GENETICS AND ANIMAL BREEDING RESEARCH UNIT

1. Using tissue pools for DNA extraction and implementation in genetic evaluation

Scientist: J. W. Keele, Molecular Computational Biologist

Background information: There are large amounts of data observed in the commercial sector (beef processing plants and feedlots) that can be used to improve rankings of expected progeny differences in bulls produced in the seedstock sector by exploiting SNP microarrays, DNA sequencing, and DNA pooling to bridge the gap between commercial and seedstock sectors. Traits observed in the commercial environment and not in the seedstock include liver abscess and lung lesions observed in beef processing plants and respiratory disease treatments observed in the feedlot. We can genotype pools of animals with extreme phenotypes and use the genetic connections between pooled animals and seedstock animals as an avenue to genetically evaluate seedstock animals with accurate rankings of expected progeny differences in the commercial environment. Achieving equal representation of each animal in a pool is important for accurate genetic rankings. Extracting DNA on individual animals prior to making pools is too expensive; hence, we need to achieve equal representation of animals without extracting DNA on individual samples.

Project Description: This project is part of our genomes to phenomes project in the Genetics and Animal Breeding Research Unit to improve beef cattle performance by combining genetic and genomic approaches using DNA pooling to cost effectively evaluate seedstock bulls based on expected progeny differences in the commercial environment. Accuracy of genetic evaluation depends on achieving nearly equal representation of animals in pools. The student will conduct a series of experiments that evaluate low-cost strategies of pooling for achieving low variation in individual animal representation to pools.

Duties and Responsibilities: The student selected for this project will identify and evaluate various strategies to equally represent animals in pools based on tissue without extracting DNA on individual animals. In the first 3 weeks, the student will collect pig or beef lung samples from the abattoir. The student will pool fresh lung tissue from multiple animals while employing various labor saving and low-cost techniques to achieve equal representation of animals in pools. In addition, individual animal lung tissues will be saved and frozen for individual extraction and genotyping. In weeks 3 through 4, pools and individual animals will be extracted to obtain DNA. DNA samples will be checked for quantity and quality and sent to NeoGen for genotyping with 50K SNP array for pigs or 100K SNP array for cattle. Weeks 5 through 8 will be spent analyzing data and preparing for intern seminars at the end of July. We

have experience with all the steps in this process so we believe the intern will be able to complete the proposed project in the eight-week time frame.

Applicants for this position should be interested in and have taken coursework that encompasses biology and genetics. Applicants should also be willing to learn laboratory techniques, laboratory safety procedures, and how to use DNA information to improve cattle genetics.

2. Evaluating rumen microbial community variation in animals originating in a common environment and moved into different backgrounding and finishing systems

Scientist: T. McDaneld, Research Geneticist

Background: It is well established that the rumen microbial community plays an important role in the degradation of feedstuffs. More recently, variation in this microbial community has been reported to be associated with feed efficiency and is influenced by diet and the host. For this project, animals born at USMARC were transported to other ARS locations after weaning to be fed in grower/stocker systems reflective of management practices in their region. Cattle are subjected to dry lot backgrounding at USMARC, wheat grazing at the Grazing lands Research Laboratory (GLR; El Reno, OK) or winter range at the Livestock and Range Research Laboratory (LARRL; Miles City, MT).

Project Description: Rumen samples were collected at fall weaning from approximately 135 spring-born cattle in 2018, 2019, and 2020. The animals were divided into groups of 45 and placed on one of three backgrounding x location allocations: dry lot silage at USMARC, winter range grazing at LARRL, and grazing winter wheat at GRL. Rumen samples were collected after acclimation to the backgrounding regime (minimum 28d) and after allocation to a subsequent finishing regime (minimum 28d).

Duties and Responsibilities: The student will identify bacterial populations present in the rumen samples at each location and time point by learning and implementing a variety of laboratory methods. The student will accomplish this by first learning and using laboratory techniques that include basic microbiology techniques for working with bacteria, DNA extraction, polymerase chain reaction (PCR), and basic sequencing protocols. In the first two weeks, the student will become familiar with sequence analysis software by assisting a scientist to evaluate 16S sequence data collected from a previous project. In the remaining six weeks, the student will (1) extract DNA from the rumen samples collected, (2) identify bacterial populations present in the rumen samples through initial 16S sequencing of the DNA and (3) identify changes in bacterial populations with different feeding regimes. As this project involves

standard protocols performed in our lab, we believe that the intern will be able to complete this proposed project in the eight-week time frame. Applicants for this position should be interested in and have taken coursework that encompasses biology, microbiology, and genetics.

MEAT SAFETY AND QUALITY RESEARCH UNIT

3. Determination of the impact of placement errors on VBG-7L assessment of marbling score.

Scientist: *S. Shackelford, Food Technologist*

Background information: The beef grading camera is used in packing plants to assess marbling score and yield grade traits to assist the grading process. A recent technology upgrade to the camera allows for quantification of errors in beef carcass grading camera application due to ribbing errors and camera operation errors. There are several potential types of camera operation errors in how the instrument is positioned on the carcass side as the ribeye cross-section is imaged. However, it is not known how those errors impact marbling score determination.

Project Description: This project will conduct research both at the U.S. Meat Animal Research Center and in commercial packing plants for this study. Ribbed beef carcass sides will be imaged multiple times with the VBG-7L beef carcass grading camera with the camera: 1) properly positioned, 2) nose up, 3) heel up, 4) tilted left, 5) tilted right, 6) not on the cross section (AKA shooting from the hip, AKA John Wayne). Multiple images will be collected on each side with each positional variation to assess both the impact on the mean and distribution of values and the repeatability of marbling assessment.

Duties and Responsibilities: Applicants for this position should be interested in and have taken coursework that encompasses biology, animal, and meat science, and/or ag engineering. The incumbent will be expected to participate in research endeavors in a variety of environments including livestock production settings, packing plants, abattoirs, sensory laboratories, and research laboratories. The incumbent will be responsible for thorough and accurate collection and analysis of data while adhering to stringent personal, livestock, and food safety protocols. The student will be responsible for making sure that images are collected and numbered in an orderly fashion, analyzing the data and preparation of a report of the findings. The intern will also assist in collection of carcass data, at large-scale commercial beef packing plants, as part of large-scale beef genetic studies.