Evaluation Of Genomic Selection For Functional Traits In Horse Breeding Programs

F. Sitzenstock[*], S. König, F. Ytournel and H. Simianer

Introduction

Genomic selection was formulated by Meuwissen et al. (2001) as a novel concept for based on breeding values using dense marker maps, and it is under way to be implemented in dairy cattle breeding programs (Hayes et al., 2009). The benefit of genomic selection relative to conventional breeding programs has been demonstrated for dairy cattle (Schaeffer, 2006; König et al., 2009) as well as for pigs (Simianer, 2009). The advantage of genomic selection in sport horses may be limited because of the long generation intervals, due to late onsets in breeding and long reproductive lifetimes (Hamann and Distl, 2008), which may be difficult to reduce. However, such a selection procedure may be useful for functional traits in sport horses. Selection for functional traits, for example osteochondritis dissecans (OCD), gets indeed more and more necessary because of economic aspects and animal welfare. OCD is a multifactorial disease of limb joints in young animals (Jeffcott, 1991). The estimated heritability for OCD is moderate in riding horses (0.06 to 0.33) (Stock et al., 2007; Winter, 1995). A potential for selecting German Warmblood riding horses based on radiographic findings was demonstrated (Busche, 2005; Stock et al., 2007). However, many horses undergo surgery for OCD, and such horses cannot be identified and are thus false negatives.

The general objective of the present study was to assess the efficiency of genomic selection for a functional trait (OCD) in a conventional breeding program for sport horses. The economic evaluation focussed on comparisons with respect to the number of genotyped animals (in one or both sexes), the costs for genotyping, and accuracies of genomic indices.

Material and methods

The studied population comprised 20,000 mares (M) generating a selection pool of 4,000 reared female foals and 2,000 reared male foals per year. Selection criteria of 100 three year old stallions (young stallions, YS) are pedigree information and results from own performance tests. Final selection of 75 stallions (old stallions, OS) at the age of seven years is based on results of progeny. Half of mares are mated with OS, the other half are mated with YS. The yearly selection of 2,000 mares at the age of three is based on pedigree information and own performance testing. Selected stallions and selected mares were used for a breeding period of seven and ten years, respectively. The breeding program was modeled with the computer program ZPLAN (Willam et al., 2007). This program combines the gene flow method (Hill, 1974), selection index theory (Hazel, 1943), and a complex economic model of costs and returns. The gene-flow between the three groups (YS, OS, M) is presented in table 1.

[*] Department of Animal Sciences, Georg-August-University Goettingen, Albrecht-Thaer-Weg 3, 37075 Goettingen

Table 1: Schematic gene flow matrix (arrows indicate the gene flow)

	young stallion (YS)	old stallion (OS)	mares (M)
young stallion (YS)		OS → YS	M → YS
old stallion (OS)		OS → OS	M → OS
mares (M)	YS → M	OS → M	M → M

Traits in the breeding goal were dressage ($h^2 = 0.3$) and jumping ($h^2 = 0.27$) with an antagonistic relationship among each other ($r_g = -0.20$), and equal economic weights per genetic standard deviation. In both scenarios (scenario I and II) genomic selection was applied for a low heritability functional trait (OCD, $h^2 = 0.15$). OCD was supposed to be genetically uncorrelated to both dressage and jumping. The economic weight per genetic standard deviation for OCD was 50 % of the economic weight for dressage or jumping, respectively. Genotyping was realized either only on the 2,000 reared male foals (scenario I) or on all 6,000 reared foals from both sexes (scenario II). Accuracies of genomic indices for the functional trait were altered within the range from $r_{TI} = 0.3$ to $r_{TI} = 0.8$. Considered variable cost parameters per mare comprised costs for the organization of the herdbook, for performance testing, and for X-ray examinations of all reared male foals, which are mandatory for selling. Costs for genotyping were varied between 100 € and 250 € in increments of 50 €.

The main criteria to evaluate the various breeding programs was the discounted profit (DP) reflecting the discounted returns (DR) minus discounted costs (DC) per mare. Discounted return is the monetary value of the genetic superiority expressed by improved animals in the whole population over the time of investment (50 years).

Results and discussion

Discounted costs augmented with increasing costs for genotyping, especially when genotyping in both sexes (table 2). For each scenario and each genotyping cost, the DC is constant. Therefore we use the DP for comparing the results.

Table 2: Discounted cost per mare for different costs of genotyping

	costs for genotyping			
	100 €	150 €	200 €	250 €
scenario I	105,34 €	109,96 €	114,59 €	119,21 €
scenario II	114,59 €	137,69 €	151,57 €	165,44 €

The DP with the modelled accuracy of the genomic index and the different costs for genotyping are shown in figure 1. With the increase of the accuracy of the genomic index, the DP rose up in both scenarios. As expected, it decreased with higher costs for genotyping. Scenario II provided higher DP than scenario I for genotyping costs of 100€ per animal, but the inverse was observed when the genotyping costs were highest. With intermediate genotyping costs, scenario II achieved better DP than scenario I with accuracies between 0.5 (genotyping costs=150€) and 0.7 (genotyping costs=200€). These accuracies can be achieved with genomic information in functional traits (France Génétique Elevage, 2009). The realized DP and the best genotyping strategy (all reared horses or only the male foals)

