

The Basics of Genomics

Given that the genetic information of every animal is contained in its DNA, technology now available allows for genotyping males and females for over 58,000 different markers across the whole genome. The laboratory analysis provides a DNA profile for each animal, which is unique except for genetically identical sibs, such as twins produced from split embryos, for example.

For calculating genomic evaluations in the Holstein breed, Canadian Dairy Network (CDN) currently uses a group of over 2,200 sires that have an official proof in Canada plus another group of over 4,700 sires with only a MACE evaluation in Canada, which are mainly sires already proven in the United States. The genotypes for this pool of nearly 7,000 proven sires results from a joint research initiative between Canada and the U.S. with involvement from various major A.I. companies in North America. The basis for estimating genomic evaluations for young bulls, heifers and cows comes from a comprehensive analysis of associations between the DNA profiles for the pool of reference proven sires and their proof for each trait of interest. Currently, CDN estimates genomic evaluations for over 60 different traits that are included in existing genetic evaluation systems for dairy breeds in Canada.

Combining Information

The end product of the new genomic calculations at CDN is a Direct Genomic Value (DGV) for each trait for every genotyped animal. On a trait-by-trait basis, each animal's DGV is combined with its traditional genetic evaluation, which may be a Parent Average (PA), an official domestic evaluation (EBV) or a MACE proof (MACE). After blending, the resulting genomic evaluations to be officially published starting August 2009 will be labelled in Canada as **GPA**, **GEBV** and **GMACE**, respectively. In Canada, the blending step weights the DGV and the traditional genetic evaluation in proportion to their respective Reliability. For young sires and heifers, the weight on the genomic information in their GPA is approximately 65% and the remaining 35% comes from their traditional PA. For young cows in first or second lactation, the relative weighting is roughly 55:45 on the DGV versus the traditional EBV. For older cows and proven sires, both the DGV and EBV receive similar weightings close to 50%.

Gains in Accuracy with Genomics

While Canada and United States are using a common pool of genotyped animals for estimating genomic evaluations, the final results in each country may often

be different. These discrepancies come from different PAs or EBVs for many animals in each country as well as slightly different technical details associated with calculation data and methods. For genetic selection decisions in Canada, genomic evaluations from CDN should be used over those from the United States. Gains in accuracy of evaluations with genomics vary by trait and sub-group of animal in the population. For young sires and heifers, the average Reliability of their GPA for LPI is 60%, which is a gain of 29 Reliability points over the average of 31% for traditional PA LPI. While this doubling of accuracy is very significant and young sires with genomic evaluations should be used with more confidence than PA young sires previously, caution is still warranted. It is important to note that the average Reliability of proven sires with their first crop of daughters also increases with genomics from an average of 83% for LPI to 88% for their genomic LPI (GLPI). Gains for first and second lactation cows are from 51% Reliability for LPI to 68% for GLPI.

Accuracy Gains as Daughter Equivalents

Rather than looking at the increases in Reliability with the inclusion of genomics, it is also possible to equate those gains to daughters in their proof. For example, the average Reliability of GLPI for young sires is 60%. With traditional genetic evaluations, a bull with a Reliability at this level would have, on average, less than 10 daughters in his production proof or, about a dozen classified daughters.

Accuracy Versus Risk

The additional accuracy from genomics leads to better mating decisions compared to using PA alone, but it is advisable to use a limited number of doses from any one GPA young sire and select several of them. Theoretically, with a 60% Reliability, 10% of all young bulls with a genomic evaluation are expected to have a true LPI that is at least 725 points higher or lower than its estimated GPA for LPI.

Future Top LPI Listings

With the official publication of genomic evaluations starting August 2009, the top lists will be modified. For proven sires, those with a GEBV will be indicated by a "G" code on all top lists. For cows and heifers, the current Top LPI lists will include only animals that have their genomic information included. Non-genotyped females will be listed separately, in descending order of LPI (or PA LPI for heifers), on a new report entitled the "Top LPI Genotyping Candidate" list to assist owners in identifying females in their herd they should genotype.

Use Genomics to Improve Genetic Selection Decisions & Genotype Key Animals!