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Original Paper

The use of new technologies in horse selection

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Most successful selection strategies are not in use in horse selection. This study describes the use of current strategies of selection in horse breeding and tries to answers why well known, scientifically proven selection strategies are still not implemented. In the era of genomic selection (GS) in animal breeding, decision making in horse selection, even classical breeding values (BV), are not fully taken advantage of. Breeding organizations (BO) which implement BVs as selection criteria in their breeding programs show great success in genetic gain. However, a horse's achievements and the popularity of its relatives still plays an important role in selection level. Genomic based selection tools in horse breeding have limitations in quantitative traits since it is difficult to establish reference population. Mendelian traits have been studied for several years, especially those related to horse health and functional longevity (long sport or race careers), yet there are still only a small number of validated mendelian traits offered for horses. The important benefit of GS is the prevention of related mating based on genomic data, in addition to pedigree data. The specialty in horse breeding is the use of cloning. From the point of view of genetic variability, cloning is useful in enabling geldings or non-genetically infertile animals to carry genes to next generations. In sport and race BOs, breeding stallions from foreign BOs are frequently used. In such cases a need for comparable BVs exists. These factors were the motivation behind the establishment of Interstallion 20 years ago. Due to difficulties in BO collaboration, Interstallion has not been as successful as planned. On the whole, it is expected that the sector of horse selection will need to change considerably in the future.

Keywords: breeding value, cloning selection, genomic selection, inbreeding, strategies

1 Introduction

Horse selection is not much younger than horse domestication. Breeders most commonly use foals for the next generation of breeding mares and stallions if they show positive traits such as: health, fast growth, easy handling, temperament attuned to the intended use, etc.

The variety of possibility of horse use is one of the largest in any domestic animal species. From domestication through the Industrial revolution, horses have been used mainly for food, transport, work in agriculture and forestry, work in the military and for other different kinds of work. More recently, the main role of horses in developed countries has been changed and their previous roles have become much less important. Today, the most economically important industries involving horses are those of racing and sport. However, most people involved in the horse industry are leisure riders. A growing use of horses can also be found in tourism, equine assisted activities and therapies (EAAP), and the niche use for meat and milk production. Additionally, in the last few decades, there has been an interest in returning to an almost forgotten use of horses in agriculture and forestry (Liljenstolpe, 2009).

For a long time, breeders for selection have made decisions based purely on phenotypic observations. These points of interest have mostly been conformation traits. In the middle of the 20th century, the first study on how to estimate the additive genetic effect, known as BV, was done by Henderson (1953). From a scientific point of view BV is the most powerful tool for efficient selection. In comparison with phenotypic value, which is the measurement of the animal itself, BV describes the expected value of offspring (Koenen et al., 2004).

The first use of BV estimation was done for Islandic horses (Árnason, 1984) after finding 30 years of theoretical basis. At the time, BV estimation was used in dairy cattle, where recording different economically important traits was widely in use. In a short period of time, BVs in dairy cattle have become the main selection criteria and bull semen has been priced according to their BVs. Consequently, the

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knowledge and importance of BV for successful selection has spread from science to practice. In the horse sector, this has not happened yet. Breeders do not trust BV and horse prices are still tailored predominantly according to phenotypic measurements than BVs. Several examples have shown that the use of BV in horse breeding programs have had equal success as in cattle. Both BOs, as well as some breeders within BOs, who use BVs in their breeding decisions have had great success; examples include the Islandic horse, Swedish warmblood, and Royall Dutch sport horse (KWPN) (Koenen, 2005).

The aim of this study is to describe the use of current strategies of selection in horse breeding and to find answers to why well known, scientifically based selection strategies, routinely practiced in cattle selection, are not in use in horse selection.

Selection strategies in horse breeding

It is well known that the most successful breeding programs in dairy cattle cannot be reproduced in horses. The main reasons are: significantly smaller populations, longer generation intervals, more traits – some of which are difficult to measure – and the strong effect of preferential treatment. On the other hand, pedigree data in horses is more complete and most traits are measured for both genders. These facts need to be taken into consideration in selection programs for horse populations (Koenen et al., 2004).

Classical selection

Today, classical selection involves the use of BVs as selection criteria, which are estimated based on phenotypical records and pedigree information.

