P1 - Almeida

Project Title: *The efficacy of competitive exclusion culture to control contemporary enterotoxigenic strains of E. coli in the face of an outbreak*

Principal Investigator(s): Marcelo Almeida

Collaborating Investigator(s): Pablo Pineyro; Rodrigo Paiva; Nubia Macedo; Eric Burrough; Darin Madson; Philip Gauger;

Veterinary Scholar Abstract:

Enterotoxigenic Escherichia coli (ETEC) strains are considered the most important cause of post-weaning diarrhea (PWD) in the United States, and pigs have become more difficult to treat because of increased antibiotic resistance. Data from 3,199 ISU-VDL ETEC isolates (F4 and F18 strains) demonstrate that the antimicrobial susceptibility has decreased over the past twelve years for multiple antibiotics. Due to concerns over the development of antibiotic-resistant bacteria and seeking novel approaches to the prevention and treatment of ETEC, the use of competitive exclusion (CE) culture has been developed. Although the potential of CE culture has been observed previously, studies to assess this concept using contemporary ETEC strains are needed to provide relevant information to the swine industry to control PWD. We hypothesize that CE culture can be used as an alternative strategy to reduce shedding and clinical disease related to highly virulent, multi-drug resistant ETEC F18+ strains. A challenge study will be performed to investigate different uses of CE in controlling post weaning colibacillosis

P2 - Beck

Project Title: *Identification of the apicomplexan target of triazine antiprotozoals and mechanism of drug-resistant coccidiosis*

Principal Investigator(s): Josh Beck

Collaborating Investigator(s):

Veterinary Scholar Abstract:

Coccidiosis is an intestinal infection caused by coccidian parasites of apicomplexan phylum that results in major losses in domestic livestock production as well as disease in companion animals and humans. Triazines are an important class of anticoccidial drugs widely used to control coccidiosis but resistance to these compounds threatens to undermine their effectiveness. Judicious management of triazine use to curb resistance and development of improved compounds is limited by the lack of known mode of action or mechanisms of parasite resistance for these drugs. Apicomplexa is a large group of protozoa of veterinary and medical importance which also includes the human malaria parasite Plasmodium falciparum. Interestingly, triazines are effective against a broad range of apicomplexans, including P. falciparum and we hypothesize that the target(s) of these compounds is conserved among these related parasites. Here, we propose to exploit the tractability of P. falciparum as a model apicomplexan to identify these conserved targets and/or mechanisms of resistance. In aim 1, we will use an established approach for in vitro evolution of resistance to triazines by culturing P. falciparum with sublethal drug concentrations followed by whole genome sequencing to identify resistance-conferring mutations, revealing candidate triazine targets. In aim 2, we will determine the biological function of these candidates using reverse genetic approaches in P. falciparum and evaluate target orthologs in relevant coccidian species to verify their importance for triazine resistance in the species that cause coccidiosis in production animals. Collectively, this work will reveal targets and/or mechanisms of resistance for an important class of anticoccidials.

This project remains consistent with the 2024 ILHAC research priorities to address Coccidiosis in Poultry, Sheep and Goats as well as and the IVMA priority to address the threat of antiparasitic resistance for all species.

P3 - Bell

Project Title: *Determining cell signaling events following influenza or Rift Valley fever virus (RVFV) infection for the development of antiviral countermeasures*

Principal Investigator(s): Todd M. Bell

Collaborating Investigator(s):

Veterinary Scholar 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 countermeasures to be better prepared for emerging viral diseases.

During the summer of 2025, the emerging viruses we will be focusing on are influenza and RVFV. We will be infecting 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. Antiviral treatments will be aimed at these uncovered cellular pathways to determine drug efficacy. 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.

P4 - Bellaire

Project Title: *Support for ISU's HPAI BSL3 Research Community*

Principal Investigator(s): Bryan Bellaire

Collaborating Investigator(s): Todd Bell

Veterinary Scholar Abstract:

Participate within HPAI research community and multidisciplinary activities.

P5 - Caceres

Project Title: *Host range and binding profiles of Influenza A(H5N1) in livestock species*

Principal Investigator(s): C. Joaquin Caceres

Collaborating Investigator(s): Silvia Carnaccini

Veterinary Scholar Abstract:

Influenza A (FLUAV), family Orthomyxoviridae, is a relevant pathogen for livestock species, including poultry, swine, and, more recently, cattle. FLUAVs are classified into subtypes based on their two main glycoproteins: hemagglutinin (HA; H1-H18) and neuraminidase (NA; N1-N11). Some subtypes, such as H5N1, are gaining attention due to their broad host range and impact on Public Health. Since 2022, more than 130 million poultry have been affected with highly pathogenic avian influenza (HPAIV) H5N1, encompassing 1,300 flocks in 50 states. In addition, HPAIV H5N1 was confirmed for the first time in dairy cows in 2024, and 919 cases have been confirmed so far, affecting 16 states.

