Dairy Cluster Projects

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Students: Audrey Martin, Kerry Houlahan, Lucas Alcantara, Colin Lynch

Project 1: Main Goals

- Assess the current breeding structure in Canadian dairy cattle (economic and genetic aspects); useful predictions on medium and long-term impacts of the current strategy
- In-depth analysis and prognosis regarding implementation of new methods and technologies
- Recommendations on how to incorporate novel traits in current and new breeding schemes to optimize breeding programs, maximizing genetic gain and ensuring sustainability and genetic diversity

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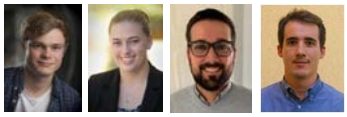
Current Analyses (Project 1)

Assess the current breeding structure in Canadian Dairy Cattle



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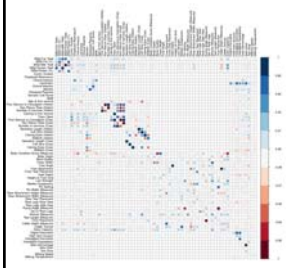
Genetic Parameters



- 67 traits evaluated on heifers and first lactation Canadian Holstein cows
- 500,000 records
- Pedigree: 1980 to 2019
- 2,211 bivariate combinations of traits

Oliveira et al., submitted

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Conclusions

- Estimates required for
  - building new indexes
  - updating existing selection indexes
  - predicting correlated responses due to inclusion of novel traits in the breeding programs

Current Analyses (Project 1)

Assess the effect of synchronized breeding on genetic evaluations of fertility traits in dairy cattle

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Simulation Results

Results:

- All parameters changed unfavorably and proportionally to the increased use of Timed AI
- Long-term effect on genetic trends
- Methods for adjustment should be considered

Conduct analysis with Real Data

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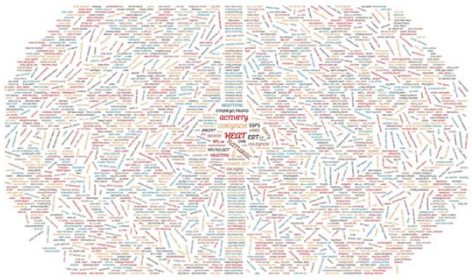
Breeding Protocols



Conclusions

- Standardized measures of recording breeding methods required to improve accuracy and quality of breeding records
- Large re-ranking of bulls when using timed AI records vs Heat detection records, indicates a bias does exist
- Methods to account for this bias to help improve the accuracy of genetic evaluations of fertility traits
- Alternatively, fertility traits split via management technology, (one trait solely uses Timed AI records with the other using heat detection records in a multiple trait analysis

Current Analyses (Project 1)

To assess the changes in genetic parameters for dry matter intake, energy corrected milk and metabolic body weight over a lactation

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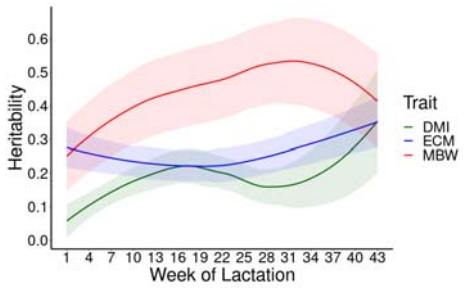
Heritability



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Conclusions

- Genetic variability throughout lactation for traits related to feed efficiency
- Using a model that allows for the dynamic nature of the traits to be considered is important when estimating genetic parameters
- Changes in correlations between weeks of lactation need to be considered when selecting for feed efficiency

Current Analyses (Project 1)

To assess the association of conformation traits with Pro$

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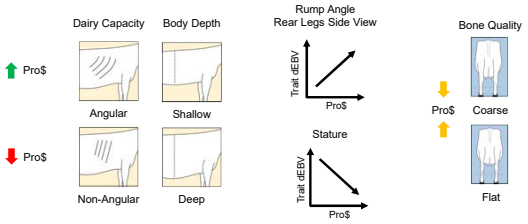
Conclusions

- Type traits explain 65% of variance for Pro$



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Project 2: Main Goals

Designing a reference population to accelerate genetic gains for novel traits in Canadian Holstein

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Current Analyses (Project 2)

- Create an enlarged female reference population for genomic prediction of novel/existent traits with limited EBV accuracy with ssGBLUP
  - 6,300 animals genotyped in 9 months out of 25,000 planned
- Generate tools for maximizing the rate of genetic progress for novel/existent traits with limited EBV accuracy
  - E.g.: Utilizing genomic epistatic effects for fertility/health traits
    - Exploiting the “missing heritability”

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Acknowledgements

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DAIRY RESEARCH CLUSTER 3 GRAPPE RECHERCHE LAITIÈRE 3
Lactanet
DAIRY FARMERS OF CANADA / LES PRODUCTEURS LAITIERS DU CANADA
THE Efficient Dairy GENOME PROJECT
THE Resilient Dairy GENOME PROJECT

