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IMPLEMENTATION OF MARKER ASSISTED EPDs

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INTRODUCTION

Genomic information, in the form of Single Nucleotide Polymorphisms, has always held the promise to increase the accuracy of Expected Progeny Differences (EPD). This promise has finally been realized for those breeds that incorporate this information into their EPD calculations. For those breeds that have not, genomic information for complex traits (those controlled by many genes) is available to producers in a disjoined context and is published separately from EPD. Depending on the accuracy of the genomic test (as measured by the proportion of genetic variation explained) Marker-Assisted (or genomic enhanced) EPD can increase the accuracy of animals and lead to faster rates of genetic change.

BACKGROUND

The US Beef Industry has witnessed considerable evolution in terms of the genomic tests available in the market place. The tests that are currently being included in EPD are comprised of either 384 SNP or 50,000 (50K) SNP, although the research community is commonly using 50K or 770K genomic tests for discovery of "novel" traits (i.e. feed efficiency, disease susceptibility). The American Angus Association (AAA) began including genomic predictions into EPD calculations to producer Marker-Assisted EPDs (MA-EPD) in 2009. The list of traits for which this is done has continued to grow and can be found in table 1. The American Hereford Association (AHA) is on the verge of releasing MA-EPD and it is likely other breeds that wish to remain competitive will follow the lead of these two.

A common, and fair, question is to ask why genomic predictions are available for heavily recorded traits (i.e. growth) and not "novel" traits such as different measures of efficiency or disease susceptibility. In order to develop genomic tests, there must exist phenotypes to "train" the markers, where training is simply determining if there is an association between each marker and the trait of interest and quantifying that effect. Consequently, the first genomic tests focus on those traits for which vast phenotypic resources exist. There are large USDA funded projects currently underway that are focused on the two "novel" traits mentioned above.

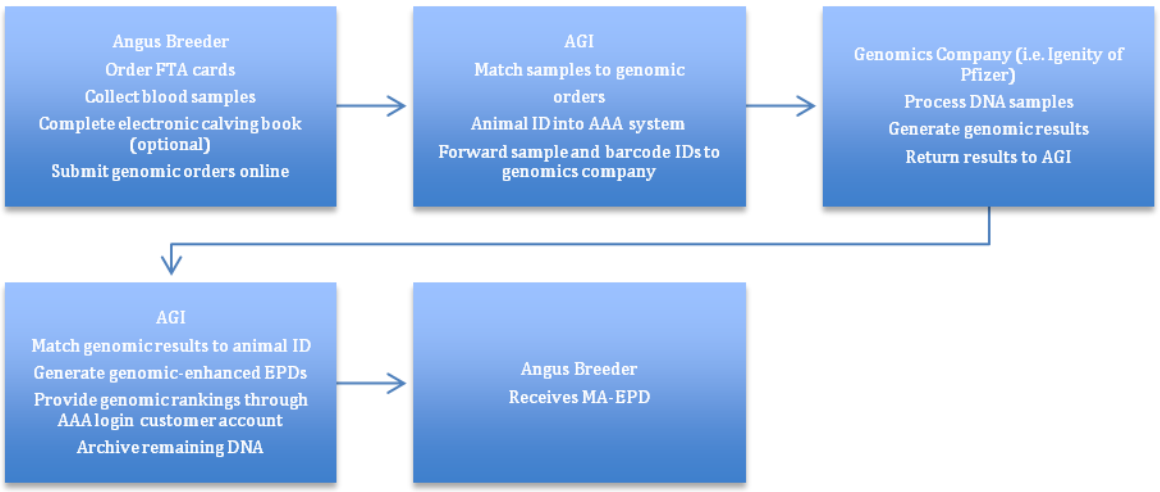
Table 1. Summary of traits for which the American Angus Association uses genomic results in EPD estimates by company.