Given the relevance of H5N1 for animals, particularly the ones most affected and impacting the U.S. economy and food chain, it is essential to understand the pathogenesis of H5N1 and the host range in relevant species such as poultry, cattle, and swine. Regarding the FLUAV host range, the HA is responsible for the attachment to the host cell sialic acid receptors, which is critical for beginning influenza replication, directly implicated in the FLUAV host range. Because of this, the Caceres lab is interested in the binding profiles of different H5N1 derived from poultry, cattle, and swine to tissues from various livestock species. To investigate this, we will engineer different H5N1 viruses by reverse genetics with modifications that will allow a safe manipulation under BSL2 conditions. Next, we will use those viruses to characterize the binding profiles on fixed tissues from chickens, turkeys, dairy cows, and swine. The summer scholar will work alongside the PI to generate the proposed viruses and perform the different binding assays using the already available fixed tissues.

P6 - Carnaccini

Project Title: *Development of an avian metapneumovirus reverse genetics system for the generation of modified live vaccines*

Principal Investigator(s): Silvia Carnaccini

Collaborating Investigator(s): Yuko Sato, Mohamed El-Gazzar, Zhang Jianqiang, Joaquin Caceres

Veterinary Scholar Abstract:

Avian metapneumovirus (aMPV) subtypes A and B were reported for the first time in the United States at the end of 2023 and since then they have spread across 29 states causing significant economic losses to the poultry industry. These viruses cause an acute respiratory disease in turkeys and chickens with increase morbidity and mortality and predisposition to secondary bacterial infections. While aMPV virus genome can be detected longer after infection by PCR, virus isolation from PCR-positive samples is seldom successful. This is problematic because virus isolation is crucial to understand the virus biology and develop efficacious vaccines. We aim to develop a system to obtain live viruses from the aMPV sequences obtained from PCR-positive field samples via reverse genetics (RG). RG is a technique that allows to generate live virus from complementary genomic data inserted into plasmid and using specific cell cultures. This approach is routinely used in our laboratory to study avian influenza virus. Therefore, we plan to develop and validate an improved reverse genetics system to produce replicative-competent aMPVs subtypes A and B entirely from a single large, cloned segment of complementary DNA (cDNA). With this technique we will be able to make modifications to the virus genome directly to understand the functions of specific genes, obtain a safe and stable modified live vaccine, or to make a vaccine more immunogenic. Only a handful of reverse genetic methodologies have been published to generate metapneumoviruses from synthetic constructs. These are overall laborious and outdated, requiring multiple passages in vitro and low success rates (<10%). With our system, we expect to increase the yield of the viruses we generate and by testing the viruses in cell cultures we will confirm that they maintain the same phenotypical characteristics and kinetics growth of the field isolates.

P7 - Desaulniers

Project Title: *Enhancing boar fertility in the face of climate change through the mitigation of in utero heat stress*

Principal Investigator(s): Amy Desaulniers

Collaborating Investigator(s):

Veterinary Scholar Abstract:

Each year, six million pregnant sows in the United States have an increased risk of heat stress due to climate change. Notably, IUHS impairs boar sperm production and semen quality. Because the swine industry almost exclusively utilizes artificial insemination, a single boar affects the reproductive outcome for thousands of sows. Therefore, the boar has the greatest cumulative impact on reproductive performance and drives genetic progress in the herd. The overall goal of this USDA-funded project is to better understand how IUHS impairs boar reproductive physiology while simultaneously testing a novel IUHS mitigation strategy — genomic selection for heat tolerance. The specific hypothesis is that IUHS impedes testis function by reducing gonadal steroidogenesis, a requisite for fertility. Using a unique cohort of pigs divergently selected for heat tolerance, Objective 1 will determine how IUHS impacts boar reproductive endocrinology. Objective 2 will examine sperm health and function in IUHS boars. Objective 3 will assess how IUHS alters the cellular/molecular mechanisms underlying porcine testicular function. This work will advance our understanding of the biological pathways affected by IUHS in the boar. The proposed research is significant because implementation of this new knowledge is expected to lead to novel methodologies to enhance gonadal function of boars. Ultimately, these outcomes will increase boar fertility, swine reproductive efficiency, and the sustainability of U.S. pork production.

