A1 – Bell

Principal Investigator(s): **Dr. Todd Bell**

Project: Protein signaling in cells treated with the MP12 vaccine strain of Rift Valley Fever Virus

Abstract:

Most emerging viral infections over the past 20 years have been zoonotic spillover events, and Iowa State University, with its research focus and animal health expertise, is uniquely positioned to lead the way in understanding this zoonotic interface. The Bell lab, in collaboration with other ISU partners, is focused on uncovering host-viral interactions at the cellular and systemic levels to develop antiviral therapeutics and next generation vaccines to be better prepared for emerging viral diseases. During the summer of 2024, the emerging virus we will be focusing on is RVFV. We will be infecting mouse and human liver cells with different emerging viruses to better understand the cellular switches each virus is turning on inside the host to reproduce and evade the host's immune system. You will learn about viral infection in a cell culture system, and you will be immersed in various cellular assays that will teach you how to quantify virus, determine cell signaling, and even test drugs in cell culture against pathways that are turned on in response to viral infection. Laboratory tasks and tests you will be exposed to include: General lab safety and working with viruses in BSL-2; Viral plaque assays for viral quantification; Polymerase Chain Reaction (PCR) for viral quantification; cell culture techniques; cell toxicity assays; drug effectiveness assays (effective concentration 50 assays); Western blotting for protein quantification and pathway mapping; laboratory ordering and organization; laboratory weekly meetings. Hard work, positivity, and a team first approach are a must for the Bell lab.

A2 – Brewer

Principal Investigator(s): **Dr. Matt Brewer, Dr. Katy Martin**

Project Title: Vaccination of cattle against a cysteine protease from *Tritrichomonas foetus*

T. foetus is an obligate reproductive tract parasite of bovines that causes early embryonic death. One approach to controlling *T. foetus* includes vaccination that produces IgA in cervical mucus. In this project we will address cysteine protease 8 (CP8), a virulence factor from the parasite. In this study, CP8 expressed in *E. coli* will be used to immunize cattle. We will conduct ELISAs to detect anti-CP8 in serum and reproductive fluids. The student will optimize and conduct ELISA/Western blot to compare immune responses in different vaccine groups. The student will also use anti-CP8 antibodies to detect antigen from clinical samples in order to produce a prototype diagnostic test.

A3 – Dewell

Principal Investigator(s): **Dr. Grant Dewell, Dr. Renee Dewell**

Collaborating Investigator(s): **Emiline Sundman, Dr. Suzanne Millman**

Project: Intensive assessment of animal welfare and outcome of hospital and chronic feedlot cattle

Abstract:

This study aims to provide feedlot producers and veterinarians with evidence to inform husbandry protocols and to better determine the appropriate clinical decision for cattle in chronic pens. One unexplored area, particularly for beef cattle, is the care of compromised and non-performing (chronic) cattle in feedyards. Newly arrived calves may experience challenges associated with changes in diet, disease exposure, mixing with new cattle and finding resources in unfamiliar environments. The overarching goal of this project is to investigate animal welfare, economic, and production outcomes of calves that are pulled from feedlot pens into chronic pens. At the conclusion of this project we expect to 1) characterize demographics of typical chronic pens, 2) determine animal-based outcomes associated with primary diagnosis and 3) develop decision aids to improve animal-based outcomes regarding treatment and euthanasia.

The summer scholar student working on this project will primarily assist in behavior data collection from video recordings of cattle housed in chronic pens on a commercial feedlot. Additional responsibilities include data management, and contributing to scholarly works through literature review and technical writing. Candidate should be familiar with beef cattle production and interested in animal welfare/behavior. In addition to participating with this project the student is expected to assist research group with other relevant research projects.