Trait	Igenity	Pfizer
Calving Ease (Direct and Maternal)	X	X
Growth (BW, WW, YW, Milk)	X	X
Residual Average Daily Gain (RADG)	X	X
Docility	X	
Carcass (CWT, MRB, RIB, FAT)	X	X

IMPLEMENTATION

Figure 1 depicts the flow of information from a breeder beginning with a DNA sample and ending with a MA-EPD. This is the model that AAA uses, but the model that AHA will use is considerably different and will not require involvement of genomic companies.

Figure 1. The flow of information from a DNA samples to a Marker-Assisted EPD in the model currently used by the American Angus Association.



The underlying question commonly asked by producers is "does it work?". It is critical to understand that this is not a valid question, as the true answer is not binary (i.e yes or no). The important question to ask is "how well does it work?", and the answer to that question is related to how much of the genetic variation the marker test explains. The magnitude of the benefits will depend on the proportion of genetic variation (%GV) explained by a given marker panel, where the %GV is equal to the square of the genetic correlation multiplied by 100. Table 2 shows the relationship between the genetic correlation (true accuracy), %GV and BIF accuracy. Table 3 summarizes the genetic correlations for the two tests that AAA currently utilizes.

Table 2. The relationship between true accuracy (r), proportion of genetic variation explained (%GV), and Beef Improvement Federation (BIF) accuracy.

R	%GV	BIF
0.1	1	0.005
0.2	4	0.020
0.3	9	0.046
0.4	16	0.083
0.5	25	0.132
0.6	36	0.200
0.7	49	0.286

Table 3. Genetic correlations (rg) between traits and their genomic indicators used by the American Angus Association by company.

Trait	Igenity rg (384 SNP)	Pfizer rg (50K SNP)
Marbling	0.65	0.57
Ribeye Area	0.58	0.60
Fat	0.50	0.56
Carcass Weight	0.54	0.48
Birth Weight	0.57	0.51
Weaning Weight	0.45	0.52
Yearling Weight	0.34	0.64
Milk	0.24	0.32
Dry Matter Intake	0.45	0.65
Docility	0.47	---

MacNeil et al., (2010) utilized Angus field data to look at the potential benefits of including both ultrasound records and MBV for carcass traits in genetic evaluations. The MBV evaluated were produced specifically for Angus cattle and provided to AAA by Igenity. The MBV were developed using genotypes and EPD from 1,710 Angus bulls. The genetic correlations between the MBV and carcass traits are reflected in table 3 above. Although the genetic correlations between the MBV and the Economically Relevant carcass traits are moderate, they are not perfect predictors.

In contrast to the thought process of DNA marker panel results being a separate and disjoined piece of information, these test results should be thought of as a potentially useful indicator that is correlated to the trait of interest. As such, the MBV can be included in NCE as a correlated trait following methods of Kachman (2008). This is the approach that AAA is currently using. Other methods have been proposed including "blending" the EPD and MBV which is the equivalent to forming an index of the two where the index weights reflect the accuracy of the two components. Yet another approach is to use the actual SNP genotypes to form a genomic relationship matrix that could allow for known relationships between animals based on genotypes across SNP loci. The latter approach requires access to the genotypes, not just the MBV. Combining these sources of information, molecular tools and traditional EPD, has the potential to allow for the benefits of increased accuracy and increased rate of genetic change.

Figures 2-5 illustrate the benefits of including a MBV into EPD (or EBV which is twice the value of an EPD) accuracy (on the BIF scale) when the MBV explains 10, 20, 30, or 40% of the genetic variation (GV), which is synonymous with R^2 values of 0.1, 0.2, 0.3, and 0.4. The darker portion of the bars shows the EPD accuracy before the inclusion of genomic information and the lighter colored portion shows the increase in accuracy after the inclusion of the MBV into the EPD calculation. As the %GV increases, the increase in EPD accuracy becomes larger. Additionally, lower accuracy animals benefit more from the inclusion of genomic information and the benefits decline as the EPD accuracy increases. Regardless of the %GV assumed here, the benefits of including genomic information into EPD dissipate when EPD accuracy is between 0.6 and 0.7. On the other hand, when %GV is 40 an animal with 0 accuracy could go to over 0.2 accuracy with genomic information alone. This would be the same as having approximately 4 progeny for a highly heritable trait or 7 progeny for a moderately heritable trait (Table 4).

