

Where are we going with genomics? What about inbreeding?

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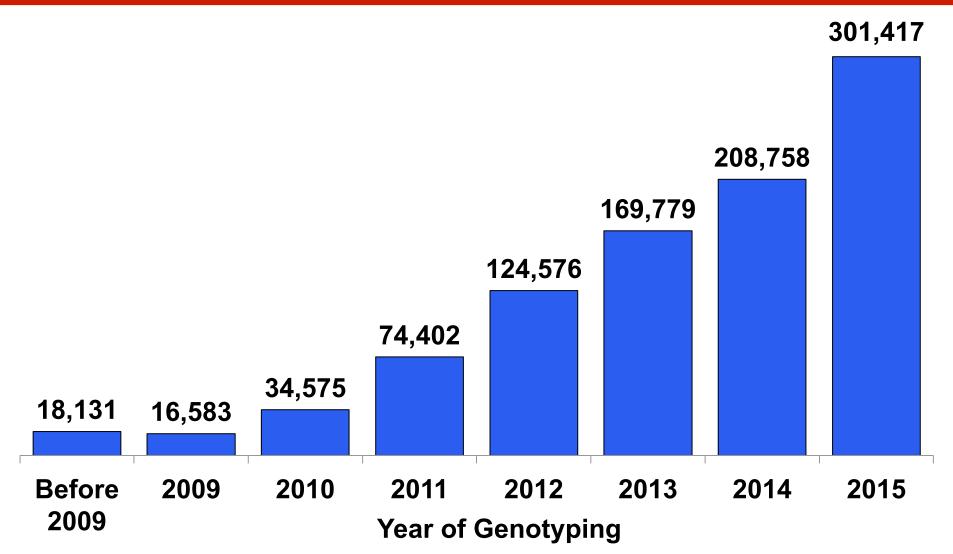
Total Genotypes at CDN - March 2016 -

Breed	Genotypes	Percentage
Ayrshire	5,732	0.5%
Brown Swiss	21,610	1.8%
Guernsey	2,644	0.2%
Holstein	1,060,214	86.0%
Jersey	143,166	11.6%
Total	1,233,366	100%

Over 1 Million Holstein Genotypes!



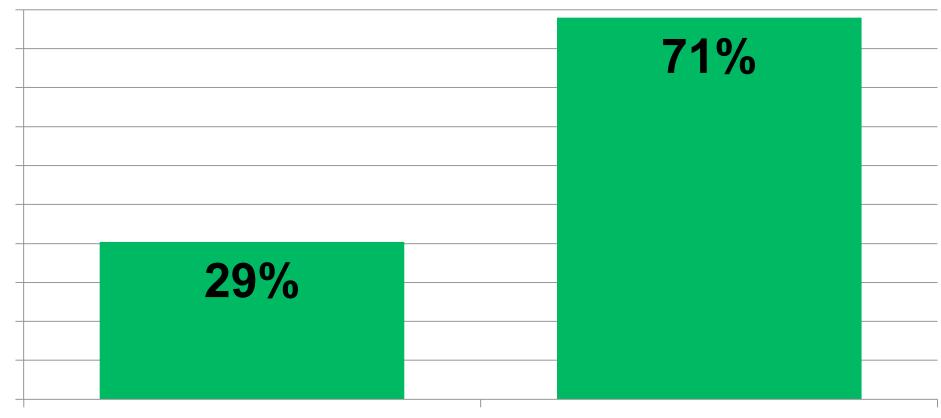
No. Holsteins Genotyped per Year in North America