The Veterinary Scholar will participate in all aspects of the project including semen collection/evaluation via CASA, surgical cannulation of swine, and serial blood collections. Students will also assist with necropsy and tissue collection. The successful student will learn how to conduct radioimmunoassays and lead the quantification of two reproductive hormones (e.g., testosterone and LH). Students may also learn other laboratory techniques (e.g., IHC, western blot) to augment their educational experience.

P8 - Dewell

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

Principal Investigator(s): Grant Dewell

Collaborating Investigator(s): Renee Dewell, Suzanne Millman, Emiline Sundman

Veterinary Scholar 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.

P9 - El-Gazzar

Project Title: *Investigating a Potential Role for Wild Turkeys in the Epidemiology of the Emerging Avian Metapneumovirus Outbreak in Commercial Poultry.*

Principal Investigator(s): Mohamed El-Gazzar

Collaborating Investigator(s): Yuko Sato – Silvia Carnaccini – Eman Gadu – Rachel Ruden

Veterinary Scholar Abstract:

Avian Metapneumovirus (aMPV) subtypes A and B emerged in the commercial poultry industry in late 2023 and rapidly spread unhindered across the continent. Sequence data shows that both subtypes remain virtually unchanged indicating that horizontal transmission is the main route of transmission of a single event introduction outbreak. While poultry movement and lapses biosecurity measures can explain a portion of the ongoing horizontal transmission, the speed and scale with which the virus has spread across the states remains unexplained. Wild birds have been proposed to play a role in aMPV spread; however, that role remains undefined. Wild turkeys (*Meleagris gallopavo*) are one of the most evolutionally related species to domestic poultry amongst the *Galliformes* birds. We hypothesize that wild turkeys played a role in the rapid spread of aMPV across the continent. A bank of sera and tissue samples from 2021 – present time are available to us for testing. We will continue collecting samples in spring and summer of 2025. Acute exposure will be detected by testing tissues with quantitative real-time Polymerase Chain Reaction (qPCR). Chronic exposure will be detected by testing sera using Enzyme-linked Immunosorbent Assay (ELISA). Time of exposure and location will be interpreted in the context of the aMPV outbreak timeline. This data could elucidate any potential role of wild turkeys in spreading of this costly disease and inform the risk of spillover into a population already in decline. Ultimately, this information in turn could guide the development and implementation of effective biosecurity measures toward the prevention and possibly the eradication of this emerging infectious disease.

P10 - Fasina

Project Title: *Parvovirus RNA processing and epitranscriptome*

Principal Investigator(s): Olufemi Fasina

Collaborating Investigator(s):

Would the proposed project be in-person or virtual: In-person

Veterinary Scholar 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.

P11 - Gorden

Project Title: *Evaluation of an Innovative Dairy Cattle Vaccine for High Path Avian Influenza*

Principal Investigator(s): Patrick Gorden

Collaborating Investigator(s): Lucas Huntimer, Chief Scientific Officer, Genvax Technologies, Inc.

Veterinary Scholar Abstract:

The emergence of H5N1 highly pathogenic avian influenza (HPAI) in dairy cattle poses serious risks to animal health, public health, and the dairy industry. The virus's presence in cattle, confirmed human cases, and detection in milk products highlight its potential for widespread impact. To address this urgent issue, Genvax Technologies, Inc. (GTI) is developing a self-amplifying RNA (saRNA) lipid nanoparticle (LNP) vaccine targeting the hemagglutinin (HA) gene of H5N1. This innovative platform has demonstrated safety and immunogenicity in dairy cattle, offering a promising solution to control viral transmission, protect public health, and reduce economic losses for producers. This project focuses on evaluating the immune response in lactating dairy cattle following immunization, contributing to improved preparedness against this USDA-designated livestock disease of concern.

P12 - Jergens

Project Title: *Effect of different tissue fixatives on preservation of the canine mucosal microbiota*

Principal Investigator(s): Albert E. Jergens DVM, PhD, DACVIM

Collaborating Investigator(s): Diapk K. Sahoo PhD, Eric Cassmann DVM, PhD, Craig Willette DVM; Maria Merodio DVM

Veterinary Scholar Abstract:

Background

Tissue fixation is the first required step towards preservation of tissues and analysis of the spatial organization of the intestinal microbiota. Historically, formalin has been the most used fixative due to availability, cost, and its broad application in clinical and research settings. However, tissue preservation methods can also influence the integrity of the mucus layer which serves as a habitat for bacterial populations.