Table 4. Approximate number of progeny needed to reach accuracy levels (true (r) and the BIF standard) for three heritabilities (h^2).

Accuracy		Heritability Levels		
r	BIF	h^2 (0.1)	h^2 (0.3)	h^2 (0.5)
0.1	0.01	1	1	1
0.2	0.02	2	1	1
0.3	0.05	4	2	1
0.4	0.08	8	3	2
0.5	0.13	13	5	3
0.6	0.2	22	7	4
0.7	0.29	38	12	7
0.8	0.4	70	22	13
0.9	0.56	167	53	30
0.999	0.99	3800	1225	700

Figure 2. Increase in accuracy from integrating genomic information that explains 10% of the genetic variation into Estimated Breeding Values (EBV).

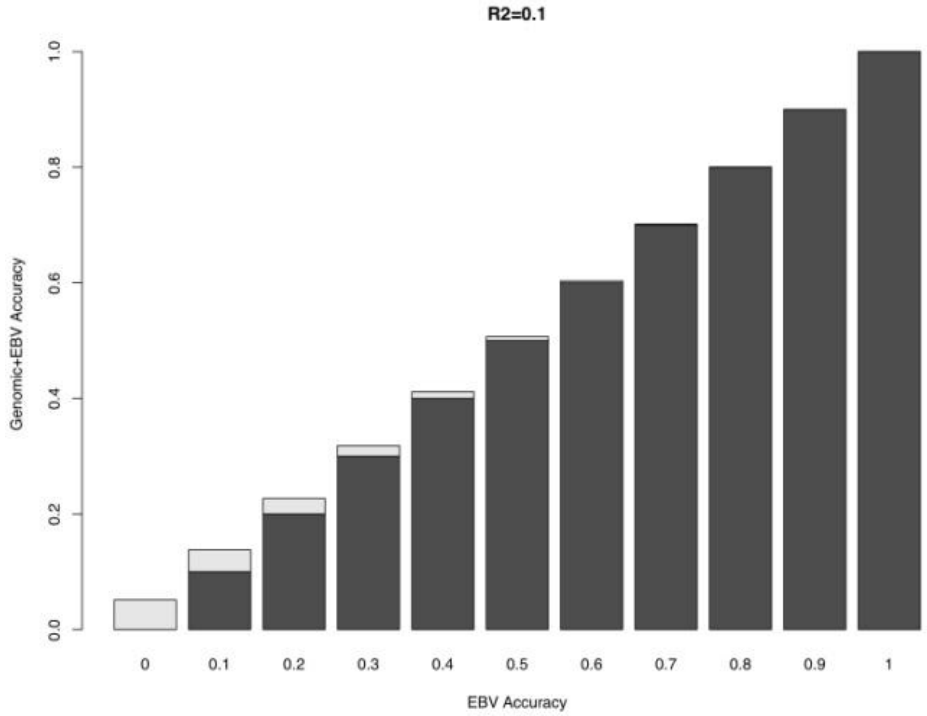


Figure 3. Increase in accuracy from integrating genomic information that explains 20% of the genetic variation into Estimated Breeding Values (EBV).

