Carlson College of Veterinary Medicine
Department of Biomedical Sciences

BIOMED INSIDER

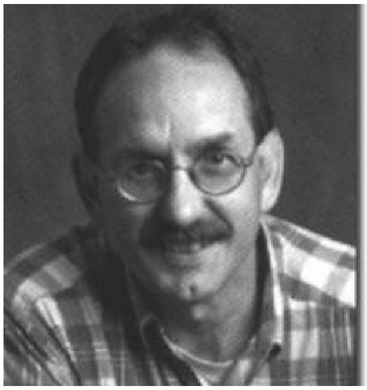
ISSUE N.06 | FALL 2021

RESEARCH NEWSLETTER

Artwork by Sally Byrd, M.D.

LETTER

from the Department Head of Biomedical Sciences



In this new issue of Biomed Insider, we showcase work that veterinary students participated in last summer. What an amazing collection of projects, adding knowledge to both veterinary medicine and human medicine!

Upon reading the descriptions of the scientific experiences, it becomes clear what the excitement of faculty mentors and the motivation and hard work of students can accomplish. The projects range from comparative immunology of sheep, investigation of chlamydia infection in surrounding forms, ecology of infectious organisms in animals, epidemiologic study of hospital-associated infections, fish parasitic diseases, stem cell research in canine osteosarcoma, kidney function in cats, the role of selenium in nutrition, experimental treatment of herpes infection, bovine tuberculosis, diarrhea in buffalo, inflammation, and much more. Congratulations to all involved!

The student participation in research, which gives them the chance to learn laboratory techniques and the appreciation as well as interest in the development of medicine, is only one facet of what knowledge is generated in the college laboratories and hospital facilities. Faculty and students participate in many diverse projects, encompassing the signature areas of research in the college: regenerative medicine, global infectious diseases, metabolic diseases and inflammation, cancer, cardiovascular diseases, and neuroscience.

Scientists make discoveries every day that increase our understanding of biological systems and lead to new technologies, new surgical techniques, and innovative therapy to restore functions to fight disease and improve the quality of life in humans and animals. With each advancement, we gradually open the black box of biology.

Sincerely,

Dr. Luiz Bermudez, M.D.
Department Head of Biomedical Sciences

CONTENTS

POST-TREATMENT OUTCOMES OF LASER ABLATION OR SURGERY TREATED FOR ECTOPIC URETER IN FEMALE DOGS

A retrospective review conducted by Dr. Stacie Summers and collaborators compares the complication rates and post-procedural owner-reported continence of female dogs receiving surgery or transurethral cystoscopic-guided laser ablation for intramural ectopic ureter. They presented the abstract at the 2021 American College of Veterinary Internal Medicine Forum.

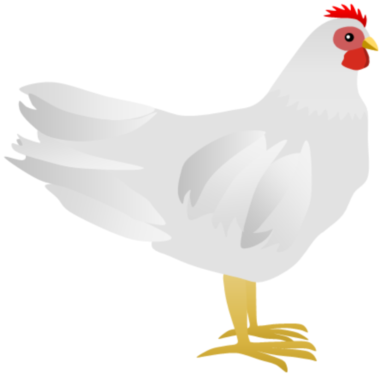
They found that dogs that underwent surgery had a higher risk of post-treatment complications and spent more time in the hospital after the procedure. However, follow-up reports by owners revealed higher rates of improvements or resolution of urinary continence from dogs that received surgery.

BENEFITS OF INCORPORATING HEDGEROWS FOR PASTURE-RAISED BROILER CHICKENS

Incorporating hedgerows into pastures improves pasture conditions and feed efficiency for pasture-raised broiler chickens, according to a new study. This method could help increase profit margins and improve animal welfare for small farms that practice pasture-rearing.

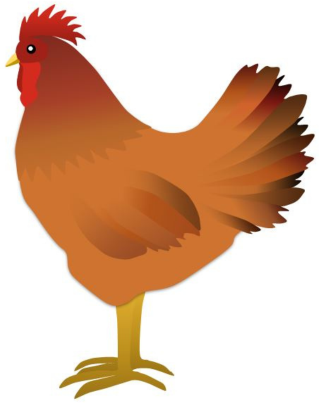
Dr. Brianna Beechler, Dr. Anna Jolles, Caroline Glidden, Eilea Delgadillo, Marissa Pollak, and Holly Rysenga, of Oregon State University, demonstrated how incorporating hedgerows into pastures can affect the overall health status and production performance of U.S. slow-growing Red Ranger broiler chickens and fast-growing Cornish Cross broiler chickens.

The study shows that on average, Cornish Cross with hedgerow access gained weight faster than Cornish Cross in a bare pasture. There was no significant difference in feed intake between those two groups, which could help improve the economic gain of small farms, as hedgerow access can increase the rate of gain in Cornish Cross without incurring extra feed costs. Red Ranger with hedgerow access, on average, demonstrated greater ability to



Cornish Cross Broiler Chicken

- The most common of chickens and known as the modern broiler chicken
- Cornish Cross is not a breed, but a hybrid bred for commercial meat production
- They have a big appetite, and as a result, are muscular and heavy
- Their wide leg stance help support their body weight
- They grow rapidly and can reach harvest weight in 6-7 weeks
- Their sparse white feathers make plucking easy
- The chicken meat you purchase at the grocery stores are most likely Cornish Cross



Red Ranger Broiler Chicken

- Red Rangers are dual-purpose chickens with them primarily being meat chickens, but can also lay eggs
- They are active birds with very good foraging abilities
- Red Rangers have strong and muscular legs
- They grow slowly and can reach harvest weight in 12-14 weeks
- Their fully feathered body makes them suited for the outdoor living environments, but makes plucking more difficult
- Red Rangers are popular among those who raise free-ranging and pasture-raised chickens

neutralize *Escherichia coli* in whole blood and a lesser degree of hemodilution than Red Ranger in a base pasture. This indicates that hedgerow access improved immune function and led to a lesser degree of heat stress in Red Rangers. Hedgerows can provide shade and shelter to combat effects associated with uncontrolled environmental conditions, such as reducing predation losses and heat stress on production.

The results of the study are consistent with a phenomenon that has been documented, where a genetic trade-off exists between maximum production performance and the ability to adapt to environmental challenges in broiler chicken. The fast-growing Cornish Cross are evolved to have maximum growth rates in conventional indoor poultry houses. In contrast, slow-growing Red Rangers retain the ancestral ability to distribute resources to develop vital and adaptive mechanisms such as immune surveillance and hemodynamic cooling.

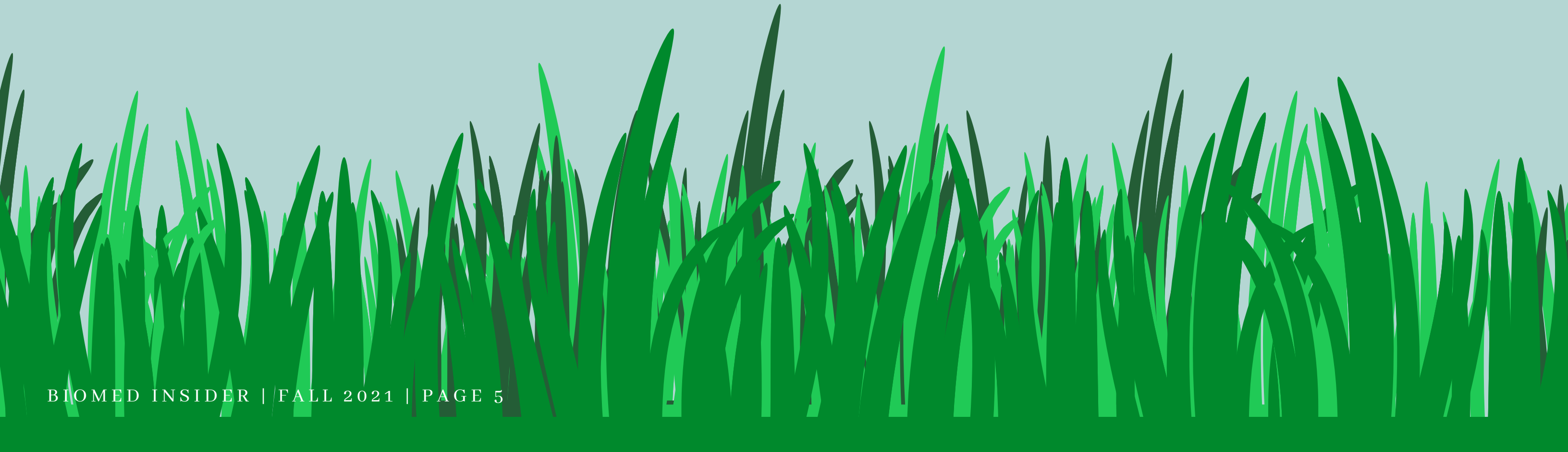
The results and information from the study build onto the body of knowledge on how to use natural environmental enrichment such as hedgerows to improve pasture conditions. The researchers hope commercial poultry farmers can maximize the genetic potential of their flock by optimizing existing landscape features.

AGRONOMIC SELENIUM BIOFORTIFICATION OF OREGON FORAGES

Plants and soils in the Pacific Northwest are low in selenium concentrations and as a result, livestock that feeds on the locally-grown forages are deficient in selenium. Traditional methods of injecting selenium and/or feeding selenium-enriched supplements to increase the selenium status of livestock are often unable to sustain adequate selenium whole-blood concentrations.

Agronomic selenium biofortification is a different method that uses fertilization to increase the selenium content of feed sources. Dr. Jean Hall and colleagues used this approach in a two-year study to investigate the effects of using traditional nitrogen-phosphorus-potassium-sulfur (NPKS) fertilizers enhanced with sodium selenate on forages across Oregon with low selenium concentrations.

The study was conducted from 2017 to 2018 across four representative forage types in Oregon: an alfalfa and a grass mixture in Union, a grass-clover mixture in Roseburg, and orchardgrass in Terrebonne. A split-plot design was used with double-repeated measures of first, second, third, and residual harvest cuts for each year. These measures were analyzed to determine the effects of NPKS fertilization and springtime selenium foliar application rates on total selenium concentration and beneficial selenium species in



the different forage types.

Dr. Hall and colleagues noticed a linear increase in forage selenium concentrations with increasing springtime foliar selenate application across the different forage types. The majority of the forage-incorporated selenium from foliar selenate application was found in the first and second cuts, and the bulk of applied selenate was metabolized into selenomethionine.

The effects of NPK/PK fertilization were found to decrease forage selenium concentrations in second and later cuts of forages from selenium-amended fields. Sulfur fertilization decreased forage selenium concentrations from fields without selenium amendment. Of the four Oregon forage types, alfalfa had greater selenium concentrations under low soil selenium conditions. Grass-dominated forages had higher selenium concentrations after selenium-amendment.

The use of springtime sodium selenate foliar application can be a cost-efficient agronomic selenium biofortification method for increasing forage selenium concentrations and specifically selenomethionine concentrations. Implementing this method can help increase selenium whole-blood concentrations in Oregon ruminant livestock for optimum health and productivity.

This photo is from another study of Dr. Hall's, but it illustrates the principle of selenate fertilization.

ANALYSIS ON INFECTIONS AND ANTIBIOTIC USE IN ANIMAL PATIENTS WITH CANCER

Animal patients with cancer commonly develop infectious diseases. Yet, there is limited information about infection in animals who have tumors and are undergoing treatment. Understanding these infections may provide veterinary oncologists information on the causes of the infections and insight on effective treatment options.

