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

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Speaker: Filippo Miglior

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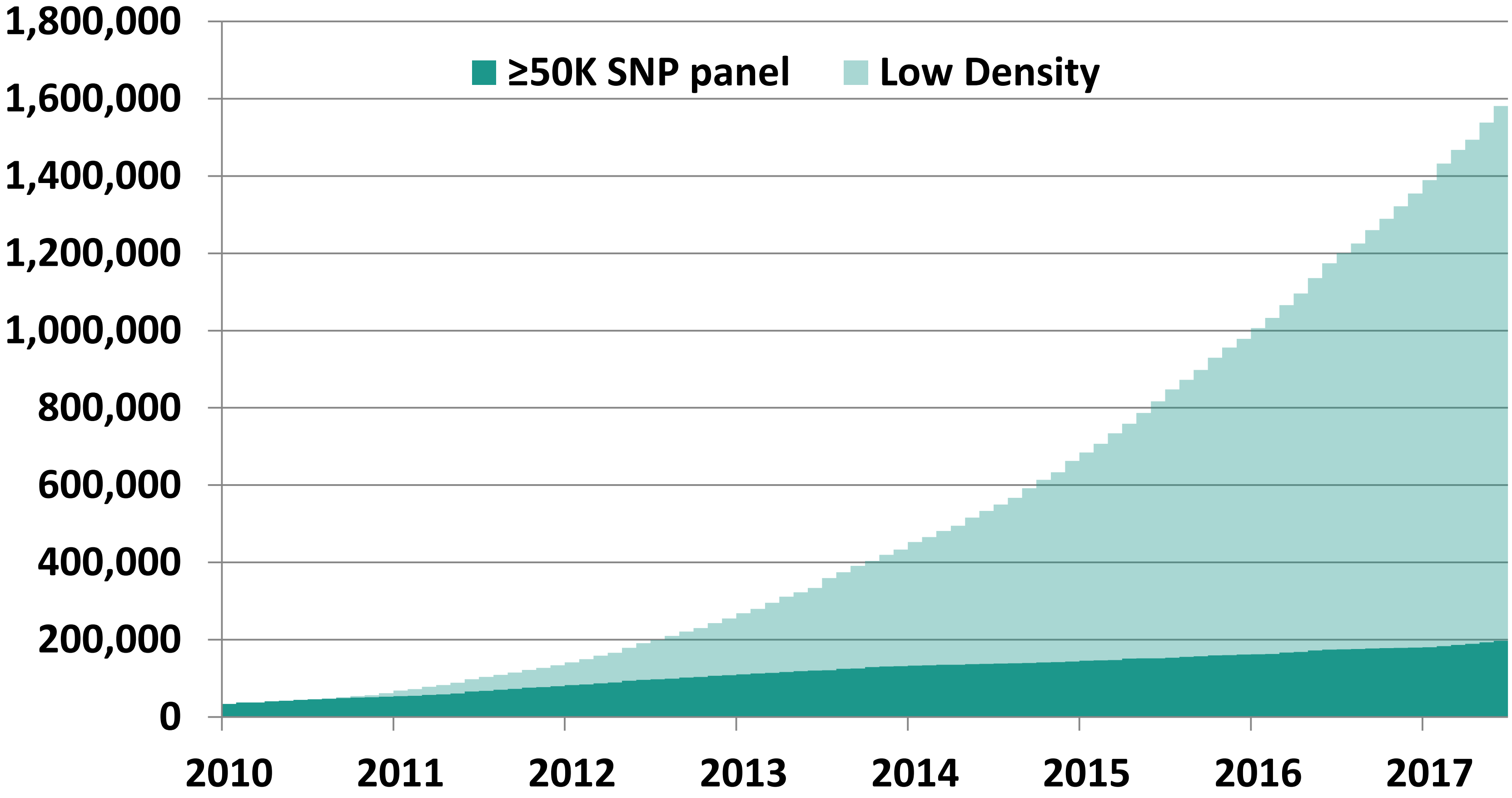
Evolution of Genotype Data Base



