kg CO₂e)



Trait Relative Emphasis in a GHG Index (w/o Herd Life)



Modernized LPI - April 2025



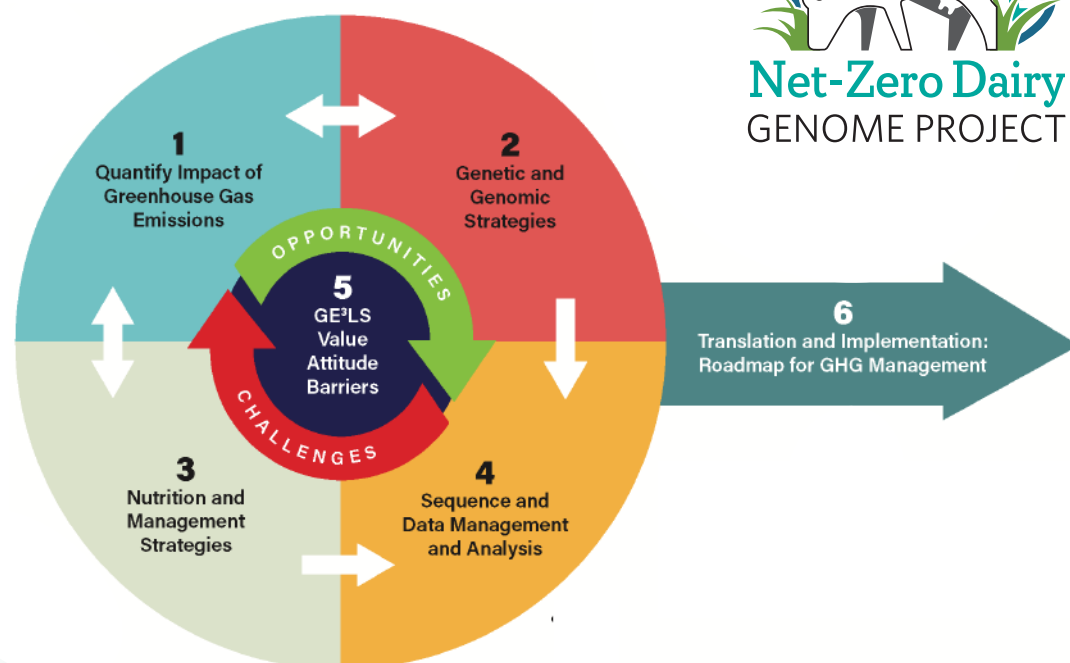


GenomeCanada

Net-zero Dairy Genome Project

GOALS

- Consolidation of existing methane emissions data (including beef)
- Estimate animal and herd-level emissions
- Quantify potential GHG reductions through genetic and nutrition strategies
- Enhance CH₄ genomic evaluations
- Understand public attitudes/behaviours to emissions reductions
- Develop and implement CH₄ herd monitoring and benchmarking tools
- **Develop a roadmap for CH₄ mitigation**