A4 – El-Gazzar 1

Principal Investigator(s): **Dr. Mohamed El-Gazzar**

Collaborating Investigator(s): **Dr. Yuko Sato, Dr. Amro Hashish, Dr. Mostafa Shelkamy**

Project Title: Investigating the pathogenicity of Avibacterium paragallinarum through live chickens challenge study

Abstract:

Infectious Coryza (IC) continues to pose a substantial challenge to the layer industry in the US. leads to a significant loss in egg production. IC is caused by Avibacterium paragallinarum (AP), a Gram-negative bacterium, which is a primary pathogen for chickens. This means its presence should lead to clinical disease in naïve flocks. However, positive qPCR results and bacterial isolation was reported from multiple-layer flocks without any history of clinical signs or vaccination in different states across the US. The absence of any clinical signs from these naïve flocks proposes the non-pathogenicity of these strains, hence dubbed non-pathogenic Avibacterium paragallinarum (npAP). However, confirmation of the lack of pathogenicity of these new npAP strains requires pathogenicity testing in live chickens. A total of 135 SPF chickens will be obtained and housed at the ISU animal facility. Birds will be allocated randomly into five groups. Fifteen birds in the negative control group (G1) will be inoculated with 200µl BHI broth via oculo-nasal inoculation route. Each of G2, G3, and G4 (n=30) will be challenged with 3 different ntAP-selected isolates. G5 (n=30) will receive 200µl BHI broth via oculo-nasal route delivering ~ 107 CFU/Bird of AP type strain and will serve as a positive control group. Coryza scores and respiratory scores will be recorded for seven days post-challenge. Daily choanal swabs will be collected and will be tested for AP using qPCR, bacterial load will be measured using a standard curve in order to understand differences in replication rates between the isolates and then positive samples will be sequence typed. Confirming the non-pathogenicity of these strains would help better understanding of this bacterial population and assist in improve the diagnostics for this disease.

A5 – El-Gazzar 2

Principal Investigator(s): **Dr. Mohamed El-Gazzar**

Collaborating Investigator(s): **Dr. Yuko Sato, Dr. Amro Hashish, Dr. Eman Gadu**

Project Title: Enhancing the molecular diagnostic capacity of ISU-VDL through the validation of Real-Time PCR for poultry Bacterial and Viral pathogens

Abstract:
The poultry industry in Iowa and across the US faces significant challenges due to the prevalence of bacterial and viral infections that can severely impact the health and productivity of flocks. Conventional diagnostic methodologies, often characterized by insufficient sensitivity and expediency, present limitations in effectively managing and controlling these diseases. Molecular diagnostic assays, such as Real-Time Polymerase Chain Reaction (qPCR), offer a compelling solution by overcoming these limitations with their numerous advantages.

In response to that, this study focuses on enhancing the molecular diagnostic capacity of the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL) through the validation of qPCR for identifying bacterial and viral pathogens in poultry. Within the spectrum of pathogenic agents, this study narrows its focus to three distinct entities significantly affecting the turkey industry. Ornithobacterium rhinotracheale (ORT), a bacterial pathogen, and two viral agents, Turkey coronavirus and Avian metapneumovirus, constitute the primary subjects of scrutiny.

ORT infection leads to considerable economic losses in the turkey industry. Identification of the organism using routine bacteriologic examination is challenging due to the fastidious nature of the organism. The molecular diagnostic of ORT using qPCR offers a good alternative. While an existing qPCR assay for ORT is available, our research team has developed a novel qPCR demonstrating heightened sensitivity in detecting ORT from clinical samples. However, validation of this assay utilizing ISU-VDL reagents remains an essential prerequisite. Moving to the two viral agents, multiple qPCR assays are available, however, validation of them is still required.

The validation of these three qPCR assays promises to augment ISU-VDL's diagnostic capacity significantly. This enhancement equips the laboratory to effectively address the diagnostic demands from the turkey industry not only within Iowa but also on a broader scale.