Most sport BO publish BVs for economically important traits. Important BV for trotters do the same. However, the making of selection decisions, based on a horse's performance and that of its relatives (their phenotype) still plays an important role. A unique situation in selection can be seen in thoroughbreds. The only selection criteria there is phenotype. A good example is one of the best thoroughbred stallions in the southern hemisphere, Savabell born in 2001. He has excellent performance and is a long standing carrier stallion, having produced more than 1,000 offspring. None of his offspring have reached or surpassed his results but at the age of 17 years his mating price is still growing (Waikato, 2018). There is general agreement that there is no longer any genetic progress in thoroughbreds. On the other hand, there are several strategies on how to breed good race horses with inbreeding. The most well-known is the so-called Rasmussen Factor, developed by Leon Rasmussen, which occurs when there is a duplication of a female ancestor between an individual's sire and dam, within five generations or closer (FMITCHELL07, 2009).

Conversely, selection decisions based on BVs have proven to be successful in sport horses. After the KWPN BO separated the selection goals for dressage and show jumping horses, at the beginning of the 21st century, it become the first BO in the World Breeding Federation of Sport Horses (WBFSH) rankings which was classified as the best BO in dressage and show jumping in 2009 and remained the best BO for both disciplines for three years. To date, no other BO has reached such success (WBFSH, 2018).

In several other BO which are not mainly selected for sport (local breeds) BVs are also estimated mainly for conformation traits. Of course, in these breeds BVs are even less reliable since populations are smaller than in sport horses and data recording is most often less consistent. In smaller populations prevention of related mating is most important. For these purposes breeders mostly check the pedigree information and do not use stallions with a common ancestor of the broodmare in at least the first three generations.

The fact, in horse breeding, is that the value of a horse is generated mostly based on their and their relatives' results, as well as their conformation regardless of the fact that BVs are scientifically and practically better criteria for selection decision making.

Genomic selection

The main advantage of GS, according to classical selection, is the reduction of the generation interval. Although the reliability of BVs based on genomic data (GBV) are lower, the expected genetic gain is higher because reduction of the generation interval is so high (Eggen, 2012). Those of us who know that the generation interval in horses is much longer than in dairy cattle, where GS has been in routine use, with great success, during the last decade, also have high expectations for horse selection (Reed, 2018). However, a lot must be done to gain enough quality reference population for quantitative traits. For this, there are not many strategies. A single horse BO is not large enough to set up its own reference population. The only option seems to be to merge the data between BO with similar breeding goals. This idea is quite old and resulted in the founding of the Interstallion organization 20 years ago (Thorén Hellsten, 2008). Unfortunately, it has yet been unable to compound a common data set for international BV evaluation. In the Brown Swiss cattle population this problem was solved with the successful Intergenomics project, the results of which have been in routine use since 2012 (Jorjani et al., 2012).

Other options for GS are more realistic for implementation in horse selection schemes. Reducing gene frequency for genetic disorders, increasing the frequency for desired mendelian traits; and prevention of related mattings according to functional inbreeding which is based on genomic data (Mark, 2013).

Mendelian traits have been studied intensively for several years. There is huge interest within BO to include mendelian traits which are related to horse longevity, into breeding programs. The work investment with young horses is quite high, especially in sport and race horses, so a payoff with a long sport and race career is desirable (Mark, 2013). Nevertheless, there is still a lack of reliable results from genomic associated studies in comparison with other species. The OMIA database has only 57 mendelian trait entries in horses, but 312 in dogs and 246 in cattle (OMIA, 2018). The reason is probably well known in horse breeding – lack of collaboration; in this case a lack of data exchange.

The prevention of related mating is very important for all horse breeds. In larger populations the reason for inbreeding is too often the use of popular stallions and, in indigenous breeds, the size of the population. Traditionally, breeders check the common ancestors between their mare and potential stallions or the relationship coefficient based on pedigree data and the inbreeding coefficient of each breeding animal. Pedigree based inbreeding and relationship coefficients are not as reliable as genomic based coefficients, while pedigree information is never complete and mistakes are common. Genome based relationship coefficients express relationships between animals based on the degree of gene function equality. This is the reason that management of inbreeding in a population is much more under control with the use of genomic data which motivates BO to implement such methods in their breeding programs (Reed, 2018).