A team of researchers at the Carlson College of Veterinary Medicine reviewed a database of cats and dogs with cancer for concurrent infections, which may provide insight on the causes of common infections and their susceptibility to antibiotics in these cancer patients.

Joelle Jacob, and Drs. Haley Leeper, Luiz Bermudez, Katie Curran, and Kathy O'Reilly reviewed patients seen for an oncologic disease from 2013 to 2018 in the Veterinary Teaching Hospital at the Carlson College of Veterinary Medicine. A total of 153 patients had concurrent bacterial infections. Infection agent, site of infection, and susceptibility to antibiotics were identified from those cases and analyzed.

Out of the 153 cases, a majority of the infections were caused by bacteria commonly seen and associated with that particular location site of the body, with antibiotic susceptibilities that are as expected. Site of infection included abscesses and wounds, airways and lungs, eyes and ears, and urine. The majority of the bacteria isolated in these cases are predominantly associated with either the skin or possibly acquired in a hospital environment.

In general, the most common pathogen linked to infections was *Escherichia coli (E. coli)*, except *Staphylococcus pseudintermedius* was often identified as a pathogen related to wound infections. Although *E. coli* infections are expected, it was surprising to see *S. pseudintermedius* as a possible skin contaminant. Urinary tract infections caused by *Enterobacter sp., Enterococcus sp., and E. coli* were anticipated as they are regularly observed as etiology bacteria commonly linked with urinary tract infections in cats and dogs.

It was unexpected to see *E. coli* and *Proteus mirabilis* isolated from bronchoalveolar lavage fluid since these are uncommonly observed microorganisms isolated from the respiratory tract. It was also uncommon to see infections in cancer patients caused by opportunistic bacteria, aside from the specific cases of wound infections that were mostly acquired in the hospital.

An analysis of antibiotic activity against infections showed that amikacin overall had good activity in all the various infections. Amoxicillin plus clavulanic acid also demonstrated effective activity and could be an alternative to treat most infections until there are available bacteriologic results. The team noted that respiratory tract infections linked to *Pasteurella* would respond fairly well to antibiotics typically used to treat *Pasteurella* infection. On the other hand, if the respiratory infection is caused by *E. coli,* these bacteria may be multi-resistant and require treatment of the aminoglycosides class of antibiotics. Significant resistance to available antibiotics was seen in bacteria isolated from wounds. In comparison, abscesses resulted from antibiotic susceptible bacteria.

These results could provide information and guidance to veterinary oncologists treating their patients. The information on the common microorganisms causing these infections may help limit and narrow the spectrum of antibiotic treatments in patients with cancer, preventing unnecessary antibiotic use and decreasing the effect of antibiotic resistance as a result.

VISCOUS WATER INCREASES WATER INTAKE IN CATS


Photo by suju-foto from pixaby

Researchers explored the idea of giving viscous water to cats to increase water intake, thereby reducing the risk of urolithiasis.

Urolithiasis is the formation of urinary stones (kidney and bladder) and is a common condition responsible for lower urinary tract disease among cats. Increasing water intake in cats may reduce the risk of developing the condition. Corresponding author Dr. Jean A. Hall and her colleagues blended 1% methylcellulose, which is a chemical compound that can be used as a thickener, to deionized water to make viscous water.

The study, published on July 15, 2021, in *Animals*, found that cats provided with viscous water had increased water intake compared to cats that were provided with control deionized water. The increase in water intake resulted in lower serum creatinine, blood urea nitrogen, and triglyceride concentrations, and urine-specific gravity. The researchers also noticed a decrease in urine calcium concentrations, as well as increased resistance to oxalate crystal formation.

The use of viscous water may potentially help cats reduce the risk of urolithiasis and, as researchers noted, the benefit of viscous water is that cats do not have to change their natural drinking habits to increase water intake.

2021 SUMMER PROGRAMS

Through the summer programs at the Carlson College of Veterinary Medicine (CCVM), professional veterinary and undergraduate students conducted summer projects with CCVM faculty mentors and presented their results on Research Week 2021.

Here is a recap of some students' work!

Rachel Moore

Rachel Moore at the OSU dairy farm where she was worked alongside Dr. Joseph Klopfenstein to join on Rural Veterinary Practice farm calls.

Rachel Moore is a third-year DVM Candidate at the Atlantic Veterinary College at the University of Prince Edward Island in Canada. Rachel came across the Summer Research Program at the CCVM with an interest in working on the topic of immunology. She has an interest in obtaining board certification in laboratory animal medicine. She hopes to use her veterinary degree to improve animal and human health by working in the field of biomedical research, specifically immunotherapies and medical device research.

Over the summer, Rachel worked with Dr. Brian Dolan and Brandy Nagamine, a graduate student in the Dolan Lab, on identifying mucosal-associated invariant T cells in bovine peripheral blood. She was also able to join OSU clinical veterinarians on the Rural Veterinary Practice service rotations to work on large animal clinical cases across the Corvallis area.

Identification of mucosal-associated invariant T (MAIT) cells in bovine peripheral blood

Abstract: Mucosal-associated invariant T (MAIT) cells are innate T cells that are highly conserved across mammalian species and express a semi-invariant αβ T cell receptor that recognizes derivatives of riboflavin synthesis (produced by bacteria and fungi) presented by the antigen-presenting molecule, MHC class I-like protein (MR1). MAIT cells have been identified in mice, non-human primates, and humans, but the studies that support the presence of MAIT cells in cattle are limited. This study seeks to identify and characterize the presence of MAIT cells in bovine peripheral blood samples using the potent MAIT cell ligand, 5-(2-oxopropylideneamino)-6-D-ribitylaminouracil (5-OP-RU), which is presented by MR1 and is a derivative of bacterial and fungal riboflavin biosynthesis. The research has not yet been completed as of summer 2021, but preliminary data supports the presence of MAIT cells in cattle and further research will be necessary to understand the role of MAIT cells in immunity and infection, especially during the economically important zoonotic disease of cattle.


Alexandra Behnke with Sansa

Alexandra Behnke

Alexandra Behnke is a third-year DVM Candidate at the CCVM. Alexandra dedicated the summer to work in the Jin Lab on investigating whether an inhibitor of cullin RING ubiquitin ligases, MLN494, can be used against koi herpesvirus infection. She worked with Dr. Ling Jin, who was her mentor, Xisheng Wang, a faculty research assistant in the Department of Vet Biomedical Sciences, and Gloria Petri, a DVM Candidate who also participated in the Summer Programs.

Treatment of MLN4924 against latent koi herpesvirus reactivation

Abstract: Cyprinid herpesvirus 3, or koi herpesvirus (KHV), is a highly contagious virus that infects the common carp (*Cyprinus carpio*), with those infected suffering from high rates of morbidity and mortality.

Currently, there is no antiviral drug available that can protect koi from KHV infection. However, recent studies have shown that herpesviruses manipulate Cullin RING ubiquitin ligases (CRLs) to weaken the innate immunity of the host. MLN4924 is a Nedd8-Activating Enzyme (NAE) inhibitor that can prevent CRLs from being conjugated. Thus, it was hypothesized that MLN4924, the NAE inhibitor, can prevent KHV infection in koi.

For this study, groups of 6-month-old koi fish were treated with TPCA-1 (a STAT3 and NF-kB inhibitor) and then infected with KHV. Koi fish were subsequently treated with acyclovir (ACV), DMSO, and MLN4924. Tissue samples were then collected post-mortem for analysis.

Results showed that the fish treated with MLN4924 did not fare better than those treated with ACV and DMSO, as mortality rates and KHV viral replication levels were similar among the three groups. This indicated that MLN4924 was not an effective treatment of KHV for fish with compromised immune responses.

Dana Tsuchida

Dana Tsuchida is a DVM Candidate, Class of 2023, at the CCVM. Dana's summer project focused on researching the immunological parameters of California Bighorn sheep, with mentor Dr. Brianna Beechler and Robert Spaan, a Ph.D. student in the Department of Fisheries, Wildlife, and Conservation Sciences at the College of Agricultural Sciences.


Dana Tsuchida

Immunological Measures of Bighorn Sheep

Abstract: Bighorn sheep are an iconic species in the American West that have been heavily impacted and suffered die-offs from novel diseases in recent years (Besser et al., 2017). Understanding the health and survival pattern in these species is crucial to properly manage and protect them.

One under-researched area is understanding immune function. This is especially important in bighorn sheep because they are threatened by various infectious diseases that can lead to rapid decreases in number.

Using the data set collected by a graduate student in 2016 and 2017, which included survival for five months post-capture, the immunological functions of California bighorn sheep were assessed. The collected immunological measures consisted of diverse innate and adaptive assays performed at the time of capture from roughly 150 sheep in Oregon and Nevada. These assays included lymphocyte function, the bacterial killing ability of whole blood, total antibody titers, and white blood cell differential counts. We first asked if any of the single measures of immune function correlated to whether the sheep survived for five months after capture. Sheep with higher white blood cell counts, driven primarily by neutrophil counts, were more likely to die during the follow-up period than those with lower white blood cell counts.

It is possible these sheep were suffering from infection during capture, with led to the increased risk of death. These data should be compared to the chemistry panel values that were collected from these individuals to see if there is any correlation between immune function and the general health of the animals. No other measures of immunity correlated to mortality risk.

We then sought to create an "immune profile" using a Principal Component Analysis (PCA), allowing us to look at whether there were patterns of immune assays driving the individual differences in immunity. We will then ask whether these "immune profiles" correlate to survival on a more holistic level.

Ened McNett

Ened McNett is a third-year DVM Candidate at the CCVM. Ened devoted the summer to investigating the effects of supra-nutritional selenium-yeast supplementation of pregnant beef cows on whole blood selenium levels and nasal microbiota in their calves at weaning. Ened worked with mentor Dr. Jean Hall and collaborators from Oregon State University, Texas A&M University, and the USDA-ARS-Poisonous Plant Research Lab.

Ened McNett

Does supra-nutritional Se-yeast supplementation of beef cows during various trimesters of pregnancy affect whole blood Se levels and nasal microbiota in their calves at weaning?

Abstract: We previously reported that feeding selenium(Se)-biofortified alfalfa hay to weaned beef calves in a preconditioning program decreases morbidity and mortality during the feedlot period, leading to an increase in carcass weight and quality at slaughter. In these pre-conditioned calves, these positive outcomes were correlated with an increase in nasal microbiome abundance and diversity at weaning.

The objective of the current study was to see whether Se supplementation of cows during pregnancy affects calf whole blood Se (WB-Se) concentrations at birth and if differences persist through weaning enough to alter nasal micro-biome diversity at weaning and subsequently increase carcass weight and quality at slaughter.

This was part of a two-year study in which Angus-cross cows were supplemented with Se yeast via boluses in either the first, second, or third trimester of pregnancy. A control group that was not treated with Se-yeast boluses was also included. Treatment cows received Se-supplementation during their corresponding pregnancy trimester in the form of Se yeast boluses administered once per week for 13 weeks, with the Se dose equaling 105 mg Se/week throughout their treatment trimester.

Ten calves born from each group were chosen for studying nasal microbiome. Blood samples were taken at birth and again at weaning to measure WB-Se concentrations. Nasal swabs were collected at weaning to assess the nasal microbiome for richness and

diversity. Carcass weight and quality were recorded for each of the calves at slaughter after finishing in the feedlot.

