



# GENESTAR<sup>®</sup> MVP<sup>™</sup> TECHNICAL UPDATE

July 2009

The methodology behind GeneSTAR Molecular Value Predictions and the answer to the question: “Can an MVP predict a performance (phenotypic) outcome?”

## GeneSTAR MVPs

- GeneSTAR MVPs are Molecular Breeding Values, published in the units that the trait is measured in. They incorporate the sum total of the DNA marker effects for the traits included in the DNA marker diagnostic panel.
- Each MVP for a particular trait is also published with an average reliability value (REL%).
- The current GeneSTAR DNA marker panel includes 56 DNA markers that predict the genetic potential for feed efficiency, marbling and tenderness in beef cattle.

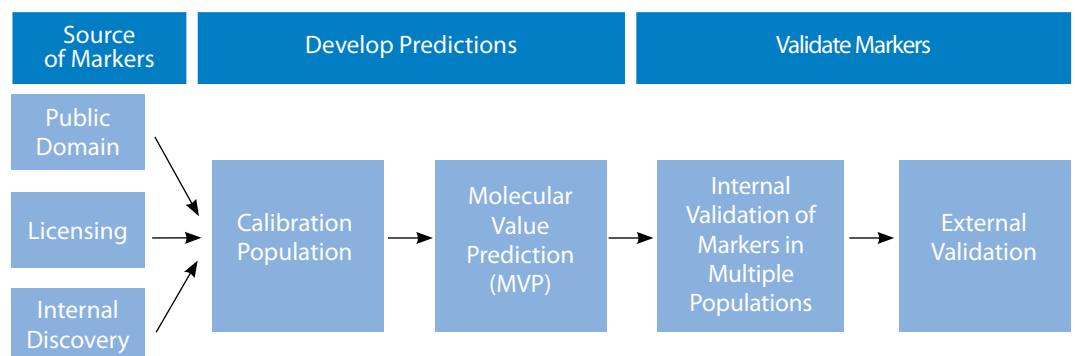
Pfizer Animal Genetics is committed to refining its MVPs to continuously improve the predictive power of this important new selection tool for customers. Integration of MVPs into existing genetic evaluation tools such as EBVs is a key Pfizer Animal Genetics commitment. The desired goal here is to increase the accuracy of EBVs by including DNA marker information.

To that end Pfizer will conduct internal and external, independent evaluations of our MVPs. That validation will be conducted over time to ensure the best predictive power for the MVP in different breed types in different environments/production systems.

This technical update is about an important outcome arising from the independent evaluation oversighted by the Beef CRC and conducted by the Animal Breeding and Genetics Unit (AGBU) in Armidale, Australia.

A recent technical meeting between Pfizer Animal Genetics scientists, AGBU and independent geneticists was held, with Meat & Livestock Australia chairing. This update describes one important outcome from that meeting. Collaborative technical meetings will be part of a process of consultation with these parties that will be ongoing.

Figure 1: Discovery and Validation Process



## Genetic parameters

EBVs (& EPDs) for particular breeds are produced using breed-specific genetic parameters such as variances, heritabilities and correlations between traits. It takes large numbers of records (5000+) before breed-specific values are calculated.

In the case of MVPs, similar genetic parameters are required and, like the EBVs, large numbers of quality records are required on the same or very similar trait to provide accurate breed-specific adjustment factors. It is important to remember that until those large numbers of records are available for a breed, genetic parameters from similar breeds may be used for genetic evaluation. Figure 1 shows the rigorous process that has been used in developing our current GeneSTAR marker panel.

The following notes discuss some of the methodology behind the MVPs and evaluation of the genetic parameters that give them their predictive power.

### Is an MVP like an EBV?

Like an EBV, half the value of the MVP on a sire or a dam is passed on to the progeny. Our expectation is that on average, half the difference in any comparison between two bulls' MVPs is translated to the performance (phenotype) of their progeny when all other things are equal (e.g., mated randomly to females, all progeny treated equally and contemporary groups recorded).

This prediction of the performance of the progeny of, say, a bull with an MVP is based on the expected performance within the group of cattle where Pfizer evaluated the DNA marker panel effects. This group of cattle is often called the 'calibration group' or population. This was a different group of cattle from those in which the DNA markers were originally discovered.