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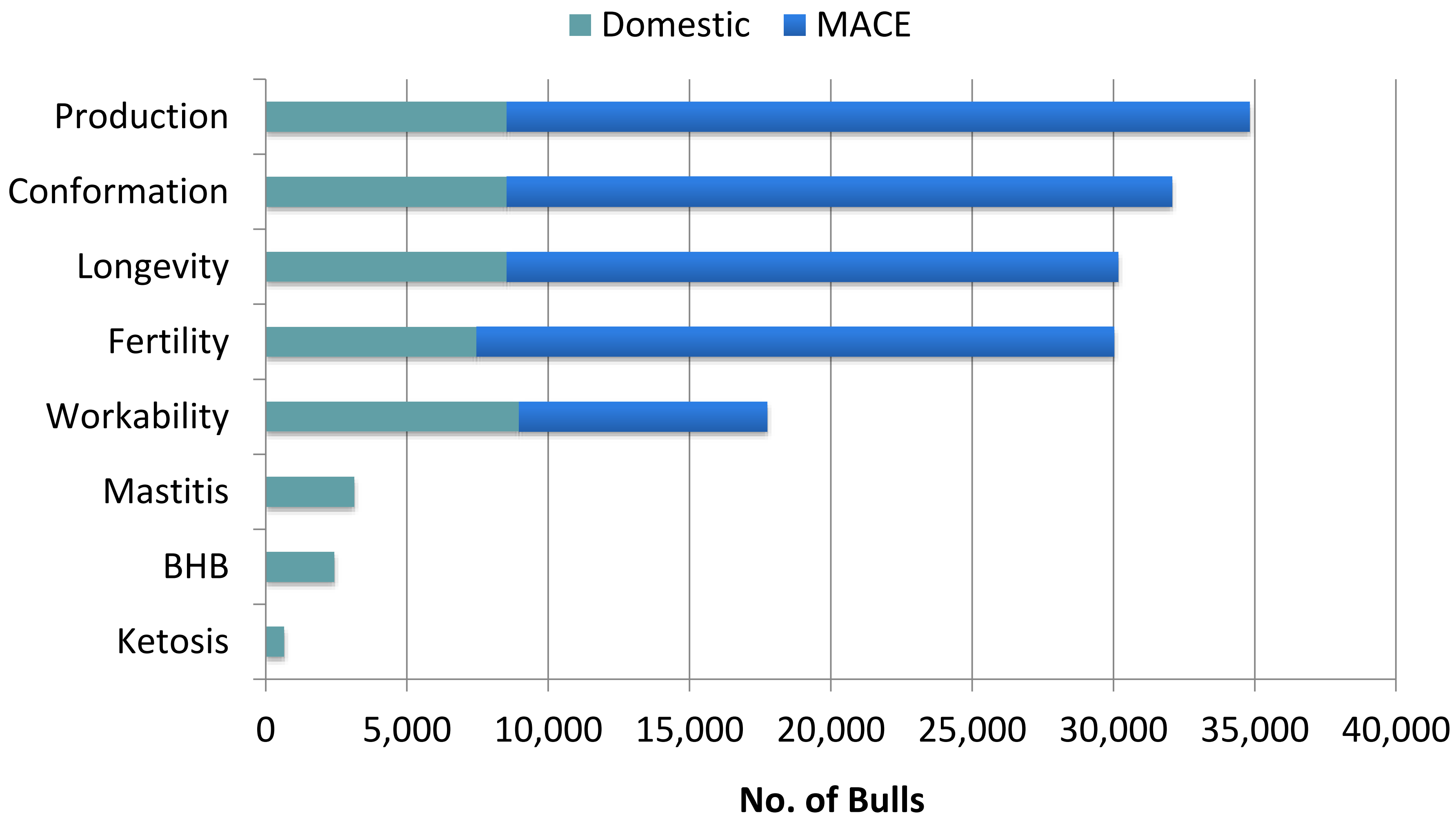