Results showed that WB-Se concentrations were significantly different at birth (P <0.05) between the control group of calves and calves born to mothers given Se treatment during trimesters two and three. WB-Se concentrations were still different at weaning between the control group of calves and calves born to mothers given Se treatment during trimester three.

No significant differences were noted between control calves and Se-treatment groups in the nasal microbiome at weaning. Carcass weight and quality information are still being assessed. These findings show that supplementing organic Se-yeast during pregnancy alters WB-Se concentrations in calves at birth, but WB-Se differences lessen by weaning such that nasal microbiome abundance and diversity are not altered at weaning. To see benefits to the nasal microbiome, calves would need to be fed Se-fortified forages again at weaning.

Jordi Moo-Fuentes

Jordi Moo-Fuentes is an undergraduate student in Animal Sciences at the College of Agricultural Sciences. Jordi worked in the Rockey Lab with Dr. Daniel Rockey, who served as his mentor, during the summer to test chlamydial detection approaches via PCR to study the differences and provide insights into this genus.

Using PCR techniques to assess genetic variability across the chlamydia trachomatis genome

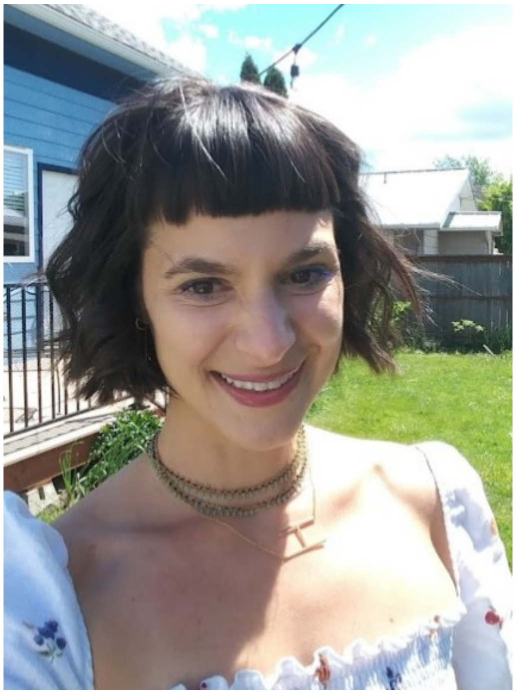
Abstract: Chlamydia possesses immense importance within both human and animal medicine when looking at pathogens. The members of the genus itself contain extremely similar methods of infection and makeup, allowing for the analysis of clinical samples through techniques such as PCR.

In this research project, chlamydial detection approaches are tested through PCR to study these differences and better improve our understanding of this genus. Sequences along a highly variable 100kb fragment of Chlamydia Trachomatis were tested through an isolated DNA template (D+) to determine if detection of the disease was possible. Once this was complete, the process was repeated with clinical samples from clinics along the West to test the PCR detection method with a highly variable infection from real patients.

Success in this project will allow us to obtain DNA greater than a 10kb length, along with increasing the overall sensitivity of DNA sequencing within chlamydial samples of both humans and animals. This would allow for more efficient chlamydial testing and a more rapid treatment process across the clinical setting.

Hilary Ann Lakin

Hilary Ann Lakin, Class of 2023 at the CCVM, participated in the 2020 Summer Research Program investigating the gross and histologic development of bovine tuberculosis in wild African buffalo. For the 2021 Summer Research Program, Hilary Ann continued the research project with mentors Drs. Anna Jolles and Brianna Beechler, focusing on the progression of pathology associated with bovine tuberculosis in wild African buffalo.



Hilary Ann Lakin

Gross and histological progression of bovine tuberculosis in African Buffalo (*Syncerus caffer*)

Abstract: Bovine tuberculosis (BTB) is a zoonotic disease of global importance that is endemic in African buffalo in sub-Saharan Africa, including Kruger National Park where the study took place. We first sought to describe the pathologic progression of bovine tuberculosis over time in infected African buffalo. We then asked if progression correlates to genotypic markers.

African buffalo were captured, fitted with a tracking collar, and tested for BTB during a 4-year-cohort study. This allowed for serial captures and BTB testing for the buffalo in the study, creating a database with known sero-conversion dates for those not infected with BTB at initial capture. At the end of the project, BTB positive buffalo were culled, and necropsies were completed. We found that as the infection progressed, more lung lobes were affected with bigger lesions, as opposed to a single lobe with bigger lesions. There is a weak positive correlation between disease progression with the length of infection, reinforcing the difficulty in developing a clear timeline for bovine tuberculosis. The probabilities of retropharyngeal and tracheobronchial lymph nodes infection mirror each other, with a high likelihood of pathology early in the disease process.

Lastly, the previously identified BTB risk allele, SNP 3195, is of particular interest in terms of the progression of lung necrosis. Lung lesions from buffalo with the homozygote genotype are less necrotic when controlled for length of infection, compared to wildtype and heterozygote genotypes. This could suggest the homozygote genotype serves a protective function within this herd.

Gloria Petri

Gloria Petri

Gloria Petri is a third-year DVM Candidate at the CCVM. She participated in the 2021 Summer Research Program working with Dr. Ling Jin, who served as her mentor, Xisheng Wang, a faculty research assistant in the Department of Biomedical Sciences, and Alexandra Behnke. During her time in the Jin lab, Gloria examined whether ML324, a histone demethylase inhibitor, can prevent koi herpes virus infection or reactivation.

Inhibitor of histone demethylases (ML324) and koi herpes virus

Abstract: CyHV-3, koi herpes virus, first appeared in 1997 in common carp and has since caused high mortality in koi that contract it. There is currently no accepted treatment for those affected with KHV.

In this research, we studied the effects of a histone demethylase inhibitor, ML324, on preventing the reactivation of KHV from latency. 6-months and 2-year-old koi were infected with KHV on day zero of this study. Our fish were separated into treatment groups as follows: 6m treated with ML324, 2yr treated with ML324, 6m treated with acyclovir, 6m treated with DMSO, 2yr control. In addition to receiving their allocated drug, an additional NF-kB inhibitor was given to all fish to simulate a concurrent infection/immune suppression.

In previous research by Dr. Jin, the ML324 treated fish seemed to have a higher survival rate than those in the acyclovir and DMSO groups. From our study, we found that the addition of the NF-kB inhibitor increased the mortality rate in all groups. When comparing the ML324 treated group to DMSO treated fish (which were to act as a control of those infected, as DMSO will not treat the KHV), ML324 significantly worsened the mortality rate compared to DMSO. This indicates that under immune suppression, the use of ML324 would not only not stop KHV reactivation from latency, but ultimately allowed for further viral replication than if left untreated.


Zoe Moulton at rice paddy fields in Vietnam

Zoe Moulton

Zoe Moulton is an undergraduate student in the Department of Biochemistry and Molecular Biology at the College of Science. Zoe dedicated the summer to work in the Morgan and Shulzhenko Lab researching the genomic regions of probiotic bacteria that improved disease outcomes when supplemented to treat hosts with metabolic diseases, such as obesity and type 2 diabetes. She worked with Dr. Shulzhenko, her mentor, Dr. Andrey Morgun, Shivani Thakor, and Jacob Pederson.

Exploring the links between functional genomic content and the phenotypic effects of "probiotic" bacterial supplementation on metabolic syndrome

Abstract: Probiotic supplementation has become increasingly popular as public trust in the proposed health benefits of live cultures increases, with extensive research being conducted to determine the possible effects of bacterial supplementation on metabolic syndrome.

The purpose of this study is to identify the most effective bacterial probiotic strains for the prevention or treatment of metabolic syndrome and to establish which bacterial genes are associated with improved phenotypes in diabetes and obesity.

Data was collected from published literature involving "probiotic" supplementation to hosts with metabolic syndrome; significant changes in expression of metabolic phenotypes were noted. Then, bacterial genomes available on online databases (NCBI, Ensembl, JCM) were annotated using eggNOG-mapper, and the Cluster of Orthologous Genes (COG) IDs was extracted for functional genomic content characterization.

Future steps include reducing the dimensionality of the collected dataset, performing analysis of COG content of genomes and phenotypic changes between bacterial strains, and building a network to identify connections between specific bacterial genomic regions or genes and phenotypic modulations.

Elizabeth Alvey

Elizabeth Alvey

Elizabeth Alvey, a third-year DVM Candidate at the CCVM, conducted a summer project exploring protocol optimization of three assays by using a model challenging cartilage with interleukin-1β. Elizabeth worked with her mentor, Dr. Katja Duesterdieck-Zellmer, and Maureen Larson.

Protocol optimization of assays used to analyze cartilage viability, cartilage matrix homeostasis, and concentration of prostaglandin E2

Abstract: Utilizing in vitro cartilage tissue culture models to mimic biological processes helps study inflammation, and challenging cartilage explants with interleukin-1β (IL-1β), an inflammatory cytokine, is a model of osteoarthritis (OA). Changes in cartilage can be detected through a resazurin salt viability assay, a dimethylmethylene blue (DMMB) assay, and a prostaglandin E2 (PGE2) enzyme-linked immunosorbent assay (ELISA).

Resazurin salt is a redox indicator used for detecting cell viability. DMMB dye binds glycosaminoglycans (GAGs), a component of cartilage extracellular matrix. PGE2 production is increased in inflammation, and PGE2 ELISA determines the concentration of PGE2 through binding of PGE2 to its antibody. Our study looked to optimize the protocols for these three assays by utilizing a model of challenging cartilage with IL-1β. Each assay needed to be sensitive enough to detect known changes between treatment groups (no IL-1β, low IL-1β, high IL-1β). A secondary objective was to determine if resazurin salt exposure affected the results of the other assays since it was used before treatment with IL-1β.

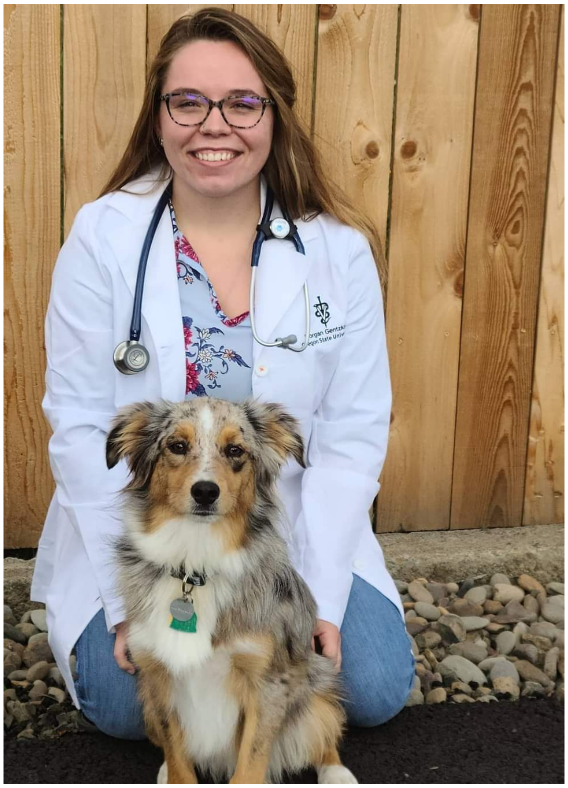
Cartilage explants were challenged with IL-1β or left unchallenged, and the three assays were performed. The resazurin salt assay was optimized by determining the correct filter set for fluorescence reading and the optimum ratio of resazurin salt solution to cartilage explant. For the DMMB assay, papain digested explants and media were used.

