Enhancing the Data Pipeline for Novel Traits in the Genomic Era: From farms to DHI to evaluation centres

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Importance of data

- Collection of data once and accurately
- Data in one centralized system
- Share of data with all stakeholders automatically
- Data are then processed for
  - Herd Management & Benchmarking
  - Genetic & Genomic evaluation
  - Research

Who collects the data on farm

	Data Centralized
Milk Recording Agencies (DHI)	✔
Breed Associations	✔
AI Organizations	✔
Veterinarians	some sharing
Hoof Trimmers	some sharing
Research Projects	rarely
Manufacturers	some sharing

Traditional Selection

- Sophisticated statistical methods are used to predict the genetic merit of individuals
  - Information from daughters, parents and other relatives
  - Genetic and environmental effects well separated
- Their application has been very successful in dairy cattle for the improvement of easily measured traits
- The success of this approach is mainly due to the feasibility of recording traits from thousands of herds across the country

New phenotypes: Novel traits

- However, this strategy is not feasible for traits that are costly to measure
- The advent of genomics provides an exceptional opportunity to genetically improve the national herd for those traits that are more costly to record
- What is a novel trait?
  - A trait that was not recorded or used in genetic evaluation before

New Data Pipelines for Novel Traits

- Health – 40% of producers **2007**
  - 8 diseases
  - Milk BHB (since **2014**)
- Milk MIR spectral data – <20% of milk vials **2013**
  - Currently two lines of FOSS spectrometers
  - All 12 FOSS lines by early 2017 – 100% of milk vials
- Hoof health **2016**
  - Hoof trimmers – currently ~35 trimmers
- Feed intake and methane emissions **2018**
  - Over 10,000 cows internationally – in progress

Systematic Health Recording

- Canada: health recording system since April 2007
  - Voluntary Recording done by producers or veterinarians
- Producers provided with disease definitions for identification and recording of the diseases
- Data collected by milk recording technicians at each test day herd visit and forwarded to the DHI
- Eight diseases are recorded:
  - **mastitis, displaced abomasum, ketosis, milk fever, retained placenta, metritis, cystic ovaries and lameness**

Index for Mastitis Resistance

- Multiple-trait evaluation including mastitis and well correlated predictors with higher heritability
  - Patterns of SCS, BCS, Udder Depth and Fore Udder
  - Increase of +30 points in reliability of EBV
- Since Aug 2014, Index for Mastitis Resistance (MR)
  - 33% CM-First + 33% CM-Later + 33% SCS
- Genomics
  - Holsteins: 2,800 reference bulls
  - Increase in reliability of +16 points for young bulls, and +8 for proven bulls

Metabolic Diseases - Evaluation

First parity cows – 2nd parity cows and later

Metabolic disease traits (5-100 DIM)

- Clinical Ketosis (**CK**) and Displaced Abomasum (**DA**)

Sub-clinical Ketosis (SCK) (5-45 DIM)

- Milk β-hydroxybutyrate (**BHB**)

Milk recording predictor traits: (5-45 DIM)

- Fat to Protein Ratio (**F:P**)

First parity cows

Conformation indicator traits

- Body Condition Score (**BCS**)

