



Update on Genotyping and Genomic Evaluations in Canada

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SNP Panel Options



- 95 for parentage verification
- 3K initial low density (LD) panel (Sept.'10)
- 6K LD panel that replaced the 3K (Oct.'11)
- 10K LD+ panel by GeneSeek (Mar.'12)
- 50K standard for genomic evaluation
- HD for imputation within breed and across breed genomic evaluation estimation
- Full sequencing



Imputation Methods



Population Based:

- Unrelated individuals
- Sharing small DNA blocks
- Computationally demanding

Family Based:

- Genotyped ancestors/progeny
- ➤ More effective for small density panels (with less than 10,000 SNP)
- Much less demanding computationally



Imputation Error Rates



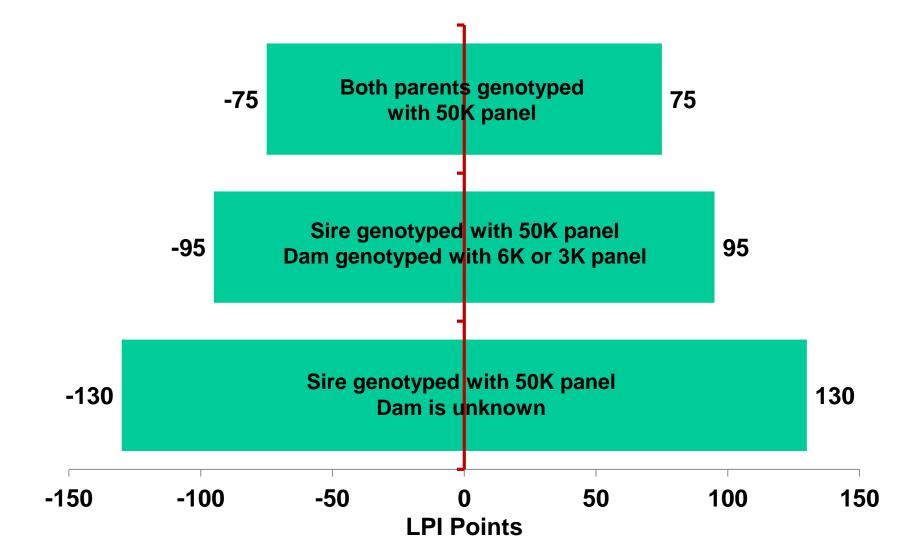


Sira Canatuna	Dom Conotyno	Average Imputation Error Ra		
Sire Genotype	Dam Genotype	3K Panel	6K Panel	
50K	50K	0.9%	0.4%	
50K	3K	1.8%	1.1%	
50K	6K	1.4%	0.7%	
50K	Not Genotyped	2.9%	1.1%	
Not Genotyped	Not Genotyped	5.9%	2.3%	
Not Genotyped	Not Known	7.7%	5.0%	



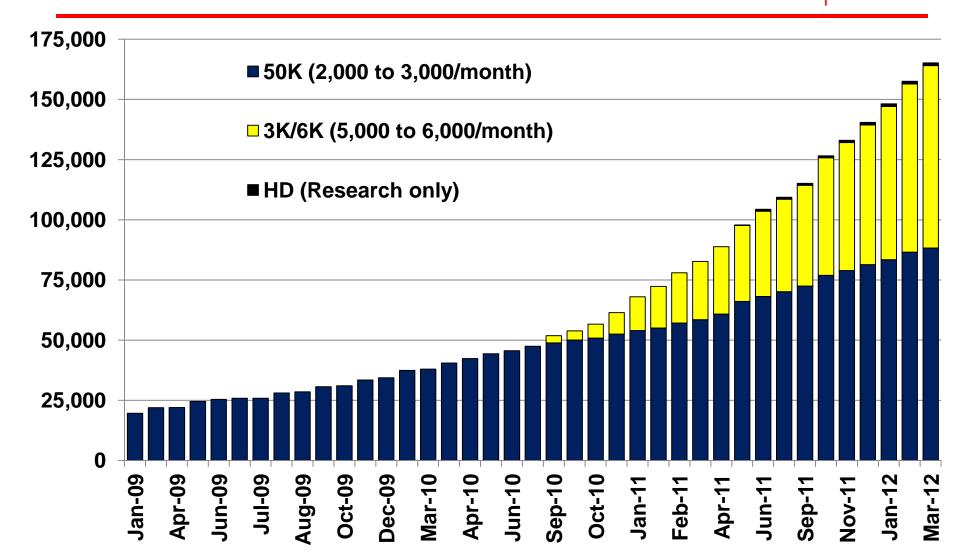
99% Confidence Range for LPI Using 6K vs 50K