We found 1:5 and 1:10 dilutions of the former and 1:5 dilutions of the latter fell within the linear portion of the standard curve. For the PGE2 ELISA, the best results were seen with 10-fold and 20-fold dilutions of media, and it was determined that synovial fluid requires purification for the ELISA. Both assays seemed to detect differences between treatment groups. The DMMB assay was unaffected by resazurin salt exposure, but the PGE2 ELISA showed differences between samples exposed to resazurin salt and unexposed samples.

We will utilize this optimized protocol for a study determining the concentration-dependent effects of botulinum neurotoxin A on cartilage explants in vitro.

Morgan Gentzkow

Morgan Gentzkow is a DVM Candidate, Class of 2024, at the CCVM. She worked with mentor Dr. Brianna Beechler and Robert Spaan, of Fisheries, Wildlife, and Conservation Sciences, at the College of Agricultural Sciences. Morgan's summer project involved completing three objectives regarding biochemical parameters of California bighorn sheep. Her results will be combined with Dana Tsuchida's results on immunologic parameters of California bighorn sheep for a scientific journal publication.



Morgan Gentzkow with Nova

Can biochemical parameters be used to predict survival in wild ungulates?

Abstract: Many wildlife species are lacking reference ranges for biochemical parameters. Having an established reference range for each species can aid in predicting the health and survival of the animal.

The objectives of this study were to (1) establish reference ranges for biochemical parameters on wild California bighorn sheep subspecies (*Ovis canadensis*), (2) determine whether biochemical parameters can be used to predict the sheep's survival eight months post-capture, and (3) determine how the biochemical parameters of an adult ewe may predict whether she can raise her lamb to a weanling.

Reference ranges for California bighorn sheep (n=135) were calculated from blood samples taken during 2016 and 2017 capture events in southeast Oregon and into northwest Nevada. The sheep ranged from age 0-11, with a mix of males and females. The calculated reference ranges tended to vary from recorded ovine reference ranges from OSU-VDL, the reference ranges that Borjesson et al. (2000) calculated for free-ranging desert bighorn sheep and the reference ranges that Whittaker et al. (2000) calculated for California bighorn sheep.

Biochemical parameters indicative of mortality in adults were potassium, chloride, phosphorus, whole blood selenium, and globulins. Biochemical parameters indicative of mortality in lambs were BUN, βHBA, and copper. Reference ranges from this study should be able to be used on other California bighorn sheep.


Mariné Lugo with Milo

Mariné Lugo

Mariné Lugo is a third-year DVM Candidate at the CCVM. The Summer Research Program allowed Mariné to improve her research skills, as she spent the summer with mentor Dr. Brianna Beechler working on a project that involved African Buffalo and bovine viral diarrhea virus.

Identifying the principal components of African Buffalo (*Syncerus caffer*) immune responses and using them to characterize the reaction to bovine viral diarrhea virus

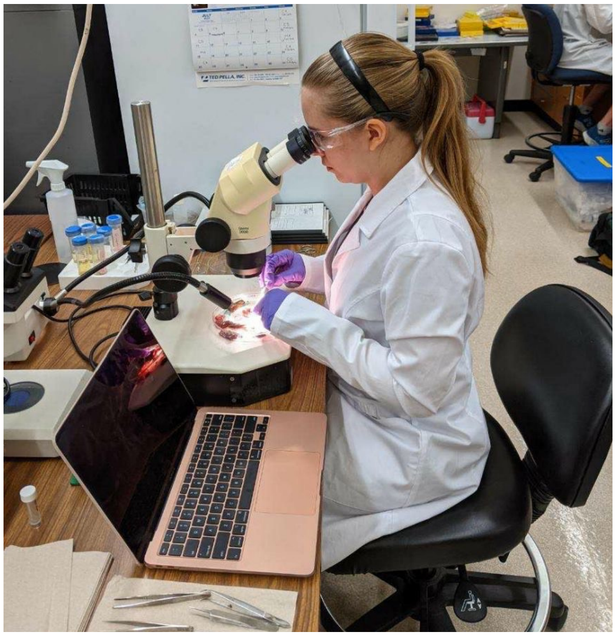
Abstract: The main goal of this research was to evaluate the main drivers of Buffalo immunity and identify correlations between factors that correspond to immune responses to Bovine Viral Diarrhea Virus (BVDV). For this, we used data gathered from previous experiments on African buffalo (*Syncerus caffer*) in the Kruger National Park in South Africa.

To select the factors used in the analysis, we first ran a correlation matrix to identify and eliminate redundant or highly correlated variables. Then we ran a PCA analysis on the remaining factors to identify the primary drivers of variability within the sample. The resulting principal components were interpreted based on the highest-ranking variables within each principal component.

The first five principal components were responsible for 44.68% of the variability, so we used those to run a generalized linear model to predict buffalo immune responses to BVDV. PC4 was the most significant ($p = 0.0004$) followed by PC1 and PC5 ($p = 0.0022$, $p = 0.027$ respectively).

For every increase in PC4, PC1 and PC5 there is a log odds increase of 1.58, 1.23, and 0.69 respectively of having BVDV. PC4 represents a decrease in lymphocyte quantity but an increase in activity, while PC1 is describing an inflammatory response. PC5 is driven by haptoglobin and therefore is describing an acute inflammatory response.

To further characterize the buffalo immune response to BVDV, each factor was also used in a generalized linear model predicting disease incidence. Lymphocytes, eosinophils and globulins all had a significant effect ($p = 0.0006$, $p = 0.001$, $p = 0.004$, respectively). For every increase in eosinophils and globulins, the log odds of having BVDV increase by 0.698 and 0.757 respectively, while they decreased by 0.471 with every increase in lymphocytes.



Jessica Sheet looks into a dissecting microscope while dissecting and extracting the parasite *Eustrongylides tubifex* from Mountain Whitefish viscera.

Jessica Sheets

Jessica Sheets is a DVM Candidate, Class of 2023, at the CCVM. She dedicated her summer working in the Kent Lab with Dr. Michael Kent as her mentor and other collaborators. Her research project involved collecting and examining Mountain Whitefish from the Deschutes River, Sunriver, Oregon. The project was part of a collaborative project between Oregon State University and the Bend Science Station.

Heavy infections of Eustrongylides sp. larvae in mountain whitefish from the Deschutes River, Sunriver, Oregon

Abstract: High prevalence of the larval nematodes, *Eustrongylides tubifex*, was recently reported in the Mountain Whitefish (*Prosopium williamsoni*) in the Deschutes River system, located in eastern Oregon. *Eustrongylides spp.* is not reported to cause high morbidity and mortality to fish but do cause pathologic issues to fish-eating birds, such as fibrinoperitonitis and granulomas. Continual collections and examinations were made on Mountain Whitefish from Spring River (a section of the Deschutes River system crossing through Sunriver, OR) and a river section 3 miles south of the Wickiup Reservoir on the Deschutes River. We examined a total of 214 fish collected in the summer of 2021.

Lester (1984) summarized 6 methods for assessing parasite associated mortality (PAM) in wild fishes: Method 1 (Necropsy), Method 2 (Determining the frequency of lethal infections), Method 3, (Observing a decrease in prevalence of long-lived parasites with host age), Method 4 (Observing a decrease in the variance/mean ratio for the parasites with host age), Method 5 (Comparison of the observed frequency of a combination of two independent events with the calculated probability of their occurrence), and Method 6 (Comparison of the observed frequency of the parasite with a projected frequency based on data from the lightly-infected fish). Within the limitations of our study, we are subjecting our data to Methods 1, 3, and 6.

A total of 214 fish were necropsied and worms were counted in the viscera from each fish. Samples were also taken for histology examination as part of "Method 1: Necropsy". Histology showed nematode cysts predominantly in the submucosal and muscularis layer of the

stomach, with no other significant abnormal histologic lesions found. Parasite abundance for both the Spring River and Wickup locations resembled the parasitology Law of Aggregation, showing negative binomial distribution of parasites. However, a much higher range/mean of parasites were observed with Spring River fish (range of 0-117, mean of 18.4) compared to Wickiup fish (range of 0-15, mean of 2.4). Subjecting the data to Method 6 is pending. No statistical relationships were observed between fish length and parasite count nor condition factor and parasite count, which suggests that although some fish are heavily infected, the parasite does not severely affect overall fitness.

We will be moving forward with aging fish using scales that we collected from 78 fish to determine if there is a change in parasite burden over time (Method 3). More research is needed to explain Spring River's unusually high *Eustrongylides tubifex* abundance. A high presence of leaky septic tanks within the area is a potential cause because first intermediate hosts of the nematode are oligochaete worms (e.g., *Tubifex tubifex*), and these worms thrive in waters that are well oxygenated but have high organic loads.

Jenna Beilby

Jenna with Tashi

Jenna Beilby is a second-year DVM Candidate at the CCVM. Jenna worked with Dr. Luiz Bermudez, who served as her mentor, and fellow DVM Candidate Shelby Matsuoka over the summer analyzing *Staphylococcus pseudintermedius* biofilms in simulated hospital conditions at the CCVM's Veterinary Teaching Hospital.

Examining *Staphylococcus pseudintermedius* biofilms in simulated hospital conditions

Abstract: *Staphylococcus pseudintermedius* is a common member of canine flora but can be an opportunistic pathogen, and the rise of methicillin-resistant strains is of particular concern, as it is not as well-studied as its relative *Staphylococcus aureus*.

The purpose of this study was to gain a greater understanding of the biofilms formed by *S. pseudintermedius*, to inform preventative protocols. This was approached via three methods. We measured the biofilm mass of three pathogenic *S. pseudintermedius* strains and one *S. aureus* strain cultured in hospital-mimicking conditions. The structure of the biofilms was observed with scanning electron microscopy. Lastly, OSU VTH disinfectant protocols were tested for effectiveness in killing established biofilms on a dry surface.

Varsha Karthikeyan


Varsha Karthikeyan

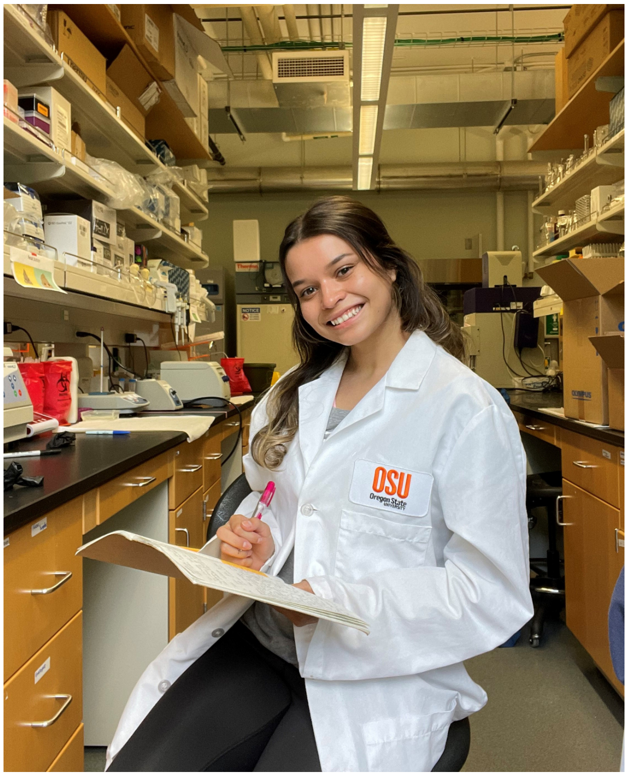
Varsha Karthikeyan is an undergraduate student in Biology at the College of Science. Varsha participated in Summer Undergraduate Research Program, working on a summer project with with her mentor, Dr. Patrick Chappell. Varsha's summer project focused on the role of exosomes in the neuroendocrine processing of estrogen positive feedback for ovulation.