A6 - Fasina

Principal Investigator(s): **Olufemi Fasina DVM, PhD, Dipl. ACVP**

Project Title: Parvovirus RNA processing and epitranscriptome

Abstract:

Posttranscriptional mRNA regulation is a critical cellular homeostatic node often hijacked by viruses for a productive life cycle and currently utilized for the design and development of two severe acute respiratory coronavirus 2 (SARS-CoV2) vaccines. Parvoviruses are linear single-stranded DNA viruses that infect animals and humans and represent an excellent tractable model for understanding virus-host cell interactions, and they are currently utilized for gene therapy and oncolytic virotherapy. Alternative RNA processing strategies including, alternative splicing and alternative polyadenylation, are modulated by parvoviruses to generate a diverse proteome, including the capsid protein, which determines the tissue specificity for gene therapy applications. We recently reported and characterized the first parvovirus non-structural protein, NP1, that modulates alternative splicing and alternative polyadenylation for efficient capsid production. This proposal will test and explore the hypothesis that a linear single-stranded DNA virus, bocaparvovirus minute virus canine (MVC) infection, modulates viral and potentially cellular RNA methylation for a productive viral life cycle in an NP1-dependent manner. RNA methylation and the epitranscriptome is a recently characterized posttranscriptional modification that regulates viral pathogenesis, cellular differentiation and transformation, and neurodegeneration. Results from this project will elucidate the interaction of the epitranscriptome with the parvovirus life cycle, generates and provide new insights and methods to enhance parvoviral capsid production with significant impact on parvovirus; adeno-associated virus (AAV), and human bocaparvovirus gene therapy, potential oncolytic virotherapy applications, and viral pathogenesis.

A7 – Jablinski

Principal Investigator(s): **Anne Jablinski, DVM, MS**

Collaborating Investigator(s): **Amanda Fales-Williams, DVM, PhD, DACVP; Kim Moss, MFA; Aliye Karabulut-Ilgu, PhD**

Project Title: A Groundbreaking Collaboration for Cutting-Edge 3D Printed Veterinary Teaching Models

Abstract:

The veterinary scholar involved in this project will have the opportunity to be part of a long-term, multi-phase project. The student will gain experience in collaborative projects across multiple colleges, in the creation of tools to enhance the learning experience of veterinary students through tactile and visual methods (namely 3D printing and models), and the implementation of educational research and methods to assess efficacy.

The project is a collaboration between the biomedical illustration program (BPMI) and the veterinary school to provide realistic 3D models for visual and tactile learning of hepatic anatomy and pathology. Veterinary scholars involved in this project should have some interest in one or more of the following: anatomic pathology, veterinary education, biomedical illustration and invention, 3D printing, and the scholarship of teaching and learning. The scholar involved in this project will be expected to spend time gathering current, pertinent data surrounding 3D printing and models in human and animal medicine. They will engage and dialogue with BPMI students to learn more about the development and design of realistic hepatic tissues through 3D printing and gauge their impressions of the process. The student will document anticipated cost and timeline of 3D printing and 3D model design and development. They will describe the 3D model creation process in their presentation and develop a plan to provide learning opportunities for vet students with 3D models and a way to evaluate effectiveness of teaching with these models. They will propose and potentially create a method to assess learning using forums, surveys, focus groups, or other modalities and serve as a mediator for veterinary students engaging with the models.

A8 – Mavangira 1

Principal Investigator(s): **Dr. Vengai Mavangira**

Collaborating Investigator(s): **Dr. David Borts and Dr. Patrick Gorden**

Project Title: Alterations in fatty acid and oxygenated metabolites in subclinical mastitis in dairy cattle

Abstract:

Mastitis negatively impacts the dairy industry with costs estimated at greater than US$2 billion annually. Factors contributing to the costs of production include decreased milk production due to mammary tissue damage, treatment costs, labor, and death or early removal of animals from the herd. Mammary tissue damage in cattle with clinical mastitis was shown to be a consequence of severe inflammation and excessive production of reactive oxygen metabolites (ROM). In addition, the excessive inflammation and ROM production are associated with severe alterations in the lipid oxygenations metabolites known as oxylipids. However, the degree of ROM production and inflammation in mastitis without clinical signs (subclinical, the most prevalent form of mastitis) is unknown. In the summer of 2023, we showed that cows with subclinical mastitis (SCM) had an increased tendency for prooxidant states in the mammary gland. Combining the prooxidant findings with published evidence of persistent inflammation during subclinical mastitis, the objective of the 2024 summer study will be to investigate the profiles of oxylipids that have the capacity to regulate inflammatory responses. The first part of the approach will be to quantify the association of persistent somatic cell counts (SCC) with inflammatory mediators in milk samples collected from cows with SCM. Next, we will perform a method development to allow for the quantification of the oxylipids. Finally, the developed method, will be applied to samples from naturally occurring SCM and also from cows that are experimentally challenged with the infusion of Streptococcus uberis bacteria into the mammary gland. The results from this study will provide preliminary information for optimizing persistent inflammation associated with SCM in order to mitigate mammary tissue damage and loss of milk production. Overall, this study will contribute to decreasing the costs of production in the dairy industry.

