Microsatellite alleles imputation from SNP genotypes for parentage verification in sport horses

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Validating genomic selection for sport traits in Dutch warmblood horses

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In recent years, genomic selection has been successfully implemented in various animal species for a number of performance traits. Horse breeding has only marginally been part of this development. Meanwhile, a reasonable number of genotypes on horses using a high density SNP panel is available within the Royal Dutch Sport Horse-population. Horse breeders are still hesitant to use BLUP techniques over phenotypic selection which is still common practice. For decision making and to increase acceptance it is important to demonstrate and quantify the advantages of genomic selection. The aim of this study was to examine the added value of genomic breeding values compared to traditional breeding values for sport performance in warmblood sport horses by means of a validation. The accuracy of EBVs obtained with either BLUP or single-step genomic BLUP (ssGBLUP) were evaluated using a leave-one-out technique. For 52 breeding stallions born since 2003 in a specialized breeding programme with at least 30 offspring competing in sport, all information of all their offspring and potential grand offspring was iteratively removed from the dataset. This has been repeated but now also omitting stallion's own performance. The accuracy of the breeding values (r_{IH}) was determined by the weighted Pearson correlation between the (G)EBV of the stallion from the evaluation where its sources of information were removed and the average pre-corrected performance of his offspring. The full dataset used for this analysis comprised 109,089 records with performance data and known pedigree in five generations; 4,273 animals had SNP genotypes. A multivariate animal model was used to estimate the (G)EBVs for the sport trait and three other performance related traits using MiXBLUP software (version 2.2). The accuracies of (G)EBVs from ssGBLUP compared to BLUP improved by 7% when omitting both own performance and (grand-) offspring performance of the stallions (49% for BLUP, 56% for ssGBLUP), and by 5% when omitting the performance of offspring and potential grand offspring only (55% for BLUP, 59% for ssGBLUP). Despite the limited size of the training data, genomic selection showed an improved accuracy for a breeding goal trait in sport horse breeding.

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Nowadays in France, microsatellites markers (MS) are used for parentage verification among all horse breeds. Studies have shown that parentage verification based on Single Nucleotide Polymorphisms (SNPs) are less prone to error, cheaper and have shorter processing times. Moreover, ISAG is working on a SNP panel to allow the transition from MS to SNP for parentage verification. The principal constraint of this transition is the cost of re-genotyping all sires and mares that are already MS-genotyped. In this study, we wanted to test a method to impute MS alleles from SNP haplotypes. A total of 6,295 horses from 3 breeds (Arabs, Selle-Français and French Totters) were used. They were MS genotyped for parentage verification and have been SNP genotyped with 54K to 670K chips. Haplotypes for markers within 500 Kb on either side of each MS were obtained using FImpute 3 by considering MS alleles as pseudo-snp. To determine SNP haplotypes that best fit a MS allele, we started by selecting 10 SNP on each side of the MS genotype, with the possibility of extending it if haplotypes matched with several MS alleles. The objective was to obtain a haplotype that always fitted one MS allele (or as little MS as possible). The haplotypes were built within breeds and across breeds. First analysis of the 9 alleles of MS AHT4 and the 166 haplotypes with 20 flanking SNPs showed mixed results. Problematic results from phasing, i.e. missing MS allele or more than one MS allele on the same haplotype, represented less than 0.5% of phased samples. Rare association (1 case) between MS allele and SNP haplotypes represented 1% of the phased samples. After removing these cases, SNP haplotypes were able to attribute unambiguously MS allele in 84% of the cases considering all breeds together (from 50% for Selle Français alone to 100% for French Trotters alone). Longer haplotypes will be tested and influence on parentage verification will be checked.