



First results on genomic selection in French show-jumping horses

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The KCNJ11 (potassium inwardly-rectifying channel, subfamily J, member 11) gene is located in BT15, near a quantitative trait loci for meat tenderness. In this study, single nucleotide polymorphisms (SNPs) were described in KCNJ11 and associated with Warner – Bratzler shear force (WBSF) at different aging times: 1 d after slaughter (WBSF0), after 7 d (WBSF7) and 14 d (WBSF14) of aging. Fourteen steers of Nelore breed, characterized as extreme for the distribution of WBSF0 in a half-sib population of 500 progenies from 32 sires, were selected for sequencing. Twenty-two SNPs were found and the disequilibrium pattern indicated the SNP 2126C>T as a principal TagSNP. Allele frequency difference between extremes of WBSF0 (Fisher test, $P \leq 0.05$) was found for the SNP 2942T>C and both SNPs were genotyped in the whole population. A mixed model was used to investigate association with WBSF. Associations were found between the SNP 2126C>T and WBSF7 ($P \leq 0.0458$) and for the SNP 2942T>C with WBSF0 and WBSF7 ($P \leq 0.0487$ and $P \leq 0.0356$, respectively). Allele substitution effects of 0.92 g on WBSF0 ($P \leq 0.0487$) and of 0.88 g on WBSF7 ($P \leq 0.0356$) were found for the SNP 2942T>C, with the T allele associated with reduced WBSF. The KCNJ11 gene appears to have an additive genetic effect on meat tenderness and may be useful for marker assisted selection in this breed.

Key Words: cattle, SNP, meat

P4047 Tissue-specific expression of porcine TFAM. Andrej Rencelj^{*} and Peter Dovc, *Department of Animal Science, Biotechnical Faculty, University of Ljubljana, Domžale, Slovenia.*

Mitochondria play a leading role in energy metabolism of mammalian cells. The number of mitochondria in the cell can change in a short time because it depends on energy requirements of the cell. The biogenesis of mitochondria is very complex process and it involves several regulatory proteins; for example, NRF-1 and NRF-2, PGC-1, TFAM, POLG, POLRMT. Irregular expression and mutations the genes coding these proteins can cause abnormal function of mitochondria, leading to the vast range of cell and organ pathologies. The purpose of this study is to develop the gene network regulating mitochondrial biogenesis and to establish their expression profiles in different tissues. Our previous experiments suggested the presence of two different splicing forms for the mitochondrial transcription factor TFAM. Because the expression of TFAM plays an important role in muscle type determination and oxidative

potential of different tissues, we developed qPCR assay for quantification of both splice forms in different tissues. Our results confirm presence of the long (whole length transcript) and short (missing exon 4) splice forms in all analyzed tissues (eye nerve, eye muscle, brain, muscle, liver, kidney, spleen). The proportion of the short form in all tissues was very low, except for the m. semispinalis capitis, where the short form represents about 20% of transcripts and eye muscle, where the short form is predominant.

Key Words: TFAM, splicing, mitochondria

P4048 First results on genomic selection in French show-jumping horses. A. Ricard^{*1}, S. Danvy², and A. Legarra³, ¹Institut National de la Recherche Agronomique, UMR1313, Jouy-En-Josas, France, ²Institut Français du cheval et de l'Equitation, Exmes, France, ³Institut National de la Recherche Agronomique, UR 631, Castanet-Tolosan, France.

Genomic selection could be highly interesting for horse breeding because it would reduce the currently high generation interval, at a low cost compared with the value of an animal. The aim of this study was to estimate the observed accuracies of genomic estimated breeding values. 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, 44444 SNP were retained. From whole population BLUP-based estimated breeding values and their reliability, a specific procedure was developed 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 CII, 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). Results showed low advantage of genomic evaluation. On the validation sample SF+FH+AA, the correlation between de-regressed proofs and GBLUP or BayesCII predictions was: 0.39, 0.37, 0.51 according to the different validation data sets compared with 0.36, 0.33, 0.53 obtained with BLUP predictions. GWAS analysis would be performed on the same data.

Key Words: horse, genomic selection, jumping

P4049 Association of the single nucleotide polymorphisms in cholecystokinin type A receptor gene with growth traits in Japanese Hinai-dori crossbred chickens. Kazuhiro Rikimaru^{*1,2}, Megumi Komatsu¹, Daiki Takahashi¹, Keiichi Suzuki², Yoshinobu Uemoto³, Hisato Takeda⁴, and Hideaki Takahashi⁴, ¹Akita Livestock Experiment Station, Daisen, Akita,