

Experiences in Validating Genomic Evaluations

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Abstract

Several approaches were used to validate genomic evaluations for Holstein bulls in Canada. Four year old data was used to calculate estimated breeding values both with and without including genomic information and these breeding values were compared to current official domestic proofs. Results showed that using genomic information improved the accuracy of estimated breeding values for young bulls but these accuracies remain much lower than accuracies of progeny tested bulls.

Keywords: genomic evaluations, validation, Holstein

Introduction

Canada has been working on implementing genomic evaluations for all traits in the Holstein breed for official release in August 2009. As part of this process genomic evaluations need to be validated. Genomic proofs will be used by different people for different purposes and as a result different validation methods may be required. Most of the validation methods (Schenkel *et al.*, 2009, Sullivan, 2009) have looked at improvements in accuracy within a group of young bulls without any progeny information. This is important when selecting young bulls for a progeny testing program but this is not an appropriate method when young bulls are going to be compared to proven bulls. Therefore, different approaches to validating genomic evaluations were applied with the aim of obtaining results that are easy to understand and have practical meaning to the industry.

Data and Methods

The basis for all validation methods used was to see how well proofs based on four year old data predicted the current official domestic bull proofs. Data used were estimated breeding values (EBV) for Holstein bulls as they were officially published in Canada in February 2005 including both domestic proofs and MACE proofs on the Canadian scale. These proofs were used as the input for genomic evaluations using the software (VanRaden, 2008) and method as implemented in Canada in August 2009 (Van Doormaal *et al.*, 2009) with the exception that the weight on the polygenic effect was 5% rather than 20%. Resulting direct genomic values (DGV) were

combined with the original EBV (Sullivan, 2009) using a weighted average with the reliability of each proof used as the weight to obtain the genomic breeding values (GEBV). The three sets of breeding values were validated by comparing them to the Canadian August 2009 domestic bull proofs (EBV) for officially proven bulls.

Results

Results presented in this paper were calculated using genotyped bulls with an official Canadian domestic proof in the August 2009 run. In addition, bulls needed to be matched to their proof from four years ago which resulted in a total of 2344 domestically proven bulls with an LPI that could be used. Of these bulls 75 had a MACE proof, 1276 already had a domestic proof four years ago and 993 only had a parent average (PA) four years ago. Proofs from four years ago were base adjusted using the 1276 bulls that had an official domestic proof in both runs. Base adjustments were performed using genotyped bulls with an official domestic proof for each specific trait. Therefore, exact counts varied across traits but were fairly similar except for traits without MACE evaluations using USA proofs. All results included in this paper are based on these groups of bulls and bulls that have not yet been genotyped were excluded from the analysis.

R-Square

The R-square is used frequently in validating genomic evaluations. Typical usage has been to look at the R-

square for bulls that only had a parent average (PA) several years ago but have an official proof now and examine how much the R-square increases when adding genomic evaluations to the PA. This approach certainly has its benefits in that it is easy to apply and shows whether direct genomic values (DGV) or genomic parent averages (GPA) evaluations improve the PA accuracy for young bulls. Accuracy of selection among young bulls is very important since it affects the genetic level of bulls entering progeny testing programs and as a result an improvement in ranking will have a big impact on genetic gain. The disadvantage of this method is that although it shows the improvement in the accuracy of breeding values for young bulls it does not consider how the breeding values of young bulls compare to progeny proven bulls. The R-square is a useful tool for validating genomic proofs of young bulls when selection is performed within this group of bulls. Comparing R-square values for different methods showed (Figure 1) that genomic evaluations resulted in a more accurate ranking of young bulls. There was an improvement for nearly all traits but for traits without MACE proofs or without the USA contributing to the MACE proofs there was a much smaller increase in the accuracy due to genomic evaluations. There was not much difference in R-square between the DGV and GPA for these bulls.

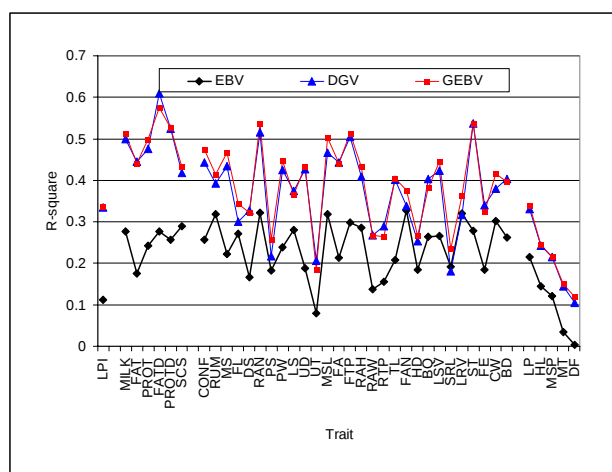


Figure 1. R-squares when using three different methods to calculate 4-year old parent averages to predict current official domestic bull proofs for various traits.

