Réseau laitier canadien

Canadian Dairy Network

Comparing DGVs and Traditional Evaluations

Since genomic breeding values were officially released more than one year ago, many have tried to decipher the exact relationship between an animal's Direct Genomic Value (DGV) and its traditional genetic evaluation, especially in cases where the DGV is much higher (or lower) than expected. In order to maximize the accuracy of selection decisions made today by breeders and A.I. companies purchasing young bulls, research determined that the most appropriate way to use genomic information was to blend the estimated value from the DNA profile with the animal's traditional genetic evaluation. The significant gains in accuracy achieved by incorporating genomic information were greatest for young bulls and heifers, where reliability of genomic values nearly doubled compared to their Parent Averages (PA), which averaged around 35% traditionally. Gains in accuracy for proven sires were much lower, as their traditional breeding values were already extremely reliable and incorporating genomic information only provided minimal added insight.

Genotypes are static but Direct Genomic Values can change

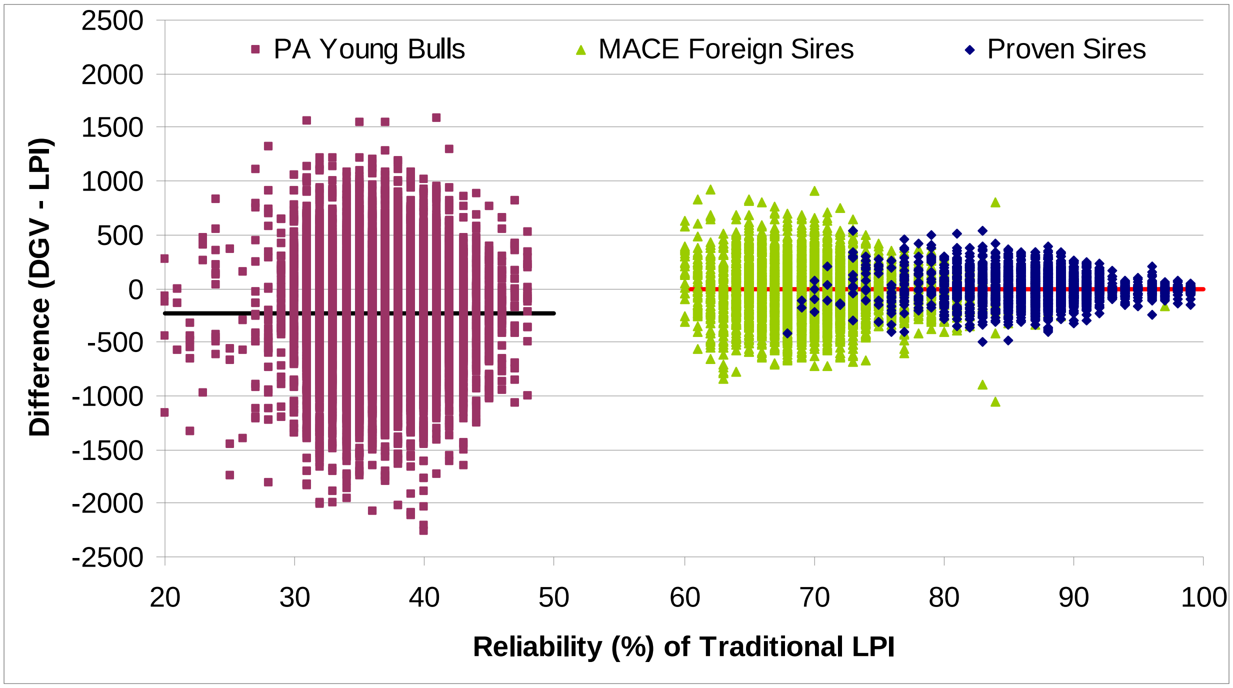
Although an animal's genotype does not change, the relationship between its genotype and how this specific combination of genes is expressed in the evaluated population of proven sires can change. DGV are calculated by first comparing the proof for all genotyped proven sires to trends in their DNA profile at each of the 50,000+ markers. Next these known associations between DNA profiles and bull proofs are applied to all genotyped animals, including young sires, heifers, cows and proven sires. Therefore, as traditional bull proofs change from run to run and new bulls receiving official proofs are constantly added, the associations to proven bull genotypes are modified, subsequently altering the DGV for most genotyped animals. Animals most likely to experience change in their DGV are daughters of newly proven genotyped sires, or dams of such sires. Additional sources of change to DGV include the annual genetic base update applied to traditional evaluations as well as changes in methodology.

To that extent can DGV and traditional values differ?

In order to help explain the relationship between genomic and traditional values, all animals that were genotyped in North America that received a genomic evaluation in Canada in August 2010 were investigated. Difference between DGV LPI and traditional LPI were calculated for several groups of animals. Results are shown in Figures 1 and 2 plotted by reliability of traditional LPI for males and females respectively.

As reliability of traditional LPI in males increases, the range in difference between DGV LPI and what we would have expected without the inclusion of genomic information decreased or narrowed. Younger males can have a DGV LPI that is more than 1500 points higher or 2000 points lower than their PA, whereas, this range of difference in domestically proven sires is less than ±400 LPI points. As we continually incorporate daughter records over time, a sire's traditional LPI becomes highly reliable and significantly dictates what his DGV LPI will become. On average, a young bull's DGV was 231 points less than its traditional PA LPI, whereas there was no overall downward bias in this difference for domestically proven or MACE foreign sires.