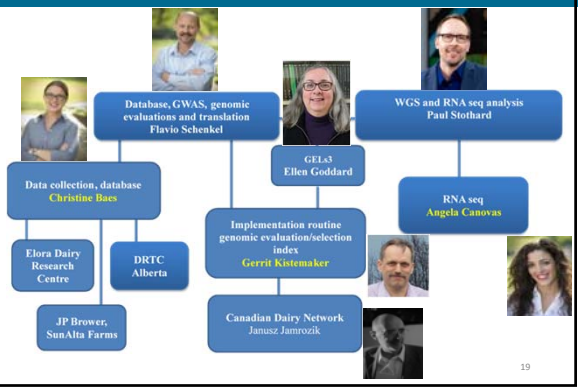
UNIVERSITY OF GUELPH — DEPARTMENT OF ANIMAL BIOSCIENCES — CGIL — DAIRY at GUELPH — THE Efficient Dairy GENOME PROJECT

Efficient Dairy Genome Project
Project Highlights

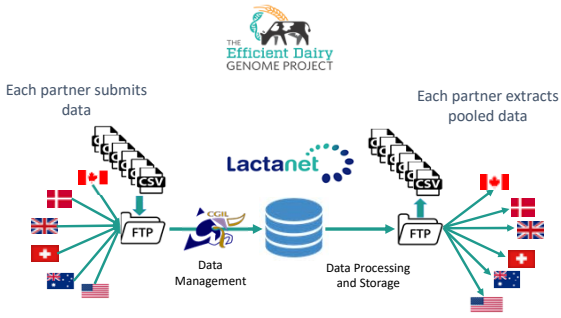
Tatiane Chud

Project leaders : Flavio Schenkel, Paul Stothard, Filippo Miglior

Activities



Database fully functional



Database in numbers

- Pedigree: **22,204** animals
- **1,091,212** DMI records; **5,609** cows
- **352,119** BW records; **4,305** cows
- **381,313** ECM records; **7,018** cows
- **14,059** ME records; **1,433** cows
- **5,139** animals genotyped
- **93,654** milk MIR spectra records; **2,128** cows

The EDGP database will continue grow via the RDGP.

Sequencing and variant discovery

- 55 animals whole genome sequenced.
- Novel CNV and SNP/Indels were identified.
- Several software pipelines to process sequence data and SNP chips were developed.

RNA-Seq and functional studies

- 55 cows (24 high RFI and 31 low RFI) were RNA sequenced.

RNA-Seq analysis on milk somatic cells will be used to identify differentially expressed genes (DEG) and causal variants between high and low RFI dairy cows.

Genetic evaluation for FE

- Improve FE not simply reduce feed intake.
- Need to take into account energy required:
  - **Maintenance**
    - MBW= (Body Weight)$^{0.75}$
  - **Production**
    - ECM = (0.25 x Milk) + (12.2 x Fat) + (7.7 x Protein)
- Minimize reduction in feed intake in early lactation when animals usually have a negative energy balance.
- Using both national and International datasets.

Genetic evaluation for FE – April 2021

- Single-Step genomic evaluation.
- A recursive model for estimating **EBV for residual feed intake.**
- The model for FE defines three traits:
  - DMI
  - ECM
  - MBW
- Two lactation periods: 5-60 days and 61-305 days in milk.

(Chud et al., 2019; Jamrozik & Kistemaker 2019)

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Methane emissions – Canadian data

- Need more data → MIR predictions.
- Milk MIR spectra used to predict weekly ME (r≈ 0.70). – (Shadpour et al. 2020. JDS. In preparation)
- Heritability of predicted weekly ME = 0.20.
- Residual methane production is been investigated as an alternative trait using recursive models.

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GE^{3}LS research

A positive willingness to pay (WTP) for increased FE exists, but with a WTP ~ zero for reduced ME. There is additional value from a ME trait when it is offered as a bundle with a FE trait.

(Jones, K. 2018. MSc Thesis)

Use of genomic technologies to select for FE and reduced ME is likely to be profitable, risks of negative returns can be substantially reduced when predictive accuracy is > 0.40.

(Worden and Hailu. 2020. Agricultural Systems)

Current levels of prediction accuracy for FE are >> 0.40, given confidence in the adoption of genomic evaluation for FE.

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Ongoing studies at CGIL EDGP + RDGP

- Collar rumination records and their association with FE and ME.
- Copy number variants as a new source of genomic markers.
- Feasibility of MIR predicted ME for large scale genetic evaluation for ME.
- Integration of other omics information into the genomic evaluation for FE.

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Project in numbers

Publications	
Papers	16
Theses	8
Seminar/Conferences	40
Outreach/Media	63
Invited Presentations	6
HQP	
MSc students	6
PhD students	4
Post-docs	9
Research Assistants	5
Undergrad students	59

New Collaborations	
Projects	3
Other	2
Main awards	
Research members of project	6

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Final Remarks

The EDGP project ended with lasting impact on:

- **Dairy industry**: Timely genetic evaluation for FE, possibility to evaluate/monitor ME, and foundation for future collaborations.
- **HQP formation**: Many people finished and several will conclude their programs in the future.
- **Research**: Database created the basis for future research and collaborations.

