Realistic Expectations of Genomics and Current Applications

Matt Spangler, Ph.D.
Department of Animal Science, University of Nebraska-Lincoln

Introduction

DNA information has proven very beneficial in both the seedstock and commercial sectors for identifying carriers of genetic defects and other simple recessive alleles (i.e. red color, horns) and for resolving uncertain paternity. Genomic information, in the form of Single Nucleotide Polymorphisms (SNP), also holds the promise to increase the accuracy of Expected Progeny Differences (EPD) and add "novel" traits to our suite of available EPD. However, the deployment of Marker-Assisted EPD (MA-EPD) is currently limited to the American Angus Association (AAA), although other breeds are moving rapidly towards this goal. The development of selection tools for traits such as feed efficiency, disease resistance, and other novel traits have been slow to develop. In order for these genomic tools to develop and evolve, large resource populations that have these phenotypes collected are required both for discovery and validation of SNP associations with these traits. Consequently, we have seen the development and deployment of genomic tools for traits that we have phenotypes routinely recorded for.

Without the seamless integration of this technology into EPD calculations, we find ourselves in the context of being faced with two disjoined pieces of information: traditional EPD and marker panel results. In this scenario, it is impossible to directly compare EPD to marker panel results. Table 1 shows the relationship between the genetic correlation (true accuracy), proportion of genetic variation explained (%GV) and BIF accuracy. One example to the contrary is the American Angus Association producing MA-EPD using Angus specific panels from both Igenity and Pfizer Animal Genetics. The genetic correlations between the genomic test and the trait of interest is detailed in table 2.

Table 1. 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

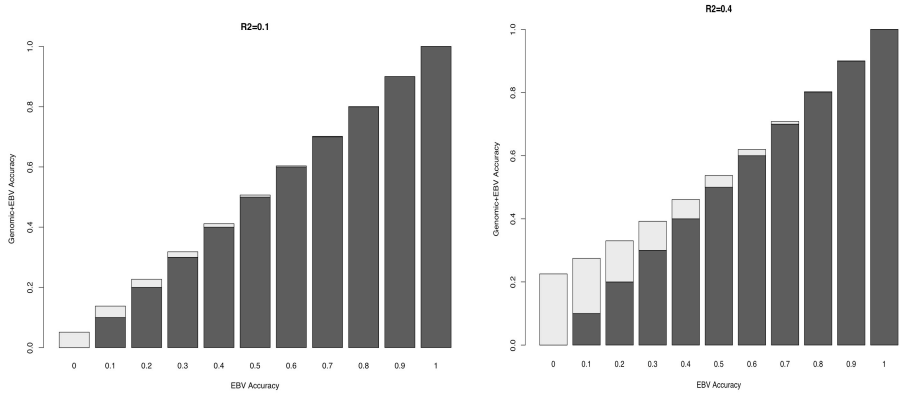
Table 2. Genetic correlations (rg) between traits and MBV using two commercially available tests as reported by the American Angus Association

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	---

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 Molecular Breeding Value (MBV) can be included in National Cattle Evaluations as a correlated trait following methods of Kachman (2008). This is what AAA currently does. Other methods have been proposed including using SNP genotypes to

form a genomic relationship matrix that could allow for known relationships instead of those estimated by pedigree or forming an index of MBV and EPD in a "blending" approach. 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. The magnitude of the benefits of Marker-Assisted Selection (MAS) will depend on the proportion of variation explained by a given marker panel.

The figures below illustrate the benefits of including a MBV into EPD (or EBV which is twice the value of an EPD) on accuracy (on the BIF scale) when the MBV explains 10 (figure on left) or 40% (figure on right) of the genetic variation which is synonymous with R^2 values of 0.1 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. 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.



It is important to understand some limitations in the current application of MAS. Current marker panels are likely to work best in the populations where discovery occurred, but will potentially decrease in predictive power as the target population becomes more genetically distant from the discovery population. 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