Role of exosomes in the neuroendocrine processing of estrogen positive feedback for ovulation

Abstract: The hypothalamic-pituitary-gonadal (H-PG) axis controls female reproductive functions and the neuropeptide kisspeptin (Kiss-1) is positioned at the center of this axis. Currently, it is known that hypothalamic Kiss-1 acts at the GnRH neuron via the G Protein-coupled kiss-1 receptor (Kiss1R) to stimulate the release of GnRH. GnRH, released into the portal circulation, reaches the anterior pituitary and then stimulates the release of the gonadotropins, LH and FSH. This pathway is required for normal pubertal development and reproduction.

For this project, pre-isolated exosomes from kisspeptin neurons, exposed previously to various estrogen conditions, were used to treat cultured GnRH neurons (GT1-7 cells).

Real-time PCR was then used to evaluate gene expression changes in the Kisspeptin receptor gene. The premise tested in this project is whether it's possible for GnRH neurons treated with exosomes from kisspeptin to make more kisspeptin receptors. Future directions include identifying what's in the exosomes that could lead to this potential increase.


Lineth Trujillo Morales at the Dryden Hall 101 Lab

Lineth Trujillo Morales

Lineth Trujillo Morales is an undergraduate student in Biology at the College of Science. Lineth collaborated with her mentor, Dr. Brianna Beechler, over the summer to investigate the population connectivity and the plasma bacterial killing ability assay in subpopulations of desert bighorn sheep in the Mojave Desert.

Desert Bighorn Sheep (*Ovis canadensis nelsoni*) Population Connectivity and the plasma bacterial killing ability assay

Abstract: Desert Bighorn Sheep (DBH) within the Mojave Desert, in southeastern California, is a fragmented system of connected sub-populations. The previous tracking of DBH demonstrated that more isolated populations had increased incidence of *Mycoplasma ovipneumoniae*. Additionally, it was found that more isolated populations had poorer immune responses when compared to DBH populations that were not as isolated. This could be attributed to greater genetic diversity within these populations.

Participation in fieldwork within the Mojave Desert allowed me to gain a further understanding of DBH and population connectivity. The purpose of this project is to investigate the immunological competence of these populations, by analyzing plasma bacterial killing capacity (pBKA) (an indicator of the immune response) from sheep captured in 10 populations in Fall of 2020. How pBKA varies by population will be evaluated, and if it varies with genetic diversity and connectivity as expected.

Cindy Zurita Cruz

Cindy Zurita Cruz is a recent graduate of Bioresource Research at the College of Agricultural Sciences. Cindy spent the summer completing a research project with mentor Dr. Jean Hall, as well as Dr. Brian Dolan, Department of Biomedical Sciences, and Dr. Gerd Bobe, Department of Animal and Rangeland Sciences.

Effects of Selenium Supplementation During Different Trimesters of Pregnancy on Natural and *Vibrio coralliilyticus* Specific IgM Antibody Concentrations in Beef Cows at Parturition

Abstract: The immune response to microbial infections is compromised in beef cattle at parturition. Innate and adaptive immunoglobulin M (IgM) serve as initial antibodies during microbial infection before the generation of adaptive immunoglobulin G (IgG). Selenium (Se) is an essential micronutrient required by all mammals, which can improve immune responses in beef cattle.

To determine the best time during pregnancy to supplement beef cows with organic Se to optimize immune function at parturition. We hypothesized that feeding Se yeast to pregnant beef cows in each of the three trimesters of pregnancy would alter total and *Vibrio coralliilyticus* specific IgM concentrations in cows at parturition.

A total of 79 black Angus and Angus cross beef cows were used in the study. All of the cattle were housed and obtained routine care including deworming and vaccinations at Oregon State University Soap Creek Ranch, Corvallis, OR.

Twenty-three cows were in the control group; they did not receive any Se-yeast boluses. Twenty-one cows were in Group 1. These cows received three 52.5g Se-Yeast boluses once weekly in the first 3 months of their pregnancy. Fifteen cows were in Group 2. These cows received three 52.5g Se-Yeast boluses once weekly in the second trimester of pregnancy from months three to six. Twenty cows were in Group 3. These cows received three 52.5g Se-Yeast boluses once weekly in the third trimester of pregnancy, from months six through nine. Thus, all cows except control cows received 105 mg Se/week from the three boluses administered during their specific treatment trimester, equating to five times the upper limit for US FDA Se administration regulations. Blood was collected at parturition from all cows.

A commercial ELISA kit was used to measure total IgM antibody concentrations in the serum of beef cows at parturition (Bethyl Bovine IgM Kit). To test for *Vibrio coralliilyticus* specific IgM antibody concentrations and whether differences in concentration occur with the timing of Se treatments during gestation, an ELISA protocol was

also developed for detecting *Vibrio coralliilyticus* specific IgM antibodies.

Total and *Vibrio coralliilyticus* specific IgM concentrations were highly correlated ($r = 0.78$; $P < 0.0001$). Compared with values of Control cows, cows treated with Se in the first, second, or third trimester of pregnancy, respectively, had similar serum total IgM concentrations ($P = 0.43$; $P = 0.86$, and $P = 0.19$, respectively) and similar *Vibrio coralliilyticus* specific IgM concentrations ($P = 0.47$; $P = 0.55$, and $P = 0.67$, respectively).

These findings show that weekly organic Se-yeast supplementation using a 105 mg Se/wk dosage during different trimesters of pregnancy does not affect IgM concentrations in beef cows after parturition. We do not provide evidence for Se-yeast bolus Se supplementation of beef cows during pregnancy impacting IgM production at calving.

Tasman Flora

Tasman Flora is a second-year DVM Candidate at the CCVM. Tasman's interest to investigate the efficacy of botanical treatments in veterinary medicine prompted the summer research project she worked on with Dr. Michelle Kutzler, a professor in the Department of Animal and Rangeland Sciences at the College of Agricultural Sciences.

A review on botanical anti-inflammatories for the treatment of osteoarthritis

Abstract: Botanical treatments for disease have been used for centuries, and there has been increased interest in their use in veterinary medicine. However, little is known about how and if these compounds work or if they are safe to recommend.

The purpose of this study was to evaluate botanical anti-inflammatories for pain management in cases of osteoarthritis. It was hypothesized that the efficacy of botanical treatments for the management of osteoarthritis would not differ from the efficacy of using conventional, synthetic treatments (e.g., NSAIDs).

The goals of the study were to review published in vivo research and report on the mechanism of action, efficacy, side effects, and pharmacokinetics of each botanical. Two hundred and fifty-nine botanical compounds were identified with in vivo anti-arthritic, anti-inflammatory, anti-oxidative, or anti-nociceptive properties that improved the symptoms of osteoarthritis.

Nearly all of these (257/259) used laboratory animals (rats, mice, rabbits). About a fifth of these studies (46/259) used human patients. There were only four relevant studies in dogs. To serve as a guide for practitioners, the botanicals were grouped according to their mechanism of action and properties displayed. The current project has identified where gaps existed relating to the use of botanicals for osteoarthritis in veterinary medicine.

Reagan Jagosh on the left and Jessica Sheets on the right. They are standing next to the Spring River, located in Sunriver, Oregon. The raft provided by the Oregon Department of Fish and Wildlife allowed Reagan and Jessica to collect fish for their summer research projects.

Reagan Jagosh

Reagan Jagosh is a DVM Candidate, Class of 2023 at the CCVM. Over the summer, Reagan investigated if Giemsa imprints are as sensitive as histology and could be used as an alternative method for diagnosis of *Ceratonova shasta*. She worked with mentor Dr. Michael Kent, Dr. Elena Gorman, Stephanie Nervino, Jessica Sheets, and the Oregon Department of Fish and Wildlife.

Diagnosis of *Ceratonova shasta*, a common intestinal parasite of adult salmon: sensitivity and specificity of giemsa imprints compared to histology

Abstract: Chinook Salmon are native to Oregon rivers across the state, providing a food source to people and animals alike, proving to be a vital part of the ecosystem. Pre-Spawn Mortality (PSM) focuses on the fish that die between the time they return to the rivers from the ocean in the late spring/early summer, up to the point when they spawn in the fall months, and subsequently die naturally. Those fish that die before reaching spawning grounds are unable to contribute to future healthy fish populations, leading to an overall decline in numbers.

Dr. Kent and colleagues have been working on the problem since 2009, with roughly 500 salmon collected thus far. One of the major causes of PSM is excessive pathogen abundance, this project focuses on the parasite *Ceratonova Shasta* and aims to determine of sensitivity and specificity of Giemsa stained imprints compared to histology samples.

Current diagnostic recommendations outlined in the FHS Blue Book suggest a combination of wet mounts and PCR as the best way to detect *C. shasta*. In contrast to this, Dr. Kent and colleagues showed that histology was much more sensitive than wet mounts for detection of spores and that juvenile fish often show infections with only presporgonic forms (which wet mounts are unable to detect). Should imprints prove to be of similar sensitivity to histology, it could be a faster, cheaper, more readily available method for diagnostic purposes of *Ceratonova Shasta* in adult Chinook Salmon.

Vanessa Gramlich


Vanessa Gramlich

Vanessa Gramlich is a third-year DVM Candidate at the CCVM. Vanessa worked with Dr. Lia Danelishvili, who served as her mentor for her summer research project. Over the summer, Vanessa got to learn and better understand the pathophysiology and virulence of *Mycobacterium avium* subspecies *paratuberculosis.*

Macrophage response to *Mycobacterium avium* subspecies *paratuberculosis* infection

Abstract: Johne's disease is a common infectious disease in dairy cows and is caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP). Infected calves become chronic carriers and, years later, are capable of shedding 50 billion bacteria per day in their manure and milk when clinical signs are already obvious. MAP can infect and survive in macrophages, but these phagocytic cells effectively kill the nonpathogenic mycobacteria, for example, Mycobacterium smegmatis.

Here, we wanted to understand how innate immune cells respond to MAP infection by analyzing macrophage proteomics during a) pathogenic MAP and b) nonpathogenic *M. smegmatis* infection and identify innate immune signaling pathways that promote MAP survival within phagocytic cells. Through literature review, we identified the RIPK3/MLKL pathway, key mediators of necroptosis, and the PI3K/mTOR/CTH pathway, inductors of the reverse transsulfuration pathway, as potential pathways used by MAP as a mechanism for immune escape.

To test this, macrophages were pretreated with inhibitors for mTOR, CTH, and MLKL and subsequently infected with MAP. The bacterial colonies from one replicate were counted and analyzed. Data from qRT-PCR demonstrated these genes as highly expressed. This project is still ongoing; however, preliminary findings suggest new pathways that can be manipulated to reduce MAP pathogenicity in phagocytic cells.

Nicole Sipple


Nicole Sipple with Bailey

Nicole Sipple, a second-year DVM Candidate at the CCVM, worked in with her mentor, Dr. Jennifer Johns, Dr. Shannon Phelps, and Dr. Caroline Allende over the summer. Nicole's summer research project concentrated on the immunomodulatory qualities of mesenchymal stem cell-derived extracellular vesicles on canine peripheral blood mononuclear cells, as it may be a possible alternative to whole stem cells therapy.