Objective

To compare the effects of two tissue fixatives, 10% neutral-buffered formalin (NBF) and Carnoy's solution (CS), on preservation of the mucus layer and mucosal microbiota in dogs.

Animals

Six adult laboratory reared dogs.

Methods

Gastrointestinal (GI) endoscopy with collection of mucosal biopsies from the duodenum, ileum, and colon of each dog will be performed. Eight endoscopic samples from each intestinal compartment will be placed in biopsy cassettes for fixation, with the first half of the biopsies immersed in NBF and the second half immersed in CS. Tissues will be routinely processed, paraffin embedded, sectioned at 4 µm, and stained with H&E and Alcian blue to evaluate tissue morphology, goblet cell number, and thickness of the inner/outer mucus layers. Fluorescence in situ hybridization (FISH) will be performed using a universal bacterial probe (EUB338) to visualize and quantitate the mucosal microbiota. Data will be analyzed statistically.

Expected results

We expect to see differences in thickness of the mucus layer and bacterial counts in intestinal compartments between the two fixative methods.

Conclusion and clinical significance

Use of the optimal fixative for GI tissues is crucial for defining the biologically relevant spatial relationships of the mucosal microbiota that mediate GI health and disease in dogs.

Student tasks: performance of mucosal FISH, bacterial quantification using Metamorph® software, assist with pathological studies and data analysis, SS poster construction and presentation

P13 – Kreuder (Gorden, McGill)

Principal Investigator(s): Dr. Amanda Kreuder

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

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

Veterinary Scholar 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.

P14 - Kreuder 2

Project Title: *Investigation of the role of biofilm formation* Campylobacter *colonization*

Principal Investigator(s): Amanda Kreuder

Collaborating Investigator(s): Brandon Ruddell (post-doctoral scholar)

Veterinary Scholar Abstract:

Our lab investigates the colonization, persistence, transmission, and control of *Campylobacter*, a common pathogen transmitted via contaminated food products from animals including poultry and small ruminants to humans resulting in foodborne illness. This project will use the *C. jejuni*- chicken animal model of infection to determine if *C. jejuni* gene products related to biofilm formation contribute to the ability to colonize animals. In this project, the summer scholar will gain experience both in microbiology laboratory techniques and as well as be directly involved in completing an animal colonization study. The main component of this study will involve a 4-week chicken colonization study where the scholar will gain experience handling chickens, collecting cloacal swabs, and performing necropsies to collect ceca content. Additionally, scholars will learn how to prepare and utilize selective culture media in the lab to culture *C. jejuni* from the animal samples, as well as preserve RNA from samples collected from the chickens using a commercial RNA kit. This work aims to enable a hands-on experience for the scholar to perform hypothesis-driven experiments in both a microbiology laboratory and an animal study setting.

P15 - Martin

Project Title: *Evaluation of the efficacy of the essential oils geraniol and carvacrol against Haemonchus contortus*

Principal Investigator(s): Katy Martin

Collaborating Investigator(s): Matt Brewer, Shivani Choudhary, Alan Robertson

Veterinary Scholar Abstract:

Haemonchus contortus is a gastrointestinal nematode of sheep and goats that causes severe anemia and death. Anthelmintic resistance across all major drug classes is common in populations of this parasite. Novel treatment options are necessary to control H. contortus and reduce clinical disease and losses. This project aims to evaluate the efficacy of the essential oils geraniol, an cyclic monoterpene alcohol found in a variety of plants, and carvacrol, a cyclic monoterpene phenol present in thyme and oregano. Our previous studies have confirmed the activity of these compounds at nAChR. Larvae collected from the feces of infected sheep will be used in motility assays to determine EC50s for each compound, as well as the compounds in combination. This will provide a dosage to be evaluated in experimentally infected animals. This study will evaluate geraniol and carvacrol, in vitro and in vivo, with the goal of providing a novel treatment option for small ruminant producers in the face of multi-drug resistant parasites.

P16 - Olds – 1

Project Title: *Voluntary Semen Collection and Preservation Techniques for the Bonobo (*Pan paniscus*)*

Principal Investigator(s): June Olds DVM, DACZM, Theresa Beachler DVM, PhD, DACT

Collaborating Investigator(s): Olivia Striklin DVM, MS, Katie Newman DVM, Tressa Reiner, DVM, Sara Skiba PhD, Jared Taglialetela PhD

Veterinary Scholar Abstract:

