Answering Your Questions About Genomics in Canada

The January 2010 genetic evaluation release represents the second publication of official genomic evaluations for the Holstein breed in Canada. Given the rapid evolution of this technology in the dairy cattle industry, research has continued since the August 2009 implementation for Holsteins as well as for the possible future application in other breeds. The following are up-to-date answers to common questions posed by dairy producers and industry personnel regarding the current genomic evaluation methods and results in Canada.

How Many Animals Are Now Genotyped?

As of the end of December 2009, genotypes from a total of 34,323 Holsteins, 3,689 Jerseys and 993 Brown Swiss animals from across North America have been received at Canadian Dairy Network (CDN) for inclusion in genomic evaluation calculations. For the Holstein breed, these counts include 2,727 proven sires with an official LPI in Canada, 5,699 foreign proven sires with a MACE LPI in Canada, nearly 15,000 young bulls with a Parent Average in Canada and over 10,000 heifers and cows. Of these females, 22.5% were born in Canada and the remainder were nearly all born in the United States. Recall that any male or female genotyped in either Canada or the United States becomes part of a shared North American database of genotype profiles for use in calculating genomic evaluations in each country. In terms of young bulls, there are currently over 4,500 being genotyped in North America each year by authorized A.I. companies, from which roughly one-third are selected for purchase, semen collection and marketing.

How Does CDN Estimate Direct Genomic Values (DGV)?

In Canada, only sires with an official progeny proof in Canada or an official MACE evaluation in Canada are used to estimate the associations between trends in genotype profiles and genetic evaluations. The resulting associations are interpreted in terms of prediction equations that can be applied to cows, heifers and young bulls based on their own genotype profile to derive their Direct Genomic Value (DGV). For January 2010, a total of 8,426 progeny proven sires were used to estimate the prediction equations, which is an increase of 928 (12.4%) proven sires compared to the August 2009 calculations. An important difference between genomic evaluation methods in Canada and the United States is that they also include genotyped cows in the process for estimating the genomic prediction equations while research has shown that this reduces the accuracy of prediction for the Holstein breed in Canada.

What is the Gain in Reliability Due to Genomics?

As expected, the largest gains in accuracy of genetic evaluations are realized for young bulls and heifers, which traditionally would only have a Parent Average. Table 1 shows

the average Reliability for LPI for various sub-groups of animals in the Canadian Holstein population. With an average LPI Reliability of 61% with genomics, young bulls and heifers now have more accurate evaluations than cows used to have with traditional genetic evaluations prior to genomics (i.e.: 54%). On the other hand, genomically tested young bulls have GPAs for LPI that are still significantly less accurate at 61% Reliability compared to genotyped proven sires with only their first crop of daughters, which average 89% Reliability for GLPI. Genomics also has an important impact for increasing the accuracy of published evaluations for milk-recorded and classified cows in Canada as well as foreign cows and bulls with MACE evaluations on the Canadian scale.

Table 1: Average Gain in LPI Reliability for Holsteins by Population Sub-Group			
Sub-Group	Average Reliability (%) for LPI		
	Traditional	Genomics	Gain
Young Bulls and Heifers (2007-2009)	34	61	27
Younger Cows in 1st or 2nd Lactation	54	68	14
Foreign Cows with MACE in Canada	43	65	22
1st Crop Proven Sires in Canada	86	89	3
Foreign Sires with MACE in Canada	70	80	10

Does Genomics Affect Proofs for Progeny Proven Sires?

For proven bulls with many daughters and Reliability levels over 95%, the addition of genomics has very little impact compared to their traditional proof. For sires that are younger and newly proven within the past year or two, the story is somewhat different. While they may have several daughters contributing to their production and type proofs, these more recently progeny proven sires still have less daughter information for some traits such as Herd Life and Daughter Fertility. For this reason these two traits, along with Daughter Calving Ability and Milking Temperament, experience significant gains in accuracy due to genomics for proven sires (i.e.: 7 to 13 points for Reliability). Even type traits with lower heritability levels, such as Feet & Legs, achieve Reliability gains of 5% or more for genotyped progeny proven sires.

How Can Direct Genomic Values Change Over Time?

From one official genetic evaluation release to another, it is possible for DGVs to change for any genotyped animal. The most important contributing factor is the regular changes that can occur in traditional bull proofs from run to run, which also affect the resulting prediction equations used to calculate DGVs for cows, heifers and young bulls. The addition of more genotyped proven sires, such as the 900+ added in January compared to August, into the genomic evaluation system can also have an impact. Daughters of newly proven genotyped sires, or dams of such sires, are more likely to experience changes in DGVs as this genetic information on male ancestors or descendants is added to the estimation of genomic prediction equations. In addition to the annual genetic base update applied to traditional evaluations, it is possible that changes in methodology over time can also affect resulting DGVs.

What is the Status of Genomic Evaluations for Breeds Other Than Holstein?

At CDN, the genotypes for the Jersey and Brown Swiss breed have been used to estimate research-based genomic evaluations. This has been done monthly since September 2009 on an unofficial basis for Jerseys with official implementation currently aimed for April 2010. Analysis of the first genomic results for Brown Swiss has been initiated at CDN while researchers at the University of Guelph have launched a genomics project for Ayrshires and other breeds of small population size in Canada.

Summary

Following the first official release of genomic evaluations for Holsteins in August 2009, there has been strong producer interest and acceptance of genomics as a new important tool for increasing the accuracy of Canadian genetic evaluations. With the rapid evolution of this technology, producers must be aware of updated answers to common questions to ensure a comprehensive understanding of how genomics can improve their genetic selection decisions.

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