Immunomodulatory activity of mesenchymal stem cell derived extracellular vesicles on canine peripheral blood mononuclear cells

Abstract: Mesenchymal stem cells (MSC) are used for immunomodulatory therapy, but have drawbacks including potential embolism and variability of product. MSC-derived extracellular vesicles (MSC-EV) are a potential alternative therapy with easier storage and administration, decreased risk (vs. injecting MSC), and a more uniform product. MSC-EV contains numerous molecules involved in cell signaling pathways and may have immunomodulatory activities similar to the parent MSC. The purpose of this study is to evaluate the immunomodulatory effects of MSC-EV on canine peripheral blood mononuclear cells (PBMCs). We have found that MSC-EV causes increases in viable canine PBMCs.

We hypothesize that MSC-EV increases cell proliferation of stimulated canine PBMCs and this change can be measured via an ATP assay. Further characterizing MSC-EV induced changes via flow cytometry, qRT-PCR, and multiplex analysis of secreted products are important next steps to understanding immunomodulatory effects of MSC-EV on canine PBMCs.

Shelby Matsuoka with Shuri

Shelby Matsuoka

Shelby Matsuoka is a DVM Candidate, Class of 2024 at the CCVM. Her research project over the summer involved the examination of infections caused by *Staphylococcus pseud-intermedius*, a commensal bacterium isolated from skin and mucous membranes of companion animals, at the CCVM's Veterinary Teaching Hospital. Shelby worked with Dr. Luiz Bermudez, her mentor for the project, and fellow DVM Candidate Jenna Beilby.

Staphylococcus pseudintermedius as a source of hospital infections

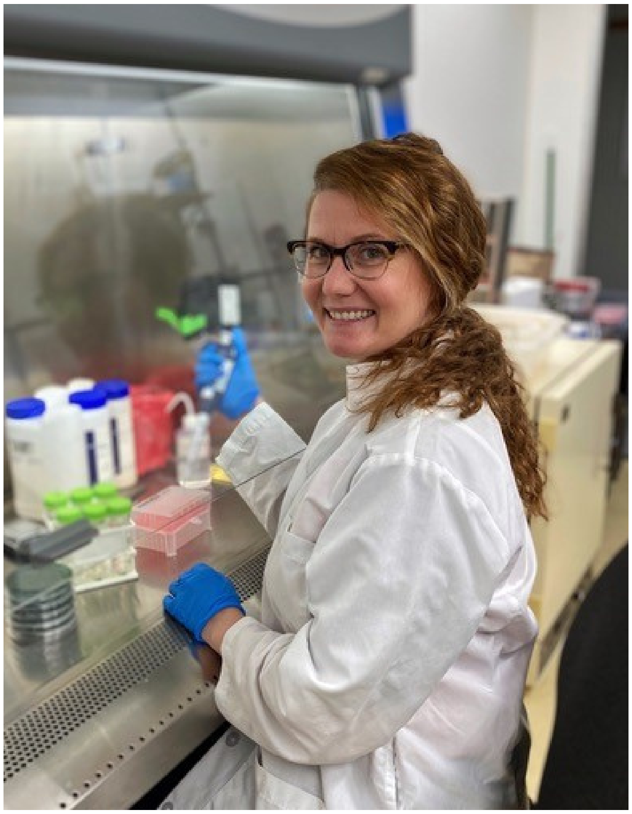
Abstract: A retrospective analysis of the Diagnostic laboratory submissions from 2016 to 2020 was performed to assess the patterns of resistance/susceptibility of *S. pseudintermedius* and determine which location in the hospital might potentially be acting as environmental source(s) for the bacteria.

Data were obtained regarding the site of infection, locations visited in the hospital, antibiotic treatment, and outcome. In addition, samples were taken of the hospital environment by swabbing areas in the intensive care unit and anesthesia preparation room in the VTH at OSU.

The colonies were isolated and species identified after being amplified via PCR. Virulent strains were then tested to look for differences in resistance/susceptibility to antibiotics, and how biofilm formation impacts their strains of *S. pseudintermedius* obtained from the hospital were used to infect human and mouse macrophages. We determined how well the bacteria survive inside the cells and compared the results to *S. aureus*.

Tiffany Spendiff

Tiffany Spendiff is a non-traditional undergraduate student in Microbiology at the College of Science. After a 12-year gap in her education, Tiffany rediscovered how much she enjoyed marine biology. Her interest in shellfish research has led her to work in the Schubiger Lab during the summer. Dr. Carla Schubiger served as Tiffany's mentor for the summer research project. She also worked with Ph.D. student Spencer Lunda and MS student Jennifer Hesser, both of whom are part of the Schubiger Lab.



Tiffany Spendiff preparing cultures of bacteria (*Vibrio parataemolyticus*) used to research food safety of raw oysters.

The purge: application of probiotics in depuration for reducing *Vibrio parahaemolyticus* in pacific oysters (*Crassostrea gigas*)

Abstract: A probiotic “cocktail” of four indigenous marine strains was evaluated for its effectiveness in reducing *Vibrio parahaemolyticus* concentrations in adult oysters via depuration. Depuration is a post-harvest procedure to let adult oysters purge sand and microbial contaminants in sterile seawater. The human pathogen *V. parahaemolyticus* is prevalent in the marine and estuarine environments and causes foodborne illness through the consumption of raw or undercooked seafood.

For the experimental trials, Pacific oysters (C. gigas) were inoculated with 6.76 x 104 CFU/ml of a nonpathogenic *Vibrio parahaemolyticus* “cocktail” comprised of equal additions of the strains S13-052, S13-059, S13-060, S13-075, and S13-078. After 24 h, the oysters were individually immersed in the probiotic cocktail at a concentration of 1.02 x 107 CFU/ml for another 24 h in triplicates, then shucked, diluted 2:1 with phosphate-buffered saline, and serially plated on LBS agar plates for enumeration. After 24 hours, oysters treated with probiotics did not have a significant reduction in *V. parahaemolyticus* when compared with non-probiotic treated controls.

Further directions include the evaluation of different probiotic candidates or changes to the depuration parameters (temperature, salinity, flow rate, etc.).

Jieun Hong

Jieun Hong

Jiuen Hong is a DVM Candidate, Class of 2024 at the CCVM. Over the summer, Jieun worked with her mentor, Dr. Kathy Magnusson, and Emily Sackinger, a graduate student in Comparative Health Sciences. Jieun worked in the Magnusson Lab to examine the effect of cannabidiol on NMDA receptors and cognitive function in 5XFAD mice.

Protein Assay of 5XFAD mice treated with Ibuprofen and CBD

Abstract: Alzheimer's disease (AD) has impacted about 36 million lives worldwide by reducing their quality of life and will continue to do so at a rapidly growing rate. It has been observed that a significant number of amyloid-beta plaques and neuroinflammation are closely related to the cognitive decline in AD.

Certain drugs such as ibuprofen (IBU) and cannabidiol (CBD) have been tested to alleviate AD symptoms. IBU is a non-steroidal anti-inflammatory drug (NSAID) that is known to protect neurons against glutamate toxicity, decrease the production of proinflammatory cytokines, and suppress neuritic plaque pathology and inflammation in the AD brain (Dokmeci D. Ibuprofen and Alzheimer's disease. Folia Med (Plovdiv). 2004;46(2):5-10.).

Meanwhile, CBD has recently been shown to protect against the neurotoxic effects of beta-amyloid peptide (Aβ) in cell culture and cognitive-behavioral models of neuro-degeneration (Hughes et al., Cannabidiol Reverses Deficits in Hippocampal LTP in a Model of Alzheimer's Disease. Neurochemical Research. 2019;44:703-713.).

In these IBU and CBD studies, we aim to reduce amyloid plaques and the degree of neuroinflammation as well as to reduce hyperactivity of N-methyl-D-aspartate receptor (NMDAR) responses that we have characterized at an early age in the 5xFAD mouse model of amyloid overexpression.

This presentation will include Western blot analysis of NMDA receptor protein expression in brains of 5xFAD mice fed 375 ppm ibuprofen (the human equivalent of 2.2 pills per day) in the chow or regular chow for 2 months and Morris water maze data analysis of cognitive function in 5xFAD mice fed CBD in chow or regular chow for 2 months. The results of these studies may help with the development of early treatments to prevent the onset of Alzheimer's disease.

Kyndall Zieglowsky performing an Ophthalmology exam on a great horned owl.

Kyndall Zieglowsky

Kyndall Zieglowsky is a DVM Candidate, Class of 2023 at the CCVM. Over the summer, Kyndall worked on a study regarding rehabilitation success patterns in common birds of prey species. She collaborated with fellow Summer Programs students, Salene Freeman and Kayla Christy, as well as their mentor Dr. Brianna Beechler. Kyndall spent time at the Liberty Wildlife Center in Phoenix, Arizona collecting data for the study.

Kayla Christy

Kayla Christy, a third-year DVM Candidate at the CCVM, worked at the Chintimini Wildlife Center in Corvallis, Oregon during the summer, collecting information on the rehabilitation success of birds at the center. It was Kayla's first experience working at a raptor center. She was able to collect data with the help of Dr. Claire Peterson, Director Erika, and Katie, the technician at the center.

Dr. Claire Peterson on the left and Kayla Christy on the right.

Salene Freeman

Salene Freeman is a DVM Candidate, Class of 2023 at the CCVM. Salene worked with the Teton Raptor Center in Wilson, Wyoming during the summer to track their rehabilitation success patterns at the center. One interesting experience Salene had while working at the Teton Raptor Center was seeing a radiograph of a bird with fractures on the left ulna and right metacarpals.

Salene Freeman with a juvenile American kestrel that was successfully released on 7/20/21.

Rehabilitation success patterns in common birds of prey species

Abstract: Our study aimed to track rehabilitation success in common species between Liberty Wildlife Center in Phoenix, Arizona, Chintimini Wildlife Center in Corvallis, Oregon, and Teton Raptor Center in Wilson, Wyoming. Common species among the three rehabilitation facilities included *Buteo jamaicensis* (Red-Tailed Hawks), *Falco spar-verius* (American Kestrels), and Strigiformes (all owl species). This study allows rehabilitators to determine which injuries have a good, guarded, or poor prognosis, thus improving treatment and release success for birds of prey.

Primary causes of morbidity were classified into 10 categories: Infectious disease (viral, bacterial, parasitic), entanglement (twine, netting), head trauma (window strike, car strike, building strike), eye trauma, body trauma, emaciation (keel BCS 1/5), electrocution, displaced juvenile (nestling, fledgling, hatch-year, and human abduction), orthopedic issues (fracture, metabolic bone diseases, luxation, nerve damage), and unknown/undetermined.

Final dispositions were labeled as Successful Rehabilitation: Released and Unsuccessful Rehabilitation: Euthanized in 24 hours, Euthanized + 24 hours, DOA (Dead on Arrival), Died in 24 hours, Died + 24 hours, and Unreleasable/ Placement into an education program. A total of 85 patients from all three rehabilitation facilities were analyzed both prospectively and retrospectively. Standardized intake forms, weekly check-in forms, and food charts were shared among the three facilities.

When comparing rehabilitation success between classes of raptors, 38.5% of all admitted American Kestrels, 13.8% of Red-Tailed Hawks, and 13.3% of owls resulted in successful rehabilitation and release back into the wild. Additionally, 15.4% of all admitted American Kestrels, 27.6% of Red-Tailed Hawks, and 16.7% of owls are currently residing in flight cages intended for release.