The reproduction of wild animals in human care is challenging. Often, animals are moved from one facility to another for breeding purposes, which could have negative impacts on individual animal welfare. In the endangered bonobo (*Pan paniscus*), movement of males is contrary to the natural social behavior of the species, which can result in poor welfare outcomes for the individual male and group. Collection of semen for cryopreservation and artificial insemination may offer opportunities to preserve genetic diversity while avoiding the welfare concerns of animal movement. Previous studies of cryopreservation techniques in bonobos and chimpanzees (*Pan troglodytes*) have been limited and yielded poor overall results. Collection of semen from captive wild animals often requires electroejaculation under general anesthesia, which further increases health and welfare concerns. Therefore, development of methods for voluntary semen collection and improved semen preservation techniques may be critical to the long-term survival of bonobos in human care. This study hypothesizes that 1) Male bonobos can be trained to use an artificial vagina (AV) for the collection of semen voluntarily and 2) Collected semen samples can be assessed for viability and methods for preservation can be compared to develop improved protocols regarding cooling techniques and post-thaw motility following cryopreservation. Students will gain experience with routine semen collection and the assessment of routine semen evaluation parameters, including concentration, subjective and objective CASA motility assessment, and morphology. Students will also gain experience with freezing techniques in various domestic species.

P17 - Olds 2

Project Title: *Hematologic Reference Ranges of Select Bufonidae Species*

Principal Investigator(s): June Olds, DVM, DACZM & Laura Kleinschmidt, DVM, DACZM

Collaborating Investigator(s): Ariel Nenninger, DVM, PhD, DACVP, Cheryl Auch DVM, MS, DACVP, Mark Morton, DVM DACVP, Taylor Yaw, DVM, CertAqV, DACZM

Veterinary Scholar Abstract:

Hematology is utilized extensively in veterinary medicine as a critical diagnostic modality to evaluate animal health. Unfortunately, few reference intervals are readily available for clinicians to evaluate the health of amphibians. Limited information available in the literature has largely focused on various frog species from the Dendrobatidae, Pipidae, Ranidae, and Myobatrachidae families. However, there is wide species variability and thus reference intervals are needed for "true toads" in the family Bufonidae. In this study, students would gain experience in appropriate venipuncture techniques, blood sample processing, and interpretation of clinical pathologic findings in select species from the Bufonidae family, which could include the Puerto Rican Crested Toad (*Bufo lemur*), Boreal Toad (*Anaxyrus boreas*), Wyoming Toad (*Anaxyrus baxteri*), and Asian Spiny Toad (*Duttaphrynus melanostictus*), at Omaha's Henry Doorly Zoo & Aquarium.

***Student must have own transportation to commute to Omaha, NE, and be prepared to spend at least 2 weeks in Omaha for the collection of samples for this project. Housing will be provided at no expense to the student. ***

P18 - Pieper

Project Title: *Evaluation of owner preferences regarding shampoo characteristics for their animals*

Principal Investigator(s): Jason B. Pieper

Collaborating Investigator(s): Kevin Kasza

Veterinary Scholar Abstract:

Previous studies have been performed in the human field to determine what shampoo characteristics are important to the purchaser. While we feel there may be some similar opinions, it has never been evaluated in veterinary medicine. While efficacy is considered very important, some veterinarians and owners may prefer to choose which shampoo to stock or purchase based on other properties. The goal of this study is to take a survey of client's perceptions of which shampoo they would prefer when they are provided with a variety of options. Some of the characteristics that we aim to evaluate for a variety of shampoos are latherability, smell, color/appearance of shampoo, and appearance of the bottle. This information can be beneficial in helping companies focus on what is most important to client's and also help veterinarian's stock what would be preferred for their clientele.

P19 - Pineyro

Project Title: *Validation of viability-qPCR (v-qPCR) on clinical samples to enhance the detection of viable Mycoplasma hyopneumoniae to improve gilt acclimatization protocol*

Principal Investigator(s): Pablo Pineyro

Collaborating Investigator(s): Rachel Derscheid; Calvin Ko

Veterinary Scholar Abstract:

Mycoplasma hyopneumoniae (M. hyopneumoniae) is the primary agent of enzootic pneumonia in swine, leading to significant economic losses in the global pork industry. Traditional diagnostic methods, such as color-changing units (CCU), are time-consuming and labor-intensive, making them less effective for this slow-growing pathogen. Real-time PCR (qPCR) offers rapid detection but cannot distinguish between viable and non-viable cells, a critical limitation for inoculum testing in acclimatization programs. Viability quantitative PCR (v-qPCR) addresses this challenge by selectively detecting viable bacteria through the use of membrane-impermeable dyes like propidium monoazide (PMA), which intercalate with exposed DNA in non-viable cells, preventing their amplification during PCR. Impact of M. hyopneumoniae and importance of the problem: • M. hyopneumoniae causes chronic respiratory disease in swine, reducing performance and increasing antimicrobial use. • Co-infections with M. hyopneumoniae worsen respiratory diseases, leading to greater production losses. • Traditional diagnostic methods cannot assess bacterial viability, hindering effective acclimatization strategies. • Improved diagnostics are crucial for successful colonization and uniform immunity in swine herds. This project aims to validate the use of v-qPCR for detecting M. hyopneumoniae in clinical samples, focusing on optimizing acclimatization protocols by correlating viable bacterial counts with long-term clinical outcomes and refining homogenate preparation. We hypothesize that v-qPCR is a superior diagnostic tool for assessing bacterial viability, offering rapid, accurate assessments of inoculum quality for gilt acclimatization programs. This approach will refine inoculation practices, improve eradication outcomes, ultimately facilitating faster achievement of disease-free herds, benefiting swine health and production. To test the hypothesis that viability-qPCR (v-qPCR) can provide accurate assessment of inoculum quality, we will conduct a series of comparative analyses. Clinical samples, including tissue homogenates and tracheobronchial swabs, will be collected from swine herds undergoing gilts acclimatization protocols. Each sample will be subjected to both conventional qPCR and v-qPCR to detect total bacterial DNA and viable bacterial counts, respectively. The v-qPCR method will incorporate membrane-impermeable dyes, such as propidium monoazide (PMA), to selectively inhibit amplification of DNA from non-viable cells. To validate the accuracy of v-qPCR, results will be compared with traditional culture-based methods, such as color-changing units (CCU), and advanced techniques like flow cytometry, which enable direct enumeration of live bacteria. By improving the detection of viable bacteria, v-qPCR is expected to enhance inoculum testing, streamline acclimatization protocols, reduce program failures, and accelerate the establishment of disease-free swine herds.

P20 - Rued

Project Title: *Examining streptococcal persistence and antimicrobial resistance incidence in veterinary clinics.*

Principal Investigator(s): Britta Rued

Collaborating Investigator(s): N/A

Veterinary Scholar Abstract:

Streptococci are a major constituent of both human and animal microbiomes. These highly adaptable organisms can easily morph from simple commensals to pathogens capable of causing serious infections such as pneumoniae and meningitis. In addition to this, they have the propensity to jump between vertebrate species. For instance, *S. suis* can easily transit from swine to humans during outbreaks in herds, and the species *S. canis* has been shown to be able to cause disease in both companion animals and human hosts. Despite this group organisms' amazing ability to jump between hosts and cause severe disease, data on their incidence in veterinary clinic settings is lacking. Most studies have concentrated on examining the incidence of other bacterial spp. or provided a cursory overview of streptococci detected in the environment. As such, data on the speciation and nature of these organisms has not been defined. The goal of this project is to examine the incidence, persistence, and level of antibiotic-resistant streptococci in a clinical veterinary setting, and to use this as data to provide rationale extend this to greater Iowa region for health benefits for companion and livestock animals. Published data indicate that these organisms are regularly detected in these environments, but little else is known about their persistence. This study will provide important knowledge for veterinary clinicians and research scientists on the rate at which these organisms are detected in the environments they work in, the need for increased environmental cleaning procedures, as well as the epidemiology and incidence of these organisms in veterinary clinics.

P21 - Sato

Project Title: Establishing Avian Metapneumovirus subtype A Turkey Infective Dose 50 ($TUID_{50}$) for 3-Day-Old and 12-Day-Old Turkeys

Principal Investigator(s): Yuko Sato

Collaborating Investigator(s): Mohamed El-Gazzar, Eman Gadu, Jianqiang Zhang, Silvia Carnaccini, Joaquin Caceres

Veterinary Scholar Abstract:

Avian metapneumovirus (aMPV) is a highly contagious virus that causes acute upper respiratory disease, with characteristic sinusitis and swollen heads in turkeys and chickens. The virus is classified into four subtypes (A–D) based on nucleotide sequence of G protein sequence. aMPV subtypes A and B have never been reported in the US until a recent emergence of aMPV-A in California and aMPV-B in North Carolina in turkeys and broilers. Both subtypes A and B have now spread to commercial poultry in 29 states. The great majority of cases in Iowa is from subtype A, with a few reported B cases. Both MLV and inactivated vaccines are available for subtypes A and B worldwide, but only subtype C vaccine was conditionally available in the USA. Iowa State University – Veterinary Diagnostic Laboratory (ISU-VDL) has successfully isolated subtypes A and B in primary cell lines and successfully adopted them to continuous cell line (Vero cells), and attenuation via serial passages is underway. However, the regulatory pathway to domestically produce MLV vaccines will require further research and time. The Iowa turkey industry is interested in using subtype A isolated from Iowa turkeys in an early exposure (3 – 12-day-old) feedback setup as a stop-gap measure until the MLV are commercially available. There is anecdotal evidence of cross-protection against subtype B using subtype A vaccine, although published studies are scarce. However, appropriate dose for effective and safe exposure remains unknown.