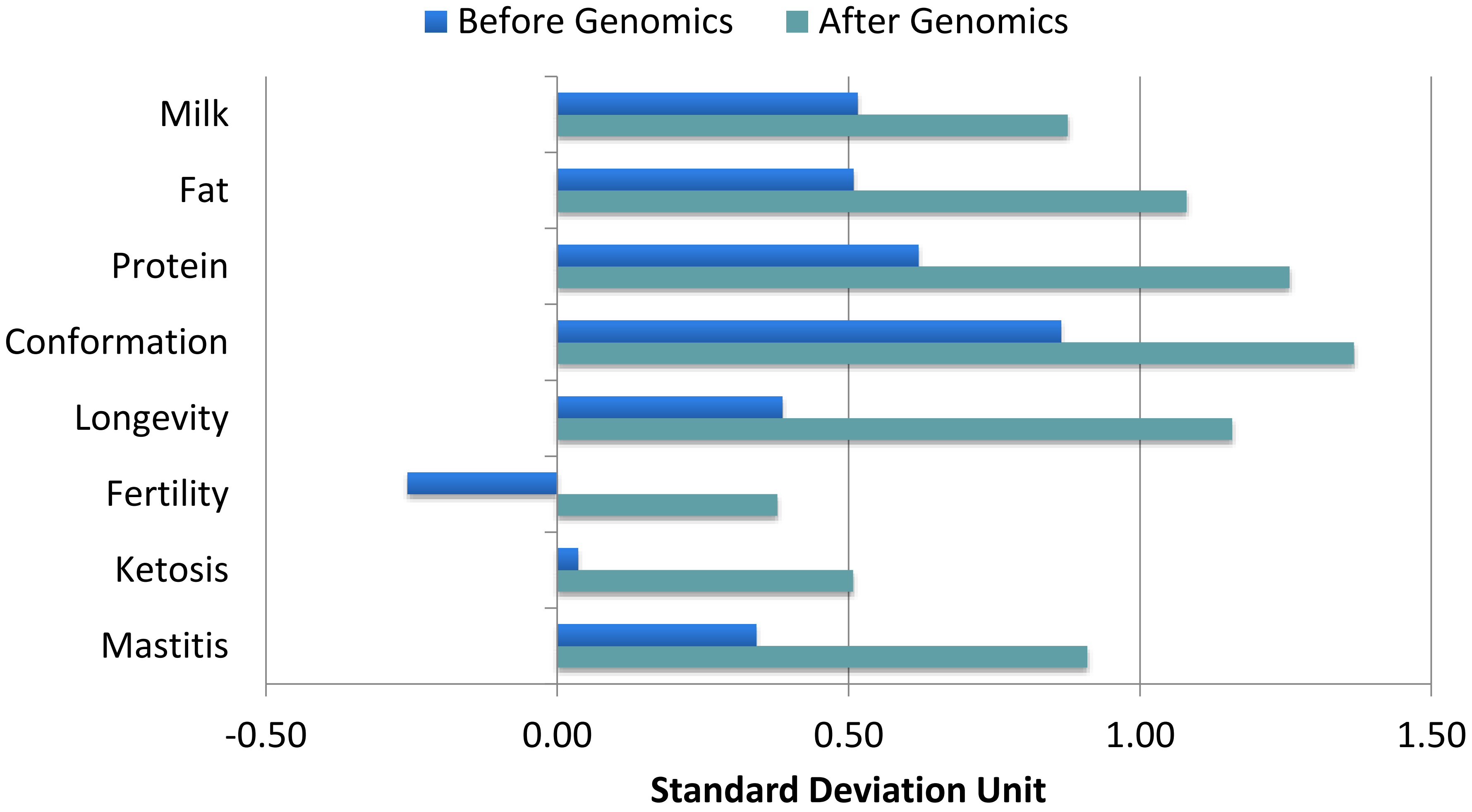
Large Bull Reference Population

