Western University
OF HEALTH SCIENCES

College of
Veterinary Medicine

ANNUAL COLLEGE RESEARCH DAY

OCTOBER 2025

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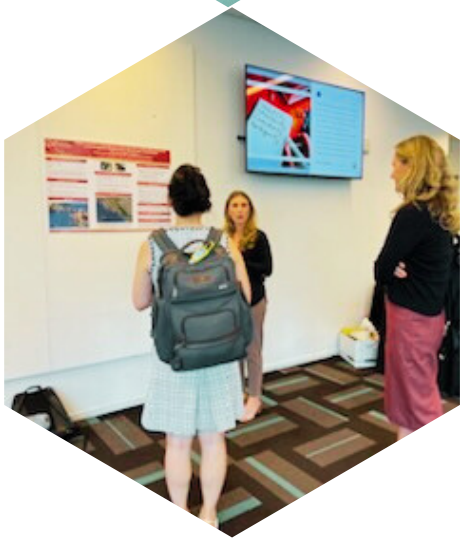

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Schedule

25-26 Annual College Research Day|October 20, 2025|HEC Lecture Hall

12:00pm-12:50pm	**Sign-In, Lunch Reception, Poster Presentations,**
1:00PM	**Welcome Introduction by Dr. Yvonne Drechsler, WesternU CVM**
1:05PM	**Andreasen, Gretchen** *"Veterinary Care Deserts: How to Quantify Professional Availability"*
1:15PM	**Wasielewski, Samantha** *"Evaluation of the Efficacy of Acupuncture in Stimulating Luteolysis in Jennies Undergoing Early Pregnancy Termination"*
1:25PM	**Truong, Lyly** *"Comparative Bioinformatics Study of Genomic Traits for Language and Memory in Humans, Dogs, and Cetaceans"*
1:35PM	**Laxa, Jeselle-Ann** *"Histological Comparison of the Immune Response between BQ and B19 Chickens After Coccidiosis Inoculation"*
1:45PM	**Marecek, Samantha** *"Developing Chemical Inhibitors that Selectively Target FOP-ALK2 Mutants Without Disrupting Wild-Type ALK2 Physiological Signaling"*
1:55PM	**Turner, Reese** *"Barcoded Magnetic Beads: Advancing Tick Borne Disease Molecular Diagnostics and Surveillance in Canines"*
2:05PM	**Keynote Speaker: Dr. Jonathan Chapman "Research Opportunities at San Diego Humane Society"**
2:55PM	*Raffle/Break*
3:05PM	**Sanders, Devin** *"Novel Drug Combinations for Addressing Polymicrobial Biofilms InVitro"*
3:15PM	**Onedera, Anita** *"Compatative InVitro Study on Selective Effects of Honeybee (Apis Mellifera) Venom on Canine Cancer Cells"*
3:25PM	**Irizarry, Kristopher (Jr)** *"Emotional Phennotyping Companion Animals from Conversations"*
3:35PM	**Cheng, Lauren** *"Identification and quantification of Calf Behavior using Labgym Artificial Intelligence"*
3:45PM	**Q & A of Presentors**
4:00PM	**Closing Remarks by Dr. Drechsler** **End of Program**

Keynote Speaker: DR. JONATHAN CHAPMAN, DVM, MPH, CPH, DACVPM

TITLE OF TALK: “Research Opportunities at San Diego Humane Society”

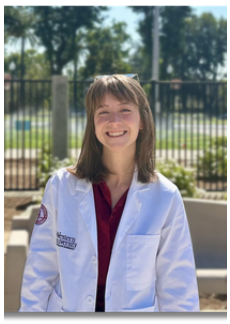
Director of Veterinary Education
Dr. Chapman oversees San Diego Humane Society's DVM residency, internship, and externship programs and provides mentorship and support to the DVMs in those programs — including one to two residents, three to six interns, and 40 to 50 veterinary students annually. He also collaborates with various universities and veterinary medical programs across the country to train the next generation of veterinarians. Dr. Chapman graduated from Ross University School of Veterinary Medicine and received his master’s degree in public health from the University of Minnesota. He is also among the approximately 10% or fewer veterinarians to hold specialty board certification. Dr. Chapman is board-certified in Public Health and Preventive Medicine by the American College of Veterinary Preventive Medicine. He is also a clinical associate professor of veterinary medicine in the College of Veterinary Medicine at Western University of Health Sciences.