Objectives: Using previously established challenge models, we aim to determine the Turkey Infective Dose 50 ($TUID_{50}$) and evaluate homologous and heterologous protection of aMPV subtypes A in 3 and 12 days old turkeys using a live challenge model.

P22 - Singh

Project Title: *Mechanism of therapeutic molecules for the treatment of genetic disorders.*

Principal Investigator(s): Ravindra Singh

Collaborating Investigator(s):

Veterinary Scholar Abstract:

Gene function is intimately linked to the production of coding and/or non-coding RNAs. In most instances, a single gene produces multiple RNAs due to alternative splicing, alternative transcription start and/or stop sites. Antisense oligonucleotides (ASOs) and small molecules that modulate transcription and/or splicing are becoming powerful tools to treat genetic diseases. The appropriate application of ASOs and small molecules for therapeutic application requires the target identification and characterization. It is also important that the off-target effects of ASOs and small molecules are properly understood before their use in clinics. Summer scholar in Singh lab will learn how to identify therapeutic targets and off-target effects of ASOs and small molecules. This collaborative project will employ a variety of techniques, including high throughput sequencing, bioinformatics, RT-PCR, molecular and cellular biology techniques. Findings of the successfully completed project by the summer scholar will be published in a peer-reviewed journal and summer scholar will have opportunity to earn co-authorship in the publication.

P23 - Thippeswamy

Project Title: *The role of Fyn-tau interactions in experimental models of epilepsy*

Principal Investigator(s): Thimmasettappa (Swamy) Thippeswamy

Collaborating Investigator(s): None

Veterinary Scholar Abstract:

Seizurogenic neurotoxins such as domoic acid (rich in certain seafood) or organophosphate pesticides exposure at high concentrations cause seizures and epilepsy in humans and animals. Acute exposure, in the long-term, will cause irreversible brain damage due to hyperexcitability of neurons, reactive gliosis, and neurodegeneration. If these are not adequately controlled at a very early stage, they will lead to the development of epilepsy, cognitive dysfunction, and other neurological deficits. Currently, there is no treatment for the long-term neurotoxic effects of these chemicals. The symptomatic drugs atropine, oxime, and midazolam (MDZ) are inadequate to prevent OP-induced long-term brain injury. MDZ controls seizures but not neuropathology. We have found that OP-induced seizures or domoic acid analog, kainate, cause reactive gliosis and increase the levels of reactive oxygen/nitrogen species (ROS/RNS) in the hippocampus. We have also discovered Fyn/Src family tyrosine kinase (SFK) as a major source of disease promoter (epilepsy) in rats exposed to these neurotoxins. Incidentally, our studies in the rat model suggested that saracatinib, a potent and highly selective Fyn/SFK inhibitor, is blood-brain barrier permeable and ameliorates long-term neuropathology in the rat kainate model of epilepsy (PMID: 34087381). Therefore, our overarching hypothesis is that Fyn/SFK is a potential target for disease modification in epilepsy. To test the hypothesis, we will use our established diisopropylfluorophosphate (OP agent) or kainate rat model to replicate a real-life scenario of chemical poisoning. In the proposed study, Veterinary Scholar will perform video-EEG analyses for seizures and utilize various histological and biochemical assays of brain samples to investigate the pathogenesis of chemical-induced epilepsy and the long-term neuroprotective effects of Fyn/SFK inhibition through a blocking peptide or vector-mediated fyn knockdown approach.

P24 - Udomteerasuwat

Project Title: *Accuracy and efficacy of alcohol neurolysis for localized anesthesia in calves*

Principal Investigator(s): Nutnapong Udomteerasuwat

Collaborating Investigator(s): Suzanne Millman

Veterinary Scholar Abstract:

Alcohol neurolysis, also known as an ethanol nerve block, is widely used in human medicine for pain management but remains largely underexplored in veterinary medicine. This project aims to assess the accuracy and efficacy of alcohol neurolysis for regional anesthesia, focusing on cornual nerve desensitization, with confirmation through pathological analysis.