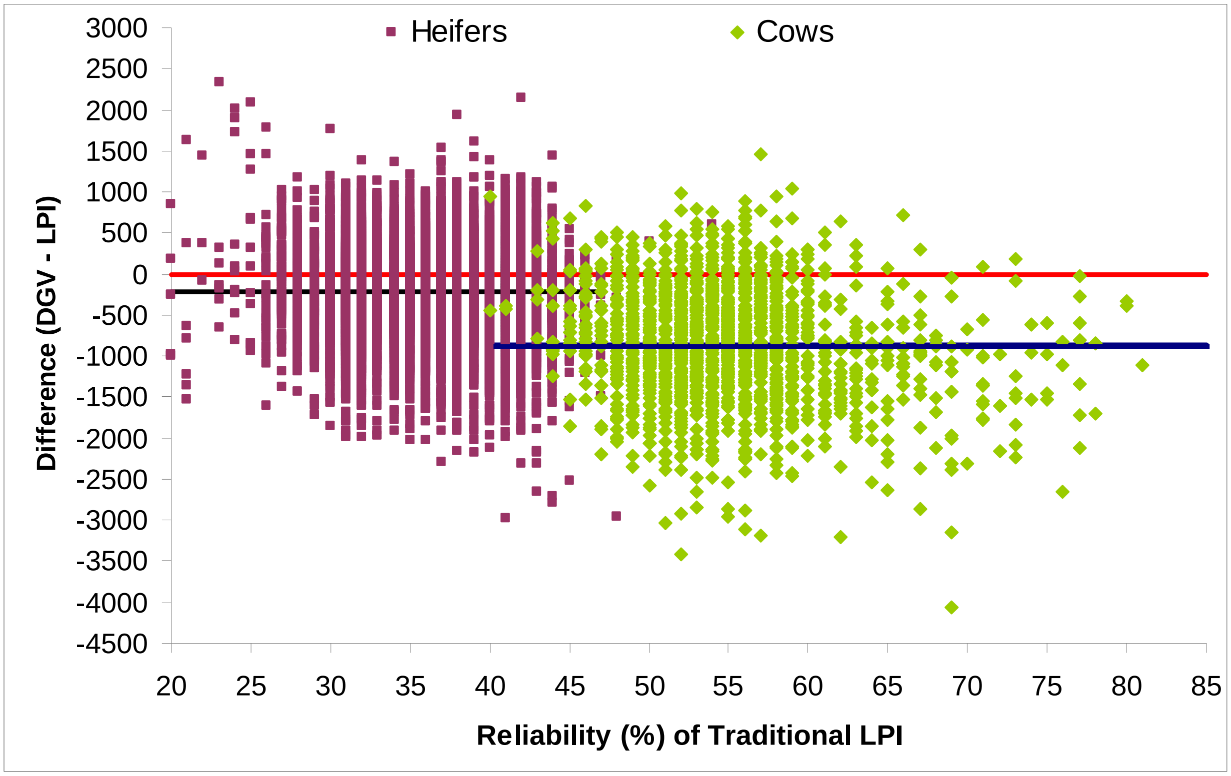
Figure 1. Difference between DGV and Traditional LPI in Holstein Males



For females, the range in difference of DGV from the traditional evaluation was similar to males but the average change was more negative. DGV LPI in heifers can range from about 1500 above to 2000 points below their PA LPI. Difference between DGV LPI and traditional LPI in cows ranged from about 1000 points above to 3000 points below. DGV LPI in females tended to be lower on average compared to their traditional LPI. This average drop was 211 LPI points in heifers and 860 LPI points in cows. It is important to reaffirm that official published breeding values on genotyped animals are a combination of DGV and traditional evaluations. Differences (drops or increases) realized in the published evaluations once an animal is genotyped would therefore be approximately half of the differences shown here. In young animals, DGV LPI contributes 65% to the weighting in officially published genetic evaluations and the PA contributes the remaining 35%. These pieces of information are weighted equally in proven sires.

Genomics has brought a huge amount of accuracy to the estimation of a female's breeding value, especially early in life. Average increase in reliability of LPI by including genomic information was 28 percentage points in heifers and 15 points in cows in August. However, since traditional cow indexes have tended to be overestimated, having more accurate genomic-enhanced information brings an average decrease in published values. Most marketers of elite females and embryos from elite females have more than accepted this average down-shift in the genetic evaluations of females and have placed a much higher value on the boosted accuracy of the information, especially in young animals.

Figure 2. Difference between DGV and Traditional LPI in Holstein Females



Summary

Genomics has given breeders and A.I. organizations an incredible tool to select and market animals more accurately nationally and internationally. The most appropriate use of genomic information remains in combination with traditional evaluations using pedigree and performance data. Young animals tend to have a large variation in how their genomic LPI compares to their traditional PA. On average, DGV LPI in heifers and young bulls is lower than their PA. Genomics pulls the breeding value of these young animals closer to how we would expect them to perform in the future long before their own or daughter performance can be recorded. Proofs for domestically proven sires are extremely reliable with or without the inclusion of genomic information, but even in this select group of animals their DGV LPI and traditional proof can vary by up to 400 points.

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