

Genomic selection in the horse industry: Examples of applied research in the Swiss Franches-Montagnes breed

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1. Introduction

Over the last decade, the sequencing of entire mammalian genomes and progress in the field of molecular genetic techniques have led to high throughput DNA chip technology. High-throughput technology allows for the cost-effective, parallel genotyping of thousands of single nucleotide polymorphisms (SNPs) per animal. Subsequently, bioinformatics, statistics, access and enormous gain of genetic information on the individual or even the population level is revolutionizing animal breeding and genetics, and thus, also impacts the horse industry.

2. Goals and Resources

Our objective was to investigate the suitability of genome-wide SNP data for breeding, genetic diversity, trait mapping, and selection purposes in a small, genetically closed, and indigenous livestock population: the Swiss Franches-Montagnes (FM) horse breed. To do so, we had access to data of 43 conformation and performance traits evaluated in the routine breeding program, and of about 1'200 FM horses with genotypes or sequence information available.

3. Results

We first evaluated the genetic diversity of the FM breeding population based on pedigree information as well as from different molecular markers using different statistical procedures. SNPs allow for the calculation of a genomic relationship matrix. We found marker information especially beneficial in situations where no pedigree data is available, or when existing pedigree data needs verification.

Secondly, genome-wide analysis revealed association signals for height at withers and other conformation traits on chromosomes 3 and 9, respectively. Together, the detected quantitative trait loci (QTL) explain ~18% of the heritable variation of height in horses, whereas all chromosomes together account for ~70% of the genetic variance. Furthermore, we detected a QTL on chromosome 6 for correctness of gaits, and we identified seven QTLs affecting white markings. Together, the seven loci explain 54% of the genetic variance in total white markings, while two of them alone account for 26%.

Thirdly, informative FM horses were selected for whole-genome sequencing and subsequent imputation of FM horses genotyped on a 50 k SNP chip only. In order to optimize the imputation of missing genotypes we investigated different imputation scenarios and programs. After imputation we ended up with around 13 million SNPs for ~1,100 FM horses. Thus, the imputation pipeline results in unprecedented marker densities in the FM sample. Based on the imputed data set we re-performed genome-wide association studies (GWAS). Several QTLs were identified for a total of 19 traits, also confirming our previous findings.

Finally, our study on genomic selection (GS) in the FM revealed that the genotypic value of an animal can generally be predicted more accurately and earlier in life using genomic breeding value estimation compared to conventional evaluation schemes. The average reliability of genomic estimated breeding values (GEBVs) was found to be 0.59 ± 0.05 , 0.60 ± 0.18 , and 0.56 ± 0.15 , for white head and leg markings, performance and conformation traits, respectively. These values are clearly higher than the average reliability of conventionally estimated breeding values (EBVs) for the same traits - 0.41 ± 0.01 , 0.28 ± 0.04 , and 0.30 ± 0.04 , respectively.

4. Conclusions

High-throughput genotyping technology, new sequencing methods, bioinformatics and appropriate data management and analysis, comprise huge potential for application in the horse industry. However, many questions remain unresolved so far concerning implementation of GS in practice: the necessary industry framework? Balance of investments and expected benefits? Know-how within breeding organizations? Small local breeds? Limitations in the number of horses available? Quality of phenotypes? Data ownership and legal issues? Commercialization of horses with low genetic merit or unfavorable genotype? Acceptance of new technologies by horse breeders, buyers and by the general public?

References

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