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Genomic Selection in Horse Breeding

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Abstract

The aim of this paper was to present the general aspects of genomic selection in horse breeding and also to provide an overview of existing applications in horses breeding, with particular emphasis on the challenges of implementation and long-term use. Based on conducted review, it could be concluded that breeding organizations must convince horse breeders that genomic selection can be a valuable tool to increase selection success either in sports or in other horse breeding. Genomic selection (GS) allows breeders to evaluate the important traits of offspring even before its birth. GS uses genetic markers to test all relevant traits, including those that are currently very difficult to measure, such as disease resistance, meat quality, horse's crest height, etc. Finally, to establish the relevant genomic selection in individual breeds or breeding types of horses, it is necessary to create a network of collaboration between breeding associations in order to gather all necessary data.

Key words: genomic selection, horse breeding, breeding associations

Introduction

Genomic selection represents a new tool in the selection of horses in order to obtain more reliable breeding values of breeding animals, especially stallions. Prediction of phenotypes is not only used for selection and breeding in animal and plant populations, but also for the evaluation of specific phenotypes, particularly predispositions for genetic diseases and disorders in a population (e.g. mutations). The use of genetic markers has been shown to be useful for predicting and selecting phenotypic traits (Petersen et al., 2013, Signer-Hasler et al., 2012).

The concept of using genetic markers for prediction of breeding values or phenotypes has been suggested many decades ago. However, the use of marker selection is limited by the small number of genotyped markers and the small number of confirmed quantitative properties (QTLs) that can be selected. Genomic selection uses dense genetic markers throughout the genome to predict a phenotype because all QTLs can be assumed to be in imbalance with at least one marker.

Genomic selection allows the selection of genetically best organisms without the need to confirm with the QTL. The concept of genomic selection was proposed in 2001, and since then it has been further developed and applied. Today, genomic selection is widely applied in breeding populations of plants and animals for the selection of future breeding animals. Prerequisites for genomic selection are genotyping platform and horse reference population. Furthermore, genomic selection strategies can contribute to significant reduction in generation intervals in horse breeding programs (Haberland et. al., 2012, Eggen, 2012). The aim of this paper was to present general aspects of genomic selection in horse breeding and to provide an overview of existing applications in horse breeding, with particular emphasis on the challenges of implementation and long-term use in horses.

The basis of genomic selection

With the start of research aimed at better understanding of the structure and function of the human genome, the revolutionary development of animal breeding was also initiated. In the last decade, parallel advances in molecular genetic technology and bioinformatics have enabled the establishment of genomic selection as a new tool to increase genetic gain in breeding animals. The entire genome sequencing that has been consuming and costly for a long period extremely time is a part of standard laboratory services now. Knowledge referring to DNA sequences of multiple species was the basis for accelerated research advancement and the use of information. The use of genomic information for improving the selection in the animal breeding has already been proposed in the late 1960s (Smith, 1967) and made possible the identification of most genes or genetic markers linked to the quantitative trait loci (QTL). The idea of exploiting genetic markers in livestock appeared in 1983 whereas selection supported markers or MAS (Marker Assisted Selection) was developed in the nineties. The aim of genomic selection, as described in Meuwissen et al. (2001), is to take advantage of connection imbalance between QTL and markers of high density across the genome to estimate breeding values in a program of genetic improvement of livestock.

Marker assisted selection (MAS) has enabled the improvement of the selection response, especially for those traits that were difficult to improve in conventional breeding programs because of low inheritance or expensive phenotypic data.

However, the cost-benefit ratio was rarely justified by MAS work. Namely, significant investments in QTL studies were required, QTL genotyping for selection was expensive, and the use of MASs in commercial breeding programs was clearly less than expected (Dekkers, 2004). According to Meuwissen et al. (2001), selection of genetic values predicted from markers could substantially increase the rate of genetic gain in animals and plants, especially if combined with reproductive techniques to shorten the generation interval. Since then, genomic breeding values and their use for selection have been widely explored all over the world. As other most successful selection methods, genomic selection has been poorly represented in the selection of horses. Genomic breeding value can be calculated for both sexes at an early stage of development of stallions and mares, and thus genomic selection can increase profitability and accelerate genetic gain in breeding sport horses, in particular by reducing generation interval. The accurate selection of genotyped young horses without their own offspring leads to significant reduction in the generation interval and thus increases the genetic response. The advantages of genomic selection are shorter generation interval, greater selection effect in traits with low heritability (h^2), and more apparent mating of inbred animals (functional mating of closely related animals). Furthermore, a large number of need animals in the database represents a lack of genomic selection.

The effects of genomic selection on breeding programs

Petersen et al. (2013) stated that intense selective pressures applied over short evolutionary time have resulted in homogeneity within, but substantial variation among, horse breeds. Furthermore, the more difficult and expensive the collection of phenotype data and the longer it takes for a breed until enough data is available for predicting breeding values reliably in conventional systems, the larger is the potential of increasing the genetic gain by genomic selection. According to Falconer (1989), in a population undergoing selection, genetic change (ΔG) is determined by the selection intensity (i), the accuracy of selection (r), the genetic variability of a trait (σ_a) and the generation interval (L) as $\Delta G = (i \times r \times \sigma_a) / L$.