Index for Metabolic Diseases Resistance

MDR = 50% SCK + 25% CK + 25% DA

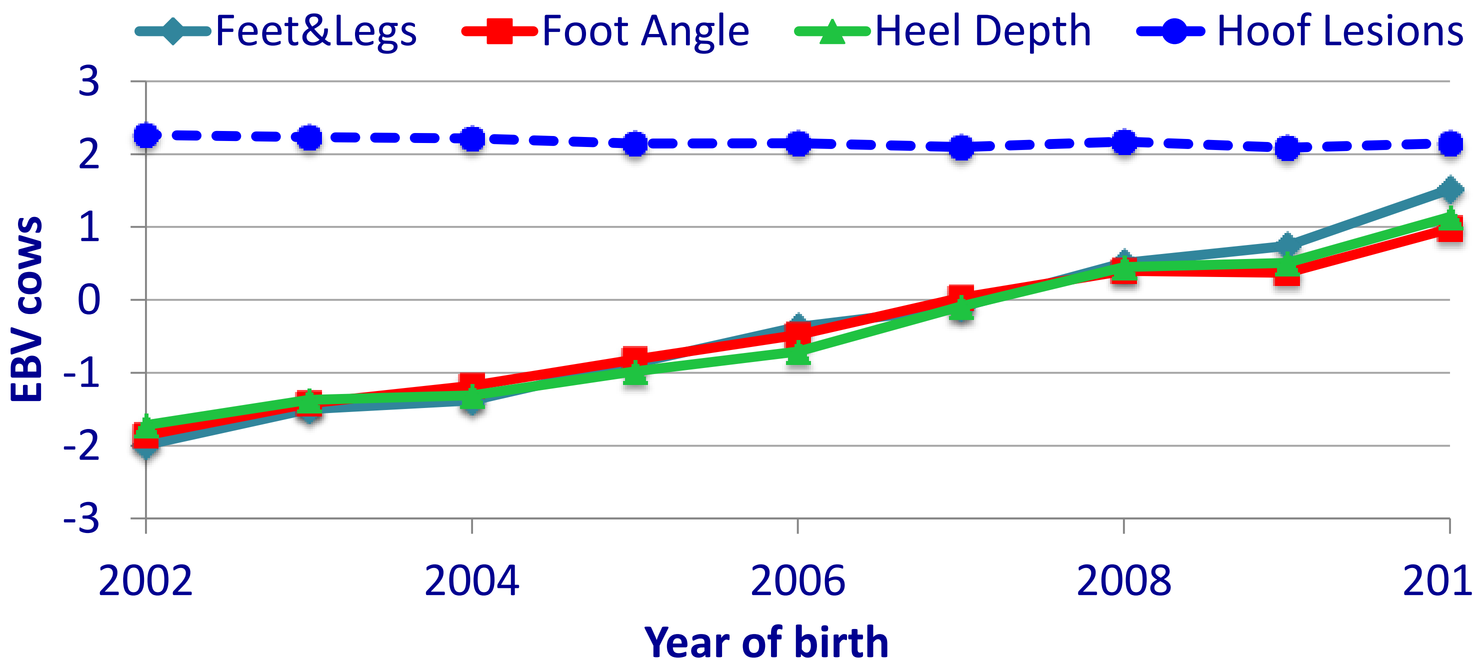
- All components: 50% EBV_1 + 50% EBV_{2+}
- Rational for above weightings
  - Higher frequency and cost of CK compared to DA
  - However, sub-clinical ketosis (SCK) more common than CK
  - Selection on SCK will induce a correlated response on CK and DA (genetic correlations)
  - Higher heritability of SCK
  - Quantity and quality of BHB records might be superior to producer-recorder health data

Next … Fertility Disorders

- Direct traits
  - Metritis (MET), Retained Placenta (RPL), Cystic Ovaries (COV)
- Predictor traits
  - None identified so far
  - Fatty Acids currently investigated
- Six EBV to be considered in the FDR index
  - Metritis (producer recorded) for first and later parities
  - Retained Placenta (producer recorded) for first and later parities
  - Cystic Ovaries (producer recorded) for first and later parities
- **FDR** index = 33%% MET + 33% RP + 33% COV
  - EBV are the average of the first and later lactation EBV of each trait

