



Search for the association of SNP in GRM8 gene with sperm quality in stallions

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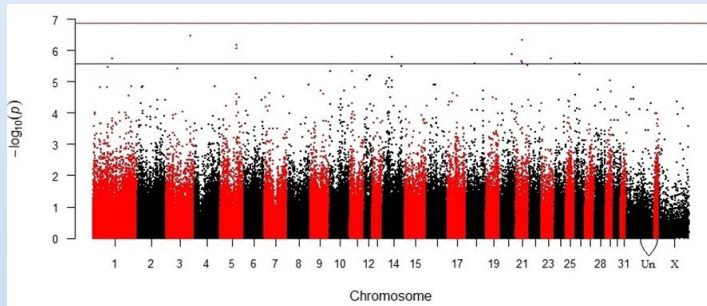


Figure 1. Manhattan plots of GWAS for VOL

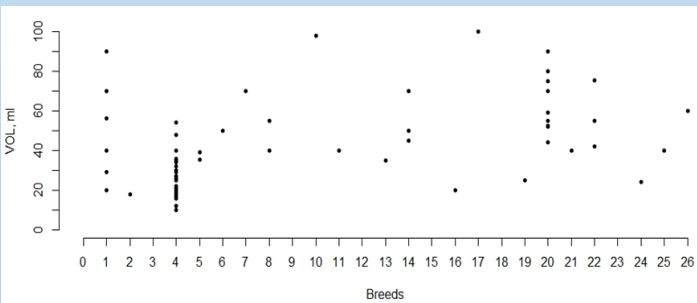
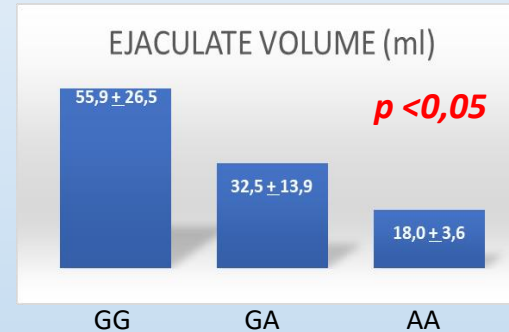
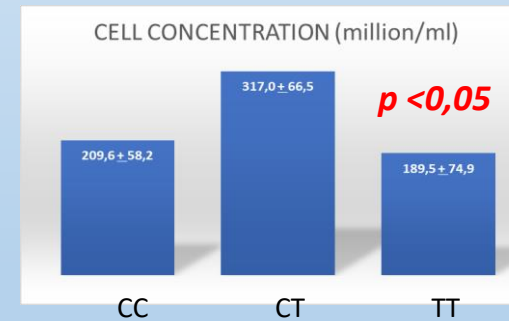


Figure 2. Distribution of VOL by breed

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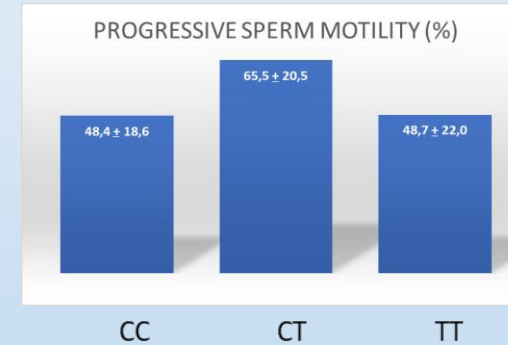
rs1147388106



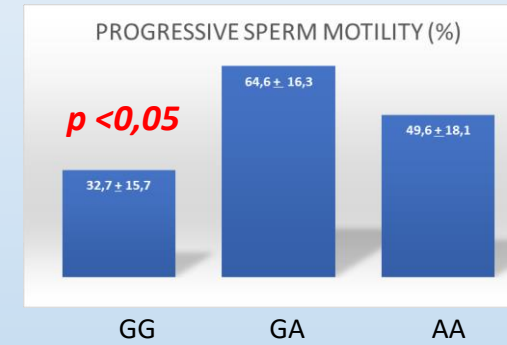
rs395286150

MATERIALS AND METHODS

The four single-nucleotide substitutions in the exon of the GRM8 gene identified during the studies and the association of these SNPs with sperm quality was carried out. Semen from 22 stallions was collected. Sperm volume, concentration and progressive motility were assessed. Sequencing of the sections of the candidate GRM8 gene was carried out using an Applied Biosystems 3500 genetic analyzer.



rs395286150



rs394524550

RESULTS

According to the identified single nucleotide substitution rs1147388106, the highest ejaculate volume was in stallions with the GG genotype (55.9±26.5 ml) compared to stallions with the GA genotypes (32.5±13.9 ml) and AA (18.0±33,6) ($p < 0.05$). When analyzing data on SNP rs395286150, stallions with a heterozygous CT genotype had the best sperm quality. Thus, the cell concentration was 317.0±66.5 million/ml in stallions with the CT genotype, 209.6±58.2 and 189.5±74.9 % with the CC and TT genotypes, respectively ($P < 0.05$). The progressive sperm motility of stallions with the CT genotype was 65.5±20.5% versus 48.7±22.0% in stallions with the TT genotype and 48.4±18.6% with CC. Analysis of data on SNP rs394524550 revealed a significant effect of the genotype on progressive motility. Stallions with the AG genotype had a progressive motility of 64.6±16.3%, and those with GG and AA 32.7±15.7 and 49.6±18.1%, respectively ($P < 0.05$).