

# FROM SHADOWS TO LIGHT

## The Promise of Genomic Selection

In Plato's Allegory of the Cave, men are chained to the wall of a cave and can see only shadows cast on the wall by a fire behind them. Images of people and objects are projected on the wall by puppeteers. Having lived their entire lives in the cave, the prisoners believe the images they see are reality rather than shadowy representations of reality.

### PLATO'S CAVE OF GENOMIC SELECTION

Horse breeding is not unlike Plato's cave in that so much of what is real and important cannot be seen, or seen clearly, by the breeder. Many important traits are hidden and others are hard to discern, especially when the horse is young. And there is no shortage of puppeteers in the industry. But the science of DNA and genomics, and their application through genomic selection, promises to change some of this. Genomic selection has revolutionized breeding of a variety of animal and plant species, and for progressive studbooks and breeders the opportunities it offers are immense.

### TRADITIONAL SELECTION METHODS

Over the years useful selection techniques have been developed to advance sport horse breeding. Figure 1 shows the method used by many

studbooks. Data obtained from each step in the pyramid is combined with competition results to calculate an estimated breeding value (EBV) for each stallion and mare in the population. This method uses a statistical model that connects all pedigree-related horses and links them to performance and other data to estimate the breeding value of the horse. All this is done using statistical methods that attempt to control for, or take into account, external factors that have nothing to do with the horse's genetics but may, for example, help or harm its sport performance.

### ESTIMATED BREEDING VALUE

While a valuable tool, traditional EBVs are limited in their usefulness for several reasons. First, like all statistical models EBVs can be only as good as the data used to estimate them, and some models continue to have poor quality data or data that sometimes have little to do with a horse's genetic endowment or true breeding value (such as auction sales prices). Second, since the models depend on competition and other phenotype data that are collected throughout the horse's lifetime traditional EBVs have low accuracy for young stallions and mares. Third, the resulting problem of 'long

generation intervals' slows down the possibility of genetic progress. Fourth, traditional EBV models have been mis-specified because until recently they have not been able to include genetic data. So in a sense we have been using shadows on the walls of the cave rather than reality because a key component – genes – of the genetic breeding values have been excluded from the analyses.

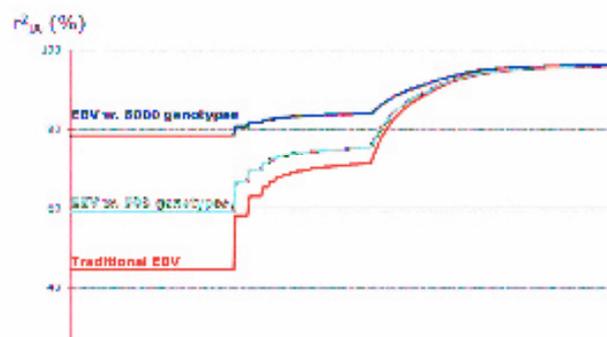
### INCORPORATING GENOMICS INTO EBVS

The information technology revolution and the dedication of genetic scientists have made genomic selection possible. The computer I am writing this article on has 131,000 times the memory of the computer I wrote my dissertation on some thirty years ago; it also has 268 million times the storage capacity. And my MacBook Pro computer costs less than two-thirds the price of my 1984 Macintosh in inflation-adjusted dollars. This technology revolution has created the opportunity for genotyping chips with 70,000 genetic markers on them to be used at a reasonable cost per tested horse, and prices will decline even more in the future. A key requirement for incorporating genetics into EBVs is to perform genomic profiles on a large number of randomly selected horses in the studbook and to link those

profiles to the existing phenotype data of conformation traits, competition results, etc. This is how a 'reference population' is created. Figure 2 compares the expected reliability of EBVs using the traditional method versus a relatively small reference population of 500 horses versus a well-designed reference population of 5,000 horses.