thus directly depend on the accuracy of the genomic information and the genotyping costs. Genotyping all foals from both sexes is more sensitive to these variations than genotyping only the male foals.
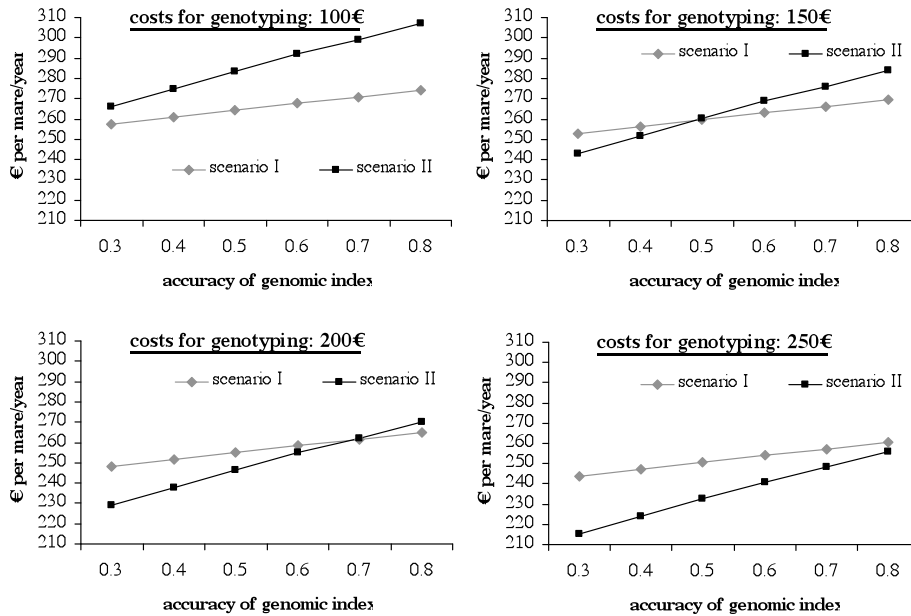

Figure 1: Discounted profit (DP) in € per mare/year for scenario I and II with different accuracy in the genomic index and costs for genotyping of 100€, 150€, 200€ and 250€

Because of the elusivness of economic weighting for the traits in the breeding goals, the genetic gain (GG) of the functional trait is even more important. Figure 2 shows this GG in genetic standard deviation per year (σ_G). It is obvious that scenario II is superior over scenario I for all accuracies of the genomic index. The GG for jumping and dressage were quite constant (around 0,025 σ_G and 0,02 σ_G, respectively).

According to these results, the implementation of genomic selection for functional traits in addition to performance traits dressage and jumping is recommended. The possibility of selecting against OCD has already been suggested (Busche, 2005; Stock et al., 2007). The problem in phenotypic selecting of OCD is the fact that horses with arthroscopic treatment are false negatives. Using molecular data would limit the possibility of hiding an affected animal and should thus be more successful. As a basis for this implementation, secure phenotypic information in functional traits must be recorded. Reliable genomic breeding values could only be estimated with this information (Hansen and Simianer, 2008). With low accuracies and high genotyping costs (realistic assumptions) scenario I realize the highest discounted profit. But supplementing the genetic gain, scenario II seems to be the best choice. Moreover, implementing a genomic selection on OCD should not alter the performances in dressage and jumping.
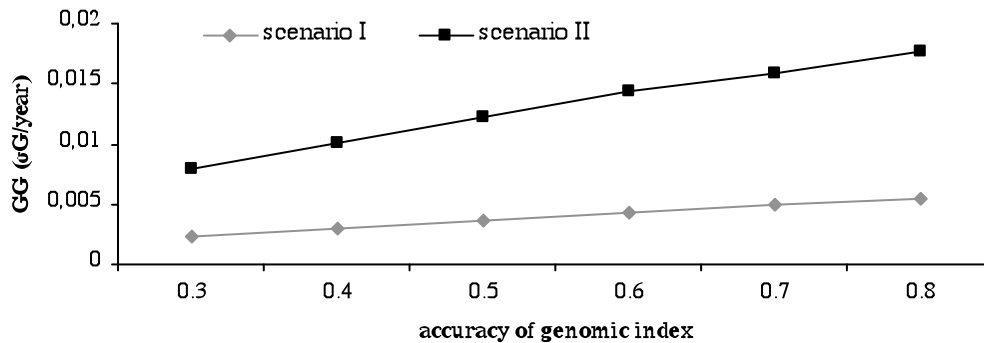
Figure 2: Genetic gain (GG) in genetic standard deviation (σ_G) per year in the functional trait in scenario I and scenario II

Conclusion

This study demonstrates the potential for genomic selection in a functional trait in addition to the performance traits jumping and dressage. The costs for the additional genotyping and the accuracy of the genomic index greatly influence the profit per mare. Genotyping all potential breeding horses promises a much higher genetic gain than genotyping male foals only. However, with high genotyping cost and low accuracies of genomic breeding values, it is economically advantageous to restrict genotyping to male foals only.

Acknowledgments

References

Busche, S.-M. (2005). *PhD – Thesis*. University of Goettingen.
France Génétique Elevage (2009). ISBN 978 – 2- 84148 – 728 – 8.
Hansen, M., Simianer, H. (2008) *Proc. 5th Uelzener Pferdeworkshop*, Uelzen, Germany.
Hazel, L. N. (1943). *Genetics* 28: 476 – 490.
Hill, W. (1974). *Anim. Prod.* 18: 117-139.
König, S., Simianer, H., Willam, A. (2009). *J. Dairy Sci.* 92: 382 – 391.
Meuwissen, T. H. E., Hayes, B., Goddard M. E. (2001). *Genetics* 157: 1819 – 1829.
Schaeffer, L. R. (2006). *J. Anim. Breed. Genet.* 123: 218 – 223.
Simianer, H. (2009). *Proc. 60th Annu. Mtg. Eur. Assoc. Anim. Prod.*, Barcelona, Spain.
Stock, K. F., Distl, O. (2007). *J. Anim. Sci.* 85: 31 – 41.
Willam, A., Nitter, G., Bartenschlager, H. et al. (2007) *ZPLAN – Manual*.
Winter, D. (1995). *PhD – Thesis*. University of Goettingen.