San Diego Humane Society

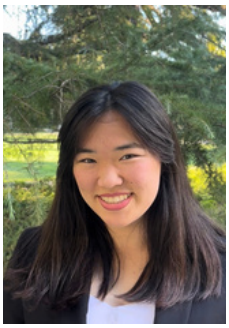
https://www.sdhumane.org/

PODIUM
PRESENTATIONS

PODIUM
PRESENTERS



Gretchen Andreasen



Lauren Cheng

Kristopher Irizarry Jr

Jeselle-Ann Laxa

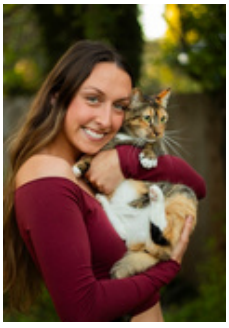
Samantha Marecek

Anita Onedera

Devin Sanders

Lyly Truong

Reese Turner



Samantha Wasielewski

Presenter: Andreasen, Gretchen

TITLE OF TALK: "Veterinary Care Deserts: How to Quantify Professional Availability"

Presenting author for Podium presentation abstract: Gretchen Andreasen, DVM 2028, margrethe.andreasen@westernu.edu, with research advisor Rhea Hanselmann, DVM, MPVM, PhD, rhanselmann@westernu.edu

"VETERINARY CARE DESERTS: HOW TO QUANTIFY PROFESSIONAL AVAILABILITY"

Gretchen Andreasen, Rhea Hanselmann

College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA

Introduction: Inequitable access to veterinary care is one of the most significant issues currently facing the veterinary profession.1-3 Identifying veterinary care deserts – areas experiencing barriers to accessing veterinary care – is a first step in combating this inequality. 1-5 A published definition of veterinary care deserts uses three metrics to assess care: accessibility, affordability, and availability.1 Accessibility and affordability can be approximated using existing geographic and income metrics.1 However, quantifying availability of veterinary care providers (i.e., the number of veterinary professionals available to provide care) has proven difficult. Previous work quantified veterinary care capacity using the number of veterinary employees per household at the county level, but counties vary widely in geographic size and population across the US and cannot describe areas with different population densities contained within the same county.2,6 Cities and census tracts offer a finer scale understanding of geographic areas, and can be used to describe rural, suburban, and urban areas more accurately.6 Thus, using cities and census tracts allows us to estimate availability of veterinary care at a level that is more reflective of the community. The objective of this project is to develop an easily implementable metric to estimate the availability of veterinary care providers using multiple data sources.

Methods: We focused on San Diego County, a large, geographically and socioeconomically diverse area, and extracted two types of publicly accessible data: active professional licenses (DVM; RVT) from the California Department of Consumer Affairs, and personnel data available on clinic websites. To understand true, current availability, we distributed a survey to all veterinary care providers with current premise licenses in San Diego County requesting data on the number and type of veterinary professionals at each facility. We will compare these survey data to the publicly accessible data to clarify their associations and inform an estimate of the availability of veterinary care providers normalized to human populations at the census tract, city, and county level.

Results: Across the 18 cities and 737 census tracts in San Diego County, we identified 1,517 DVM and 1,194 RVT licensees and extracted personnel information from 308 clinic or hospital websites. To date, we have received complete surveys from 18 clinics across San Diego County.

Discussion and Significance: By applying the veterinary care desert definition and refining the availability parameters, we take a first step in closing the gap in access that exists in veterinary care. The ultimate goal is to create a standardized tool used by veterinary services providers beyond the study area to identify communities in need, target regions with care shortage, and decrease the access to care gap.

Citations: 1 Bunke, L., Harrison, S., Angliss, G., & Hanselmann, R. (2023). Establishing a working definition for veterinary care desert. Journal of the American Veterinary Medical Association, 262(1), 1-8. 2 Neal, S. M., & Greenberg, M. J. (2022). Putting Access to Veterinary Care on the Map: A Veterinary Care Accessibility Index. Frontiers in veterinary science, 9, 857644. 3 Neal, S. M., & Greenberg, M. J. (2022). Veterinary Care Deserts: What Is the Capacity and Where Is It? Journal of Shelter Medicine and Community Animal Health, 1(1). 4 Lem M. (2019). Barriers to accessible veterinary care. La revue veterinaire canadienne, 60(8), 891–893. 5Arrington, A., Markarian, M. (2018). Serving pets in poverty: a new frontier for the animal welfare movement. Sustain Dev Law Policy, 18(1):40-43. 6 Cromartie, J. B., & Swanson, L. L. (1996). Census Tracts More Precisely Define Rural Populations and Areas. Deleted Journal, 11(3), 31–39.