Among the 85 admitted species between the three facilities, 0% of the infectious disease cases, entanglement, head trauma, eye trauma, and electrocution resulted in successful rehabilitation. Injuries that resulted in successful rehabilitation were orthopedic issues (7.4%), emaciation (10%), unknown/undetermined injuries (33.3%), body trauma (62.5%), and fledglings (87.5%).

This is the first small-scale study tracking rehabilitation success among multiple raptor rehabilitation facilities while tracking which injuries resulted in the most morbidity. The most common causes of morbidity were orthopedic issues (31.8%), emaciation (11.8%), and eye trauma (11.8%). The greatest rates of survivability were among those presenting as fledglings (87.5%) and body trauma (62.5%). The greatest rates of mortality were electrocution cases (100%) and head trauma (100%). The cases with a current disposition of "In Progress" or "Flight Cage - Intended for Release" are likely to result in successful rehabilitation, leading to data that will need to be updated in this study at a later date.

Camryn Flint

Camryn Flint is a second-year DVM Candidate at the CCVM. Camryn's interest in learning about the different fields in veterinary medicine prompted her to pursue a summer project with Dr. Benjamin Alcantar at the Wildlife Safari. She learned from Dr. Alcantar and the staff at Wildlife Safari about both the clinical and research sides of zoological medicine, from collecting diagnostic samples in the field to understanding the importance of nutritional parameters in wildlife.

Camryn Flint on the left drawing blood from the jugular vein of a fallow deer (*Dama dama*).

Determining mineral levels in ungulates at Wildlife Safari

Abstract: Determining mineral bioavailability in the diet and mineral storage in the body is an important part of animal health, especially in ungulates. Mineral concentrations in the serum versus in the liver can have many variations in domestic cattle and non-domestic bovids, and the liver is considered the best overall tissue to analyze clinically important mineral storage.

A previous study at the San Diego Zoo has found mineral deficiencies in post-mortem examinations of ungulates who showed no mineral deficiencies during ante-mortem serum testing, and reference ranges for mineral concentrations in ungulates are far and few between.

The purpose of our study at Wildlife Safari in Winston, Oregon this summer was to determine the mineral levels in exotic hoofstock at Wildlife Safari by comparing levels of multiple different minerals in the serum versus the liver to help aid zoological institutions in creating optimum programs to maintain ungulate health and accurately diagnose mineral deficiencies/toxicities.

Individuals of several species of ungulates at Wildlife Safari were chemically immobilized using the PneuDart remote capture system. A physical exam, complete blood count, blood chemistry, and blood gas analysis were performed and a serum sample and liver biopsy were analyzed for mineral concentrations at Michigan State University diagnostic laboratory.

So far, we have found that there were certainly expected discrepancies between species, and we are in the process of finishing our analysis and comparison of liver biopsies to serum. These results are important, as we can contribute to creating more data for reference values for mineral levels in non-domestic ungulate species.

Our results also showed the clinical importance of considering accuracy of methods for investigating mineral levels in non-domestic ungulates, especially because many mineral deficiencies are actively happening before an animal shows any clinical signs. Possible future directions for this project include sampling food and soil in the environment at Wildlife Safari to compare mineral intake with levels shown on diagnostic evaluation.

Eberle Yarborough

Eberle Yarborough is a DVM Candidate, Class of 2023 at the CCVM. Eberle spent the summer working with her mentor, Dr. Brianna Beechler, investigating links between desert bighorn sheep population connectivity and infectious diseases. She hopes to use the samples she collected to also look at stress physiology in the sheep.

Eberle Yarborough scanned the mountains with a spotting scope. Her field partner used telemetry to locate the sheep needed to collect samples. They found a sheep and hiked into the mountains seen in the photo.

Eco-evolutionary dynamics of infectious diseases in host population networks

Abstract: Desert bighorn sheep (DBH; *Ovis canadensis nelsoni*) are iconic desert species that live in the deserts of Southeast California. DBH live in independent populations created by fragmented terrain, creating a metapopulation where local population sizes range from tens to hundreds of individuals.

Movements between populations have been documented, driven by forage quality, predator avoidance, and access to surface water during the dry months. These DBH populations are vulnerable to diseases, many of which have been blamed on domestic sheep and goat populations nearby. DBH is an example of animal in an extreme environment facing a variety of stressors, such as disease, predation, human encroachment, and increasing ambient temperatures.

For this study, we are interested in determining how population connectivity affects disease transmission and immunogenetics. Additionally, I am interested in developing an understanding of the DBH stress response, which could be indicative of how other wildlife species respond to such stressors, and better inform wildlife management as to how to better preserve this species. This will form the basis of my Ph.D.

THE EFFECTS OF FEEDING SELENIUM-BIOFORTIFIED ALFALFA HAY TO WEANED BEEF CALVES

A study conducted by Dr. Jean Hall and colleagues, published December 1, 2020, in *Plos One*, investigated the effects of feeding selenium-biofortified alfalfa hay on fecal parasites and nasal microbiome to understand how supranutritional selenium supplementation supports calf health.

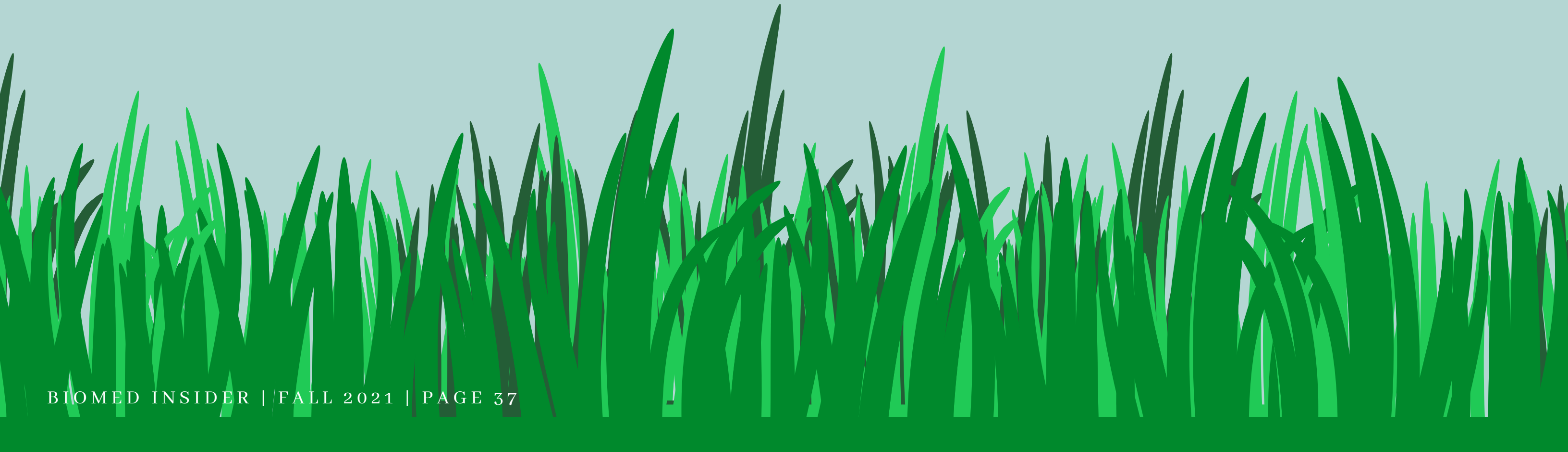
Weaned Angus-cross beef calves were split into two groups and fed an alfalfa hay-based diet in a nine-week preconditioning program. Calves consumed either alfalfa hay from a field fertilized with sodium selenate or alfalfa hay without selenium fertilization.

The researchers found that feeding selenium-biofortified alfalfa hay to weaned beef calves increased whole-blood selenium concentrations throughout the preconditioning period. The whole-blood selenium concentrations also remained higher in these calves during the initial feedlot period compared with calves that were not fed selenium-biofortified alfalfa hay.

Body weight in weaned beef calves increased when consuming selenium-biofortified alfalfa hay and showed a trend for increased hot carcass weights. Additionally, these calves had improved yield grades, higher slaughter weights, and an increased price per head.

Fecal egg counts were very low throughout the preconditioning program in these calves, thus the researchers were unable to test the effect of selenium supplementation on gastrointestinal parasite infestations.

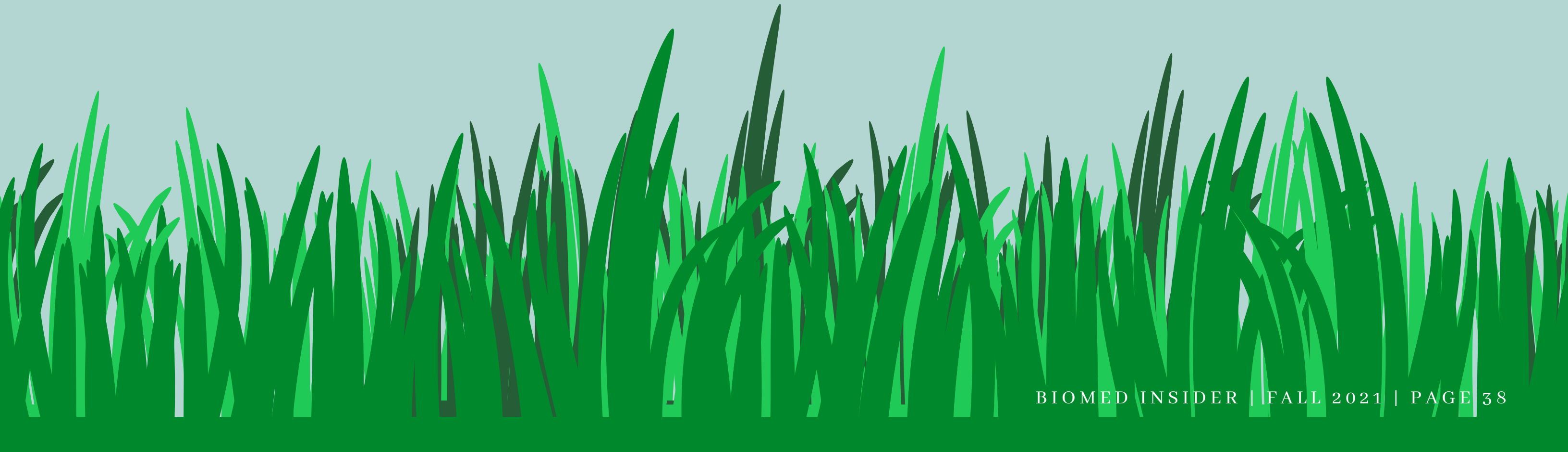
Nasal microbial diversity, particularly of the less abundant bacteria taxa, increased with selenium treatment during the nine weeks. Dr. Hall and colleagues were specifically interested in the phyla Tenericutes, as it was the only phylum with relative abundance >1% altered by selenium treatment. The proportion of the microbiota in the phylum Tenericutes, which contains genera of the *Mycoplasmataceae* family, increased significantly after calves entered the feedlot, with some calves having over 50% Tenericutes. Calves that did not consume selenium-biofortified alfalfa hay eventually caught up with the selenium treatment calves in genomic diversity in the feedlot. The researchers propose that the presence of increased nasal microbial diversity after consuming selenium-fortified alfalfa during the nine weeks, and three weeks after entering the feedlot, may provide a bacterial community element for regulating bacterial overgrowth and respiratory disease caused by *Mycoplasmataceae*.



