can conclude that thermal stress induces a pronounced transcriptional repression in sperm cells.

Key Words: sheep and related species, RNA-seq, gene expression

P37 Abstract withdrawn

P38 Abstract withdrawn

P38 Abstract withdrawn

P39 Genome-wide association study of sperm traits in Assaf rams.

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In artificial insemination (AI) centers, the volume (VOL), sperm concentration (CON) and the spermatozoa subjective motility (MOT) of rams' ejaculates are routinely evaluated before doses elaboration to ensure the fertilizing capacity of the spermatozoa and its suitability for AI. However, the relationship between these sperm parameters and ram's fertility is not clear. Moderate heritability estimates were found in sheep (David et al., 2007) for VOL, CON and number of spermatozoa (NSP) (0.12 to 0.33) and low for MOT (0.02 to 0.14). Current genomic tools could help to identify genomic regions associated with such low heritability traits, enabling to conduct a selection of the rams assisted by markers. In this work, a GWAS analysis of sperm parameters in Assaf rams was carried out using data of 27.886 ejaculates from 429 matured rams placed at OVIGEN AI center. A linear regression analysis including the ram age and herd of origin, the date of semen collection, the jump number during semen collection and the ram permanent environmental effects was conducted to obtain pseudo-phenotypes for the GWAS. The association analysis was performed with the GCTA software (Yang et al., 2011) using 342 rams genotyped with a custom 50K SNP Affymetrix microarray. The positional candidate genes were identified in the 250 Kb region on both sides of the significant SNPs. Genes and SNPs were mapped on the Oar v3.1 sheep genome. For VOL, CON and NSP, associations ($P < 0.01$) were found at the chromosome level. Putative causal genes were *TET2* (OAR6), *SLC4A4* (OAR6) and *DTNA* (OAR23) related to spermatogenesis, fertility and teratospermia, for VOL; *SERPINE3* (OAR10) and *SPEF2* (OAR16), which play role in fertility, spermatogenesis and flagellar assembly, for CON; and *GALNT14* (OAR3), *SNAP23* (OAR7), *CDYL2* (OAR14) and *SPR54* (OAR18) related to infertility, asthenozoospermia, sperm capacitation and gametogenesis, for NSP. For MOT, 5 genome regions at chromosomes 3, 7, 16, 19 and 20 showed significant associations ($P < 0.01$) at the genome level. Putative causal genes were *SEMA4F* (OAR3), *RBMS3* (OAR19) and *HSPA1L* (OAR20), which have been related to sperm fertility, teratospermia and binding of sperm to zona pellucida, respectively.

Key Words: sheep, genome-wide association, SNP, fertility, sperm traits