Evolution of Genotypes in NA Database





Genotype Database - Holstein, April 2012 -



Animal	Males			Females						
Nation	Prov	ven	Young	Sires	Cov	NS	Heif	ers	Sub-1	Γotal
Code	All	%LD	All	%LD	All	%LD	All	%LD	All	%LD
CAN	3,483	0%	5,574	20%	8,193	58%	12,032	76%	25,864	58%
USA	12,261	0%	25,330	12%	17,021	41%	49,570	80%	94,185	53%
OTHER	6,451	0%	9,307	12%	6,355	44%	19,373	73%	37,905	47%
	Sub-Total and %LD Sub-Total and %LD									
	62,406 8.3% 112,544 68.8%									
		Grand Total and %LD								
			1	74,950	47.2%					



Genotyped Holstein Young Candidate Bulls



Year of Birth	Number Genotyped
2005*	2,289
2006*	2,493
2007*	3,286
2008	5,170
2009	7,506
2010	12,241
2011	13,936

^{*} includes some bulls that are now progeny proven



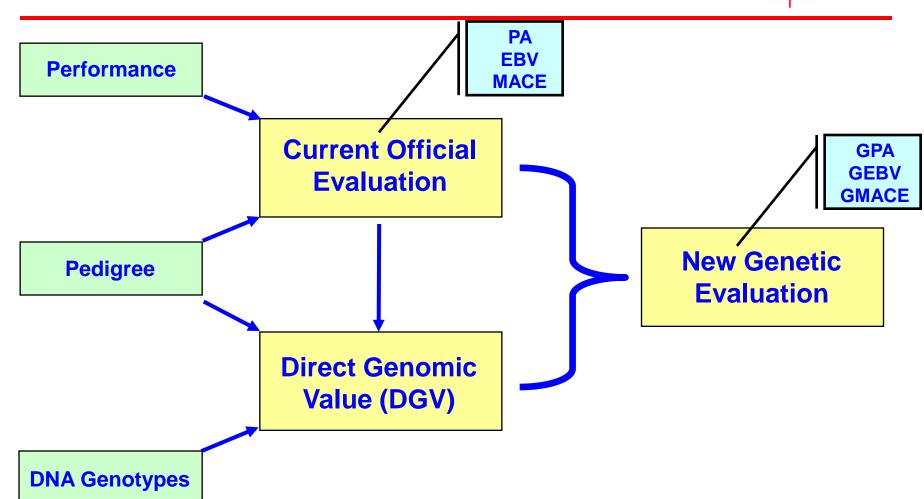
Genomic Evaluation Services in Canada



- All genotypes sent by labs to USDA for centralized quality assurance processes
 - USDA sends genotypes and pedigree to CDN monthly
 - USDA and CDN exchange female EBVs monthly
- CDN computes GEBVs every month for all genotyped animals (63 traits)
 - Compute all traditional EBVs monthly
 - >>16,000 progeny proven sires as "Training" set
 - Release new female GEBVs monthly
 - Provide candidate YS GEBVs to AI monthly



