

**W027****Genome-wide SNP Analysis of Small Ruminant Tolerance to Grazing Stress under Arid Desert****Conditions**

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Desert dwelling animals are exposed to complex biophysical stressors including heat, physical exhaustion, solar radiation, and unavailability of feed and water, which can cumulatively be referred to as grazing stress (GS). GS affect physiological parameters (PP) including rectal temperature, respiration rate, minute ventilation volume, and heat production. Changes in these traits can be used as indicators to assess (in)tolerance to GS. The genomes of desert dwellers, have been exposed to GS for millennia, may carry common chromosomal regions that non-desert animals lack. In this study, we utilized signatures of selection (SS) ("iHS" and "Fst"), and GWAS approaches to analyse genotype data generated using *ovine* and *caprine* 50K Illumina Beadchips to investigate tolerance to GS in desert sheep and goats. For SS analysis, genotype data was from 394 and 366 Egyptian desert sheep and goats, respectively and 895 and 464 non-desert sheep and goats, respectively. For GWAS, PP data from 182 and 151 Barki sheep and goats, were analyzed. Several candidate selection sweep regions were observed in both species. One of the regions on OAR10 (34-43 Mb), spanned genes associated with stress, e.g. tumor suppressors (RB1), angiogenesis and wound healing (FGF). In goats, GRID2 (neurotransmitter receptor affecting neuronal apoptosis), and PDLIM5 (ontogenesis) occurred on CHI6 (26-46 Mb). Multiple candidate QTLs affecting, for instance respiration rate change, within genes playing roles in heat generation (SLC27) and detection of temperature stimulus (NR2F6) were identified on CHI7. Results could prove useful in genomic selection and identification of genes involved in desert stress tolerance.

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