Hoof Lesions

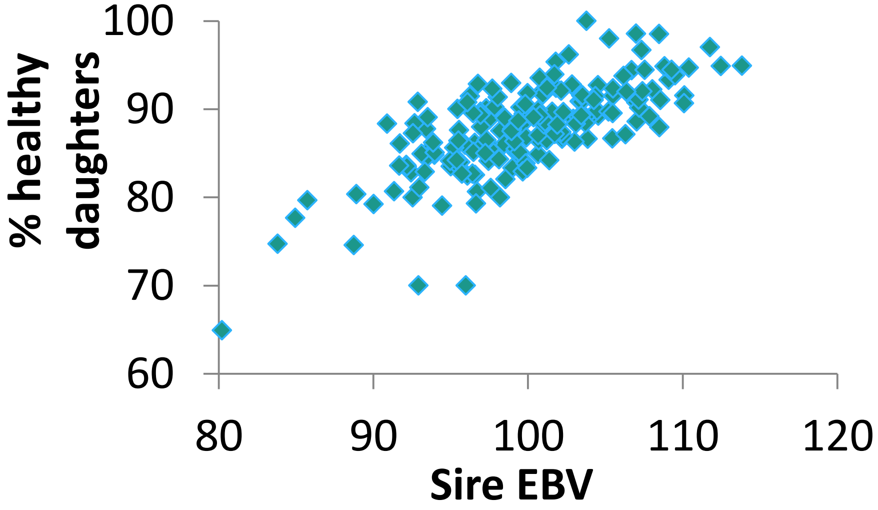
- Selection for feet and leg type traits has not resulted in any decrease of hoof lesions



New Data Pipeline

- From hoof trimmer tablets to DHI, and to CDN
- Pipeline tested with Quebec hoof trimmers
- Over 40 trimmers have been recruited
- We estimate to get 10-20% of milk recorded cows

Traits	%	h^2
Digital Dermatitis	14.0	0.05
Interdigital Dermatitis	1.3	0.01
Interdigital Hyperplasia	1.4	0.03
Sole Hemorrhage	3.4	0.01
Sole Ulcer	4.9	0.03
Toe Ulcer	1.1	0.01
White Line	3.8	0.01



Hoof Health Evaluations

- Traits included in multiple-trait evaluation
  - Most frequent hoof lesions
  - Lameness recorded by producers
  - Locomotion and Feet & Legs traits from type classification
- Work in progress for developing genetic evaluation and sub-index
- Single Step approach for genomic evaluation may be best option
- Targeted for 2018 together with index for Overall Health

Milk Spectral Records

- Data already available at DHI laboratories when milk and fat contents are measured
- Thus, relatively cheap and easy to collect for already milk recorded cows
- Prediction of many traits can be done simultaneously
- As in genomics, a reference population (gold standard) is needed to compute accurate predictions

Milk Spectral Records in Canada

- Two Foss lines out of 12 in Canada are outputting milk spectral records
- Developed a pipeline to store data at DHI labs, move to central database and then to CDN
- 3.4 million spectral records from approximately 700,000 cows currently available at CDN
- Funding from new Genome Canada project to get milk spectral data from the remaining 10 FOSS lines
  - ie. Milk spectral data for all milk recorded cows in Canada
  - Funding also to make the pipeline fully automatic

Efficient Dairy Genome Project

- Genome Canada Large Scale Applied Research Project
- Cash and in-kind funding from international and national partners to total CAD $10.3 million
  - Genome Canada, Genome Alberta, Ontario Genomics
  - ALMA, Ontario MRI, CDN, GrowSafe
- Start date Oct 2015 – End date Sep 2019
  - Led by Filippo Miglior (Guelph) & Paul Stothard (Alberta)
- **Overall objective to improve feed efficiency (FE) and reduce methane emissions (ME) in dairy cattle using genomics**

THE Efficient Dairy GENOME PROJECT

http://genomedairy.ualberta.ca

Tangible Deliverables to End Users

- **Weekly release of GEBV for FE and ME to producers and the AI industry integrated by**
  - *Newly-identified mutations or markers*
  - *New developed FE and ME predictions from MIR spectra*
  - *World's first database to routinely validate genomic predictions and continuous exchange among partners*
  - *Measurement of the farm level benefits from adopting the use of the GEBV for novel traits*
  - *Societal cost benefit analysis results from incorporating the new traits into national breeding programs*