Slope

In order for proofs from different groups of bulls to be comparable the scale of the proofs should be comparable (Sullivan, 2009). Evaluations for young bulls with a PA usually have a different scale than proven bulls. For the current usage of PA values this is not a problem since these bulls are usually directly compared. Bulls with a PA are used by AI organizations to select bulls for entry into the progeny test programs but these bulls are not compared to proven bulls. Farmers do use the PA when they select which of the young bulls they want to use as part of the progeny test program but they are aware of the lower accuracy of these evaluations and only use young bull semen for a limited number of inseminations. When genomic information is used to improve the PA and a GPA is calculated the expectation is that industry will start using these GPA bulls. Farmers might start to consider using GPA bulls in addition to or instead of proven bulls. At this stage it becomes important that the GPA values are not only accurate but are also comparable to the GEBV for official proven bulls. When comparing slopes from the regression of current proofs on old proofs (Figure 2) it can be seen that for the slope of the PA for young bulls was always less than 1. This means that the range of proofs for young bulls was overestimated relative to already proven bulls. The relative slope for PA LPI was only 0.5, which means that the range of proofs for young bulls was a factor two too high. As a result top young bulls would have an LPI which was much too high relative to proven bulls. For most traits the relative slopes for the DGV were higher (closer to 1) compared to the PA slopes showing that the scale of expression for young and proven bulls were more similar. All of the slopes for PA and DGV were still less than 1 and the ranges of these proofs were still too high for young bulls. The GPA values had relative slopes that were much closer to 1 especially for the production and major type traits, the slope for LPI was .92 meaning that the GPA for young bulls tended to be overestimated by less than 10% (relative to already proven bulls).

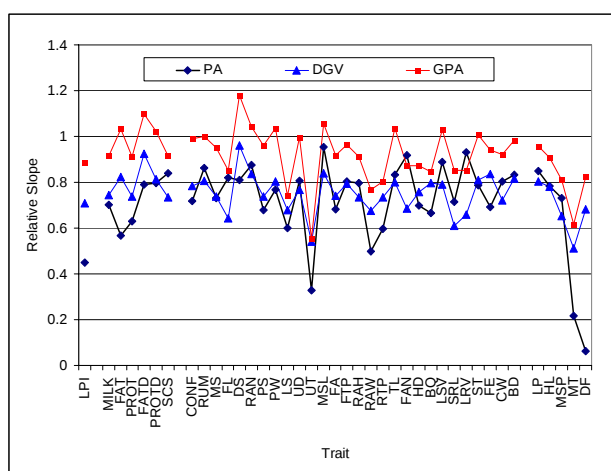


Figure 2. Slope of the regression of current proofs on 4-year old parent averages for young bulls relative to the slope for proven bulls when using three different methods to calculate parent averages.

Top Lists - Domestic Proven Bulls

Bulls on top lists are used more than any other bulls and have a big influence on both genetic improvement and the perceived accuracy of genetic evaluations. Since the most used top lists in Canada only contain proven bulls, it is useful to see how accurate these top lists are. Figure 3 shows the effect of changing proofs on the ranking of bulls for bulls that already had an official proof four years ago. The ranking in each set of proofs was based on the same group of around 1276 bulls that were genotyped and had an official domestic proof four years ago. For production and type traits, around 80% of the proven bulls that appeared in a top 100 list were correctly placed in this list and about 20% of the bulls should not have been on this list (compared to proofs 4 years later). There was not a big difference between types of evaluations which is not surprising since for these bulls the DGV was calculated using the bulls own EBV. The EBV rankings were slightly better but this is probably because the analysis compared the 4-year old proofs to the current EBV (not the current DGV or GEBV) for the same animal.

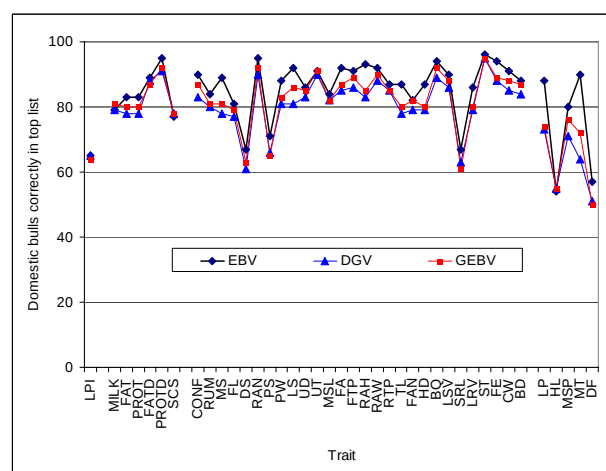


Figure 3. Number of top 100 proven bulls from four years ago that were still in the top 100 among this group of bulls four years later when using three different methods to calculate proofs.