Accordingly, the increasing genetic gain for the current characteristic can be achieved by increasing the intensity of selection, more accurate estimation of animal breeding value and by reducing the generation interval.

Significant increases in the intensity of selection include the risk of adverse effects due to loss of genetic diversity, at least in the long term, so that it may become necessary to use data from the entire genome for managing diversity and inbreeding (Cervantes and Meuwissen, 2011).

Genomic selection in practice

The role and structure of the horse industry vary considerably between countries, but there is no doubt that it plays an important economic role in countries with developed horse breeding. The occurrence of genetically-conditioned diseases in horse, such as x monosomy, chimeric karyotype, hypercalcemia periodic paralysis, lethal cleavage of the patella, occipital-atlantic-axial region malformation, narcolepsy, degenerative spinal cord injury, lethal white gene W, myoclonus, cerebral disease, haemophilia, combined immune defect, night blindness, epitheliogenesis imperfecta, melanoma, osteohondrosis, and neonatal isoelectrolysis can be prevented by application of genomic selection (Sakač, 2008).

Today it is possible to carry out genomic selection of embryos, sex selection, disease resistance rating, genomic breeding value rating, as well as rating of functional inbreeding. Petersen et al. (2013) stated that genome-wide analysis reveals selection for important traits in domestic horse breeds. Furthermore, the d_i test statistic is designed to detect signatures of selection that are at or near fixation within a population, but success in detecting such loci is dependent upon and limited by the classification of populations. Unlike the production sector of horse meat, which is economically important in some countries, but there is no structure for genomic enhanced breeding programs, horse sports industry has a clear organizational structure and well-developed breeding programs worldwide.

According to (Koenen and Aldridge 2002), routine genetic evaluations were established for sport horses in several equestrian sports with a focus on performance, while further important breeding traits have not been considered yet sufficiently due to difficulties with testing. Long generation interval in a horse implies great potential of genomic selection to increase genetic gain and at the same time to optimize the range of selection traits. The available SNP chips have already been used for researches (Schräder et al., 2012; Petersen et al., 2013) and routine use of whole genome data for breeding purposes can be expected in the near future. Collecting enough high quality phenotype data will likely be the main limiting factor, but it is possible to rely on the information on phenotypic records of relatives (Van Grevenhof et al., 2012).

However, co-operation between breeding organizations is essential for gathering all data, although the network in the horse industry may not be as close as it is in dairy cattle, where international exchange of information has already been established via Interbull. The study of Petersen et al. (2013) has demonstrated the utility of this approach for analysing the equine genome and is the first that shows a functional consequence of selective breeding in the horse. In this study, they determined the breed structure of the horse to identify regions of the genome that are significantly different between breeds and therefore may harbour genes and genetic variants targeted by selective breeding.

Furthermore, they emphasize that identification of variants in the Paint and Quarter Horse is significantly associated with altered muscle fibre type proportions favourable for increased sprinting ability. Finally, Signer-Hasler et al. (2012) reveal loci influencing height and other conformation traits in horse.

Conclusion

Finally, it could be concluded that breeding organizations must convince horse breeders that genomic selection can be a valuable tool to increase selection success either in sports or in other horse breeding. Genome selection (GS) allows breeders to evaluate the important traits of an offspring even before its birth. GS uses genetic markers to test all relevant traits, including those that are currently very difficult to measure, such as disease resistance, meat quality, horse's crest height, etc. Finally, to establish the relevant genomic selection in individual breeds or breeding types of horses, it is necessary to create a network of collaboration between breeding associations in order to gather all necessary data.

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Геномска селекција у узгоју коња

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Сажетак

Циљ овог рада био је да се представе општи аспекти геномске селекције у узгоју коња, као и преглед постојећих примјена селекције у узгоју коња, са посебним нагласком на изазове примјене и дугорочно кориштење. На основу обављеног прегледа могло би се закључити да оплемењивачке организације морају увјерити узгајиваче коња да геномска селекција може бити драгоцјено средство за повећање успјеха у селекцији за спортске сврхе или осталим типовима селекције. Геномска селекција (ГС) омогућава узгајивачима да процјене важне особине потомства коња чак и прије самог рођења. Геномска селекција користи генетске маркере за тестирање свих релевантних особина, укључујући и оне које је тренутно јако тешко измјерити, као што су отпорност на болести, квалитет меса, висина гребена коња, итд. Коначно, за успостављање одговарајуће геномске селекције код појединих раса или узгојних врста, потребно је успоставити мрежу сарадње између узгајивачких удружења у циљу прикупљања свих потребних података.

Кључне ријечи: геномска селекција, узгој коња, узгајивачка удружења