B1 - Beck

Principal Investigator(s): Dr. **Josh Beck**

Project Title:

Project Summary:

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 mechanisms of action or 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 (year 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 (year 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 importance class of anticoccidials. This project is consistent with the 2023 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.

B2 – Gorden

Principal Investigator(s): Dr. **Patrick Gorden**

Collaborating Investigator(s): **Cody Sacquitne and Phillip Jardon**

Project Title: Pilot study to validate a hand-held luminometer with indicator organism tests to enumerate bacteria in colostrum and whole milk to be fed to dairy calves

Project Summary:

According to the USDA National Animal Health Monitoring System Dairy 2014 study, morbidity and mortality associated diarrheal diseases continues to be one of the most common calf health challenges dairy producer's experiences and is the most common reason antibiotics are used in pre-weaned calves. Bacterial contamination of colostrum and milk replacer is a common, but often unrecognized cause of failure of passive transfer and/or neonatal calf diarrhea. On-farm investigation of diarrheal outbreaks in which elevated bacteria is a differential risk currently require the collection of milk samples which are later submitted to a microbiology laboratory, which has substantial time lag and cost. Adenosine triphosphate (ATP) bioluminescence (luminometry) is a common tool for performing comprehensive evaluations of feeding and housing equipment cleanliness on dairy farms. One manufacturer of bioluminescence equipment markets an indicator organism test system to monitor total bacteria, total coliform bacteria, and total *E. coli* in milk that will provide same day bacterial count results. In this proposal, we describe a two-year project to validate the use of a luminometry system to quantitate bacterial counts in colostrum (year one) and milk (year two) to be fed to calves. **Our hypothesis of this work is that the use of rapid diagnostic tests to quantify bacterial counts in colostrum and milk will improve colostrum and milk quality fed to calves.** We plan to collect 300 colostrum samples to complete the validation of a luminometry system to estimate total bacteria, coliform, and *E. coli* and compare these results to laboratory based total bacteria and total coliform counts as the gold standard. The results of this work will allow for rapid bacterial enumeration, potentially on-farm. In the end, this will help reduce morbidity on dairy farms.

B3 – Jones

Principal Investigator(s): Dr. **Douglas E. Jones**

Collaborating Investigator(s): Dr. **David Verhoeven**

Project Title: Peptide Vaccination Targeting Highly Conserved Epitopes of Pathogens

Project Summary:

The immune response towards infection often generates a pathogen specific response with the adaptive immune response targeting immunodominant epitopes that are effective for a particular subtype or variant of the pathogen. This is exemplified by the current SARS – CoV-2 pandemic as well as ongoing influenza infections. Although these 2 viral pathogens have highly conserved peptide sequences, shared amongst all Coronavirus types or Influenza strains, the immune response typically generates antibody and T cell specificity to immunodominant epitopes. One solution is to vaccinate with short peptide sequences of highly conserved regions of these pathogens. Unfortunately, peptide vaccination is notoriously inefficient and difficult, with poor adaptive immunity generated by these small amino acid sequences. We have developed an implantable vaccine platform for extended antigen release (VPEAR) that in preliminary studies demonstrates efficient vaccination using short peptide sequences. In this project the individual will use conserved peptide sequences from either SARS - CoV-2 or influenza and determine the ability of VPEAR to generate broadly neutralizing antibodies to these pathogens in mice via ELISA, flow cytometry and virus neutralization.