Top Lists - Young Bulls

Top lists for each set of proofs were based on the same group of around 993 young bulls that had a PA four years ago but currently have an official domestic EBV. Using genomic evaluations (DGV or GPA) for young bulls improved the accuracy of selecting top bulls for most traits (Figure 4) compared to using their PA. These results give an indication of how rankings are affected when bull proofs change from a parent average to an official proof. For young bulls using the DGV resulted in a ranking that was more accurate compared to using the PA especially for LPI and production traits. Combining PA and DGV into the GPA seemed to have very little impact compared to directly using the DGV. On average, only around 35% of the top bulls in this group were correctly identified when the EBV was used but rankings for LPI and production traits were less accurate. Using DGV (or GEBV) improved the percentage of bulls correctly included in the top 100 to approximately 40% for the LPI and type traits and 45% for production traits.

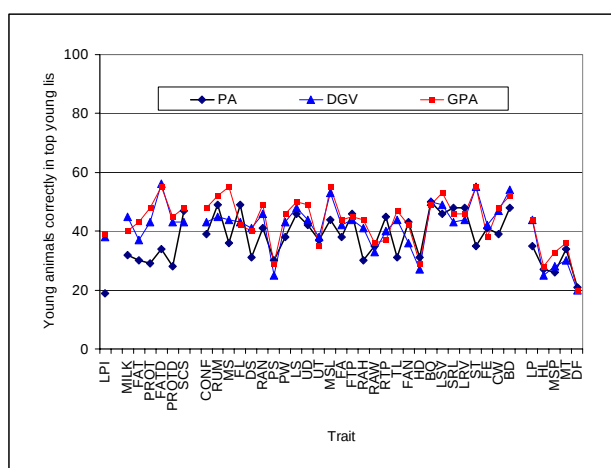


Figure 4. Number of top 100 young bulls from four years ago that were still in the top 100 within this group when they have an official proof four years later, using three different methods to calculate proofs.

Top Lists – All Bulls

When genomic evaluations are published it is very likely that selection is going to shift towards selecting a combination of progeny tested and younger bulls. Therefore, it is important that the top list across these groups of animals includes the best bulls. Figure 5 shows the effects of changes in proofs for genotyped bulls that currently have an official domestic proof (around 2344 bulls) compared to the proof they had four years ago regardless of whether that proof was domestic, MACE or just a parent average. The ranking of bulls improved when using the DGV or GEBV compared to using the EBV especially for the LPI the production traits. Comparison with Figure 3 shows that identifying top bulls within this group is much more difficult then when just looking at progeny proven bulls. When using bulls from this list there is about a 50% chance that the selected bull remains among the top 100 bulls four years later (within the same group of bulls).

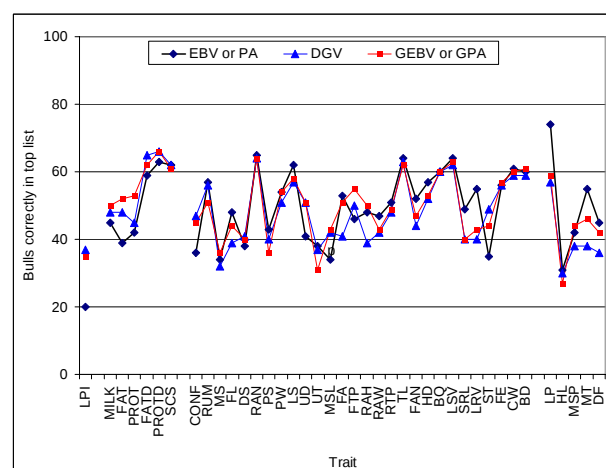


Figure 5. Top 100 bulls from four years ago that are still in the top 100 four years later when using bulls that are genotyped and currently have an official domestic proof, using three different methods to calculate proofs.

Summary and Conclusions

Results show that including genomic information into genetic evaluations increases the accuracy of resulting proofs. Different methods can be used to help validate these proofs and the method that is most suitable depends on the use of the resulting evaluations (comparison across groups of bulls or just within each group). Although GPA are more accurate than PA for young bulls it is important for the industry to realize that the accuracies of GPA proofs for young bulls remain much lower than the accuracies of proofs for progeny tested bulls. Therefore, if at this stage there is a large shift from the usage of proven bulls to the usage of a few selected GPA bulls this may result in a lot of people being disappointed with genomic evaluations.

References

- Schenkel, F.S., Sargolzaei, M., Kistemaker, G., Jansen, G.B., Sullivan, P.G., Van Doormaal, B.J., VanRaden, P.M. & Wiggans, G.R. 2009. Reliability of genomic evaluation of Holstein cattle in Canada. *Interbull Bulletin* 39, 51-58.
- Sullivan, P.G. 2009. Options for combining direct genomic and progeny test results. *Report to Genetic Evaluation Board of CDN, June 24, 2009 (Unpublished)*.
- Van Doormaal, B.J., Kistemaker, G.J., Sullivan, P.G., Sargolzaei, M. & Schenkel, F.S. 2009. Canadian implementation of genomic evaluations *Report to Interbull Open Meeting, Barcelona, Spain, August 21-24, 2009. Interbull Bulletin* 40, 314-318.
- VanRaden, P.M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91, 4414-4423.