A Fully Integrated Partnership

UNIVERSITY of GUELPH

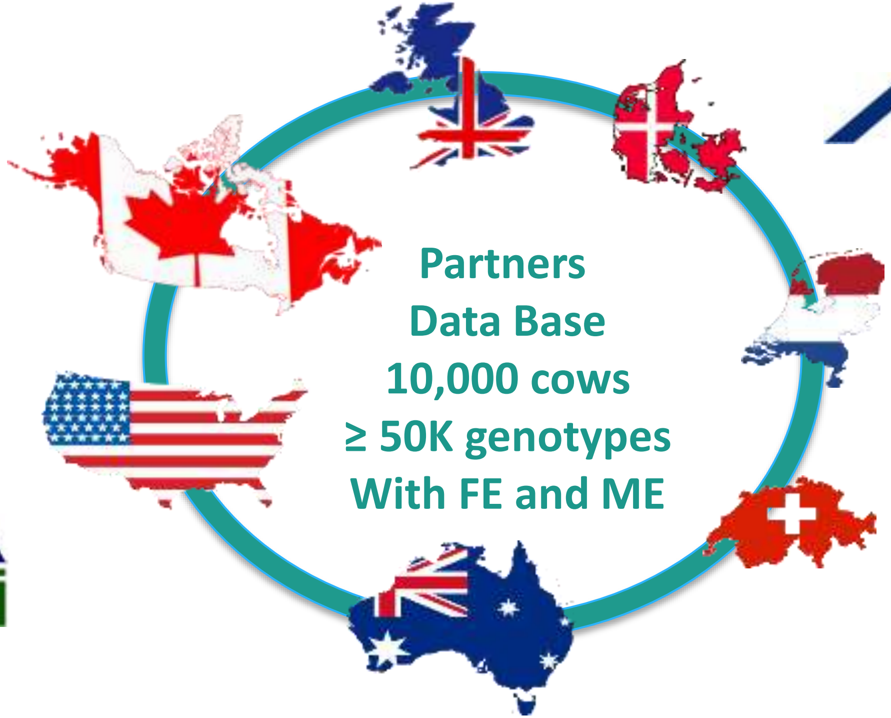
UNIVERSITY OF ALBERTA

Réseau laitier canadien
CDN
Canadian Dairy Network

GrowSafe SYSTEMS

USDA

SRUC



Partners
Data Base
10,000 cows
≥ 50K genotypes
With FE and ME

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Integrated Solution for Greener Dairy

- Genomics provides an opportunity to select for higher feed efficiency and decreased methane emissions
- ➢ Will lessen the environmental impact of dairying
  - – Reduction of emissions and feed waste
  - – Less feeds (less land) used for dairying
- Compelling opportunity to make dairy greener worldwide, through strong collaboration
- Whereas at same time benefiting dairy producers
  - – Reduction of feed costs
  - – Potential credits for cutback in methane emissions

Conclusions

- Genomics offer rapid industry-wide benefits
  - *Targeting expensive traits*
  - *Delivering High efficiency and immediate uptake*
  - *Genetic progress has more than* ***doubled*** *since genomics*
- However, it is critical to develop cost-effective pipelines to collect and store new phenotypes
- Cow reference populations provide reliable genomic evaluations of expensive and novel phenotypes
  - *Needed size of reference population depends on trait heritability*

Participating Organizations

GenomeCanada

GenomeAlberta

Ontario Genomics

NSERC
CRSNG

Dairy Research
for a Healthy World

ALMA
Alberta Livestock
and Meat Agency Ltd.

Ontario
MINISTRY OF RESEARCH & INNOVATION

Ontario
Ministry of Agriculture,
Food and Rural Affairs

Agriculture and
Agri-Food Canada

Agriculture et
Agroalimentaire Canada

Canadian Dairy
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