In the genetic evaluation of the effect of a particular DNA marker and its prediction power, a statistical technique called regression analysis is normally used. In examining the relationship between the DNA marker for a trait and progeny performance for that trait, the

prediction power in the calibration group should, by definition, be 1.0 or 100%.

### Is it 1.0 for other cattle groups?

Moving outside of the calibration group to another group of cattle (see Figure 1) in a different production system or environment or another breed or crossbreed raises the question, "Will the predictive power still be 1.0?"

In other cattle groups the same regression technique can be used to examine predictive power of the MVP on the performance of the animals for the particular trait. However, if the difference between sires' MVP and progeny performance is not fully reflected in the performance of the progeny, then the regression will be less than 1.0.

That now means for every unit of MVP, the change in progeny performance is expected to be less than 1.0 for the unit of performance.

### Why may the regression value be less than 1.0?

There are basically four potential reasons:

1. Scale Effects: There may be scale effects due to the traits actually measured across the groups being slightly different and any adjustments made may overestimate the relationship between MVP and progeny performance.
2. Transportability Between Groups: There may be fundamentally different genetic relationships in the traits between the calibration group and this other group (e.g., different breed populations).
3. Population Size: It may simply be that the numbers of animals in the group are too small. This could happen also for EBVs, (e.g., IMF% EBVs based on real-time ultrasonic scanning), relating those EBVs to actual carcass measures, but based on small numbers of carcasses.
4. Phenotype Precision: The performance records or carcass measures may have been poorly measured.

### Scale effects:

In evaluating the effects of the DNA markers between different groups of cattle, the question

**Table 1:** Example of where there can be scale effects in Marble Scores in different groups of cattle.

Trait	Source	No.	Average	Min	Max
Marble Score	CRC 1	1,454	1.18	0	4.3
Marble Score	CRC 2	1,808	0.76	0.1	3.8
MS (AUS, MSA)	PAG Calibration	2,759	3.23	0	9

It can be seen that the average Marble Score in the calibration group (3.23) was much higher than the two Beef CRC independent evaluation groups (1.18 and 0.76).

must be asked 'are we predicting the same trait'?

Some actual examples may help us interpret the recent independent evaluation results.

a) Marbling example:

The calibration group for the Marbling MVP was dominated by Australian long-fed *Bos taurus* cattle in feedlots targeting AUSMEAT Marble Score 3 or higher. The independent evaluation by AGBU used Beef CRC cattle (i.e., *Bos Taurus*, *Bos Indicus* and indicus-derived, plus tropical *Taurindicus* composites) fed for three different market end-points (i.e., Domestic, Korean and Japan). However, even in the long-feds, the average level of AUSMEAT Marble Score was low (see Table 1); they were on a different scale to the Pfizer calibration groups.

b) Tenderness example:

A similar trait definition issue can occur with Tenderness. For instance using the Tenderness MVP based on a calibration group where the beef was aged for 14 days, but then attempting to predict based on meat aged for 2 days (the Beef CRC standard). This means in effect that the trait or records being predicted are again on a different scale to that of the MVP.

## Transportability between groups

Here we need to consider the effect of there being a different frequency of the favourable alleles between different cattle groups and these frequencies having particular and different effects. This can mean that the prediction equation

for the MVP is different (i.e., does not transport or translate between the different groups). An example of this may be across breeds that are not included in the calibration populations.

## Small numbers in evaluation groups

As discussed above, when looking to calculate breed-specific genetic factors for breed EBVs large numbers of animal records are required for each trait. The same is true for MVP calculations. However, in the case of Net Feed Intake records there are limited actual phenotypic records. When estimating the genetic values to develop the prediction equations that drive the MVP on a small number of animals, those values have the chance of being disproportionately high or low simply due to the small numbers of animals in the group.

## Implications

In these early days of calculating if an MVP can predict progeny performance in populations that may be less than optimal, some allowance has to be made for the factors mentioned above that can lead to the regression coefficient being less than 1.0.

In some cases the MVP as calculated in a new group or breed will have to be adjusted back by the regression co-efficient calculated in that group. In other cases, the decision will be to go with the calibration group's prediction equations.

As has been the history in traditional national genetic evaluation programs, until we have larger numbers of high-quality records with identical trait definition and similar allele frequencies, these factors must be considered when interpreting and using the published MVP information.

Pfizer Animal Genetics will continue to evaluate and improve MVPs both internally and externally. This will ensure the best possible predictive power of MVPs for our customers.