Réseau laitier canadien
Canadian Dairy Network

Genomics North and South of the 49th Parallel

Within the North American agreement related to genomic evaluations, both Canada and the United States share a common set of genotypes for use in each country. This means that any animal genotyped in either Canada or the United States is included in the genomic evaluation calculations done by Canadian Dairy Network (CDN) in Canada or by the Animal Improvement Programs Laboratory of the United States Department of Agriculture (USDA). Now that both countries have official genomic evaluations published in the Holstein breed, it is valuable to review the similarities and differences between the calculation methods and implementation strategies.

Starting at the Beginning

Currently, more than 31,000 Holsteins have been genotyped in North America with an average of nearly 1,200 new animals being genotyped every month. In Canada alone, there has been an increasing trend in the number of genotyped animals per month, which is currently between 250 and 300 in total. All of these genotypes, which provide the DNA profile for over 50,000 markers for each animal, are used as the starting point for genomic evaluations in both Canada and the United States.

Estimation of Associations

While both countries started their development of national genomic evaluations with common computer programs written by USDA scientists, the research done on each side of the border has led to some differences in methodology and implementation. One major difference between the procedures used in each country relates to the estimation of associations between genetic evaluations and patterns in DNA profiles from genotyping. In the United States, these associations are estimated using genetic evaluations for all genotyped proven sires (mainly from the US and Canada) as well as genetic evaluations for genotyped cows in the US and Canada. Research in Canada, however, has shown that the accuracy of genomic evaluations in Canada is reduced when cow evaluations are used in addition to bull proofs for estimating associations between proofs and DNA profiles. While this difference in data used may not seem important from a practical perspective, it does have a substantial impact on other decisions related to genomic evaluation methods used in Canada compared to the United States. Another factor contributing to differing genomic evaluations in each country for a given genotyped animal is the fact that proven bulls do not have identical evaluations in both countries. There are many examples of bulls with a progeny proof in Canada is that substantially different, either higher or lower, than their proof based on daughters in the United States. When genotyped animals have different genetic evaluations in each country, the resulting genomic evaluations for those animals as well as others will also be different.

Direct Genomic Values and Combining with Traditional Evaluations

The end result of the associations analysis, performed by CDN in Canada and by USDA in the US, is prediction equations that are applied to translate the DNA profile for each genotyped animal into their Direct Genomic Value (DGV) for each trait. Alongside this process is also the estimation of a Reliability value to reflect the accuracy of the DGV. Research in both countries, however, has shown that these Reliability values are overestimated and therefore need to be reduced accordingly. Due to the aforementioned differences in data and methods used in Canada and the United States, there is no expectation that both countries apply the same degree of adjustment to the DGV Reliability values. One outcome, however, is that the level of published reliability values associated with genomic evaluations in each country may not be directly comparable. Recent research at CDN following the August 2009 genomic evaluation release has identified enhancements to improve the accuracy of prediction of genomic evaluations. This is expected to increase the average Reliability of GPA LPI values for young bulls and heifers to over 60% with the January 2010 release.

Another difference between the genomic evaluations on each side of the 49th parallel relates to how the information from traditional and genomic evaluations gets considered in the final published evaluations in each country. In Canada, since the estimation of associations is based only on proven sires, the genetic evaluations from the female side of the population need to be considered in combination with each animal's DGV. Based on research at CDN and the University of Guelph, the optimum approach for using all sources of genetic evaluation information is to combine the traditional evaluation with its DGV based on weights proportional to the Reliability of each value. In this manner, Genomic Parent Averages (GPAs) for young bulls and heifers have roughly two-thirds weight on DGV and one-third on its traditional Parent Average. In the United States, since both bull and cow evaluations are already included in the methodology for estimating marker associations and prediction equations, there is very little gain in information by considering traditional genetic evaluations over and above the DGVs.

Publication and Labelling

In addition to differences in genomic calculation methods used in Canada and the United States, the publication and labelling of genomic evaluations also varies. In the United States all genomic evaluations are labelled as a GPTA instead of the traditional PTA, regardless of whether any data on the animal itself or its daughters is included. In Canada, CDN has always identified different types of genetic evaluations as being an EBV (official domestic bull proof or cow index), a MACE evaluation (for foreign sires and dams) or a Parent Average (for young males and females). With genomics, genotyped animals now have the letter "G" added to this evaluation code to become GEBV, GMACE or GPA, respectively. Associated with this distinctive labelling in Canada, top young bulls with a GPA LPI are not presented on the same list as top GLPI progeny proven sires and the same policy is used for top GPA LPI heifers versus top GLPI cows. In the United States, care is required when looking at some lists of top animals where those without performance or progeny (heifers and young bulls) are mixed together with those with performance or daughters (cows and progeny proven sires) since all have evaluations labelled as a GPTA.

Ending With the Bottom Line

The North American agreement for sharing genotypes for the calculation of genomic evaluations in Canada and the United States has been a huge step forward. This level of international collaboration has been mutually beneficial since both countries are among the first in the world to include genomics into their routine national genetic evaluation systems. While harmonization of genotypes used in Canada and the United States is efficient in terms of data exchange and the elimination of duplication, the fact that each country has its own national traditional genetic evaluations that are often different even for the same animal means that genomic evaluations will not be identical. Ongoing research and development in each country has also led to the implementation of differing methods for computation of Direct Genomics Values, which also affects how these DGVs are used in combination with traditional evaluations to produce published genomic evaluations. The end result is that each country aims to provide the most accurate genetic and genomic evaluations for use by their respective producers and industry personnel. Therefore, the bottom line for anyone in Canada interested in using genomic information for genetic selection decisions is to consult the official evaluations freely available on the CDN (www.cdn.ca) or Holstein Canada (www.holstein.ca) web sites.

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