Incorporating DGVs into Genetic Evaluations





Gain in LPI Reliability



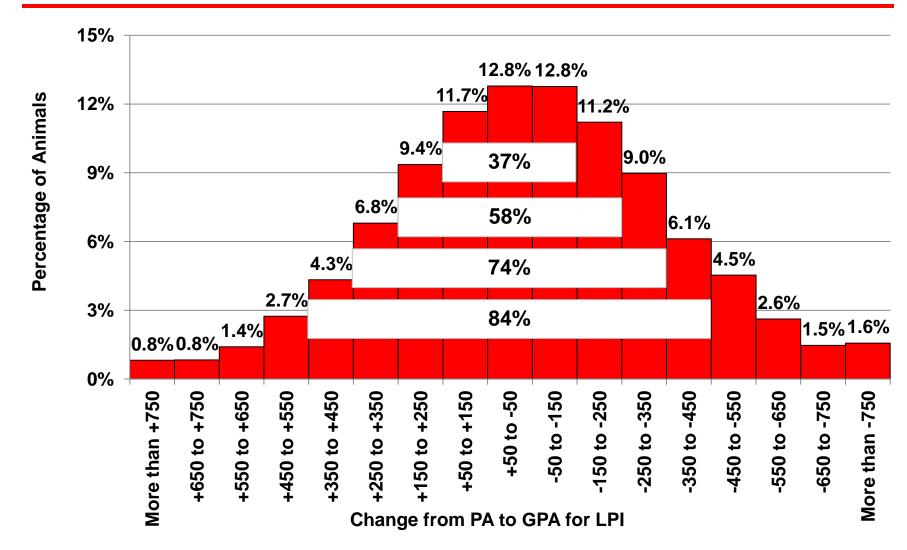


Sub-Group for	Average LPI Reliability (%)						
Holstein Breed	Traditional	Genomics	Gain	DGV Weight			
50K Young Bulls and Heifers (Born 2009-2011)	38	69	31	64%			
3K or 6K Heifers (Born 2009-2011)	35	64	29	65%			
Younger Cows in 1st or 2nd Lactation (50K)	54	73	19	57%			
Foreign Cows with MACE in Canada	42	71	29	63%			
1st Crop Proven Sires in Canada	85	90	5	51%			
Foreign Sires with MACE in Canada	70	83	13	54%			



Distribution of Change from PA to GPA for LPI





Genomic Evaluation Details

50K

GEBV 12*APR

COMESTAR LAUTAMIRE PLANET

HOCANF105753016

PRODUCTION

Protein Yield (kg)

Fat Deviation (%)

Milk Yield (kg)

Fat Yield (kg)

Genotype Panel:

Born 28	B-JUN-09	ET BW			6.77%	13%
Sire:	HOUSAM60597003		ENSENADA TABOO PLANET-ET	03-MAR-03	7.21%	12%
Dam:	HOCANF104226402		COMESTAR LAUTAMIA BOLTON	02-JUN-07	6.25%	13%
MGS:	HOUSAM131823833		SANDY-VALLEY BOLTON-ET	11-SEP-01	6.05%	11%

%INB

Direct

Genomic

2387

77

82

-0.09

Reliability

Increase

+16

+23

+20

+23

%R

Genomic
Evaluation
Details

Genotype Panel:	SUK	Genomic Evaluation	(%)	with Genomics	Value (DGV)
LIFETIME PROFIT INDEX	GEBV 12×APR				
GLPI		3584	70	+22	3124
PRODUCTION		2470	73	+21	1970
DURABILITY		1106	68	+24	1066
HEALTH & FERTILITY		8	60	+74	88

2951

100

98

-0.05

Official

Genomic

Reliability

74

73

73

73

www	.cd	n.ca	

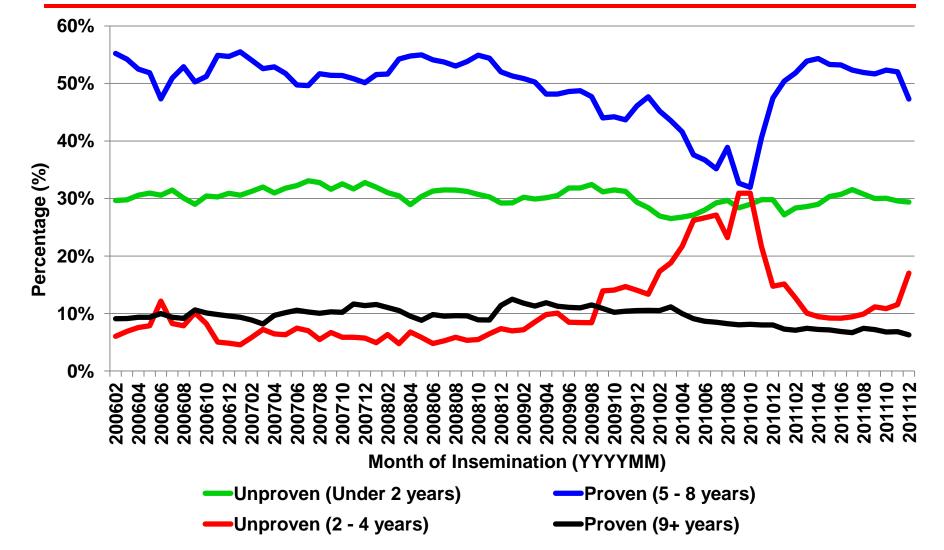
Protein Deviation (%)		0.01	73	+20	0.03
CONFORMATION	GEBV 12×APR				
Conformation		12	69	+24	11
Mammary System		12	70	+23	10
Feet & Legs		14	65	+26	15
Dairy Strength		7	70	+23	6
Rump		1	66	+20	-2

