Réseau laitier canadien
Canadian Dairy Network

Predictability of First Proof Using Genomics

The release of proofs in August 2010 commemorates one full year since the official incorporation of genomic information into the calculation of genetic evaluations by CDN for Holsteins. In total, almost 50,000 genotypes are now being shared in North America and incorporated into genetic evaluation procedures on both sides of the border. More recently, in April 2010, official genomic evaluation procedures in the Jersey breed were also released for the first time in Canada. Since successful inclusion of genomic information into evaluations procedures was achieved, research has consistently shown a remarkable gain in accuracy of predicting breeding values given the enhanced at-birth knowledge we now have that can relate genotypes to animal performance. Now that we have enjoyed an entire year of enhanced genetic evaluations and selection possibilities due to genomics, it's an appropriate time for a look at how these tools have affected our ability to predict a bull's genetic worth.

Tools for Estimation

The ideal scenario is to have increased confidence in the merit of a bull when he is being considered for inclusion into further testing and proving procedures (i.e., semen collection and progeny testing). Prior to August 2009, the primary selection and mating tools for young animals on farm and in the A.I. industry for decades was limited to Parent Average and performance of relatives. Traditional genetic evaluation calculations try to isolate the component of an animal's recorded performance that is due solely to genetics, by attempting to remove any known management and environmental factors. Only this estimated genetic component is what can be transmitted from parent to progeny. Genomics is giving us the ability to isolate this genetic component much more accurately and may become the greatest tool to boost selection decision confidence since the advent of artificial insemination more than 70 years ago.

In order to receive an official LPI, a bull has to have a minimum number of daughters and herds (for Holsteins it is 20 daughters passed 120 days in milk in at least 10 herds) as well as pass minimum reliability levels for both production and type. A total of 225 genotyped Holstein bulls passed these requirements in either April or August 2010 to receive their first official progeny proof and were included in this study. Both the predictability of traditional Parent Averages (PA) and those with the inclusion of genomic information (GPA) were considered for three consecutive proof runs prior to these bulls receiving their first official LPI. It is important to note that the primary selection tool for entry into A.I. for this group of newly proven bulls was limited to traditional methods, including PA. No genomic information would have been available at the time of their birth. Bulls expected to receive their first proof in late 2013 will be the first group to have had the opportunity to have been selected using their first official GPA LPI in August 2009. In addition to sharing genotypes, foreign female information is now exchanged across the border, increasing the accuracy of information for influential dams from non-domestic sources.

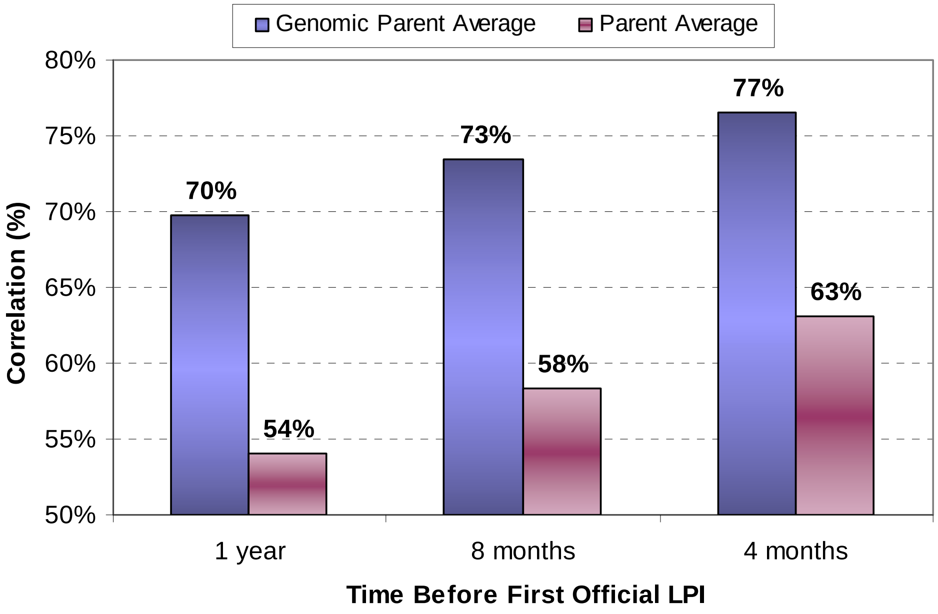
Overestimation of LPI Using PA Versus GPA

In general, Parent Average, with (GPA) or without (PA) genomics, tends to overestimate the eventual LPI when first proven. In other words, bull merit most often drops from the time of selection to the time of first proof. However, this drop is much less severe with genomics. On average, the PA LPI a year (3 proof runs) prior to reaching official release status was 393 LPI points higher in this study compared to the traditional LPI they would have received. With the improved accuracy of GPA, this overestimation of young sire evaluations was decreased by 62%. The average difference between their first official GLPI and their GPA LPI a year earlier was only 149 LPI points. Even when bulls are only four months (1 run) from reaching official status, PA was overestimating their first proof by more than 300 LPI points and including genomics removed nearly 70% of this average bias. In addition, the range in difference from GPA to first official LPI was much narrower than with traditional PA regardless of the time period in advance.

Predictability of LPI Using PA Versus GPA

As shown in the chart, predictability of first official LPI using GPA was higher at twelve, eight and four months prior to official release compared to only having traditional PA information. Genomics improved the predictability of eventual LPI over a traditional PA by 14-16 percentage points depending on how much time was to elapse before the release of the first official LPI. Even four months prior to official release, a traditional PA was only 63% related to the eventual LPI, whereas with the inclusion of genomics, this prediction increased to 77% correlation.

Predictability of First Official LPI using PA or GPA



Final Note

With the eminent launch of genotyping services using the new 3K panel, the expectation is that the number of animals genotyped (especially cows and heifers) will increase dramatically. At the farm level, this newly commercialized panel represents increased opportunities to capitalize on genomic information at a cheaper price. Research indicates that genotypes obtained from low density panels can be included in genomic evaluation to increase predictability of the genetic potential with almost no loss in accuracy as compared to the current standard of genotyping with the larger 50K panel. As more panel options are offered commercially for wide spread use, the prospects to mate animals more appropriately and have increased confidence in selection for A.I. becomes much more precise. One year prior to receiving an official LPI, a bull's GPA is already 70% correlated to his eventual first proof. Prior to the availability of genomic evaluations we would have only been 54% sure of the next great one coming one year away!

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