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Anne Ricard, S. Danvy, Andres Legarra

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First results on genomic selection in French show-jumping horses

Ricard, A.¹, Danvy, S.² and Legarra, A.³, ¹INRA, UMR1313, 78352 Jouy-en-Josas, France, ²IFCE, Recherche et Innovation, 61310 Exmes, France, ³INRA, UR 631, 31326 Castanet-Tolosan, France; anne.ricard@toulouse.inra.fr



Genomic selection could be highly interesting for horse breeding because it would reduce the nowadays high generation interval, at a low cost compared to the value of an animal. The aim of this study was to estimate the observed accuracies of genomic estimated breeding values in a representative set of show jumping horses. A sample of 908 stallions specialized in show jumping (71% Selle français (SF), 17% Foreign sport horses (FH), 13% Anglo Arab (AA)) were genotyped. Genotyping was performed using Illumina Equine SNP50 BeadChip and after quality tests, 44,444 SNPs were retained. From whole population BLUP-based estimated breeding values and their reliability, a specific procedure was developed in order to obtain de-regressed proofs combining own performances and performances of relatives outside the genotyped sample. Two methods were used for genomic evaluation: GBLUP and Bayes C π , and 6 validation data sets were compared, chosen according to breeds SF+FH+AA or SF+FH, family structure (more than 3 half sibs), reliability of sires (>0.97) or sons (>0.72). In spite of a favorable genetic structure (linkage disequilibrium equal to 0.24 at 50Kbp), results showed low advantage of genomic evaluation. On the validation sample SF+FH+AA, the correlation between de-regressed proofs and GBLUP or BayesC π predictions was: 0.39, 0.37, 0.51 according to the different validation data sets compared to 0.36, 0.33, 0.53 obtained with BLUP predictions. Correlations were much lower on the SF+FH sample. No practical applications are proposed at present. Research is pursued in order to improve the number of pairs sire-son with high number of measured progeny and to improve methodology in this context, less favorable than dairy cattle breeding.

The myostatin sequence variant g.66493737T>C detects evolution and domestication in horses

Dierks, C.¹, Mömke, S.¹, Philipp, U.¹, Lopes, M.S.² and Distl, O.¹, ¹University of Veterinary Medicine Hannover, Institute for Animal Breeding and Genetics, Buenteweg 17p, 30559 Hannover, Germany, ²University of Azores, Biotechnology Centre of Azores, Rua Capitao Joao D'Avila, 9700-042 Angra do Heroísmo, Portugal; ottmar.distl@tiho-hannover.de

Myostatin (MSTN) is a negative regulator of muscle growth. Partial or complete loss of function of MSTN leads to muscle hypertrophy. We determined the presence of the sequence variant g.66493737T>C polymorphism and the promoter insertion g.66495327-[Insertion227b]-66495326 of MSTN associated with sprinting ability in thoroughbreds, donkeys and 19 different horse populations. In addition, we analyzed the haplotypes surrounding these MSTN-polymorphisms using the genotyping data from the Illumina Equine 50K beadchip. The C-allele was found in all domestic horse breeds but not in Przewalski horses and donkeys genotyped here. The frequency of the promoter insertion was quite low (0.5%) and not in linkage disequilibrium with the g.66493737T>C polymorphism. AMOVA for donkeys and the 19 horse populations showed that 25% of the variance of the g.66493737T>C SNP is due to species and population differences and 75% of the variability can be attributed to differences within species and populations. Nei's standard genetic distances among donkeys and the 19 horse populations ranged from 0 to 0.29. Genetic distances were lowest among Przewalski and Arabian, Lewitzer, Lusitano, Hanoverian, Westphalian, Exmoor and Icelandic horses (0-0.01). Genetic distances were largest among Przewalski and Sorraia as well as Black Forest horses. Cluster analysis revealed five main clusters for the C-allele frequency. The analysis of the C/T-polymorphism of the MSTN gene highlights an east to west increase of the C-allele and indicates that this MSTN mutation arose in the West European E. ferus or during domestication in western European horses. In conclusion, the g.66493737T>C polymorphism seems to be a good indicator for differentiating domestic horses due to their western or eastern origin.

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