- In Canada, National health collection program and research projects led to recording many novel traits
  - Diseases, milk quality, feed efficiency and methane emission
- Benefits of genomic selection associated with shorter generation interval due to GEBV increased reliability
- This is the result of a large reference bull population used for production, conformation, and some fertility traits
  - ~35,000 bulls from Intercontinental consortium (Canada, US, Italy, UK, Switzerland and Japan)
  - Using Canadian proofs for Canadian bulls and Interbull MACE results for non-Canadian bulls

Size of Male Reference Population by Trait
Canadian Holsteins



Impact of Genomics on Genetic Progress



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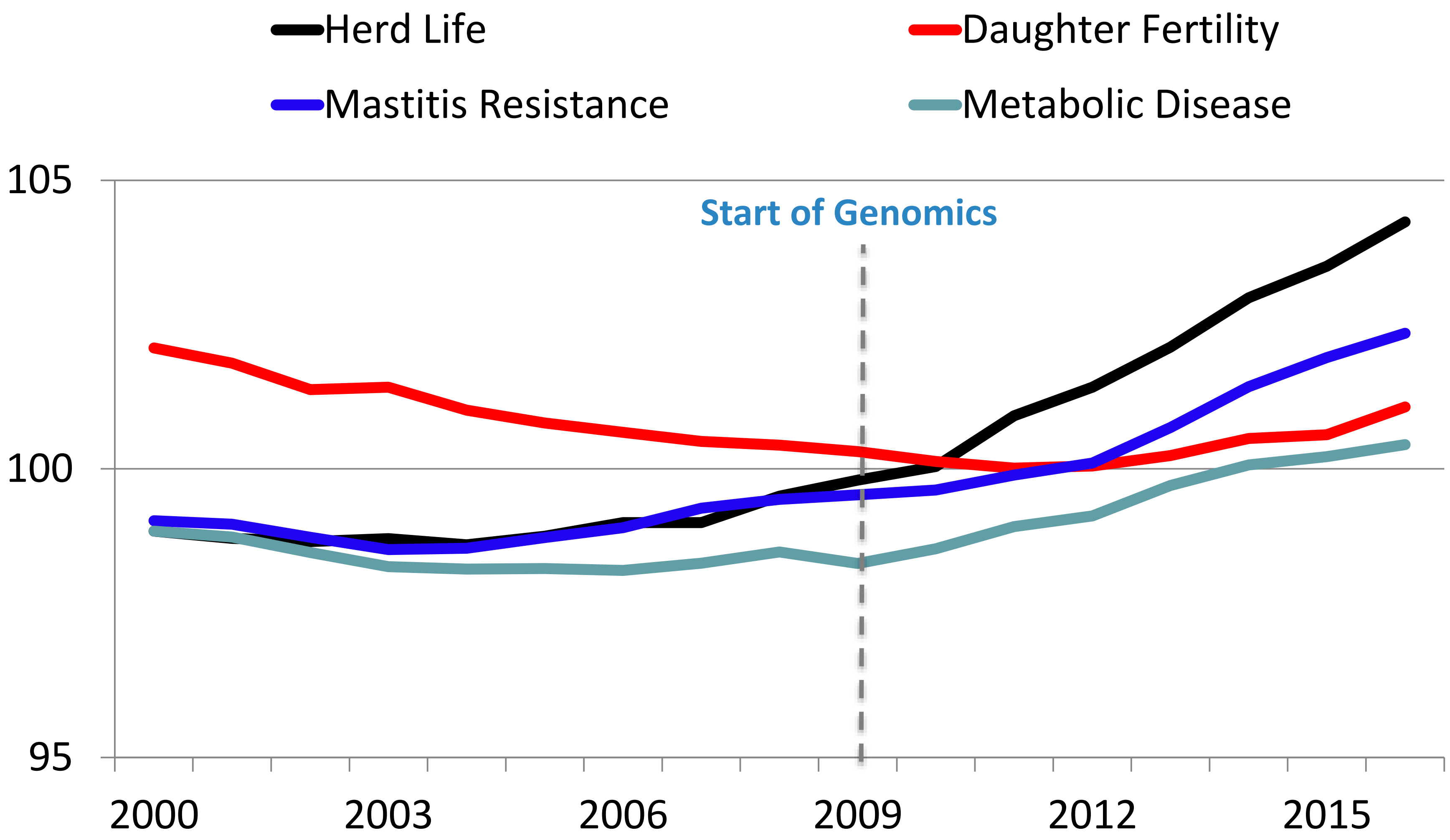
Genetic Trend