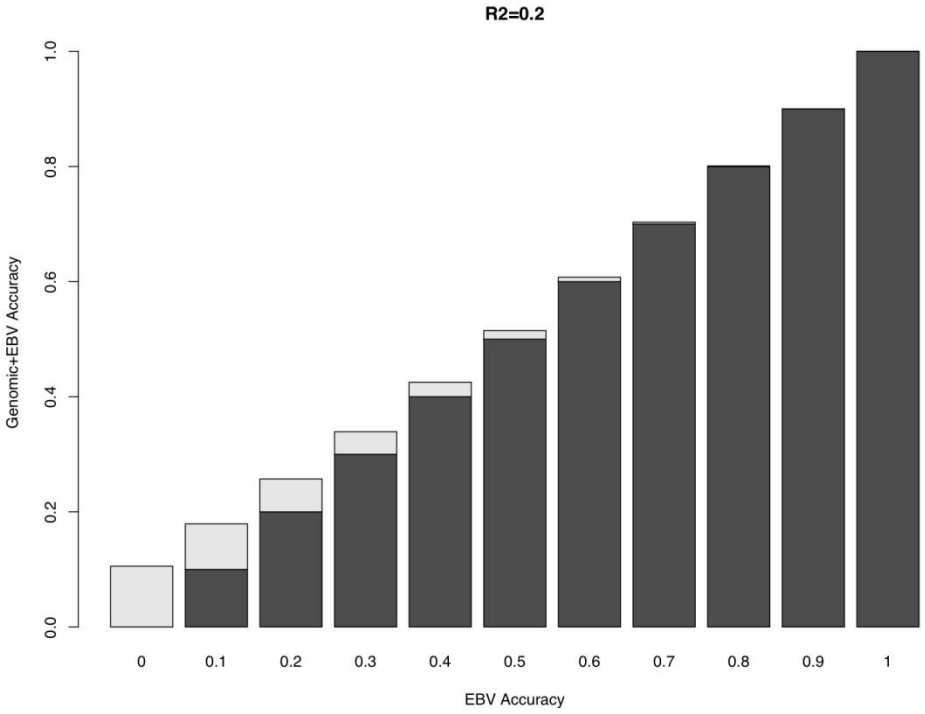


Figure 4. Increase in accuracy from integrating genomic information that explains 30% of the genetic variation into Estimated Breeding Values (EBV).