FUNCTIONAL	12×APR				
Herd Life	GPA	107	63	+26	108
Somatic Cell Score	GEBV	3.13	71	+36	3.07
Lactation Persistency	GPA	103	61	+21	103
Daughter Fertility	GPA	101	59	+23	103
Milking Speed	GPA	99	58	+19	99
Milking Temperament	GPA	110	57	+19	110
Calving Ability	GPA	104	73	+28	105
Daughter Calving Ability	GPA	107	58	+21	110



Trend in Holstein Sire Usage by Age Category









Launch of



Program







New service for producers that wish to:

- Catch up on Herdbook registration
- Start regular Herdbook registration
- Use genotyping to learn more about the genetic potential of their females
- Available initially for Holstein producers

Launch date: <u>June 1, 2012</u>







- Application form and instructions will be available on Holstein Canada web site www.holstein.ca
- Each animal requires an application form
- DNA collected (tail hair, nasal swab or blood)
- DNA submitted to Holstein Canada with completed application form
- HC does initial QA, inputs producer information, and sends to lab for genotyping







- Results come back to HC and CDN
- CDN conducts parentage discovery (Al sires and dam if genotyped) and provides genomic and genetic evaluations
- HC creates an animal record in Herdbook using pedigree data from discovery process
- Results on a herd basis also available to producers on confidential online account
 - Genomic evaluations for LPI and 60+ traits
 - Report with animals listed, purity and discovered parents







- Application form for each animal must include (sample):
 - Unique lifetime ID number from tag
 - Birth date and Breed
 - Herd management number (also name if desired in the naming of animal)
 - Dam ID if known
 - ➤ Birth codes including indication of Multiple Birth/Twin and Embryo Transfer (ET)
 - >Animal's coat colour







Genotyping is likely under two strategies:

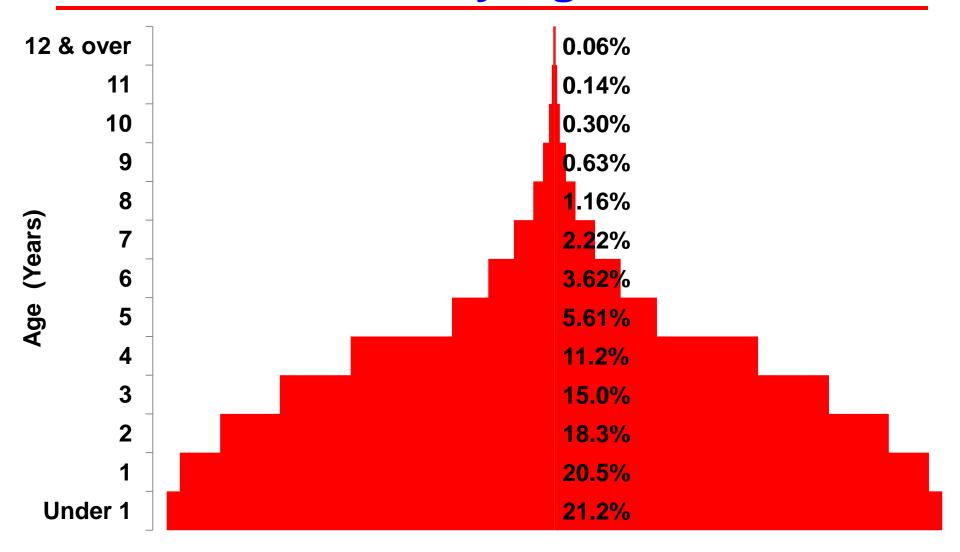
- ➤ Genotype all heifers under a year of age, or perhaps the youngest cross-section of the herd not yet in the herdbook
- Genotype the entire herd of heifers and cows

Key advantages of this "whole herd" strategy to the herd owner include

- Maximum discovery of lineage and level of recordation
- More accurate estimates of inbreeding for animal and herd
- Genetic evaluation of all animals for production, conformation and functional traits, which contributes to effective herd management and sire mating



Typical Herd Structure by Age





Typical Lineage Discovery by Whole Herd Genotyping