Holstein Reference Sires for Genomics in Canada

≈28,000 Reference Sires

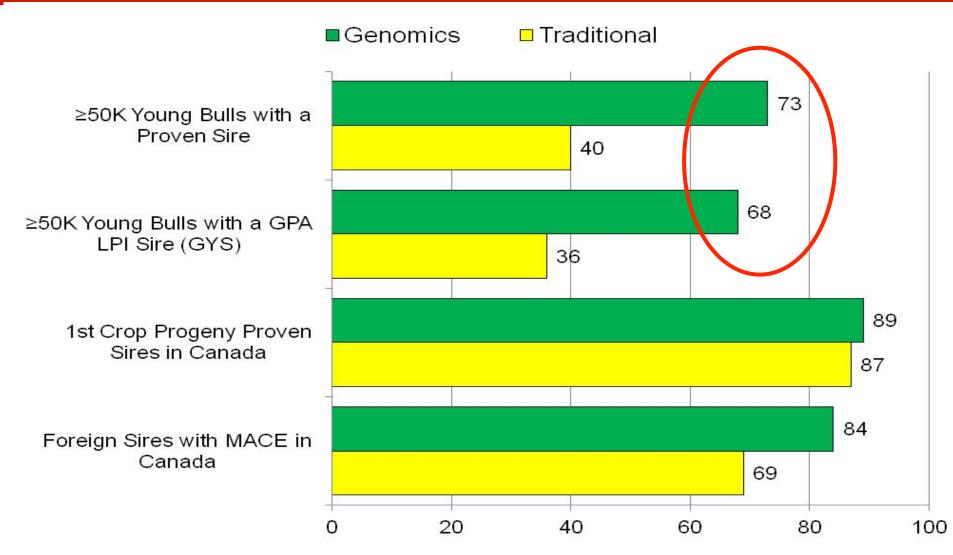


Domestic Proven Sires

Foreign Proven Sires with MACE

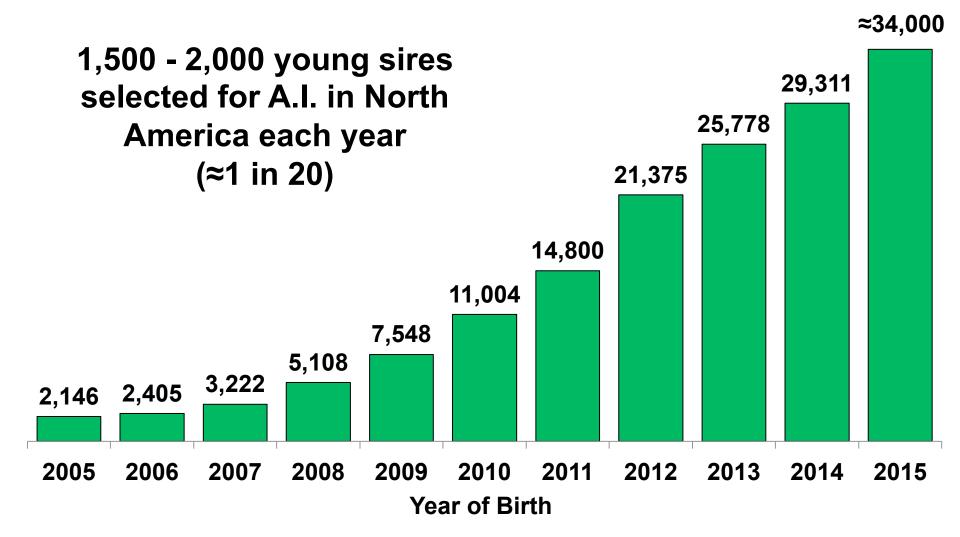


Gain in LPI Reliability with Genomics – HO Bulls



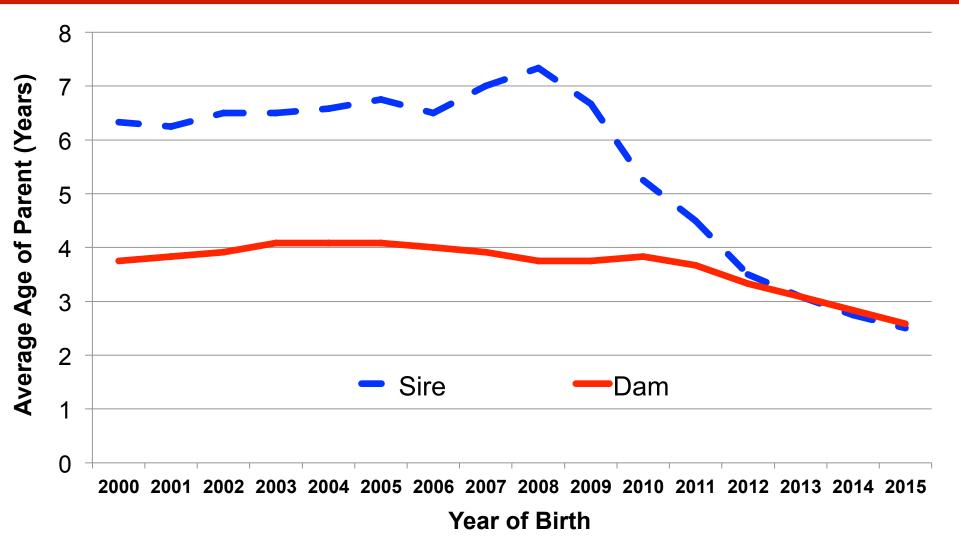


No. Young Bulls Genotyped in North America



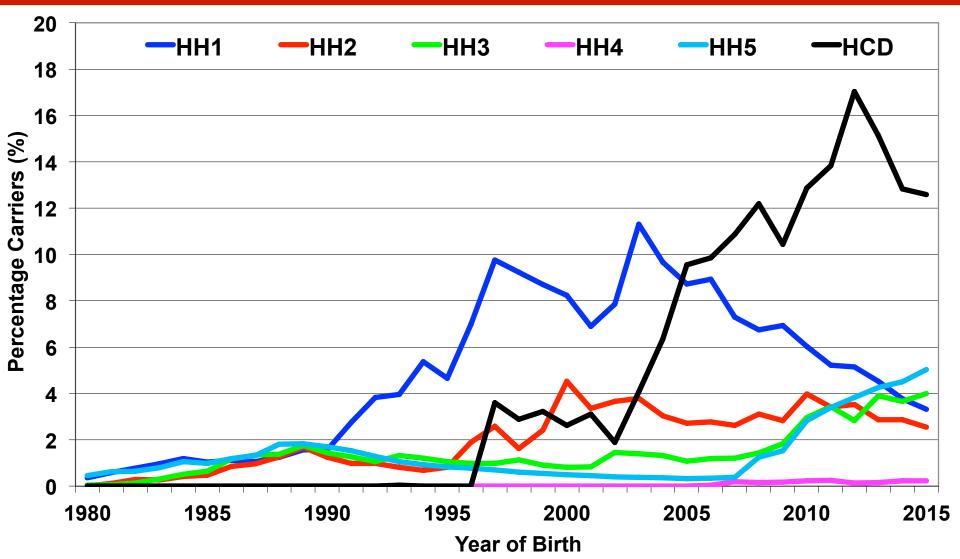


Average Age of Parents of Genotyped Holstein Bulls



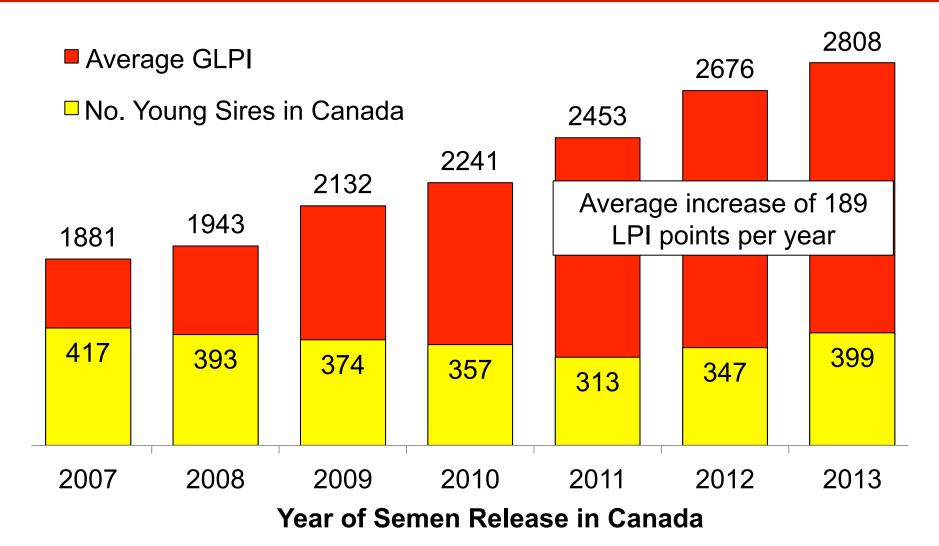


Discovery of Holstein Haplotypes - Percent Carriers





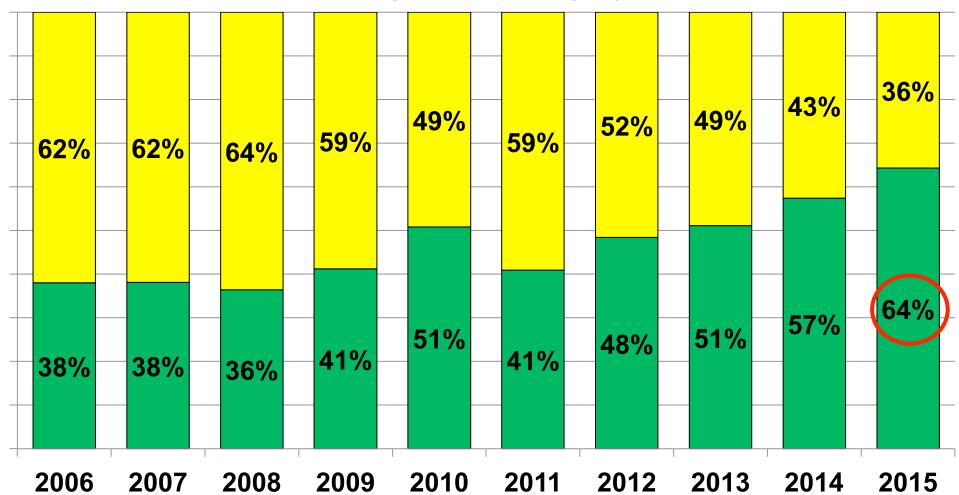