A9 – Mavangira 2

Principal Investigator(s): **Dr. Vengai Mavangira**

Collaborating Investigator(s): **Dr. Karin Allenspach-Jorn and Dr. Jon Mochel**

Project Title: Utilizing 3D Organoid Technology to Model Bovine Mastitis In vitro

Abstract:

Bovine coliform mastitis is a major contributor to production losses to the dairy industry by decreasing milk production, early removal of cows from the herd, and deaths from systemic illness. Decades of research have failed to improve effectiveness of current therapies because of lack of appropriate *in vitro* approaches to explore the mechanisms of coliform mastitis. The current *in vitro* approach consists of using 2-dimensional (2D) bovine cell cultures and immortalized murine cell lines, which have significant drawbacks and lack direct translational relevance to natural coliform mastitis. Therefore, there is a ***critical need*** for better *in vitro* modeling platforms which more closely mimic natural disease. The advent of organoid technology presents an exciting opportunity to better model coliform mastitis *in vitro* with the potential for advanced development of practical and effective treatments for clinical mastitis.

We hypothesize that bovine mammary gland organoids represent physiologically superior *in vitro* models for bovine coliform mastitis compared to currently used 2D cell cultures, by reproducing key elements of epithelial inflammation such as production of inflammatory mediators and loss of lactating function.

Experimental plan and expected results: Bovine mammary tissue from healthy dairy cattle will be used to develop 3-dimensional (3D) organoid cultures in the laboratory. Cellular responses of the mammary gland organoids will be compared to those produced by common 2D cell culture models. When stimulated, we expect organoids to show inflammatory and functional changes that mimic natural coliform mastitis in a more reproducible manner. 3D organoid models will improve mechanistic understanding of bovine mastitis and generate translatable data and address the ILHAC's priorities of clinical mastitis treatments. Additionally, improved models will decrease live animal use in induced experimental disease reducing research costs and inadvertent animal welfare compromise. Pilot data from this research will support funding applications from USDA-AFRI, Diseases of Agricultural Animals program in Fall 2024.

A10 – Millman

Principal Investigator(s): ***Dr. Suzanne Millman***

Collaborating Investigator(s): ***Drs. Caleb Brezina, Grant Dewell, Renee Dewell, Anna Johnson, Derek Haley***

Project Title: Does Social Buffering Enhance Animal Welfare And Performance When Beef Calves Are Commingled In Feedyard Environments?

Abstract:

This summer scholar position will contribute to aspects of our USDA-funded project, developed in collaboration with a commercial beef feedyard, with the goals of enhancing sustainability and minimizing ecological footprint in beef production. Commingling of calves from different sources presents biological and behavioral stressors, and is associated with increased risk for Bovine Respiratory Disease. Social buffering refers to the phenomenon of enhanced recovery from distress in the presence of a conspecific, with known neuroendocrine mechanism. In this proposal we explore whether preferential relationships among beef feeder cattle produces social buffering, with positive animal welfare, health and performance outcomes. In Objective 3, impacts of social buffering on behavior, health and performance of comingled lightweight cattle on a commercial feedlot will be determined. Videorecordings of beef calves will be used to investigate social behavior amongst familiar calves (sourced as groups from the same farm) vs unfamiliar calves during the arrival period at a commercial feedyard. Behavior data will be used to assess stress and relationships to health and performance. Results from this project will provide needed guidance on commingling practices in U.S. beef operations.