The novel contribution of the study is that selenium biofortification promoted nasal microbial diversity by establishing five new minor phyla and fifty-six new genera and their unique metabolism pathways. It has been shown that bacterial communities in the nasopharynx of healthy cattle during the feeding period were more diverse than those that developed bovine respiratory disease, suggesting that management practices that increase microbial diversity may help prevent respiratory diseases in the feedlot. Microbial biodiversity corresponds to the efficiency of nutrient utilization by a bacterial community; a greater microbial diversity means greater diversity in microbial metabolism pathways, allowing for more efficient nutrient utilization. This, in turn, decreases the chances of bacterial respiratory pathogens adhering to and colonizing in the nasopharynx. This becomes very important when stressed calves enter the feedlot, and are exposed to various new pathogens.

Overall, feeding selenium-biofortified alfalfa hay to weaned beef calves during the preconditioning period was effective at building selenium reserves, optimizing growth before entering the feedlot, and improving feedlot performance. This is the second time the researchers have shown, in two independent studies, that selenium treatment of calves in a preconditioning program was able to upregulate the diversity of the nasopharyngeal bacterial community before entering the feedlot. Thus, selenium-biofortification may provide health benefits for the prevention of bovine respiratory disease in feedlot calves.

Weaned beef calves eating selenium-biofortified alfalfa hay at the Oregon State University beef ranch.



No healthy lungs, please!

A compromised lung environment may be an ideal condition for the *Mycobacterium abscessus subsp. abscessus* to thrive.

Mycobacterium abscessus subsp. abscessus infection is not observed in healthy lungs and is much more common in patients with chronic pulmonary conditions such as cystic fibrosis. Bailey Keefe, a faculty research assistant of the Bermudez Lab, and Dr. Luiz Bermudez, Department Head of Biomedical Sciences, questioned why that may be the case. They explored the relationship between *Mycobacterium abscessus subsp. abscessus* and particular lung conditions.

Biofilm formation is a key feature of *M. abscessus* infection in the lungs of patients with cystic fibrosis. The team compared biofilm formation with and without synthetic cystic fibrosis medium (SCFM), a medium made up of bacterial culture that mimics the mucus and lung environment of cystic fibrosis, and analyzed the bacterial growth with the addition of human DNA.

Their observations revealed that *M. abscessus* can form biofilms in SCFM. *M. abscessus* showed an increase in extracellular matrix staining and increased biofilm mass in the presence of SCFM. From the SCFM solutions generated for *M. abscessus* biofilm formation, they noted that magnesium acts as an indicator for biofilm formation.

The presence of a chelating agent that removes magnesium ions suppressed biofilm formation. Looking into the protein differences between varying conditions for biofilm formation showed unique proteins containing enzymes rely on magnesium as a cofactor, which suggests that magnesium is vital in SCFM biofilm formation. In the presence of SCFM and DNA, *M. abscessus* was able to replicate, indicating the ability to adapt and use host DNA as a nutrient source.

The lung conditions of patients with cystic fibrosis seem to stimulate *M. abscessus* infection. However, the absence of magnesium from the mucus and lung environment of these patients may change the ability of *M. abscessus* to develop disease.

Multi-omics analysis of influenza A virus reveals a mechanism for evading macroautophagy

Influenza A virus (IAV) is contingent on host cell machinery and viral evasion strategies for replication in the host cell.

There is significant data on cellular factors vital for IAV replication, but there lacks data on a global scale of host factors involved in IAV restriction, particularly on immune cells that are accountable for supporting immune responses against IAV. To find more information, Dr. Hong Moulton and collaborators generated a global multi-omics analysis of the host restrictome for IAV by integrating loss-of-function screening with proteomics and transcriptomics data.

Their multi-omics analysis identified densely interconnected clusters of interferon-inducible factors or constitutive mechanisms. Further examination on the interferon-inducible factors revealed enriched immune response pathways, including type 1 interferon signaling and nine validated interferon-stimulated genes not previously associated with IAV restriction. Constitutive antiviral factors revealed that cells also rely on extensive cell-intrinsic mechanisms to control IAV infection.

Of particular interest, the researchers noticed that the macroautophagy regulator TBC1 domain family member 5 (TBC1D5) was found to be a restriction factor of IAV infection. They evaluated TBC1D5 and uncovered in vitro and in vivo that TBC1D5-Rab7 binding, which permits fusion of autophagosomes and lysosomes, could control IAV replication.

Rab7 is a small GTPase that controls vesicle transport to late endosomes and autophagosomes with lysosomes.

Their data also showed an interaction between TBC1D5 and IAV M2 protein. Further analysis provided data that TBC1D5 promotes lysosomal targeting on IAV M2 protein. Interestingly, the researchers observed that IAV M2 protein evades TBC1D5-Rab7 binding by using its cytoplasmic tail and physical interaction with TBC1D5. As a result, it reduces the activation of Rab7 and stops lysosomal fusion, allowing IAV M2 protein to transport to the cell membrane to support viral budding and the growth of IAV.

Other bacterial pathogens such as *Legionella pneumophila* and *Salmonella enterica* have been previously shown to target Rab7 activation to support survival. The strategy of evading lysosomal degradation from Rab7 activation by bacteria and viruses makes this mechanism a potential therapeutic target for establishing broad-spectrum antivirals that can restore lysosomal degradation of viral cargo.

LINK BETWEEN PERIODONTAL DISEASE AND KIDNEY FUNCTIONS

A prospective study conducted by Dr. Jean Hall and colleagues offers evidence for a link between impaired kidney function, renal tissue damage, and periodontal disease.

The researchers analyzed asymptomatic cats and dogs diagnosed with periodontal disease and were recommended by their veterinarian to have a dental cleaning. Urine and serum samples were collected one week before their dental cleaning procedure, six hours after the procedure, and again one week after.

Serum samples were analyzed for biomarkers of kidney function including serum creatinine, symmetric dimethylarginine (SDMA), and blood urea nitrogen (BUN) concentrations. Urine was examined for specific gravity (USG) and protein: creatinine (UPC). Biomarkers for renal tissue damage was also assessed including serum β-aminoisobutyric acid (BAIB) concentrations and urine for cystatin B and kidney-specific clusterin concentrations.

The samples collected one week before the dental cleaning showed that increased age and the severity of periodontal disease were associated with abnormal kidney function biomarker values. For example, older animals had increased SDMA and creatinine concentrations and lower USG values. Pets with more severe dental disease had increased UPC ratios and increased urine cystatin B and clusterin concentrations.

Samples collected directly after the dental cleaning procedures revealed an increased number of cats with elevated SDMA concentrations, especially in cats with longer duration of dental procedures. The longer duration was linked to increased urine cystatin B and clusterin concentrations indicating renal tissue damage. Higher SDMA concentrations persisted in cats one week after the dental cleaning procedures, and were linked to elevated UPC ratios one week before the cleaning procedures. Kidney function biomarker values improved predominantly in younger animals. Older cats and dogs tended to have no change or worse kidney function biomarker values one week after. It is possible that more benefits of dental cleaning would have been noted with a longer follow-up period.

Results of this study provide evidence for a link between periodontal disease, biomarkers of renal tissue damage, and markers of compromised kidney function. Early stages of kidney disease are not uncommon in asymptomatic dogs and cats undergoing dental cleaning, especially when they belong to a high-risk chronic kidney disease group (older animals, male animals, and animals with more severe dental disease).

Dental cleaning procedures have the potential to improve kidney function in animals during the early stages of kidney disease if there are no other complications. However, the disease will progress if the cause of kidney inflammation is not removed. Longer-duration dental procedures in cats, specifically older animals, may carry inherent risks of kidney injury and impaired renal function. Future studies are warranted to confirm the results of their small study.

WHAT DO THE IMAGES SHOW?

Drs. Stacie Summers, Stacy Cooley, and Geghani Galustanian presented an abstract at the 2021 American College of Veterinary Internal Medicine Forum on computed tomographic (CT) features of nasal cryptococcosis in cats and dogs.

The researchers retrospectively analyzed medical records and CT images of cats and dogs diagnosed with cryptococcal mycotic rhinitis between 2010 and 2020. The most common features found in the subset of cats were the frontal sinus soft tissue attenuation, middle ear soft tissue attenuation, and a presence of a discrete nasopharyngeal mass. The most common features found in the subset of dogs included frontal sinus soft tissue attenuation and nasal mass. It was also common in dogs to find features of lysis of the cribriform plate with meningeal enhancement, lysis of the orbit, maxilla, or hard plate, and lysis of the nasal turbinates.

In general, the common feature in cats and dogs with nasal cryptococcosis is nasal mass. Nasal cryptococcosis is also more detrimental in dogs than in cats. It is encouraged to get a biopsy of nasal masses in cats and dogs to rule out cryptococcosis.

REFERENCES

03 Delgadillo E, Glidden C, Pollak M, Rysenga H, Jolles A and Beechler B (2021) The Benefit of Hedgerow Access on the Health and Growth Rate of Pasture Raised Broiler Chickens. Front. Anim. Sci. 2:649924. doi: 10.3389/fanim.2021.649924

05 Wang G, Bobe G, Filley SJ, Pirelli GJ, Bohle MG, Davis TZ, Bañuelos GL, Hall JA. Effects of springtime sodium selenate foliar application and NPKS fertilization on selenium concentrations and selenium species in forages across Oregon. Animal Feed Science and Technology 2021; 276. doi.org/10.1016/j.anifeedsci.2021.114944

07 Curran K, Leeper H, O'Reilly K, Jacob J, Bermudez LE. An Analysis of the Infections and Determination of Empiric Antibiotic Therapy in Cats and Dogs with Cancer-Associated Infections. *Antibiotics*. 2021;10(6):700.https://doi.org/10.3390/antibiotics 10060700

08 Hall JA, Vanchina MA, Ogleby B, Jewell DE. Increased water viscosity enhances water intake and reduces risk of calcium oxalate stone formation in cats. Animals 2021, 11(7), 2110. https://doi.org/10.3390/ani11072110.

37 Hall JA, Isaiah A, Bobe G, Estill CT, Bishop-Stewart JK, DavisTZ, Suchodolski JS, Pirelli GJ. Feeding selenium-biofortified alfalfa hay during the preconditioning period improves growth, carcass weight, and nasal microbial diversity of beef calves. PLoS ONE 2020 Dec 1; 15(12):e0242771. doi: 10.1371/journal.pone.0242771.

39 Keefe BF, Bermudez LE. (in press). Environment in the Lung of Cystic Fibrosis Patients Stimulates the Expression of Biofilm Phenotype in Mycobacterium abscessus. Journal of Medical Microbiology.

40 Martin-Sancho, L., Tripathi, S., Rodriguez-Frandsen, A. et al. Restriction factor compendium for influenza A virus reveals a mechanism for evasion of autophagy. Nat Microbiol 6, 1319–1333 (2021). https://doi.org/10.1038/s41564-021-00964-2

41 Hall JA, Forman FJ, Bobe G, Farace G, Yerramilli M. The impact of periodontal disease and dental cleaning procedures on serum and urine kidney biomarkers in dogs and cats. PLoS ONE 2021 July 29; 16(7): e0255310. https://doi.org/10.1371/journal.pone.0255310.

Editor: Amy Ma
Canva.com

College of Veterinary Medicine | Department of Biomedical Sciences
Oregon State University | 106 Dryden Hall | Corvallis, OR 97331