Rapid Progress in Quality of Young Sires Offered





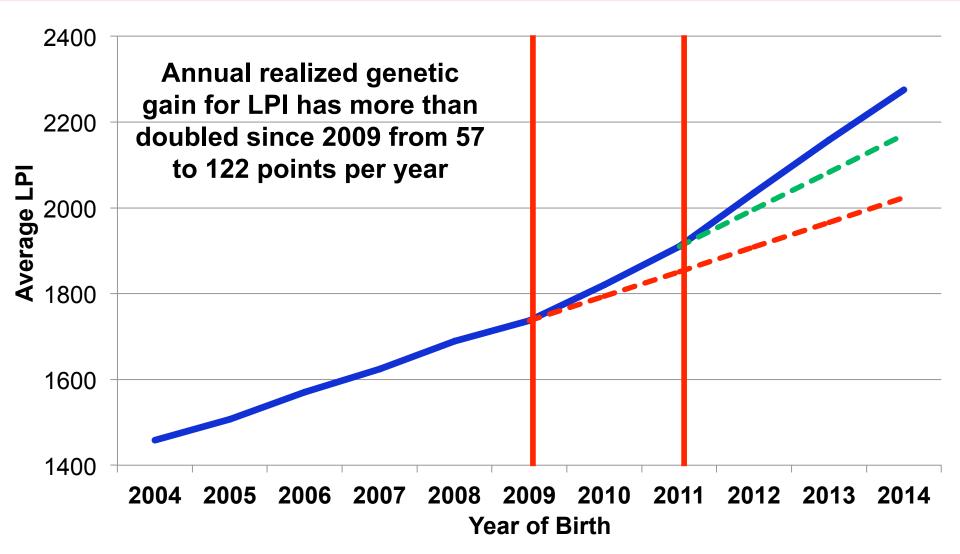
Market Share - Young vs Proven Sires -

Unproven Young Bulls Progeny Proven Sires





Impact of Genomic on Genetic Progress - LPI





Impact of Genomics

- Many GREAT things have resulted from the use of GENOMICS:
 - Higher accuracy of selection for young animals
 - Shorter generation interval between parents and the next generation of replacements
 - Both for heifers in a herd and for bulls in A.I.
 - >FASTER rates of genetic progress are a **reality**!
 - Accurate parentage verification and discovery
 - Discovery of existing genetic recessives with the ability to identify carriers to manage matings



Where is Genomics Going?

 Arguably, the BIGGEST benefit from genomics is the opportunity to improve new/novel traits of importance

Current examples include:

- Animal health and disease resistance
 - Clinical mastitis, metabolic diseases (i.e.: ketosis), etc.
- Hoof health and lameness
- Nutraceutical properties of milk (i.e.: fatty acids, cholesterol, etc.) to improve human health
- Feed efficiency and methane emissions