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Lactanet Open Industry Days
18-19 February 2021

THE Resilient Dairy GENOME PROJECT

Integrating genomic approaches to improve dairy cattle resilience:

A comprehensive goal to enhance diary industry sustainability

Christine Baes[1], Ronaldo Cerri[2], Marc-Andre Sirard[3], Paul Stothard[4]

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[3]Université Laval; [4]University of Alberta

UNIVERSITY of GUELPH

DAIRY at GUELPH

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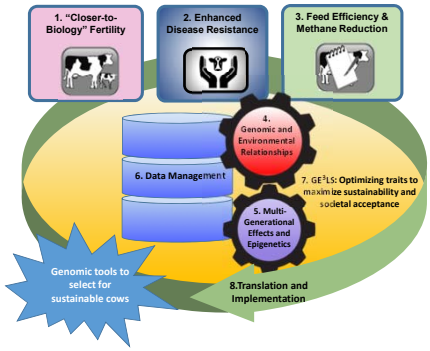
The Projects

THE Efficient Dairy GENOME PROJECT

THE Resilient Dairy GENOME PROJECT

Genomic evaluation for resilience in dairy cows: 2023

The approach



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'Closer-to-biology' fertility

1. "Closer-to-Biology" Fertility

THE UNIVERSITY OF BRITISH COLUMBIA

- Standardized phenotypes based on automated sensors
- Physiological factors affecting estrous expression and embryo survival
- Genomic markers of estrus expression and fertility

Enhanced disease resistance

2. Enhanced Disease Resistance

UNIVERSITY of GUELPH

Fertility disorders in routine genomic analyses (Lactanet, Dec 2020)

Routine phenotyping for Johne's disease

Routine phenotyping for calf health

Routine phenotyping for Leukosis

Enhanced disease resistance - Studies

- The effect of the interleukin-10 receptor alpha gene on bovine mammary epithelial cells infected with Johne's
- Genomic Evaluation for Bovine Leukosis in Canadian Dairy Cattle
- Standardizing calf health recording on Canadian dairy farms
- Development of a Canadian calf heath index to improve overall dairy cow resilience


Aisha Fong


Renee Bongers


Emma Hyland


Colin Lynch

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Feed efficiency and methane emissions

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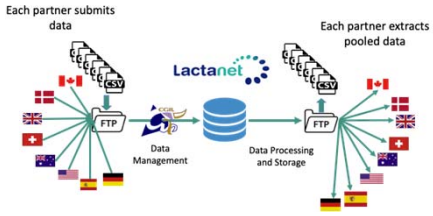
Lactanet


- Enlarging the reference population for
  - feed efficiency by +14,297 animals
  - methane emissions by +6,689 animals

See partnerships!

Database for FE and ME

THE Efficient Dairy GENOME PROJECT
THE Resilient Dairy GENOME PROJECT



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Feed efficiency and methane emissions

- Estimation of genetic parameters for feed efficiency traits (random regression)
- Correlations between FE traits and current traits
- GWAS analysis to identify candidate genes associated with feed efficiency and methane traits
- Assessment of methane emission traits in Canadian Holstein cows
- Phenotypic and genetic analysis of rumination pattern and its relationship with feed efficiency and methane emissions


Stephanie Kamalanathan


Kerry Houlahan


Lucas Lopes


Dr. Tatiane Chud

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Genomic and environmental relationships

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- Genetic parameters and prediction of EBVs of resilience traits
- Multi-trait GWAS and meta-analysis to identify genomic regions with pleiotropic effects on resilience traits

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Genomic and environmental relationships

- Investigate the effects of heat stress on important traits in Canadian Holstein cattle
- Improving knowledge and genomic predictions for resilience indicator traits using copy number variants in dairy cattle


Ivan Campos


Dr. Hinayah Oliveira

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Multi-generational effects and epigenetics

UNIVERSITÉ LAVAL

- Quantify effect of early environment (i.e,. cow's production) on resilience of daughters
- Survey for epigenetic signature on precisely phenotyped animals

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Data management

- Management of project database
- Whole-genome sequence data analysis for variants, genotypes, functional annotations
- Genome browser integration of GWAS findings, epigenetic signatures, & annotated sequence variation

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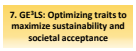
GE3Ls: sustainability and social acceptance



- Farm level decisions about tradeoffs between traits
- Farm level outcomes from selection of resilience traits
- Market level outcomes from selection of resilience traits
- Public acceptance of dairy under different breeding strategies

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Translation and Implementation

- Farm level decisions about tradeoffs between traits
- Farm level outcomes from selection of resilience traits
- Market level outcomes from selection of resilience traits
- Public acceptance of dairy under different breeding strategies
- Transparent and economically-based weighting of traits

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National and international partnerships

Team

Project leaders and Activity leaders

Dr. Christine Baes, Dr. Paul Stothard, Dr. Ronaldo Cerri, Dr. Marc-André Sirard

Dr. Flavio Schenkel, Dr. Ellen Goddard, Dr. Gerrit Kistemaker

Project Managers

Mary De Pauw

Dr. Nienke van Staaveren

More Information: **http://www.resilientdairy.ca/**

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