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Genome-Wide Scans Reveal Multiple Selection Sweep Regions in Indigenous Sheep (*Ovis aries*) from a Hot Arid Tropical Environment

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Genome-wide scans reveal multiple selection sweep regions in indigenous sheep (*Ovis aries*) from a hot arid tropical environment

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Animals living in extreme environments demonstrate the adaptive resiliency of species to diverse ecosystems. For instance, desert dwelling animals are exposed to complex interacting biophysical stressors including high temperatures, physical exhaustion, direct solar radiation, feed and water stress. The genomes of such animals are therefore adapted to perform under such conditions. In light of predictions indicating future worsening climatic conditions in arid and semi-arid environments, here we identified, using the F_{ST} derived *di* statistic and two haplotype based methods (*iHS* and *Rsb*), genome-wide candidate regions harboring signatures of positive selection and associated genes in a data set comprising 54,241 SNPs genotyped in 394 individuals from five indigenous sheep populations sampled across Egypt‘s hot arid environment. We identified 11 candidate selection sweep regions across 12 chromosomes and spanning several candidate genes suggesting that, adaptation to arid environments may be mediated by a complex network of genes. However, the physiological functions of some of the candidate genes were directly related to animal response to various stress factors associated with adaptation to arid environments, including osmotic stress (PLK3), heat stress/temperature stimuli (*EIF2B3*), regulation of homeostatic process, reproductive physiology and response to nutrient levels/digestive system process (*OXT*, *AVP*, *MICU2*, *IFT88*) as well as pigment biosynthetic process (*UROD*) and hair follicle morphogenesis (*TGM3*). This suggests that the possible selection pressures shaping the genome architecture of the study populations may be related to physiological adaptations to eco-climatic conditions and these results open avenues for the identification of genomic variants of relevance to adaptation to arid conditions.

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