Understanding the meaning of Genomic Selection and where BLUP fits in.

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The goal is to predict the genetic merit of each potential breeding animal as accurate as possible

The quest of each animal breeder is to reach the set breeding goals as efficiently as possible. Breeding goals are usually formulated based on those traits and properties that will ensure long term profitability. Traits can usually be classified formally or loosely into one or more of the following groups: Fitness traits (reproduction, survival, resistance to adversity), Growth (weights or gains to certain age intervals, efficiency of growth rate, expressed as gain per intake or gain per maintenance), Maternal ability (maternal breeding values for birth and weaning weights, weaning weight relative to cow maintenance), Type (maturity type expressed in different ways, several body measurements and linear scores), Functionality (physical description or score, prevalence of absence of specific properties) or other desirabilities (like coat colour, pigmentation).

In this quest it is important to strive for an accurate assessment of each potential breeding animal's ability to produce offspring that will perform as close as possible to these goals. This merit can also be described as the breeding value of each animal (the value as a parent for the traits of importance). There are obviously different means to increase the accuracy of prediction. Initially these predictions were purely based on visual observation. Simply put, "the biggest calves were more likely to breed the biggest or heaviest progeny". This was refined by simply weighing the calves and picking the heaviest ones as parents. By applying objective assessments breeding values were obviously more descriptive (pounds or kilograms). This was followed by assessing animals within the same treatment groups and also taking some non-genetic factors such as age at measurement, sex and age (and parity) of dam into account. This group is commonly referred to as the contemporary group. Basically each animal was rated with its contemporaries and these differences were expressed as a, so called, index (or 'ratio'). There are, however, some serious limitations to using indices as breeding value predictors. There is no real guarantee that superiority within a specific contemporary group would equal a similar feat in another. Practically expressed, if a young bull born in the spring of 2012 outperforms his peers on my farm in the 2013 weaning season there is no real certainty that he could have done the same in a different herd or in any other peer group. Other obvious questions could be linked to his mother's ability to look after him. Was his superior weaning weight the result of his merit for growth or because of the extremely good mothering ability of

his dam? Similarly, if one averages the progeny performance of a bull, will he not look superior if mated to the top cows (preferential mating) and not because of his own merit?

All these shortcomings have led to the development of more sophisticated methodologies to predict the genetic merit of farm animals.

BLUP breeding values, the breakthrough in prediction accuracy

BLUP breeding values (usually called EBVs or by other names such as EPDs or ETAs) answer all the questions related to mass (population) selection. The principle is to select individuals in a population to change the mean production levels of the population they are selected from. BLUP breeding values maximise the correlation between the predicted values and the 'true' genetic merit.

These predictions rely on a few very important principles, namely:

Related animals share the same parts of DNA

It is well known that related animals share identical parts of the genetic codes responsible for differences in genetic merit (and therefore differences in the expression or performance for different traits or properties). For example, a herd sire will share 50% chromosomal genetic material with each of his offspring. If this sire was widely used over herds and produced progeny over different years of birth he serves as a 'link' between different contemporary (peer) groups as half of him (the 50%) will be represented by each of his progeny in each group. If this fact is furthermore taken to the extreme, just about all animals in a breed could be somehow related, therefore sharing pieces of genetic pieces in the whole population.

Only part of the performance superiority can be transferred to progeny

All recording (measurement) differences among animals (even in the same peer group) are the result of two very important influences. The first influence relate to differences among animals due to their differences in genetic merit (the genes and gene interactions on their chromosomes). The second very important influence is the effect of differing environmental influences. A simple example would be to name the known non-genetic influences, from the calf's perspective, on weaning weight in beef cattle. They include, some or more of the following: Recording age (older calves are usually heavier), sex (males are usually heavier), age and parity of the dam (mature cows have more milk and are better mothers), season and year of birth, specific farm or location and any treatment different to the rest of the peer group animals.

Taking all this onto account, as well as the possibility of a random genetic 'superiority' caused by breeding practices associated with heterosis (as a result of cross breeding) or

inbreeding depression, it only expresses the genetic superiority that can be transferred to the progeny (additive genetic value). This is achieved by making use of the heritability estimates for each trait when breeding values are predicted.