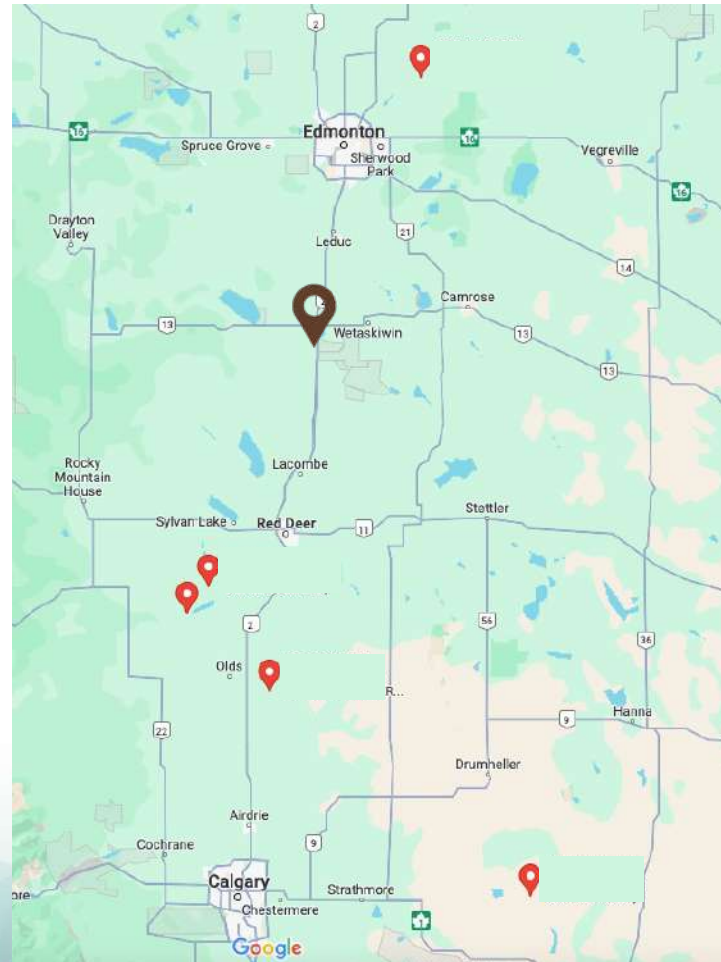


Lactanet

MooLoggers in Alberta - RDAR/Alberta Innovates

5 farms – 11 sniffers

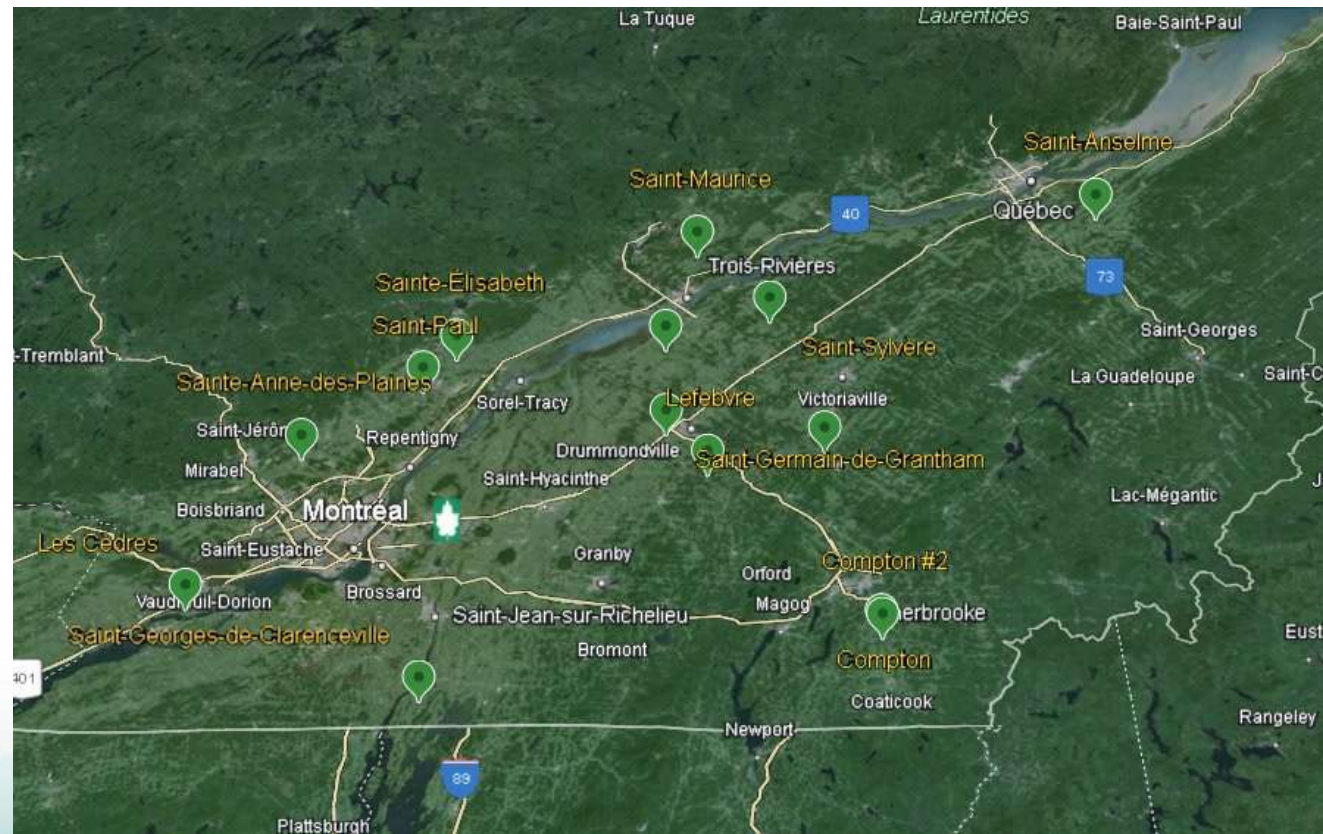
- 2-3 MooLoggers each
- 4 Holstein
- 1 Jersey
- Lely robots