### THE NEXT STEP

The Royal Warmblood Studbook of the Netherlands (KWPN) has taken this approach one step further. The studbook has been collecting linear profiles of its horses since 1989, and it has close to 100,000 profiles that are incorporated into its EBV calculations. But what must be done if the trait of concern is one that is not normally identified or investigated or seen, such as the propensity for osteochondrosis (bone chips and related developmental joint diseases)? As discussed by KWPN Director Johan Knaap in the accompanying interview, the studbook randomly selected thousands of progeny of its approved stallions and performed carefully controlled radiographic examinations on them. Combining this new phenotype data, the x-ray results, with the genomic profiles allowed them to identify the genetic markers affecting osteochondrosis (OC) and to compute an estimated breeding value for OC for



**Figure 1** Pyramid structure of the breeding program of the German Riding Horse. EBV = estimated breeding value; PTS = performance test stallions; PTM = performance test mares.

Source: Haberland, A.M., König von Borsten, U., Simianer, H., and König, S. 2012. Integration of genomic information into sport horse breeding programs for optimization of accuracy of selection. *Animal*, 6:9, pp 1369–1376.

**Figure 2** Comparison of the expected reliability of EBVs using the traditional method versus a relatively small reference population of 500 horses versus a well-designed reference population of 5,000 horses. The increase from 11 years of age is due to progeny records.

Source: Mark, T., Jönsson, L., Holm, M., and Christiansen, K. 2014. Towards Genomic Selection in Danish Warmblood Horses: Expected Impacts and Selective Genotyping Strategy. *Proceedings, 10th World Congress of Genetics Applied to Livestock Reproduction, 18-23 Aug., Vancouver, Canada.*

its stallions that incorporates this DNA information. This research and development project was very costly but now that the initial investment has been made the reference population needs to be updated only periodically as the overall population of the studbook develops.

## GENES VS ENVIRONMENTAL FACTORS

In the interview Knaap makes the point that approximately the same percentage of stallions, 14%, is excluded from approval now compared to the percentage that was excluded when x-ray exams were used to identify and exclude stallion candidates with osteochondrosis. The important point to realize is that potentially different horses are being excluded under the two regimes. Under the old system a stallion could face exclusion if he had one or more chips. The inspectors and their veterinary advisors had no way of knowing if the chips were caused by the horse's genes or by environmental factors. So stallions were at risk of being excluded from approval because of chips caused by environmental factors. With the test for OC if a horse has a breeding value above the required threshold he can be approved even if a chip is present because the likelihood is that the chip was caused by environmental factors and therefore should not be part of the selection decision. So the test will allow some stallions to be approved that heretofore were excluded. But the test will also allow stallions to be excluded from approval who have no chip but have an unfavourable genomic profile for osteochondrosis. In the past these stallions would have been approved because they were 'OCD-free' but now, based on their DNA, they will be excluded because they possess unfavourable genes that KWPN wants to control or limit in its population.

## GENOMIC SELECTION AND SOCIAL RESPONSIBILITY

Widespread use of genomic selection is a socially responsible endeavour that all breeders, studbooks, and departments of agriculture should support. Scientific networks of geneticists throughout the world are working on problems such as osteochondrosis, stress fractures, insect bite hypersensitivity, chronic progressive lymphedema, and conformation defects. If the incidence of these diseases and defects can be reduced substantial improvements will be made in horse welfare through the reduction of suffering. The use of



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genomic selection to improve sport performance and, in general terms, usefulness of various horse populations is also a socially responsible act. Too many horses are bred within studbooks of the World Breeding Federation for Sport Horses (WBFSH) that have no useful role in life because they lack the riding horse and/or athletic qualities the market demands. If the overall quality of horses can be improved through genetic selection so that each year disposable horses become more of a tail risk rather than a predictable outcome of each studbook's output horse welfare will be improved, there will be fewer losses incurred by breeders and purchasers, and less public money will be required to deal with welfare cases.

## THE WAY FORWARD

Genomic selection will present ground-breaking opportunities to advance sport horse breeding but

collaboration and an investment in the future are required. Small studbooks will find it impossible to create statistically valid reference populations in a cost-efficient way, and even large studbooks may lack the research and development expertise required to create and sustain a genomic selection program. This suggests to me that in certain countries, and especially within the European Union where intra-national and inter-national research collaboration is supported and funded, national-level or regional reference populations should be created that all relevant studbooks could access. With the emergence of increased cross-border trade in semen and breeding mares in Europe this concept becomes even more feasible.

