Effect of mitochondrial genetic variability on performance of endurance horses

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Endurance races in horse require a high level of aerobic energy production to fulfil the demand of the cardio-respiratory system and skeletal muscles. At the cellular level, the mitochondrial respiratory chain (RC) performs ATP synthesis via the phosphorylation oxidative pathway. We performed mtDNA sequencing followed by SNP calling and GWAS analysis on 434 horses (Arabian 83.4% and Anglo-Arabian 9.6%) descended from 232 sires with an average family size of 1.8 descendants per sire. The endurance performances were measured by two traits: average speed and status at the arrival (finishing or not). Among 1,268 SNP detected with some heteroplasmy, 458 were finally used after selection with minimum calling frequency of 85% and minimum minor allele frequency of 2.3%. The GWAS analysis was performed using a mixed animal model to estimate the SNP allele effects (up to 4 copies) on the two performances corrected for fixed effects (age, sex and race). Random polygenic effect was included in the model using pedigree information (5,382 ancestors). ASREML software was used. The model could detect a total of 15 SNP significantly associated (raw P-value<0.01) to the performance traits. Seven SNP were significantly associated with both average speed and status at the arrival. In these cases, the reference allele was frequent (≥89%) and its effect was favourable on both traits (from +0.30 to +0.64 in phenotypic standard deviation unit). Five SNP were significantly associated with average speed with the same configuration: reference allele frequent (>92%) and favourable (+0.40 to +0.49). Three SNP were significantly associated with status at the arrival, with high reference allele frequency (≥93%) and favourable effect of reference allele for one SNP (+0.45) and unfavourable for two SNPs (-0.39 and -0.45).