Réseau laitier canadien
Canadian Dairy Network

Improved Accuracy with DNA Genotyping

Second article in a series on including DNA information
in official genetic evaluations in Canada starting in 2009.

As outlined in the first article of this series (see www.cdn.ca, September 2008), Canadian Dairy Network (CDN) plans to incorporate information from each animal's DNA profile as a new source of data contributing to genetic evaluations, starting in 2009. The implementation of this new approach will significantly change the landscape of genetic improvement programs and strategies, as we know them today. Within the next few months and years, DNA genotyping of young sires, heifers and cows will become standard procedure for all A.I. organizations and breeders, especially those involved in the merchandising of dairy cattle genetics. Looking further into the future, all dairy animals in Canada will have a DNA sample collected, stored and genotyped for purposes of guaranteed parentage verification, animal traceability and as an added source of data for genetic evaluations, just as milk recording and type classification programs became routine sources of information during the past decades. For those not yet convinced of the reality and value of this new source of information for genetic improvement, this article should be enlightening since it focuses on the improved accuracy that results when information from DNA genotyping is added to actual official genetic evaluations in Canada rather than theoretical possibilities.

How Does DNA Genotyping Work?

A presentation earlier this year by Dr. Larry Schaeffer of the University of Guelph helped the international audience visualize how the new technology of DNA genotyping works to contribute to improve genetic evaluations. Imagine the dairy cattle genome as a very long highway running across Canada from St. John's, Newfoundland to Victoria, British Columbia (≈7,200 km). On the side of our highways there are posts that act as markers to indicate each kilometre along the way. In DNA genotyping technology, a total of 58,000 markers (known as the 50K panel) have been identified at equal distances along the entire bovine genome, which translates to one post every 125 metres along the highway. While these markers are too few, and too far apart, to identify the exact genes that act on each trait of interest for dairy cattle improvement, they do help identify areas on each of the 30 pairs of chromosomes that have some level of effect on each trait. In reality, of the 58,000 markers currently being used, roughly one-third are non-informative since they either have no significant effect on any current trait of interest or all dairy animals possess the exact same genes at these markers and no variation exists for selection. The end result of the DNA genotyping process in the laboratory is a sequence of 58,000 numerical values that indicate whether the animal carries 0, 1 or 2 copies of the specific gene located at each marker or "post" along the genome. The numerical sequence from genotyping is a unique combination for each animal (i.e.: 1020111220012… for 58,000 digits), except for groups of animals that are genetically the same, such as identical twins that occur naturally or by embryo splitting.

How Do DNA Profiles Contribute to Genetic Evaluations?

Current research in Canada for incorporating information from DNA genotypes into official genetic evaluations includes 1,560 Holstein bulls with an official LPI in August 2008. The approach used to include this new source of information into official genetic evaluations has three principle steps. First, an analysis is done using all proven sires that are genotyped to compare their proof for each trait with trends in their DNA profile at each of the 58,000 markers. In this manner, it is possible to identify the desirable profiles associated with high proofs for each trait as well as the less desirable profiles for bulls with low proofs. In the second step, these known associations between DNA profiles and bull proofs are applied to all genotyped animals, including young sires, heifers, cows and proven sires, to compute a "Direct Genomic Value" (DGV). The final step involves a process whereby each genotyped animal has its current genetic evaluation, whether it be a Parent Average (PA), an official domestic Estimated Breeding Value (EBV) or a foreign genetic evaluation expressed on the Canadian scale (MACE), combined with its DGV to derive its "Genomic" evaluation for each trait, to be labelled as Genomic Parent Average (GPA), Genomic Estimated Breeding Value (GEBV) and Genomic MACE evaluation (GMACE), respectively. These modified values will become their officially published genetic evaluations, which will also be propagated downwards to affect the published evaluations of their progeny and other descendants.

What is the Gain in Accuracy Achieved?

Table 1 shows the average Reliability values for various traits and groups of animals based on current official genetic evaluations in Canada as well as the gain in accuracy achieved by including information from DNA genotyping. As expected, groups of animals with lower current Reliabilities, namely young sires and heifers, gain the most by including their DNA profile, with Reliability increases ranging from 15 to 20 percentage points depending on the trait. Important gains in the range of 10 to 20 percent in Reliability are also realized for cows in first lactation since they do not yet have any daughters with performance data contributing to their genetic evaluation estimation. For proven sires in Canada with only their first crop of daughters included, Reliability increases are relatively small except for Herd Life, Daughter Fertility, Daughter Calving Ability and Milking Temperament, which all have a heritability of 10% or less. Genotyped foreign sires with MACE evaluations in Canada also experience gains in accuracy, mainly for functional traits.

