

# Genome-wide Analysis of Small Ruminant Tolerance to Grazing Stress Under Arid Desert

## A.S. Leaflet R3106

Ahmed R. Elbeltagy, Visiting Scholar, ISU, Senior Researcher, APRI, Egypt;  
Eui-Soo Kim, Post-Doc Research Scientist, ISU;  
Barbara Rischkowsky, Senior Livestock Scientist (Small Ruminants Management), ICARDA, Ethiopia;  
Adel M. Aboul-naga, Emeritus Chief Researcher, APRI;  
Joram M. Mwacharo, Senior Researcher, Genetics/Genomics, ICARDA, Ethiopia;  
Max F. Rothschild, Distinguished Professor, ISU

### Summary and Implications

There are three major hot and dry deserts in North America, all located in the Western United States and Northern Mexico. Desert areas are facing serious environmental challenges, most importantly drought and water shortages caused, to a large extent, by global warming which have been reducing agricultural production and rural community incomes. Therefore the need for adapted livestock populations that can cope with increasing stresses occasioned by desert climate change and still be able to produce economically to support agricultural industries in desert communities is becoming a priority.

In this study we utilized several genetic approaches to analyze genotype data generated using sheep and goat 50K Illumina SNP Beadchips to investigate tolerance to grazing stress in desert sheep and goats. For signatures of selection (SS) analyses, which detect regions in the genome under natural selection, genotype data were from 394 and 366 Egyptian desert sheep and goats, and 895 and 464 non-desert sheep and goats, respectively. For genome wide association analyses (GWAS), which detect genomic regions associated with grazing-stress-affected physiological parameters, data from 182 and 151 Barki sheep and goats, were analyzed. Several candidate regions exhibiting selection signatures were observed in both species. Results could prove useful in genomic selection and identification of genes involved in desert stress tolerance.

### Introduction

Development of livestock populations those are resilient enough to adapt to stress due to climate change while supporting livestock production in desert communities, have many biological challenges. Adaptation traits have low heritability ( $h^2 \leq 0.25$ ); are difficult and expensive to measure, and cannot be accurately measured until late in life. Such traits are therefore difficult to improve using conventional animal breeding strategies. Genomic tools offer opportunities to overcome these challenges. The hypothesis of the study derives from the fact that desert

dwelling sheep and goats are exposed to complex interacting biophysical stressors including heat, physical exhaustion, direct solar radiation, and unavailability of feed (quality and quantity) and water. These can cumulatively be referred to as grazing stress (GS). The genomes of desert dwelling livestock that have been exposed to GS for millennia are very likely to carry common chromosomal regions that are not present in non-desert animals.

GS affects major physiological parameters including rectal temperature (RT); respiration rate (RR); minute ventilation volume (MVV); tidal volume (TV) and body heat production (HP). Changes in these traits can be used to assess (in)tolerance to GS. A long term research and development (R&D) project involving scientists from Egypt's Animal Production Research Institute (APRI), Iowa State University, Ames, IA (USA) and International Center for Agricultural Research in the Dry Areas, ICARDA (Ethiopia) was launched in 2009. It was aimed at understanding the genetic basis for animal tolerance to "GS" in desert sheep and goats through a genome-wide analysis approach. The results were to be utilized in breeding programs that target to apply genomic selection for heat tolerance and adaptation to desert climates.

### Materials and Methods

Signatures of selection were studied in populations of desert sheep and goats using integrated haplotype score (*iHS*, detects long conserved stretches of chromosomal regions that could be associated with GS tolerance traits) and between desert vs. non-desert populations using coefficient of genetic differentiation ( $F_{ST}$ , determines chromosomal regions that distinguish desert from non-desert populations). These regions were investigated for the presence of functional genes associated with tolerance to GS. Genotype data were from 394 and 366 Egyptian desert sheep and goats, and 895 and 464 non-desert sheep and goats, respectively.

For GWAS, 182 sheep and 151 goats were exposed to GS (i.e. three trials each carried out between 12:00 to 15:00 pm, in July and August for 7 years; 2009-2015) involving walking at normal speed a grazing distance of 7 km under direct solar radiation while grazing poor pastures). Each animal was assessed for change in their RT, RR, MVV, TV and HP. Animal Grazing Tolerance Index (AGTI), was developed based on the changes in the 5 traits. AGTI was used to classify animals into 5 groups based on two physiological outcomes: i) respiratory (shallow rapid panting vs. deeper slower panting); ii) metabolic (increase in RT with increase/decrease in HP); vs. 3) showing no significant change. A selective genotyping approach (the most and least tolerant groups, 12.5% from each) was used.

The association study was performed using data collected from individual animals on the five physiological traits (RT, RR, MVV, TV and HP) before and after exposure to GS. Furthermore, phenotypic-correlations were estimated between 4 economic traits (body weights at weaning, at yearling and at GS-exposure, and fecundity; defined as number of offspring born/female mated) and the change in the 5 physiological traits (RT, RR, MVV, TV and HP).

**Results and Discussion**

Results indicated that lighter (U-5 Kg) desert lambs at weaning and heavier (U+10 Kg) lambs at yearling are less tolerant for GS. Desert goats did not show a detectable association between body weights and physiological response to GS. For breeding purposes, it seems that selection for tolerance to GS in desert Barki goats may not antagonize selection for their production performance. However, it is recommended to avoid light lambs at weaning and heavy desert sheep at yearling.

Several candidate selection sweep regions were observed in both species. One region found on sheep chromosome 10 (OAR10), spanned several genes associated with stress, e.g. tumor suppressors, angiogenesis and wound healing.

In goats, genes associated with stress were located in a selection sweep region (26-46 Mb) found on chromosome 6 (Figure 1).

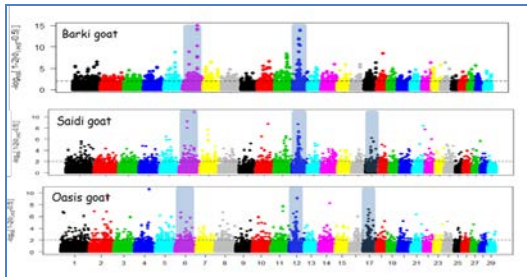


Figure 1. Genetic signatures of selection (*iHS*) In 3 Egyptian desert goat breeds

Several candidate QTLs that influence, for instance change in respiration rate, including genes with roles in heat generation, detection of temperature stimulus and homeostasis were identified on goat chromosome 7. In sheep, genes regulating cellular amide metabolic process, playing a role in single organism cell adhesion and small nuclear RNA, all present in chromosome 25 were found to be associated with RT change (Figure 2).

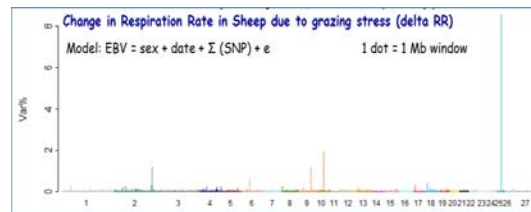


Figure 2. Genome-wide association of respiration rate change trait in Egyptian desert Barki sheep breed

These results could prove useful in genomic selection and in the identification of genes involved in desert stress tolerance. A genomic selection approach could therefore be followed to improve GS tolerance and other economic traits, e.g. growth and fecundity, to support the livestock industry within desert communities.

**Acknowledgments**

Authors are thankful for the support from ISU Ensminger Fund, State of Iowa and Hatch funding and Illumina Greater Good Initiative and GeneSeek. Appreciation is also due to the ADAPTMMap and International Sheep Genomics Consortia for providing data on non-desert small ruminant populations.