P25 - Verhoeven

Project Title: *Investigation of mRNA vaccines in animals or novel antibody development.*

Principal Investigator(s): David Verhoeven

Collaborating Investigator(s): Douglas Jones and our vaccine company Syntherna personnel.

Veterinary Scholar Abstract:

mRNA vaccines represent a novel way to quickly develop vaccines for transboundary pathogens or for viruses that have been stubborn to prevent by current vaccine technologies. We have three projects that the students can choose from: (1) development of mRNA vaccines for equine herpes and feline herpes; (2) development of mRNA vaccines for high pathologic avian influenza; or (3) development of novel antibodies for canine osteoarthritis. The first two projects would be helping with the development of these vaccines and then testing serum responses in vaccinated mice (before any equine work) or mice/cats for generation of protective antibodies. The second would be to vaccinate eggs and young chicks for HPAI and investigate the serology of vaccinees for protective antibodies. The final potential project would be to implant canine cytokines into mice, isolate the antibodies, clone them, and express them on a dog antibody plasmid.

The student, no matter the project chosen, would get lots of hands on experience with molecular biology and animal serology development and testing.

P26 - Ward

Project Title: *Implementation and Outcomes of a Patient Safety Committee and Incident Reporting System at a Veterinary Teaching Hospital*

Principal Investigator(s): Jessica Ward

Collaborating Investigator(s): Melissa Tropf

Veterinary Scholar Abstract:

Ensuring patient safety is crucial in a veterinary teaching hospital, where complex clinical and educational dynamics create unique challenges. In response to these challenges, our institution implemented a Patient Safety Committee (PSC) and a Patient Incident Reporting System in late 2021, aimed at enhancing the culture of safety and promoting continuous quality improvement. This mixed-methods research project will examine the development, implementation, and outcomes of this initiative over the three-year period since PSC formation. The project will address the committee's formation, the creation of standard operating procedures, and stakeholder education through public relations campaigns, training programs, and ongoing maintenance efforts. The analysis will highlight strategies that contributed to successful implementation, common challenges encountered, and the integration of additional safety practices such as M&M Rounds and surgical safety checklists. Initial outcomes of the PSC will be assessed by analyzing trends in incident reporting, evaluating implemented safety interventions, and exploring evidence of a "culture of safety" beyond quantitative metrics. Qualitative data from stakeholder surveys and structured interviews will be used to uncover additional context and themes to enrich quantitative data from incident reports. The Summer Scholar will gain experience in mixed-methods research, including data analysis, survey development, structured interviewing, and content analysis. Responsibilities will also involve literature review, preparing an Institutional Review Board (IRB) submission, and participating in data visualization and statistical preparation. The scholar will present findings through a research poster and draft a manuscript, contributing to the broader understanding of patient safety in veterinary medicine.

P27 - Zhang

Project Title: *Isolation and characterization of a PEDV variant strain associated with the recent outbreaks in Illinois and Iowa*

Principal Investigator(s): Jianqiang Zhang

Collaborating Investigator(s): Phillip Gauger, Marcelo Almeida, Baoqing Guo

Veterinary Scholar Focused Abstract: (300 words or less):

Porcine epidemic diarrhea (PED) continues to be an important swine disease with significant economic losses to the U.S. pork industry. Currently, two major genetically distinct PED virus (PEDV) strains are circulating in U.S. swine herds and are designated as non-S INDEL and S-INDEL PEDVs. Nucleotide substitutions, insertions, or deletions can occur in either strain although their biological functions remain unclear. Since June 2024, multiple sow farms in Illinois and Iowa have experienced new outbreaks with PED and the previously used control strategies have not been effective. Spike gene sequencing indicated that PEDV detected in Illinois and Iowa phylogenetically belonged to non-S INDEL PEDV but had a 6-nucleotide deletion in the spike gene compared to the non-S INDEL PEDV initially identified in the USA in 2013.

The objective of this study is to further characterize this PEDV variant strain. 1) Isolation of this PEDV variant strain will be attempted in cell culture and its growth curve in Vero cells will be compared to the regular non-S INDEL and S INDEL PEDV isolates. 2) The whole genome sequences of this PEDV variant present in clinical samples and cell culture isolates will be determined via next-generation sequencing technology and further analyzed. 3) The antisera previously generated against the regular non-S INDEL, S INDEL, and a live attenuated PEDV vaccine candidate in experimentally inoculated pigs will be assessed for their cross-neutralization against this PEDV variant strain. 4) The *in vivo* characterizations of the pathogenicity, duration of viral shedding, and immune responses of this PEDV variant strain in comparison with other PEDV strains will be conducted if funding is secured.