



Tropentag, September 18-20, 2019, Kassel

“Filling gaps and removing traps
for sustainable resource management”

Genetic Diversity of Nubian Ibex in Comparison to other Ibex and Domesticated Goat Species

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Abstract

Nubian ibex (*Capra nubiana*) is the only ibex species which has adapted to live in hot, arid regions. Nubian ibex was listed as a vulnerable species in 2008 by the IUCN and is currently considered as critically endangered. The objective of this study was to infer the population structure and genome wide diversity of Nubian ibex (*Capra nubiana*, n = 8) in comparison to Alpine ibex (*Capra ibex*, n = 8), Bezoar ibex (*Capra aegagrus*, n = 4), and domesticated Taggar goats (*Capra aegagrus hircus*, n = 24). Animals were genotyped by using the goat SNP50 BeadChip. The assessment of the genetic diversity in wild breeds by using the SNP chips designed for domesticated breeds is very challenging. Hierarchical clustering using Nei's genetic distances clearly distinguished between the four examined species. Surprisingly, Nubian ibex clusters closer to the Alpine ibex, than to Bezoar ibex. Principal component (PC) analysis confirmed the initial finding from clustering. The principle component 1 (PC1) accounts for 38 % of the total variation and separates the Nubian and Alpine ibex in one compact group from the Bezoar ibex and Taggar goat. The SNPs that contributed strongly to PC1 were used to pinpoint genomic regions contributing to the differentiation between breeds. Such regions are located on chromosomes 3, 6, 8, 10, and 21. Among the genes in the vicinity of those SNPs are genes coding for casein milk proteins on chromosome 6. Variation in milk protein genes likely contributes to the genetic differences between wild and domesticated species and highlights the importance of preservation and genetic analysis of these critically endangered breeds.

The first three authors contributed equally to this work.

Keywords: Alpine ibex, Bezoar ibex, genetic diversity, goat, Nubian ibex, Taggar