Traits are 'linked' through common parts of the DNA

One could say: 'no trait is an island'. In essence all traits we record in farm animals are correlated in one way or the other. This means that selection in a population for one trait will generally affect the genetic merit for other traits. Modern BLUP models consider such genetic correlations. This has a huge advantage in breeding value prediction accuracy in the following cases: sequential culling (where some animals are culled at different ages), sex limited traits (like scrotum circumference, female reproduction, maternal ability, milk, etc.) where animals could not be measured yet for some traits (still to young) or where the trait of importance is too difficult or expensive to measure for all animals (like feed intake, marbling, eye muscle, etc.).

All these factors make BLUP breeding values extremely precise and accurate in predicting genetic merit. A multitude of examples exist where genetic change happened where this methodology has been used effectively in all possible farm animal species and production systems.

The question could therefore rightfully be asked: "Why the introduction of Genomic Information in farm animal selection?"

Genomic Selection: The next step in enhancing the accuracy of breeding value prediction.

BLUP breeding values basically rely on the concept of 'family selection' as relatedness among animals are based on average values. Two collateral half sibs (for example half brothers with the same sire but born from different, unrelated mothers) are assumed to share 25% common genes (DNA). This is off course true as a common statement if it reflects the average relationship over the whole population of all half sibs. There is, however one very important fact that needs extra consideration, namely that that pieces of DNA separate relatively independent and randomly in the formation of sperm and egg cells. Some half sibs, in our example, can have a relationship of more than 25% while others are less related.

By using the additional information hidden in the genetic code in each and every animal, the 'true' relationship among all animals can be established using genomic information.

The next obvious question could be: "What could be gained by knowing more about the specific relationships among animals in a population?" This question brings one at the real crux of Genomic Selection, namely the establishment of a. so called "reference Population". Such a population consist of animals (in a breed) where the knowledge of their genetic merit is well

known. In practical terms, old animals with a large number of recorded progeny (a high BLUP breeding value prediction accuracy) form the core of such a reference. In essence the genomic values are correlated with the breeding values for animals in the reference population. Methodology has been developed where some parts of the base pairs on the chromosomes serve as 'snap shots' of the whole genome of each animal. Current 'SNP (Single Nucleotide Polymorphism) Chips' commonly used range between 50 000 and 777 000 base pairs as predictors of the approximately 3 500 000 000 base pairs on the chromosomes of most farm animals. Once these correlations are established, it can be used to enhance the prediction accuracy of BLUP breeding values for young animals. Where BLUP breeding values basically used family information, genomically enhanced BLUP breeding values add a new dimension, namely the specific separation of genes within families of animals in the population. Obviously this is even possible with BLUP alone, once breeding animals have many measured progeny. Genomic Selection, however assist in making this information available at a younger age.

Genomically enhanced breeding value predictions, commonly known as GEBVs therefore kicks off with a higher prediction accuracy, compared to BLUP alone. Knowledge of the genome information of a sire with very accurate EBV values will however be of very little use for any breeder as his progeny has already contributed to knowing his value as a parent.

The biggest benefit
The biggest benefit in using Genomic Selection is obvious. It works best in combination with BLUP breeding values and enhances the accuracy of prediction in specific cases. The biggest advantages for rapid genetic progress currently happens in the dairy industry. Previously many years passed before BLUP breeding values for potential sires could be known as milk production, its components and daughter fertility could only be recorded on the female offspring of these bulls. This has lengthen the generation interval and makes the whole process extremely expensive. The combination of genomic information and BLUP breeding values has turned this inside out as the prediction accuracy of young potential AI sires equals that of an older sire with ten measured daughters.

Many new opportunities exist. Selection for traits where recording is limited to one of the two sexes, such as milk, daughter fertility, mastitis resistance, mothering ability (eg. Beef cattle or sheep), litter size and semen quality are some examples are obvious. Other trait selection that are to benefit include those only measurable on dead animals (carcase and meat properties), are expensive and difficult to measure (like feed intake, ovulation rate, disease resistance, parasite resistance, etc.) and can only be measured late in the animal's lifetime (like longevity, lifetime production and productive her life).

Perspective

Although the use of genomic information in the breeding of farm animals have taken the world by storm it is important to keep perspective. Genomic information does not negate the need for recording of the traits and properties included in selection programs. The opposite is more true. The need for recording is as important as always as known relationships between genomic information and true breeding values change over time and is usually population (within breed and even within country) specific.

A very important issue is also to keep to well defined and logical breeding objectives when using predicted breeding values (genomically enhanced or not). In some cases, bigger or heavier might not always better. The setting up and carrying out of these objectives is a science on its own and involves knowledge of the genetic correlation among traits, their relative economic contributions and the environmental constraints (physical or due to the limitations of the production system).