MooLoggers in Quebec – Methane Quebec

14 farms – 24 sniffers

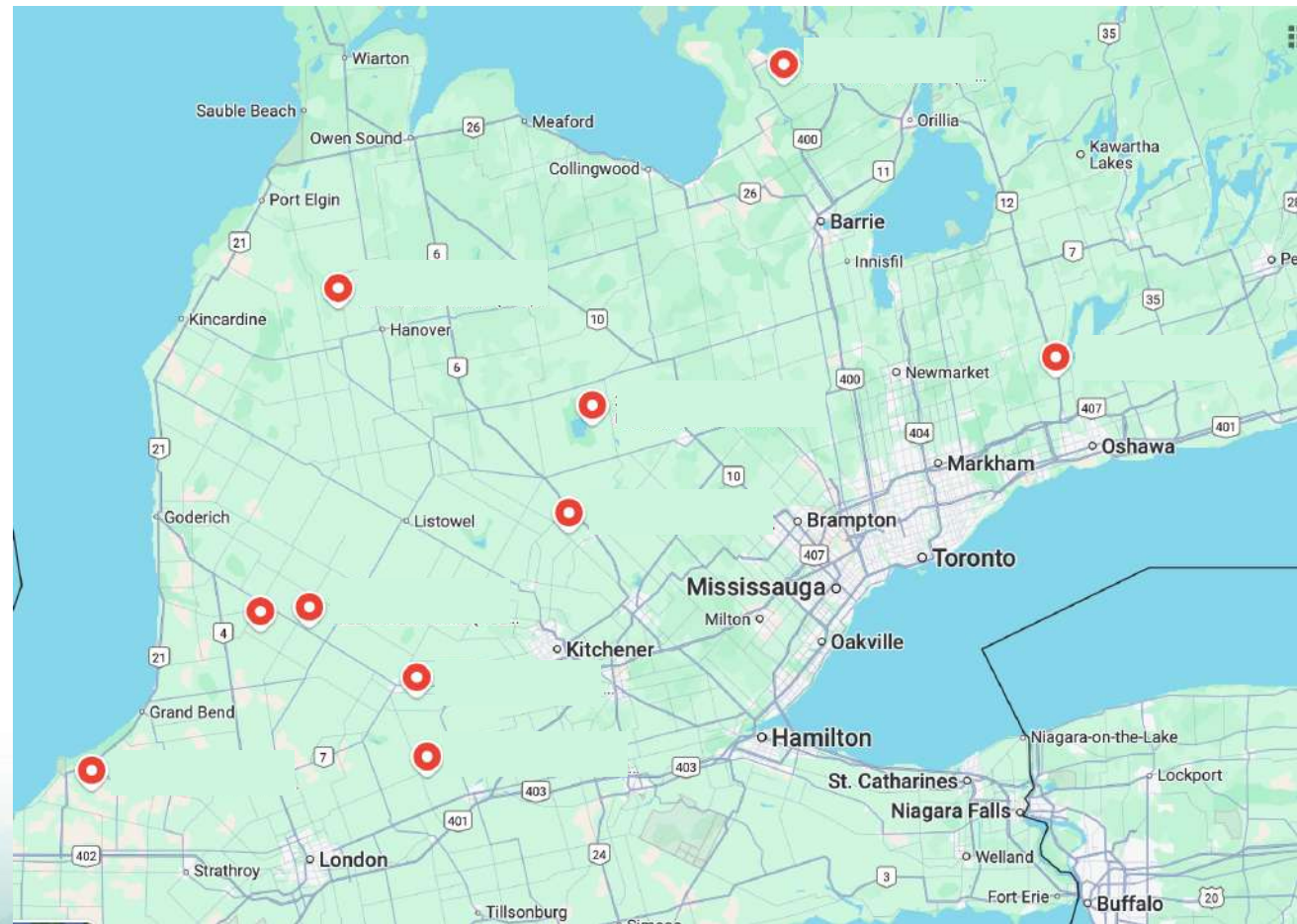
- 1-2 MooLoggers each
- 10 Holstein farms
- 2.5 Jersey farm
- 1.5 Ayrshire farm
- Lely robots



