

BREEDING TERMS EXPLAINED IN A NUTSHELL



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Breeding Value

A very simple definition for a Breeding Value could be:

“The genetic value of an animal as a parent for a specific trait (or group of traits)”.

This immediately means that such a value must be compared to a standard or a benchmark. Normal benchmarks are comparisons with:

- Other animals’ breeding values (usually those also considered as selection candidates).
- The average breeding value of a population or group of other animals (like those in the same breed, born in the same country, born in a specific year (the so-called “base year”) or even the average of animals in a herd).

A breeding value is therefore “population dependant” (the comparison of its progeny relative to the progeny of others that must perform under the same conditions or in the same population).

Usually breeding values are expressed in the unit of measurement of a trait (like kilograms body weight, mm shoulder height or scrotum circumference, days calving interval, micron fibre thickness, %butterfat, linear score units, etc.) or some form of standardised units (like standard deviation units for linear scores or an “index” value with a mean of 100 and a fixed, standardised distribution).

An **EBV** (or any of the other similar names used for the prediction of a breeding value) is therefore a prediction of an animal’s true breeding value, making use of all available and relevant information. EBVs are usually associated with the use of BLUP (Best Linear

Unbiased Prediction) methodologies to ensure that the prediction is independent of selection or mating bias. In these predictions, BLUP (multiple trait animal model) makes use of four sources of information, namely:

- Pedigrees (indication, on average, what proportion of “additive genes” are shared as relationships among all animals in the pedigree, included in the evaluation).
- Actual (phenotypic) recordings among animals subjected to the same environmental (and management) conditions (group) that contribute to average performance.
- The proportion of the differences in performance among the animals due to their genetic merit or, differently put, their breeding value differences, in relation to the total differences in performance of all the animals in the same environmental (and management) condition (group). This is called the heritability of the trait.
- The proportion of differences in breeding values for different traits influenced by the same portions of the genome (the collective of all genetic code).

This is called the genetic correlation among different traits.

The accuracy of predicting a “true” breeding value depends on the information used in such predictions, basically the accuracy and completeness of

pedigree information and the proportion of animals accurately recorded for the specific trait.

Genomically Enhanced Breeding Value

The term “Genomically Enhanced Breeding Value” is loosely used to indicate the prediction of the true breeding value by adding (mostly additional) genomic information of the animal relevant to the prediction to the BLUP breeding value predictions.

Two major different methodologies are currently used for breeding value predictions that include genomic information, namely:

BLUP breeding values based on the animal model used to be known as the Rolls Royce of breeding value predictions. Current practices, namely gBLUP (genomic BLUP) using the single step in a comprehensive multiple trait animal model, that also accounts for heterogeneous variances, additional random effects, gaps in pedigrees, non-additive gene action and complex interactions is evidence of the progress to accurately predict the true genetic merit for production animals

Two-Step (method)

This method is based on comparing a (very) large number of animals' EBVs with their genomic information and establishing a relationship between the two sources of information. This relationship is called the "SNP-key". Like, in the cases of heritability and genetic correlation estimations, the SNP-key is population dependent (breed and country population specific).

This method is called the "Two-step" as more than one step (in fact more than two steps) are needed to predict the breeding value where the genomic information is added to enhance the prediction accuracy.

Animals with known genomic information receive DGVs (direct genomic values) based purely on their genomic information's similarity to the SNP-key. Both the SNP-key and this relationship are subjected to an accuracy of prediction (as reflected by the reliability published with the DGV). The DGV is purely an interim step in the prediction as the second important step is the blending of the DGV with the EBV (as obtained from BLUP) in the proportion of the accuracy associated with the prediction of the two values. The result of this blending is called a GEBV (commonly known as a Genomically enhanced EBV).

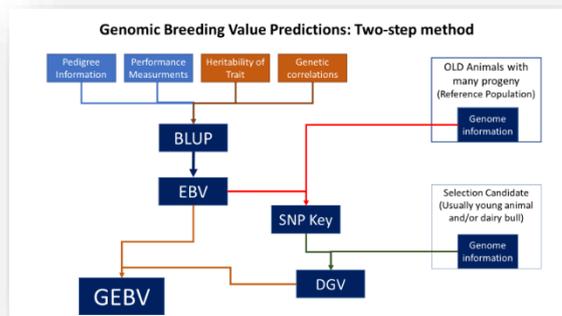


Figure 1 Illustration of the Two-step method

Single Step (method)

BLUP EBVs rely on two sources of information from breeders, namely measured records and pedigree information. Relationships among animals reflect the common parts (based on "average" assumptions) of the genome among them. The Single Step simply changes the assumed relationships among animals to the true relationships, based on their genomic information. The breeding value prediction therefore results from gBLUP and therefore the GEBVs are calculated in a different manner when compared to those from the two-step method. True relationships increase the accuracy of breeding value prediction for young animals due to the common parts of their genome with others in the population, those with high accuracy (G)EBVs, but also with others where the genomic information is included in the analyses. Each animal therefore contributes towards the accuracy of prediction.

Figure 2 explains the difference between a "traditional pedigree" versus a "genomic pedigree".

