

Wyoming Wild Sheep Foundation—Bighorn Sheep Rampage Article 2020 (resubmission of 2019)

Grant In Aid Project: Genotyping of *Mannheimia* sp. isolates from three bighorn sheep herd units in Wyoming using MALDI-TOF mass spectrometry

Funding Cycle: 1/2018-12/2019

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Graduate Student: Chris Anderson (PhD)

Rampage Article Title: Finding the Fingerprint of Pneumonia in Bighorn Sheep

Problem: Ongoing surveillance efforts for bacteria that cause pneumonia in bighorn sheep, has identified many of the same types of bacteria across multiple herds. One interpretation of this finding is that although the same types of bacteria are found in each herd, there may be certain characteristics of a bacteria that make it more likely to cause pneumonia within a particular herd. This could explain why certain herd units recover more quickly from pneumonia outbreaks (such as the Jackson herd), while others do not (such as the Whiskey Mountain herd).

Progress: Working with the Wyoming Game and Fish Wildlife Health Laboratory, and using bacteria isolated from many different bighorn sheep herd units, we can apply new technology to fine tune the identification of bacteria. Our research began with the *Mannheimia* species, which is a family of bacteria that has been associated with pneumonia in numerous bighorn sheep herds. For each bacteria isolate, we obtain their “fingerprint” using technology called mass spectrometry. Different species of *Mannheimia* have different mass spectrometry fingerprints, and we can associate a certain fingerprint with bighorn sheep herd health. While two herds may be infected with *Mannheimia*, the fingerprints may be different between the two herds. This is significant as certain bacterial fingerprints may be associated with the ability to cause pneumonia within a particular herd.

In Figure 1, we show two fingerprints of *Mannheimia*. The fingerprint A is from Jackson (blue), and fingerprint B is from Whiskey Mountain (red). While there are similarities, we focus on the differences (arrows), as that makes the fingerprints unique from one another. These differences are used to fine tune bacterial identification, and we use these fingerprints in our bighorn sheep bacterial pathogen database. This allows us to identify any *Mannheimia* species of bacteria found in bighorn sheep in a timely and cost effective manner. For future implications, individual animals can be screened for the pneumonia “fingerprint” bacteria. If the pneumonia “fingerprint” is found, management decisions could be made that decrease the transmission of this higher risk “fingerprint” to other sheep in the herd in order to better preserve overall herd health.

Future direction:

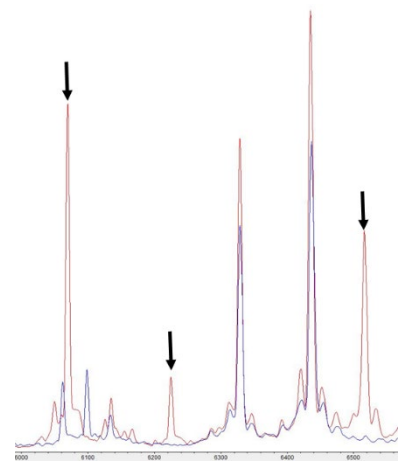


Figure 1. Bacterial fingerprint of *Mannheimia* from Jackson (blue) and Whiskey Mountain (red)

To date, over 90 fingerprints from *Mannheimia* species have been created for our bighorn sheep bacterial pathogen database. We will continue to analyze these “fingerprints” in association with other information about herd health and performance. As this important research continues, other types of bacteria associated with pneumonia including *Pasteurella multocida*, *Bibersteinia trehalosi*, and *Mycoplasma ovipneumoniae* will be used to expand the pathogen database as well as our knowledge and understanding of pneumonia in bighorn sheep.



Figure 2. University of Wyoming PhD student, Chris Anderson, collecting a nasal swab from a ewe. The swabs are used to check for bacteria that cause pneumonia.