Moologgers in Ontario – NDGP & Dairy Cluster

13 farms – 26 sniffers

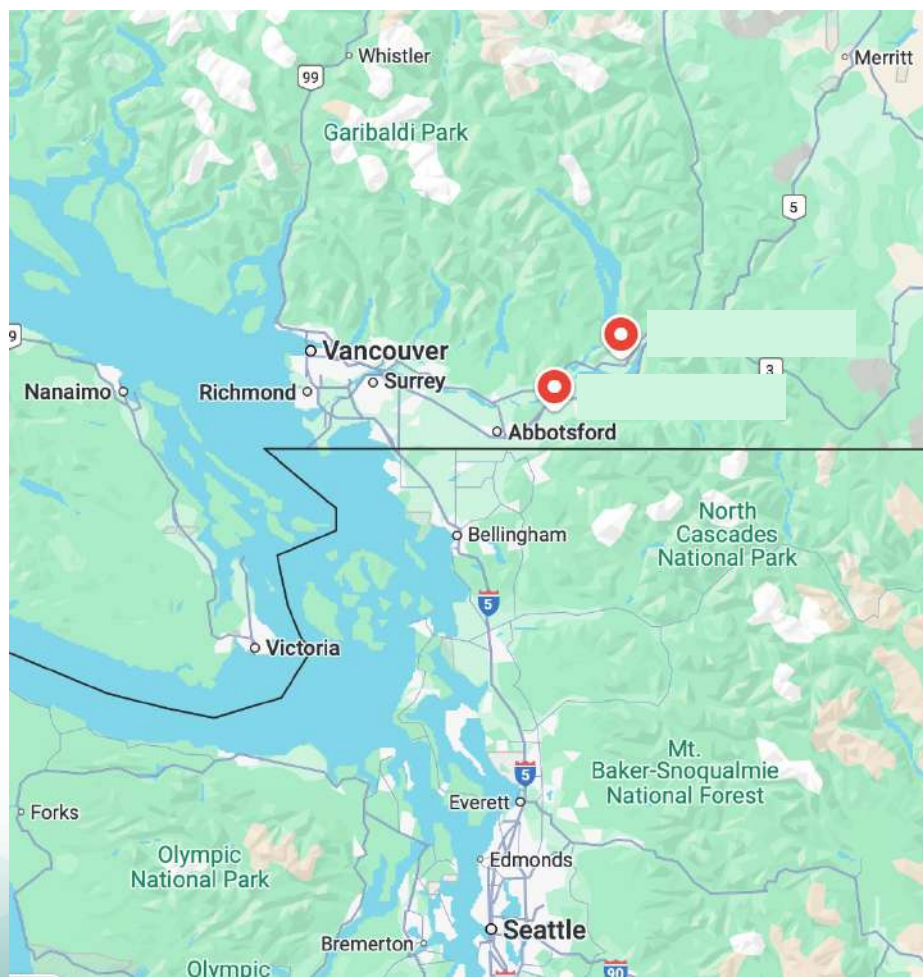
- 2 MooLoggers each
- 7 Holstein farms
- 5 Jersey farm
- 1 Ayrshire farm
- Lely robots



