

From pellets to genomes: New tools provide novel insights into mountain goat ecology and evolution

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ABSTRACT: Advancements in DNA sequencing technology combined with increased use of non-invasive sampling provide a unique lens to understand demographic and behavioural patterns in natural populations. We have several ongoing projects using these novel tools to inform mountain goat management and conservation planning. Of note, we recently characterized the fecal microbiome of mountain goats and showed how it changes within a population over time and how it could be used to distinguish populations. We have extended the microbiome assay to show how it varies with movement and space-use patterns. We have also assembled the first mountain goat genome that will be used as a backbone for understanding population and adaptive processes in this species. Our genome-wide demographic analysis has shown a dramatic reduction in effective population size during the last ice age, with no evidence of a range-wide recovery. Spatial genetic patterns assessed in 265 individuals from across the range appear to be driven almost exclusively by distance, with genetic variation strongly correlated to latitude ($r^2 = 0.83$). These new tools and analyses should be of interest to the wild sheep and goat research and management community.

Biennial Symposium of Northern Wild Sheep and Goat Council 22:133; 2020

KEY WORDS: genomics, diversity, microbiome, movement