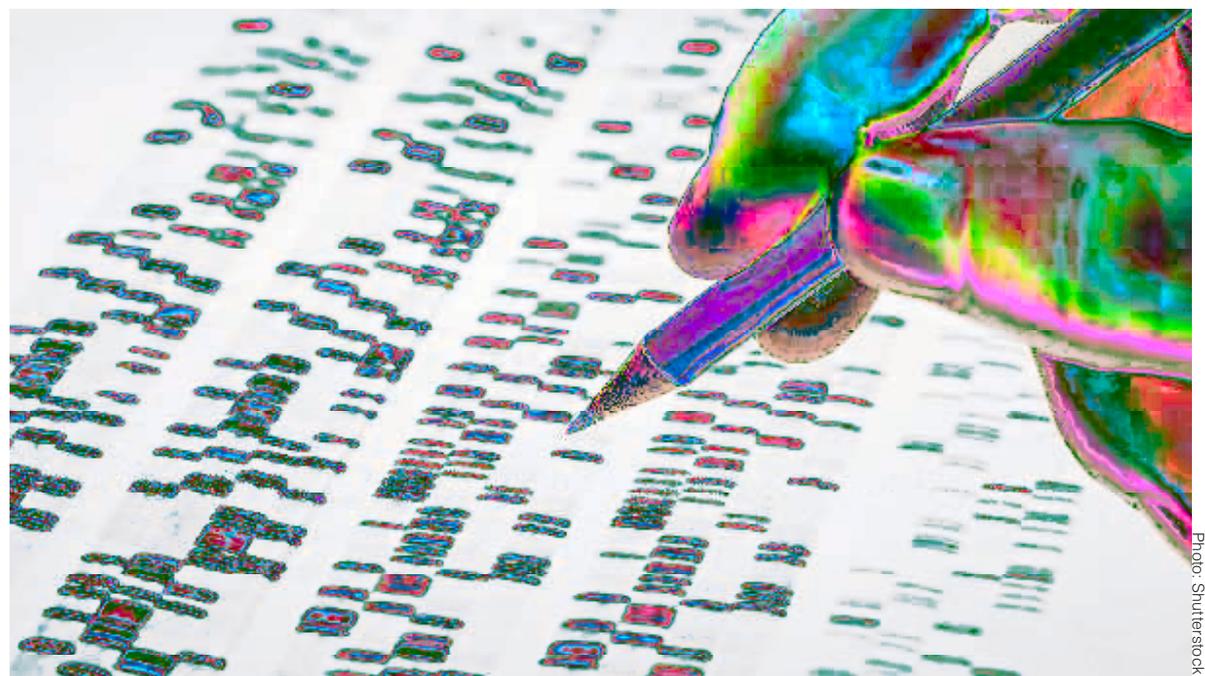
## TRUE SPORTING POTENTIAL

Last year I wrote an article for Horse International entitled The Future of the Stallion Approval Process in

which I identified three types of characteristics that a stallion approval process evaluates. The first, and for me the most important, is invisible characteristics. This is where genomic selection comes in. By shining a light on what has been invisible to breeders up to now we can create a revolution in sport horse breeding. Rather than waiting 10, 12, 15 or 18 years to discover if a stallion (or a mare!) is worth breeding to we will be able to know as a foal what its genomic profile tells us his or her expected value is for breeding. And hopefully one day, when science permits, we will know its true genetic potential for sport.

## HOPE AND PROMISE

Will there come a day when we can produce sport horses that are free or substantially free of genetically-induced osteochondrosis, laryngeal hemiplegia, and navicular disease and possess favourable genes that are associated with sound characters, trainability, and athletic prowess? That is the hope and promise of genomic selection. The prisoner in Plato's cave was blinded by the light when he was freed, and his efforts to liberate his fellow prisoners were rebuffed by them. We breeders are being invited by several progressive studbooks and scientists to join a remarkable journey and we should embrace it and advocate for it among our fellow breeders and government agencies. Traditional ways of thinking about breeding will have to be expanded but if we can combine 21st century science with traditional soft knowledge and insight the prospects for our industry are exciting and promising. ■



*Will there come a day when we can produce sport horses that are free or substantially free of genetically-induced flaws?*