Moologgers in British Columbia – NDGP

2 farms – 10 sniffers

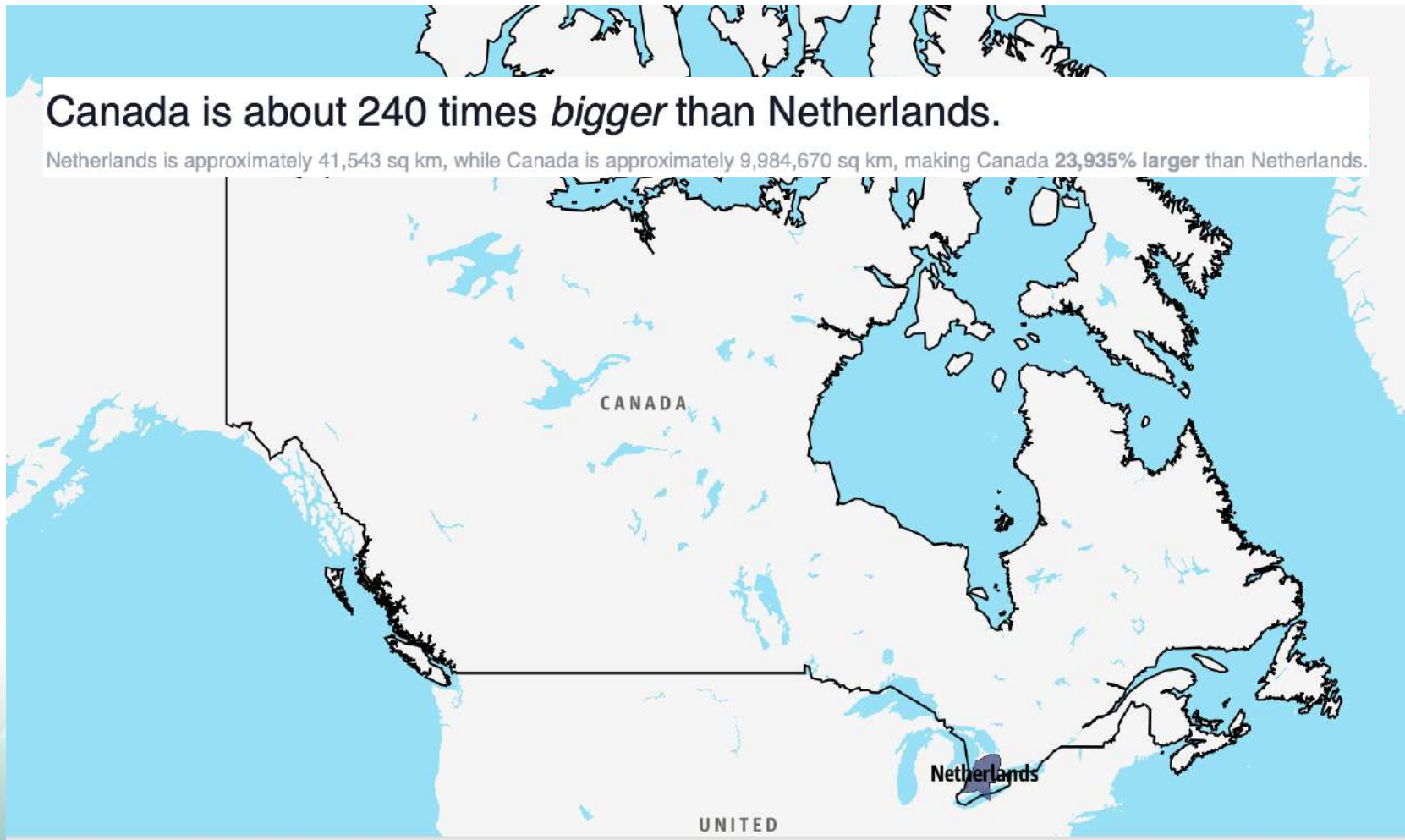
- 4-6 MooLoggers each
- 2 Holstein farms
- Lely robots



Just to put things in perspective ... ☺

Canada is about 240 times *bigger* than Netherlands.

