

Rocky Mountain Bighorn Sheep Microbiome and Associations with Host Health and Disease States

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ABSTRACT: The microbiome of Rocky Mountain bighorn sheep (*Ovis canadensis canadensis*) is relatively understudied yet has significant implications for disease management given recent population declines linked to respiratory disease caused by *Mycoplasma ovipneumoniae*. The microbiome consists of a diverse array of bacteria, protozoa, viruses, and fungi in a delicate balance of pathogenic and symbiotic organisms that contribute to maintaining host homeostasis and regulating the immune system. Metrics of the diversity of the microbiome are thought to reflect health where less diverse microbial communities are associated with dysbiosis and disease. In this project, we will investigate associations between metrics of microbiome diversity (e.g., taxon richness among and between individuals and herds) and *M. ovipneumoniae* infection status. Free-ranging Rocky Mountain bighorn sheep from herds in western Nebraska and The Badlands of South Dakota will be captured and nasal, oral, and fecal samples will be collected. We will also collect information on individual sex, age, and weight. *M. ovipneumoniae* status will be determined by real-time PCR. Lastly, we will employ PacBio sequencing methods to characterize the microbiome diversity at different taxonomic levels, from family to species. We anticipate that bighorn sheep that are RT-PCR positive for *M. ovipneumoniae* will have lower microbial diversity in their microbiomes than RT-PCR-negative individuals.

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KEYWORDS: biome diversity, disease state, microbiome, *Mycoplasma ovipneumoniae*, Nebraska, PacBio sequencing, polymerase chain reaction (PCR), Rocky Mountain bighorn sheep (*Ovis canadensis canadensis*), South Dakota.