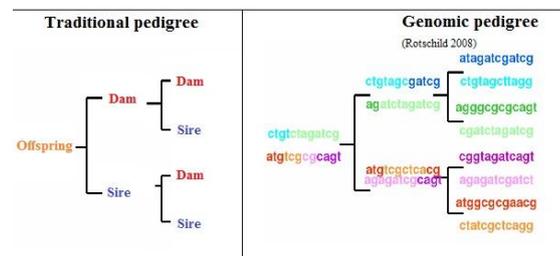


Figure 2 The difference between using traditional recording of pedigree versus genomic information in determining the relationships among animals

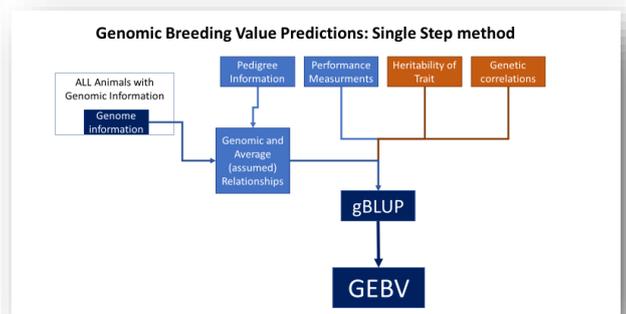


Figure 3 Illustration of the Single-step method

Selection Index (Selection Value)

It is normal in any selection program to select for more than one trait simultaneously.

This is done because of various reasons, but mainly due to each trait's contribution towards the profitability differences among progeny of different parents and the fact that all traits are genetically linked (correlated).

Not taking correlated traits into consideration might lead to unwanted selection responses.

The most effective way to reach breeding objectives when selecting for more than one trait, is to combine them in a single (selection index) value, usually expressed in monetary or standardised units.

In each case, the selection index reflects the genetic levels and variation in the relevant country as well as the pricing system for products, such as weaners or long weaners, etc. (and culled or sold animals) and variable input costs (health, raising costs of replacements, maintenance of cow herd, loss due to sickness, other involuntary culling, feed cost relative to product income).

In short therefore:

A selection index is a combination of individual EBVs (or GEBVs where genomic information is included in the BLUP calculations of the EBVs) surmised in the ratio of economic importance of, and expected correlated responses due to, selection for the contributing traits. In the case where genomic information was included (either by means of the Single Step or Two-Step) the name of the index usually reflects this by the addition of a "G" with the traditional name.

Figure 4 illustrates the building blocks of a selection (index) value.

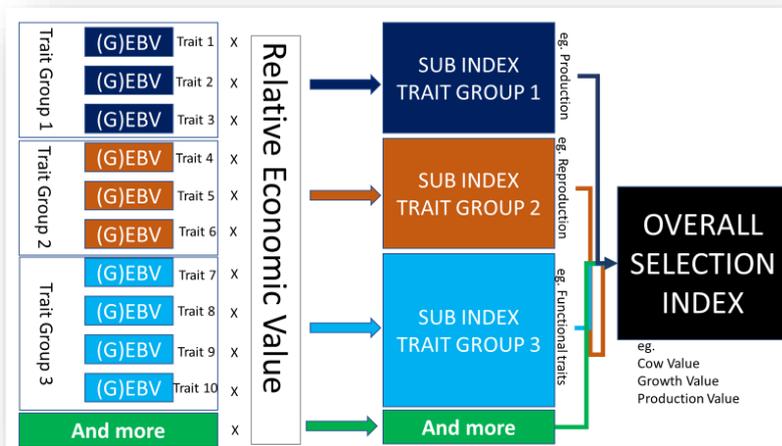
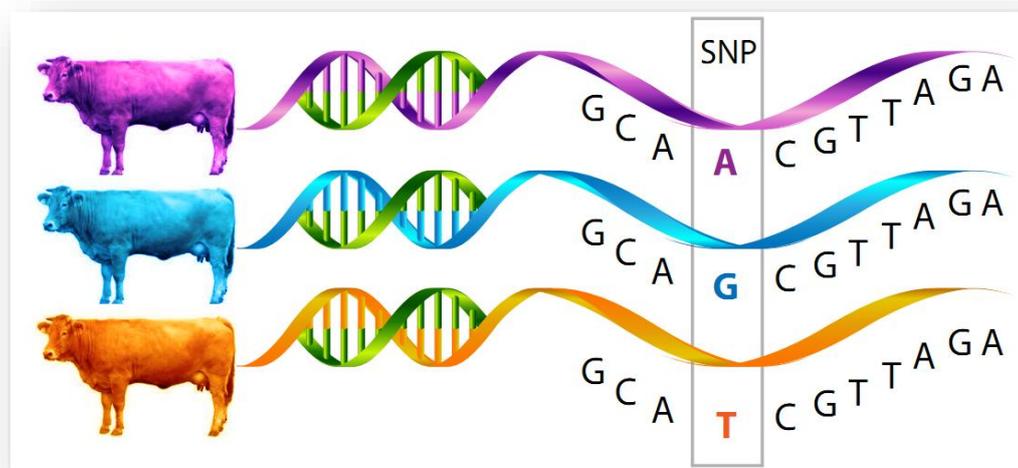


Figure 4 Illustration of the building blocks in a Selection Index



Single Nucleotide Polymorphisms (SNP), are single changes in the genetic code that are responsible or at least partially responsible for a specific phenotype. SNP differences in the same species (and breed) are used to account for genomic variation (Courtesy ICBF).