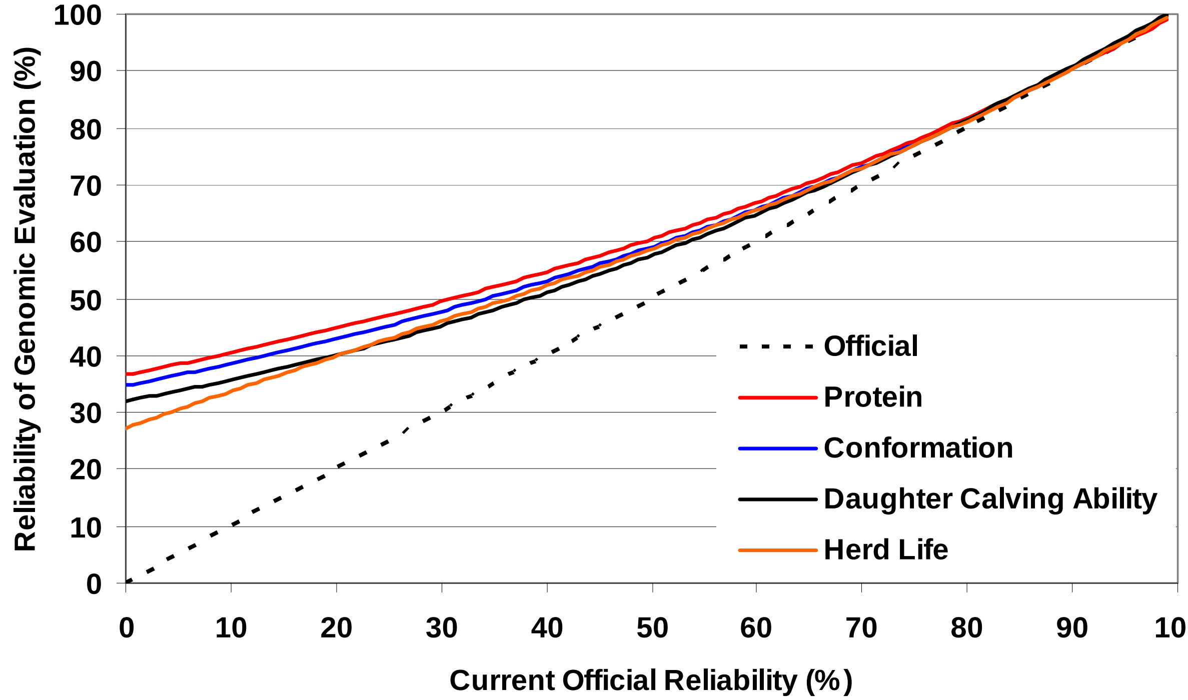
It should be noted that the accuracy improvements shown in Table 1 translate to associated changes in official genetic evaluations, which are more significant for young sires and heifers compared to proven sires. For example, the average Parent Average for young sires born since 2006 drops by an average of 240 LPI points when their DNA genotype is included in their Genomic Parent Average (GPA), which would be similar to the impact on elite heifers born during the same time period. For genotyped proven sires, the average change in LPI, or even MACE LPI, is essentially zero although individual bulls experience some change, which affects LPI rankings.

Table 1: Average Gain in Genetic Evaluation Accuracy by Including DNA Genotyping

Trait	Average Genetic Evaluation Reliabilities (%)			
	Young Sires and Heifers	Cows in 1st Lactation	Domestically Proven Sires With 1st Crop Daughters	Foreign Sires with MACE Evaluations
Protein Yield:				
• Current Reliability	38	54	89	81
• With DNA Genotyping	54	64	90	83
• Accuracy Gain	16	10	1	2
Conformation:				
• Current Reliability	35	50	84	67
• With DNA Genotyping	51	61	86	71
• Accuracy Gain	16	11	2	4
Somatic Cell Score:				
• Current Reliability	35	40	89	71
• With DNA Genotyping	52	56	90	74
• Accuracy Gain	17	16	1	3
Herd Life:				
• Current Reliability	27	29	67	56
• With DNA Genotyping	43	50	74	62
• Accuracy Gain	16	21	7	6
Daughter Fertility:				
• Current Reliability	22	29	72	43
• With DNA Genotyping	41	49	77	52
• Accuracy Gain	19	20	5	9
Calving Ability:				
• Current Reliability	31	32	80	64
• With DNA Genotyping	51	53	82	68
• Accuracy Gain	20	21	2	4
Daughter Calving Ability:				
• Current Reliability	26	29	68	34
• With DNA Genotyping	44	48	73	46
• Accuracy Gain	18	19	5	12
Milking Speed:				
• Current Reliability	24	31	80	N/A
• With DNA Genotyping	45	53	82	
• Accuracy Gain	21	22	2	
Milking Temperament:				
• Current Reliability	28	29	68	N/A
• With DNA Genotyping	46	49	73	
• Accuracy Gain	18	20	5	

To summarize the overall gain in accuracy when information from DNA genotypes are included into the animal’s own official genetic evaluations, Figure 1 shows a plot of the increase in Reliability achieved compared to that of the current official genetic evaluation. This graph clearly shows the gain in accuracy for animals with lower levels of Reliability (i.e.: less than 40%), whether they be young sires or heifers, or for a functional trait evaluation for cows. As the current official Reliability increases, regardless of the trait, the gain in accuracy by incorporating DNA profile information decreases accordingly. It should also be noted that the Reliability of a genomic evaluation essentially always surpasses the minimum of 30% even if nothing else is known about the animal's pedigree, performance or progeny.

Figure 1: Gain in Accuracy with DNA Genotypes by Reliability of Current Official Genetic Evaluation



Summary

Official Canadian genetic evaluations for all traits will include information from DNA profiles for genotyped animals as early as the April 2009 genetic evaluation release for Holsteins. Given that each animal's DNA reflects its true genetic ability, it is logical that incorporating DNA genotyping into national evaluations yields significant increases in accuracy, especially for young sires, heifers and cows. With this improved accuracy, however, also comes a major change to existing genetic evaluations for some genotyped animals, which affects current Top LPI lists for cows and heifers.

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