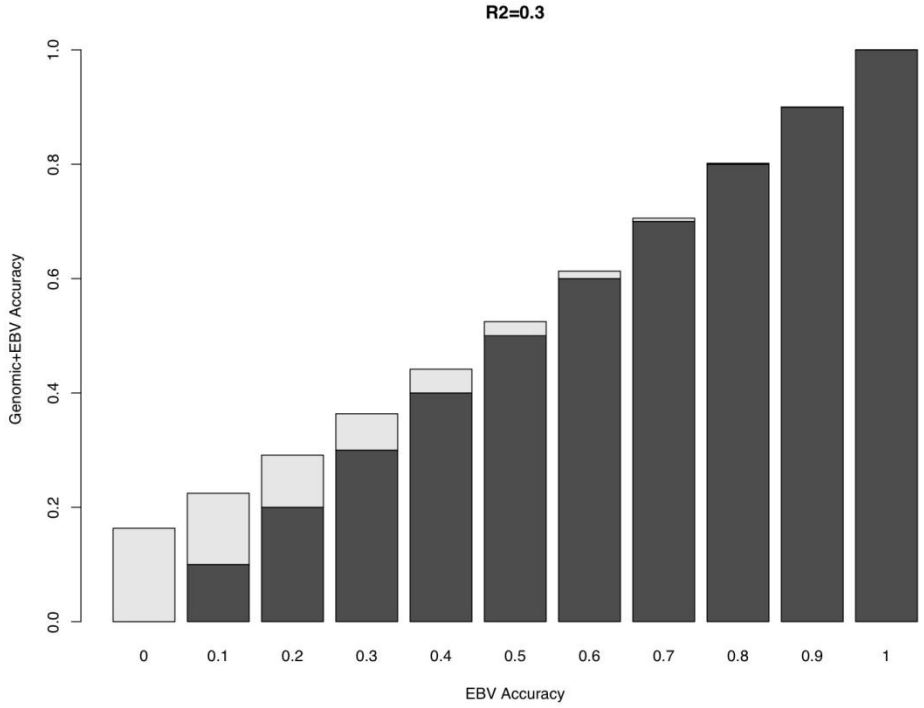
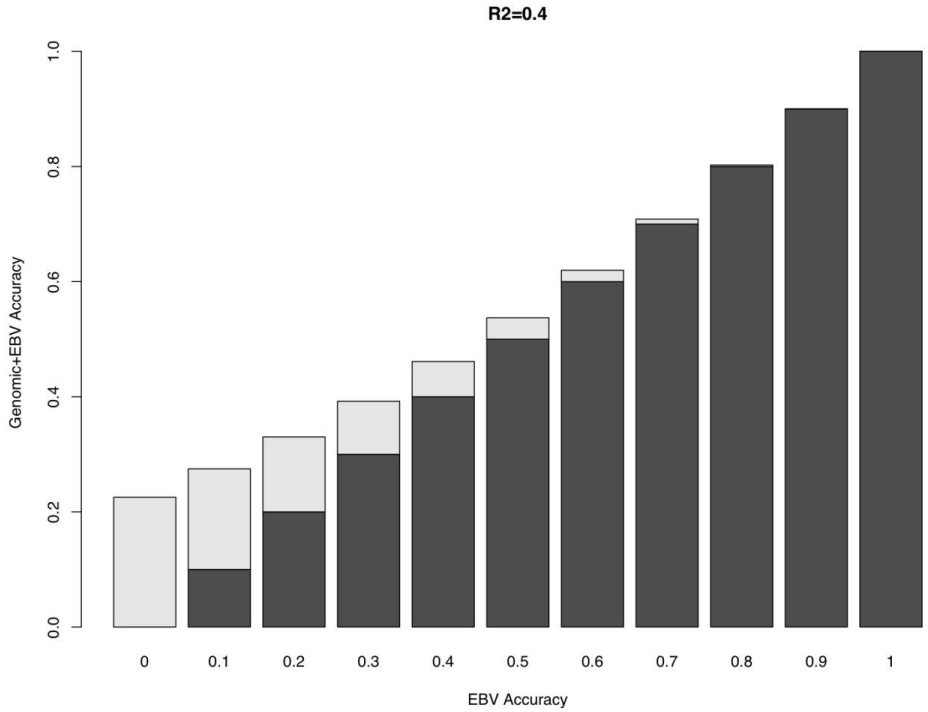


Figure 5. Increase in accuracy from integrating genomic information that explains 40% of the genetic variation into Estimated Breeding Values (EBV).



ISSUE OF ROBUSTNESS

It is important to understand some limitations in the current application of Marker Assisted Selection. For instance, current marker panels work best in the populations where training occurred, but will potentially decrease in predictive power as the target population becomes more genetically distant from the training population (de Roos et al., 2008). This has also been illustrated by Kachman et al., (unpublished) who showed that 50K based genomic predictions developed for Angus do not explain a substantial amount of variation even in a closely related breed like Red Angus. The same erosion in accuracy is likely to occur overtime as well (i.e. over generations if panels are not retrained).

Discovery	Target	
Angus	Angus	Closest relationship
Angus	Charolais	↓
Angus	*Bos indicus*	Most distant relationship

CONCLUSION

Genomics and the corresponding Marker-Assisted or Genomic-Enhanced EPD, have become a reality. Within-breed genomic predictions based on 50K genotypes have proven to add accuracy, particularly to young bulls, for several traits. The push going forward will be the adoption of this technology by other breed associations. Furthermore, methodology related to the use of this technology in crossbred or composite cattle is critically needed. The crux of adoption will be getting commercial bull buyers to see the value in, and thus pay, for increased EPD accuracy. There is a still a need to collect and routinely record phenotypic information by seedstock producers and commercial producers need to realize that EPDs, and economic index values, are the currency of the realm for beef cattle selection. Genomic technology only makes these tools stronger, it does not replace them.

LITERATURE CITED

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