Netherlands is approximately 41,543 sq km, while Canada is approximately 9,984,670 sq km, making Canada 23,935% larger than Netherlands.



Proposals in the Pipeline



Agriculture Funding Consortium - \$1.3M

- Estimate the relationship between adaptability (heat tolerance) and mitigation (methane production)
- Optimize relationships between adaptation and mitigation traits within a genetic breeding strategy
- Quantify risk/benefit associated with breeding for reduced emissions on adaptable and suitable animals for future production systems



GenomeCanada

Agriculture Agri-food Canada Methane Reduction Challenge - \$2 M

- Quantify change in methane production from daughters sired by low emitting bulls
- Validation of ME evaluations by applying ME breeding value predictions to external populations
- Include breeding values in herd calculators and national inventories

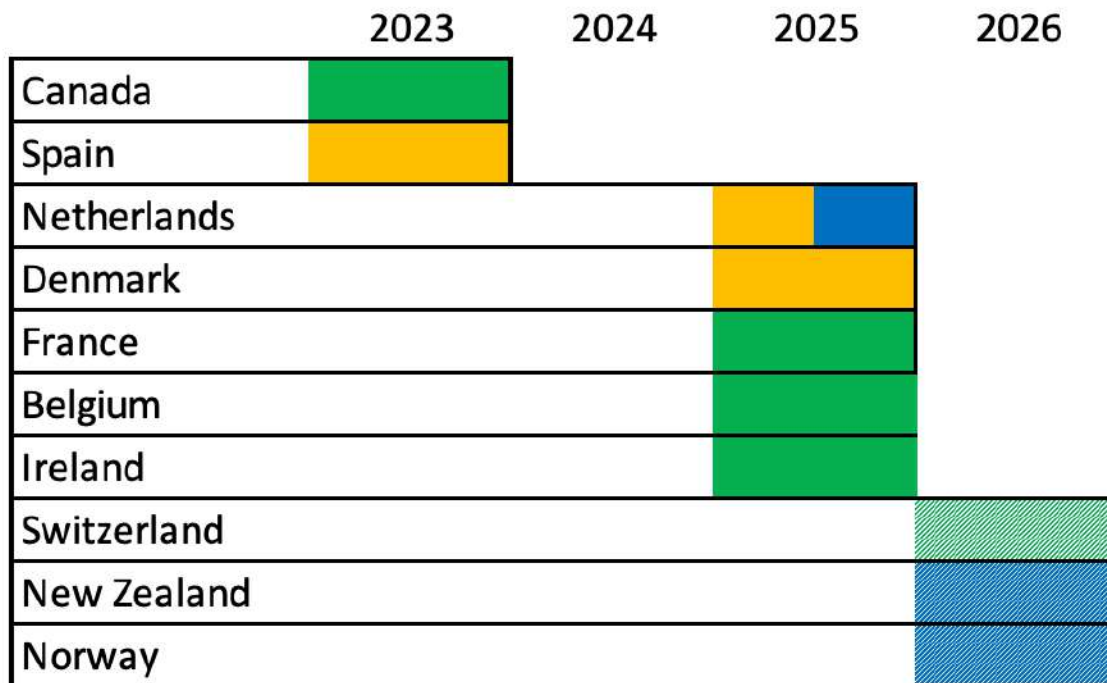


WAGENINGEN
UNIVERSITY & RESEARCH

Global Methane Genetics

- Methane phenotyping and breeding in Jerseys - \$1.7M – 6 sniffers for CAN
- Methane phenotyping and breeding in Ayrshires - \$3.4M – Nordic data to CAN

International Outlook - *Launch Date*



Legend



Acknowledgements