Cloning

Generally, cloning is not known as a useful tool in animal selection. In populations under selection programs we have a positive genetic trend towards economically important traits. Younger animals are better, on average, and there is no sense in duplicating (cloning) the old genomes. However, in sport horses the situation is somewhat different. Behavior in most types of competitions is affected by gender. Rankings of horses in many disciplines show that most top horses are geldings, especially in steeple-chase, endurance, eventing, and dressage.

With cloning we get a breeding animal out of a gelding and this is a good cost benefit for owners. For an attractive stallion (a clone of the gelding) the estimated added value would be more than two million US dollars. This amount of money can be reached in just five years if we assume 200 services per year and the cost of service at $ 2000. This economical potential motivated science and industry to introduce cloning into routine practice. Just two years after the first equine was cloned in 2003, the CRYOZOOTECH company cloned the castrated endurance champion Pieraz (Reis et al., 2012). Cruising, one of the most successful Irish sport horses, was cloned in 2011 which resulted in two colts born in 2012: Cruising Arish (ISH) and Cruising Encore (ISH), whose frozen semen is available in the US (Shelbourne Farm, 2018). In the same period, the most famous KWPN dressage stallion Jazz was cloned twice. The service of his clone Broere Jazz was available in the 2018 mating season in the Nederlands at a cost of 2,850 € (Broere Jazz, 2018).

During the time of cloning of these two famous stallions, a heated debate about cloning ethics within stakeholders of the horse industry took place (FEI, 2012). For race horses, thoroughbreds, and trotters cloning is not allowed, but the World Breeding Federation for Sport Horses allowed clones to be registered in 2012. From that time on, cloning of top sport horses has become quite popular. Not only the cloning of geldings but also stallions and mares to prolong the longevity of their genomes – for reproductive purposes.

On the other hand, the possibilities of cloning are also an issue for indigenous breeds, especially when a breeding animal becomes infertile and it is important from the genetic pool of a particular breed. For now, cloning in such cases is not practiced and breeding programs of indigenous breeds are still quite conventional since the cost benefit of the clone cannot yet cover the cloning costs.

International comparison of breeding values

In sport horses especially, where breeding stallions from foreign BO are widely in use, breeders need to compare BVs between different scales. Interstallion was founded in 1998 for this very purpose (Thorén Hellsten, 2008). It was a logical decision since Interbull, in1994, published the 1st routine evaluation of international BVs for dairy bulls and in 1996 become the official reference laboratory for BV evaluation in the EU. Interbull BVs have been widely used in national breeding programs. More than 60% of the progeny of tested bulls in Brown Swiss and Holstein populations have foreign sire (Philipsson, 2009).

In twenty years, Interstallion has not succeeded in collecting enough data from different BO to make an official international evaluation for sport horses. The main reason being that BO for sport horses tend not to share data. Considerable progress has been made with Interstallion's guidelines for standardization of publishing BV. Currently, their main objectives are to harmonize linear scoring systems for type traits between BO (Stock et al., 2015; Stock et al., 2018).

4 Conclusions

Well known and effective selection strategies and technologies in animal selection are in use in dairy cattle populations. It would be expected that such methods would also be used in the horse, especially sport and race horse populations.

In terms of GS on quantitative traits it is fair to say that it is much more difficult to produce a reference population in horses than in dairy cattle and we need time for simulation studies to be introduced and validated in practice. On the other hand, use of genomic tools to prevent genetic disorders and select for other mendelian traits in horse selection programs, seems to be in the near future. More so than in cattle selection. The reason being investment in the training of sport or race horses based to their functional longevity.

Selection of quantitative traits is still traditionally based on a horse's performance and its relatives' achievements. Herein lies an opportunity for BO, individual breeders, or companies to choose horses with imperfect results and no famous relatives but with high BVs, based on selection knowledge. Such horses are not as expensive but can produce very good offspring.

In long term selection, prevention of related mating will play an important role. The horse population is small and famous stallions are used too often, especially with new techniques (artificial insemination, cloning). To reduce the increase of inbreeding in populations, mating decisions based on genomic data will be more useful than pedigree-based ones. Cloning can play an important role in cases where a mare or stallion is not related to the population but is infertile due to non-genetic causes (too old, castrated, other fertility problems) and has no offspring.

In general, knowledge-based selection decisions need to be used more in the future in order to effectively deal with the challenges that await us in horse populations.

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