

Marker-Assisted Selection

Written by Alison Van Eenennaam

Alison Van Eenennaam, PhD
 Cooperative Extension Specialist
 University of California
 Department of Animal Science
 One Shields Avenue Ph: (530) 752-7942
 Davis, CA 95616 Fax: (530) 752-0175
 Email: alvaneennaam@ucdavis.edu



Traditional genetic evaluations have been developed using pedigree information and performance records. In the U.S. beef industry these evaluations are presented in the form of Expected Progeny Differences (EPDs). In some countries genetic evaluations present Expected Breeding Values (EBVs). EPDs can be calculated by halving EBVs (i.e. $EPD = \frac{1}{2} EBV$). The absence of any other information, the genetic merit of an animal can be predicted based on the average breeding value of its parents. This generates a low accuracy “pedigree estimate” that is typically associated with young animals prior to the collection of any information on their own performance. With only ancestor information, two flush mates or full siblings will have the same EPD. However their true values will vary as a result of the random inheritance of parental genes. One animal may by chance have obtained a superior subsample of parental alleles.

Observations on the performance of an animal, and that of its descendants, enable the development of a more accurate genetic estimate for that animal. The collection of this data takes time, especially the development of progeny test information. Because DNA-tests can be done at birth, they have the potential to increase the accuracy of genetic predictions on young animals. This is where their appeal and potential value lies, especially as it relates to the development of genetic predictions for traits that are not currently included in genetic evaluations. However, it is important to know the genetic correlation between DNA test results and the trait of interest to estimate their effect on improving the accuracy of genetic predictions.

Genetic Correlation (r)	BIF accuracy	Number of progeny records required	
		Low heritability (0.1)	Moderate heritability (0.3)
.1	.01	1	1
.2	.02	2	1
.3	.05	4	2
.4	.08	8	3
.5	.13	13	5
.6	.20	22	7
.7	.29	38	12
.8	.40	70	22
.9	.56	167	53
0.99	.93	1921	608
0.995	.99	3800	1225

Table 1. Accuracies of estimated breeding values based on (A) the correlation with true breeding values (r), and (B) the BIF standard, and the number of progeny test records required to obtain these accuracy values for traits of low (0.1) and moderate (0.3) heritability.

Marker-assisted selection (MAS) is the process of using the results of DNA testing to assist in the selection of individuals to become parents in the next generation. The genotypic information provided by DNA testing should help to improve the accuracy of selection and increase the rate of genetic progress by identifying animals carrying desirable genetic variants for a given trait at an earlier age.

The accuracy of a DNA test at predicting the true genetic merit of an animal for quantitative traits is primarily driven by the amount of additive genetic variation accounted for by the DNA test. Current estimates for this correlation and the proportion of the variation accounted for by existing tests (the square of that correlation) are generally low (<0.1) with the exception of DNA tests for tenderness where available estimates include 0.25 (Allan and Smith, 2008) and 0.016-0.299 from an Australian evaluation of the Pfizer Animal Genetics 56 SNP panel, (<http://www.beefcrc.com.au/Aus-Beef-DNA-results>).

Example 1. If a DNA test has a genetic correlation of 0.5 with the trait of interest, then a genetic estimate based on that test alone would have BIF-accuracy of 0.13. If the DNA-based prediction is for a trait that is difficult to measure, or which is obtained late in life (eg. calving ease, stayability), then having a DNA-based genetic estimate with a BIF-accuracy of 0.13 on a young animal would be of value to both seedstock producers and cow-calf producers. Bull breeders could improve genetic trend for the target trait by increasing their selection intensity and castrating inferior bulls based on the DNA-test, and commercial bull buyers could benefit from the decreased risks associated with purchasing a yearling bull with a DNA-derived genetic estimate with improved accuracy, relative to that which is typically available on young herd sires.

It is important to combine DNA test results which currently involve a relatively small number (<100) of SNP markers and typically explain a small proportion ($<10\%$) of the genetic variation associated with the target trait) with other criteria, such as EPDs (which look at the effects of many “unmarked” genes and the animal’s actual phenotype for the trait (if available), to ensure that selection is distributed over all the genes that contribute towards the trait of interest. Animals that have a good EPD for a given trait and yet are not carrying the favorable form of a marker for that trait should not be ignored. These animals are likely to be a source of good genes for the many other genes that contribute towards that trait. Ideally the information from genetic tests will become integrated into a genetic evaluation system that weighs all the information about an animal. In the future it is hoped that DNA information will enable the development of EPDs and associated accuracy values for traits that have no

DNA Tests	Industry-collected Phenotypes	
	No	Yes
No	---	EPD
Yes	EPD	EPD

phenotypic data because that are difficult or expensive to measure. Incorporating DNA information into EPDs is appealing because it makes use of the existing genetic evaluation infrastructure, and presents a metric that is familiar to producers.