A11 – Nelli

Principal Investigator(s): ***Dr. Rahul Nelli***

Collaborating Investigator(s): ***Dr. Giménez-Lirola, Dr. Gauger, Dr. Main, Dr. Halbur***

Project Title: High-throughput detection of the SARS-CoV-2 and its variants for animal testing using automated liquid handlers, robotics and portable air-samplers.

Abstract:
The COVID-19 pandemic again highlighted the importance of early detection and rapid response to outbreaks. The conventional real-time PCR method (~2000 tests in 24 h) served as a powerful molecular technique during the COVID-19 pandemic. However, during the pandemic, the traditional qPCR testing approach still lacked the high-volume testing capacity necessary to satisfy the unprecedented demand for testing capacity experienced by many public health labs. With the latest advances in instrumentation, microfluidic qPCR assays, and automation, real-time PCR assays can be scaled up for high-volume diagnostic testing (9,000 – 30,000 tests in 24 h) in a cost-efficient manner.

The main objective of this proposal is to validate the diagnostic performance and establish a cost-efficient high-volume workflow to detect SARS-CoV-2 and its variants (Alpha, Beta, Gamma, Delta, Mu, Lambda, and Omicron), in various animal specimens using cutting-edge real-time PCR instrumentation, automation and portable air-sampler devices. The validated assays will significantly increase the efficiency of VDLs and reduce some of the costs for routine surveillance and monitoring.

The established high-volume workflow will strengthen VDLs and other NAHLN labs nationwide to rapidly detect, monitor, and report susceptible animals to SARS-CoV-2. In addition, it will allow our laboratory to handle surge samples, increase disease testing capacity, and enhance laboratory emergency preparedness for SARS-CoV-2 and other emerging pathogens of economic significance (e.g., African swine fever, avian influenza) or large-scale animal food/feed emergency events identified by federal agencies. The assays will subsequently be integrated into LIMS for faster processing and rapid and timely reporting using the ISU-VDL web portal. The workflow creates the foundation for an early warning system that allows public health partners to act sooner to prevent/limit a zoonotic disease outbreak.

A12 – Olds 1

Principal Investigator(s): **June Olds, DVM, DACZM**

Collaborating Investigator(s): **Radford Davis, DVM, MPH, Diplomate ACVPM, Ganwu Li, PhD**

Project Title: Metagenomic characterization of novel viruses in big brown bats (*Eptesicus fuscus*) of central Iowa

Abstract:
Chiropterans (bats and flying foxes) are known reservoirs of emerging viruses of human and animal importance, but most viral characterization studies of bat species have occurred in Asia and Africa. In North America, the last known metagenomic study performed for native bat species was completed a decade ago on the east coast of the U.S. The big brown bat (Eptesicus fuscus) is the most common Microchiroptera species managed within wildlife rehabilitation centers in the midwest. Due to its natural ecology, this species is most likely to have environmental and direct contact with humans, wild, and domestic animals.

Bats are known carriers of lyssaviruses and paramyxoviruses, but have also been identified as the evolutionary source of most, if not all, human coronaviruses and could potentially serve as vectors of viruses of importance to wildlife and domestic animals. Considering the SARS-CoV-2 pandemic, a better understanding of the bat virome within the U.S. would aid in understanding the ecology and epidemiology of viruses they may carry, and the risk to human, wild, and domestic animal health. Oral swabs and feces were collected from 100 bats in the care of a licensed wildlife rehabilitator in central Iowa in 2020-21. These bats had been in rehabilitation for multiple months, which also put them at risk of exposure to human viruses due to frequent handling by caretakers. Samples were stored at -80°C for later analysis. The primary objective of this study is to conduct metagenomic analysis on these previously collected samples to search for known and novel DNA and RNA viruses. We hypothesize that E. fuscus in Iowa are infected with known and novel viruses that cause little to no harm to bats but may be of importance to human and animal health, reflective of their changing ecosystems under pressure from human and agriculture encroachment.

Objectives
1. Conduct metagenomic analysis on fecal and oral swab specimens that have already been collected from 99 big brown bats (E. fuscus) and one hoary bat (Lasiurus cinereus) from central Iowa.
2. Characterize the viruses found in specimens using bioinformatics.
3. Describe the association of discovered viruses to animal and human health and wildlife conservation efforts.