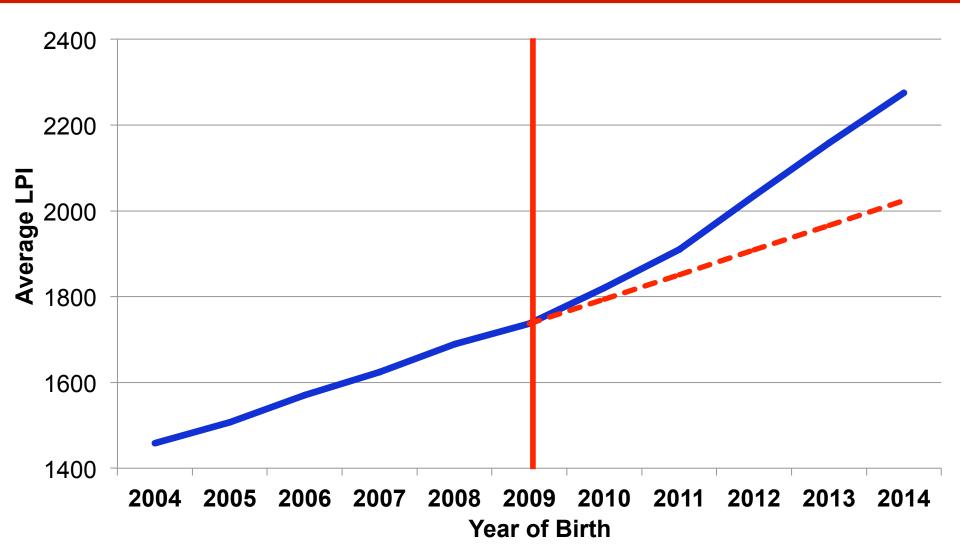


Genomic Selection for Novel Traits

- Current methods for estimation of genomics are not designed for new/novel traits
- Proven sire reference population requires thousands of progeny proven sires following decades of performance recording
- "Cow Reference Population" is the solution!
 - Performance and genotypes collected on the same animals
 - Need tens of thousands for significant accuracy gains
 - With the exception of some "expensive" traits, this approach will likely reduce international collaborations

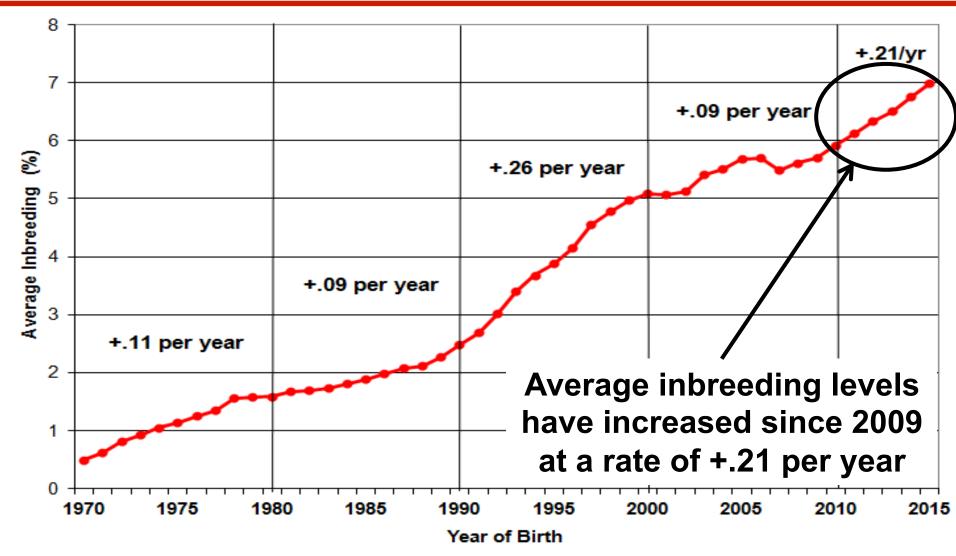


Impact of Genomic on Genetic Progress - LPI





Balancing Genetic Progress and Inbreeding





Managing Inbreeding

- The fast paced, competitive RACE for the highest genetics provides little incentive for A.I. companies to search for outcross genomic young bulls
- In general, the global Holstein population is highly related with only a few countries as exceptions
- Wide scale genotyping is required to identify new cow families and/or outcross young bulls with high genomics
- Inbreeding is best managed at the mating level!



Improved Mating Programs

Most computerized mating programs should have the ability to avoid matings that produce progeny that exceed a given level of inbreeding

Based on the genetic relationship of parents from pedigree

- With genomics, the concept of "genomic inbreeding" has been introduced
 - Based on the genomic relationship of parents from genotypes

For genotyped animals only but pedigree not used

 Concept of "Chromosome-based mating" has also been suggested





Impact of genomics is HUGE!!!

- More accurate genetic selection
- Moved focus to the youngest animals
- Increased rates of genetic progress
- Opportunities to select for new/difficult traits
- Also creates new challenges...
 - Faster turnover rate of bulls being marketed
 - Fewer breeders able sell bulls to A.I.
 - Genetic diversity and rates of inbreeding
 - New genetic and genomic evaluation systems

Tip of the iceberg!





