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Anne Ricard, Sophie Danvy, Andres Legarra

To cite this version:

Anne Ricard, Sophie Danvy, Andres Legarra. First results on genomic selection in French show-jumping horses. 63. Annual Meeting of the European Association of Animal Production (EAAP), Aug 2012, Bratislava, Slovakia. 476 p., 10.3920/978-90-8686-761-5 . hal-02746523

Session 45 Theatre 4

First results on genomic selection in French show-jumping horses

Ricard, A.[1], Danvy, S.[2] and Legarra, A.[3], [1]INRA, UMR1313, 78352 Jouy-enJosas, France, [2]IFCE, Recherche et Innovation, 61310 Exmes, France, [3]INRA, 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 SNP 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 Cπ, 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 BayesCπ 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.

Session 45 Theatre 5

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], [1]University of Veterinary Medicine Hannover, Institute for Animal Breeding and Genetics, Buenteweg 17p, 30559 Hannover, Germany, [2]University 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. Particular 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.

Book of Abstracts of the 63rd Annual Meeting of the European Federation of Animal Science

Book of abstracts No. 18 (2012)
Bratislava, Slovakia
27 - 31 August 2012