

GENETICS AND ANIMAL BREEDING RESEARCH UNIT

1. Investigation of feeding behavior patterns to assess welfare in grow-finish pigs

Scientist: B.N. Keel, Research Geneticist

Background information: From birth to slaughter, animals in the swine production system must cope with multiple stressors, including early weaning from the sow, handling, and transport, mixing with unfamiliar pigs, feed change, and exposure to pathogens. Modern animal facilities are designed for larger herds. This fact, combined with the increased cost of labor and the shortage of labor willing to work in animal facilities, makes it difficult for animal caretakers to always ensure the health and well-being of all animals under their care. Mixing is a common management strategy used to regroup pigs according to body weight or size. Previous studies suggest that mixing can impair individual animal performance and affects pig welfare because of the establishment of a new social hierarchy after regrouping. Identification of “at risk” animals due to social stress is challenging due to limited observation time of animal caretakers coupled with the fact that animals often alter their behaviors to conceal signs of distress. Feeding behavior, assessed through automated feeding systems, can be used to continuously monitor animal welfare status in real-time.

Project Description: The U.S. Meat Animal Research Center (USMARC) currently possesses feeding behavior data for more than 12,000 pigs and continues to add data for ~1,900 pigs every year. Our previous research has identified grow-finish pigs that exhibit decreased feeding behavior patterns near the time of mixing. Lesion scores have been collected at routine intervals during the grow-finish phase of production as a rapid means to estimate aggressive behavioral phenotypes. The student selected for this project will determine traits associated with decreased feeding behavior at mixing, such as lesion scores and body weight gain. In the first three weeks, the student will become familiar with the feeding behavior and performance data and learn to use the R programming language. In the remaining five weeks, the student will perform statistical analyses of the data. Over the entire eight-week period, the student will assist Dr. Keel with ongoing lesion scoring and other swine data collection. The student will also help with other ongoing projects at USMARC as time permits.

Duties and Responsibilities: The duties of the successful applicant will include a variety of computer and animal work. Animal work will include assisting Dr. Keel in data collection in the USMARC swine barns. Applicants for this position should be interested in and have taken coursework that encompasses at least two of the following: animal science, biology, genetics, statistics, mathematics, and computer science. Applicants should also be willing to learn basic computer programming.

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

Scientist: T. McDanel, 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 drylot backgrounding at USMARC, wheat grazing at the Grazinglands 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: drylot 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. Examining foodborne zoonotic pathogens present in pork

Scientist: *J.M. Bosilevac, Research Microbiologist*

Background information: A variety of zoonotic pathogens can be observed in various phases of swine production, several of which may pose a food safety threat if transferred to pork during harvest and processing. These organisms include *Brachyspira*, *Campylobacter*, *Clostridium*, *Listeria*, *Staphylococcus*, and *Yersinia*. US pork is routinely monitored by the USDA Food Safety and Inspection Service (FSIS) for *Salmonella* and aerobic plate count bacteria. Recently during their pork baseline studies FSIS examined the presence of another pathogen, Shiga toxin producing *E. coli* (STEC). The Meat Safety and Quality Research Unit has an archived set of FSIS pork baseline samples that were tested for *Salmonella* and STEC. These samples may offer the opportunity to examine this nationwide sample set for other pathogens, but detection and isolation methods for the other organisms need to be validated first.

Project Description: This work will involve inoculating pork with a pathogen (*Brachyspira*, *Campylobacter*, *Clostridium*, *Listeria*, *Staphylococcus*, or *Yersinia*) processing the sample according to the FSIS pork baseline method and determining if and at what level the pathogen can be detected. Molecular PCR screening methods and culture isolation methods will be used. After the detection and isolation methods are proven, then a set of the archived pork base line samples will be selected and examined for the pathogen.

Duties and Responsibilities: Applicants for this position should be interested in food safety and food science and have taken coursework that includes biology, and microbiology. Applicants should also be willing to learn laboratory techniques and how to use microbiological data for solving problems in food safety. The selected applicant will be responsible, with proper supervision, for sample processing in a biosafety level 2 microbiology laboratory. Activities will include pipetting, diluting, and handling bacterial cultures. Accurate data recording and willingness to learn statistical analysis will be required.