University of Nebraska Lincoln

INSTITUTE OF AGRICULTURE AND NATURAL RESOURCES
SCHOOL OF VETERINARY MEDICINE AND BIOMEDICAL SCIENCES
VETERINARY DIAGNOSTIC CENTER

23 October 2017

Dr. Kerry S. Sondgeroth DVM PhD
Assistant Professor & Veterinary Bacteriologist
University of Wyoming
Wyoming State Veterinary Laboratory

Dear Dr. Sondgeroth,

This letter is to confirm our willingness to collaborate on your research project described in the Wyoming Wild Sheep Foundation proposal entitled "Typing of *Mannheimia* spp. isolates from three Bighorn Sheep herds in Wyoming using MALDI-TOF mass spectrometry." This proposal will provide extremely valuable information to further the understanding and contributions of *Mannheimia* spp. in Bighorn Sheep diseases. This project fits with current and previous collaborative research projects undertaken by the Nebraska Veterinary Diagnostic Center (VDC) and my laboratory looking at opportunistic pathogens in ruminant respiratory and ocular diseases, specifically using MALDI-TOF mass spectrometry based proteomic approaches to compare bacterial populations.

The Nebraska Veterinary Diagnostic Laboratory is an AAVLD accredited, full-service veterinary diagnostic laboratory whose primary mission is to assist veterinarians, their clients, and others responsible for animal and public health in the detection, prevention and understanding of disease. In fitting with our mission, I believe that we can make an important contribution to your project.

Our role in the project will be to assist in comparing proteomic fingerprints generated from *Mannheimia* isolates that have been collected from bighorn sheep. Using a bioinformatics approach these fingerprints can be compared based on genotypes, phenotypes, or other comparative criteria. We also have a large number of ruminant *Mannheimia* spp. that have been added to our database which may be useful to assist in identifying these isolates to the species level.

Thank you for the opportunity to participate in this project, I look forward to a very successful collaboration that will ultimately benefit the health of Bighorn sheep populations and further our understanding of these opportunistic pathogens in ruminants.

Sincerely,

J. Dustin Loy DVM PhD Dipl. ACVM
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Dr. Kerry S. Sondgeroth, DVM. PhD
Assistant Professor & Veterinary Bacteriologist
University of Wyoming
Wyoming State Veterinary Laboratory

Dear Dr. Sondgeroth,

This letter is to confirm our enthusiastic interest in collaborating on your research project described in the Wyoming Wild Sheep Foundation proposal entitled “Typing of *Mannheimia* spp. isolates from three Bighorn Sheep herds in Wyoming using MALDI-TOF mass spectrometry.” This proposal will provide extremely valuable information to further the understanding and contributions of *Mannheimia* spp. in Bighorn Sheep diseases. This project fits with current whole genome sequencing of bacterial isolates being performed in our laboratory. We are working to be the first veterinary diagnostic laboratory to have fully validated whole genome sequencing using MinION sequencing. Virginia Tech Animal Laboratory Services is an AAVLD accredited, full-service veterinary diagnostic laboratory which offers next generation sequencing to collaborators.

Our role in the project will be to assist in sequencing isolates from *Mannheimia* isolates that have been collected from bighorn sheep. This will allow for comparison between isolates and to proteomic approaches for comparison.

I look forward to working with you on this exciting project.

Dr. Kevin Lahmers, DVM, PhD, DACVP
Associate Professor
Virginia Tech
Blacksburg, VA 24061

UNIVERSITY OF WYOMING

Wyoming INBRE Bioinformatics Core

http:/ /inbre.wygisc.org/

October 25, 2017

Dr. Kerry Sondgeroth
Wyoming State Veterinary Laboratory
Dept. of Veterinary Sciences
University of Wyoming
1174 Snowy Range Road
Laramie, WY 82070

Dear Kerry:

On behalf of the Core I would like to express our strong support for your Wyoming Wild Sheep Foundation—Grant In Aid Request "Typing of *Mannheimia* spp. isolates from three Bighorn Sheep herds in Wyoming using MALDI-TOF mass spectrometry". The proposal is a natural extension your discussions with us regarding the use of traditional diagnostic tools, genomics and ecological data to better assess herd health.

We are in an excellent position to help you achieve the objectives of your proposal given the expertise in the Wyoming INBRE Bioinformatics Core. In fact, the Wyoming INBRE program recently made a large-scale investment to develop an on campus bioinformatics group and computational resources to provide this exact type of support for University of Wyoming researchers.

I am excited to provide comprehensive bioinformatic support for your research proposal. We would propose to help you analyze your whole genome sequencing data using our computational infrastructure housed at UW's Advanced Research Computing Center. We think our newly acquired 1TB RAM nodes will be of great use to assemble the genomes of your isolates, then perform structural and functional annotation of their coding regions. Whole genome comparisons between isolates (gene order, complement, and genome architecture) may provide powerful insight as to what are the adaptive differences in the *Mannheimia* spp. in your study.

We believe that your research project is important, feasible, and consistent with the goals of the Nation Institutes of Health. We look forward to working with you on this project by providing bioinformatic support and training where necessary. If members of the Wyoming Wild Sheep Foundation have any questions regarding the informatics analysis involved in your proposal, please to not hesitate to have them contact me directly.

Sincerely,

Nicolas Blouin, PhD
Senior Research Scientist
Wyoming INBRE Bioinformatics Core