A13 - Olds 2

Principal Investigator(s): **June Olds, DVM, DACZM**

Collaborating Investigator(s): **Taylor Yaw, DVM, DACZM**

Project Title: COMPARISON OF SUBCUTANEOUS ADMINISTRATION OF ALFAXALONE–MIDAZOLAM–DEXMEDETOMIDINE WITH KETAMINE–MIDAZOLAM–DEXMEDETOMIDINE FOR CHEMICAL RESTRAINT IN ASIAN SPINY TOADS (Duttaphrynus melanostictus)

Abstract:

Few studies have investigated the efficacy of injectable anesthetic and sedative protocols for most amphibian species. To date, the most commonly used amphibian anesthetic protocols involve immersion with tricaine methanesulfonate (MS-222) or eugenol. Although immersion compounds produce relatively predictable anesthetic and sedative efficacy in most amphibians, species-specific sensitivities, including death, have been observed. Additionally, these compounds are not commonly maintained by most private practice veterinarians and may pose human health risks from respiratory irritation and local skin reactions; moreover, MS-222 can cause retinopathies in humans with prolonged exposure. Development of alternative species-specific, injectable anesthetic and sedative protocols is warranted for a variety of clinical procedures, such as diagnostic sample collection (e.g., radiographs, blood collection) and minor surgical procedures in amphibians. Although benzodiazepines, alpha-2 agonists, dissociative agents (i.e., ketamine), and neuroactive steroids (i.e., alfaxalone) are increasingly used for induction in reptile sedation and anesthesia, prospective studies evaluating their use in anuran species is limited. Incorporation of these different sedative classes into combination protocols avoids higher dosages for each drug, which avoids deleterious, dose-dependent side effects of any individual drug.

The objective of this study is to investigate practical and safe injectable chemical restraint protocols for use in Asian Spiny Toads (*Duttaphrynus melanostictus*) to achieve a moderate level of chemical restraint suitable for common clinical procedures. Similar to a previous study performed in blue poison dart frogs (*Dendrobates tinctorius azureus),* a combination of ketamine–midazolam–dexmedetomidine (KMD protocol) is hypothesized to produce a similar depth of chemical restraint as a combination of alfaxalone–midazolam–dexmedetomidine (AMD protocol). Additionally, induction and recovery times are hypothesized to be different between protocols.

****Note** The anesthesia portion of this study will be performed at the Omaha Zoo under the supervision of zoo veterinarians. The research student should expect to spend at least 10 working**

days at Omaha Zoo during the summer for data collection. Housing will be provided, but the student must provide transportation to and from Omaha, Nebraska.

A14 – Pineyro

Principal Investigator(s): **Pablo Pineyro**

Project Title: Characterization in vitro of homologous and heterologous PCV2 antibody neutralizing activity and T-cellular response induced by PCV2 commercial vaccines.

Abstract:

Porcine circovirus type 2 is a non-enveloped, single-stranded, circular DNA virus of approximately 1.7kb belonging to the family Circovirdae. PCV2 was initially described as the causative agent for the postweaning multisystemic wasting syndrome (PMWS) in Canada in the early 1990s since PCV2 has been clinically termed porcine circovirus associated disease (PCVAD), which umbrellas systemic disease, lung disease, enteric disease, reproductive disease, porcine dermatitis and nephropathy syndrome (PDNS), and subclinical infection. The high evolutionary rate and the recombination ability of multiple PCV2 subtypes in infected pigs have resulted in new subtypes. Eight PCV2 subtypes have been identified (PCV2a-i), although PCV2a, PCV2b, and PCV2d have a global distribution and high prevalence. From 1996 to the early 2000s in the US, PCV2a was the most prevalent subtype. In 2005, PCV2b outbreaks occurred in the US, becoming the most prevalent subtype, indicating a first “genotype shift” in the US (19-22). In 2014 a second “genotype shift” was described, resulting PCV2d the subtype most prevalent in the US. Following PCV2 infection, pigs develop a strong neutralizing antibody response detectable 10-28 days post-infection, coinciding with a reduction of viremia. Additionally, the number of IFNγ secreting cells is inversely correlated to viral load and lesions. While cross-protection amongst different PCV2 subtypes has been demonstrated, questions remain regarding the full immunological efficacy conferred by commercial vaccines against homologous and heterologous challenges. PCV2 vaccines became commercially available in 2004 in Europe and in 2006 in North America. The first commercially available vaccines were based on PCV2a, which included inactivated whole virus, chimeric PCV1-2a virus, and subunit vaccines. Given the most recent “genotype shift” from PCV2b to PCV2d, more recent platform advances are based on bivalent inactivated chimeric PCV1-PCV2a and PCV1-PCV2b viruses and a subunit PCV2d vaccine. Overall, PCV2 vaccines appear to effectively prevent clinical disease and lesions. However, vaccination does not prevent viral replication and infection, potentially leading to gaps in immunity caused by heterologous infection and coinfection. Thus, we hypothesize that current commercial vaccines have a differential humoral and cellular effect against different PCV2 subtypes prevalent in the field and therefore provide different levels of protection against PCV2 homologous and heterologous challenges.

A15 – Plummer (Gorden, Kreuder, McGill)

Principal Investigator(s): **Dr. Paul Plummer**

Collaborating Investigator(s): **Dr. Amanda Kreuder, Dr. Jodi McGill, Dr. Pat Gorden**

Project Title: Addressing health challenges in dairy goat operations to improve antimicrobial stewardship and sustainability

Abstract:

In this project, summer scholars will participate in a large USDA research project related to improving sustainability in the dairy goat industry. Investigators on the project are focused on antibiotic and nonantibiotic strategies to control mastitis and respiratory disease in dairy goats. Multiple positions are available on the project. The students will be responsible for collection of samples from goats with and without respiratory disease, or with and without mastitis (examples: blood, milk, nasal swabs, lung swabs, lung or mammary tissues, etc). Following collection, samples will be prepared in the lab for bacterial culture, antimicrobial susceptibility testing, metagenomic sequencing, whole genome sequencing or immunologic analyses. The students will gain experience directly working with goats to perform physical exams, diagnostic sampling, and necropsies. Additional experience culturing diagnostic samples, performing antimicrobial susceptibility testing, and extracting RNA or DNA in the laboratory will also be gained during this work.

****Note** - This project has opportunities for multiple summer scholars to participate.**

A16 – Zhang

Principal Investigator(s): **Dr. Qijing Zhang**

Collaborating Investigator(s): **Dr. Orhan Sahin, Dr. Paul Plummer**

Project Title: Isolation and Characterization of Campylobacter from sheep-National Animal Health Monitoring System (NAHMS) Sheep 2024 Study

Abstract:

Campylobacter is an important pathogen in sheep as it can cause abortion storms. It is also a foodborne agent causing gastroenteritis in humans. Currently, there is limited available data about the prevalence of Campylobacter on sheep operations in the US. To facilitate the control of Campylobacter and improve sheep health, ISU investigators and USDA APHIS have formed a collaboration to conduct surveillance of Campylobacter in sheep operations on a national scale. Sheep fecal samples collected from sheep farms across the United States will be shipped to the research laboratory at ISU. Once received, the fecal samples will processed for isolation of Campylobacter using culture media and conditions suitable for this organism. The bacterial isolates will be identified by MALDI-TOF and then undergo antimicrobial susceptibility testing. Additionally, various molecular tools will be utilized to analyze these isolates for better understanding the epidemiology of Campylobacter on farms. The work to design, implement and report out on data collected will generate novel information on antimicrobial use and antimicrobial resistance in Campylobacter found on sheep operations. The generated information will help producers to make management decisions for their sheep based on the results. Experience gained from participating this project include pathogen isolation and identification, antimicrobial susceptibility testing, antimicrobial stewardship, and molecular typing of pathogens.

****Note** - This project has opportunities for multiple summer scholars to participate.**