Small Reference Population for Bulls

- For health traits and other novel traits this is not possible
- Canada and UK are the only country within the consortium to run evaluation for health traits
- Health collection started relatively recently in Canada
  -> a much smaller group of bulls ‘proven’ for those traits
  - For Mastitis Resistance, the size of the reference bull population is limited to just over 3,000 bulls
  - Significantly lower for other disease traits and hoof health
- Such a limited bull reference population has a direct effect on the accuracy of genomic evaluations

Female Reference Population

- To remain competitive it is key to include those novel traits in future breeding programs
- A cow reference population based on animals already phenotyped seems to be the most effective solution
- Additionally, when only a small part of the population is phenotyped and genotyped
  - Single step genomic evaluation gives most accurate results
- Currently a potential female reference population of 20,000 cows for health traits, with increase of 4,000/yr

5-year Plan

Main goal is to generate tools to maximize the rate of genetic progress for novel traits by enlarging the size of the female reference population

- Identify best data-collection herds
- Develop most effective genotyping strategy
- Add novel phenotypes from complementary projects
- Perform GWAS and functional analysis
- Perform Single-Step Genomic evaluations

5-year Plan – cont'd

- Best data-collection herds must have:
  - DHI, type classification services, reproduction and health (including hoof lesions)
- Among those herds, recruit herds which already genotype animals, together with herds that have no genotyped animals
- Strategy for genotyping with mixture of LD and MD
  - Maximize number of genotyped animals at lowest cost
- Genotype additional 30,000 cows to reach a sizeable cow reference population of 50,000 cows

Novel Phenotypes from Other Projects

- Feed Efficiency and Methane Emissions
- New fertility phenotypes
  - estrus expression, pregnancy diagnosis, pregnancy loss, AMH level, progesterone at AI event and 1 week after AI
- Hoof lesions
- Key milk components for cheese transformation
- Welfare indicators

Pipeline for Imputation to Sequence

First Step (50k to HD)

- Concordance rate and allelic r^2 : 99.5% and 99.3%

Second Step (HD to Sequence)

- Concordance rate and allelic r^2 : 97.4% and 96.9%

33 new least-related bulls sequenced at high coverage

20-30 cows to be sequenced at lower read coverage

Single Step Genomic Evaluation

- Digital Dermatitis currently under development at CDN
  - To be launched in December 2017
- To be tested on health traits for non-Holstein breeds
  - And then applied to Holstein as well
- To be developed for Feed Efficiency and Methane Emissions
- Furthermore, the incorporation of -omics data will also be investigated to increase accuracy of evaluation

Conclusions

- The enlarged reference population will allow more accurate estimation of genomic evaluations
- Single step genomic evaluation is advantageous for novel traits with limited recorded populations
- By improving the accuracy of GEBVs, the rates of genetic progress will be accelerated
  - generate an additional $200 Million/year in annual net benefits to the industry
  - bringing more health, production efficiency, and welfare into Canadian dairy herds

Acknowledgments

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GenomeAlberta

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Dairy Research
for a Healthy World.

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