Presenter: Lauren Cheng

TITLE OF TALK: "Identification and quantification of Calf Behavior using Labgym Artificial Intelligence"

CVM Research Day Presentation Abstract Submission

Lauren Cheng; laucheng@ucdavis.edu
Mentors: Dr. Oakley, Dr. Reynolds, and Dr. Peralta

IDENTIFICATION AND QUANTIFICATION OF CALF BEHAVIOR USING LABGYM ARTIFICIAL INTELLIGENCE

Lauren Cheng3, Lyssabeth Lorico1, Emma Felde-Medina1, Christopher Haggard1, Kevin Lin1, Brooke St. George1, Sarah Warda1, Hoangvi Le1, Madison Miranda1,2, Jadeanna Martinez2, Isabella Fajardo3, Jose Peralta1, James Reynolds1, Brian B. Oakley1

1 Western University of Health Sciences, College of Veterinary Medicine, Pomona, CA
2 California State Polytechnic University-Pomona, College of Science, Pomona, CA
3 University of California-Davis, College of Biological Sciences, Davis, CA

Introduction

From maternal linking and early nursing, calf behaviors reflect critical biological processes, and careful observation of these behaviors can provide early warning signs of disease, distress, or poor management. Traditional methods of monitoring are time-consuming, subjective, and often impractical on commercial dairies. Artificial Intelligence (AI) tools offer a powerful solution by automating behavior identification and analysis. In this study, we sought to validate the use of LabGym, an open-source AI tool developed and published by a team of researchers at the University of Michigan, in analyzing dairy calf behavior.

Materials and Methods

Calf behavior was recorded on days 4, 9, and 14 using Kodak Play Sport and Sony HDR-AS100V video cameras mounted on tripods at the rear ventilation windows of hutches. Each recording session lasted 1.5 hours, and a standardized ethogram was developed to define behaviors, ensuring consistency across observers. Behavioral data were extracted and organized into individual tracking sheets, and videos were subsequently analyzed using LabGym for automated behavior identification and quantification.

Discussion

This study represents one of the first applications of LabGym for the automated analysis of calf behavior. LabGym successfully identified postural behaviors (i.e. laying, standing), while more active behaviors (i.e. locomotion, nursing) were also detected, but at lower accuracy. Despite these limitations, LabGym's integration into calf research and welfare-centered dairy management holds considerable promise.

Clinical significance

Monitoring calf behavior provides an early, non-invasive window into health, welfare, and developmental status. Automating this process with LabGym offers the opportunity to detect deviations from normal behavioral patterns more rapidly and consistently than human observation. Utilizing LabGym minimizes the bias introduced by observer error by providing a more reproducible measure of calf activity. Clinically, these findings have the potential to strengthen on-farm decision-making and improve calf development, while simultaneously meeting consumer expectations for welfare-centered management.

Presenter: Kristopher Irizarry Jr

TITLE OF TALK: "Emotional Phenotyping Companion Animals from Conversation"

Presenting Authors: Kristopher Irizarry
Email: irizarrykristopher@gmail.com
DVM Class (if applicable): N/A *not eligible for awards*
Research Advisors: Kristopher Irizarry, PhD; Sheema Mir, PhD; Miguel Saggese, DVM, PhD
Title: EMOTIONAL PHENOTYPING COMPANION ANIMALS FROM CONVERSATIONS
Kristopher Irizarry (Research Assistant); Natalie Titiriga, WesternU CVM; Lyly Truong WesternU CVM

Introduction: There are videos on YouTube showing interactions between humans and small animals engaged in what appears to be conversation using Augmented Interspecies Communication (AIC) devices (buttons capable of initiating a sound file that was previously recorded into the button by the owner). A recent Nature portfolio publication (Bastos et al, 2024) concluded that soundboard use by pets does not appear random and that multi-word phrases occur more frequently than randomly expected. Important questions surrounding interspecies communication are: what is the content being exchanged by the participants? And what phenotype information can be extracted computationally? As dogs and cats may exhibit clinically relevant behaviors and emotions (separation anxiety, stress), automated detection of emotional phenotypes in conversations involving small animals may be of clinical significance.
Materials & Methods: Videos were found on YouTube of dogs and cats interacting with humans through button presses. Only videos of apparently authentic interactions using AIC devices were included; videos that were primarily for entertainment purposes were excluded. Transcription then took place for each collected video using Google Sheets which included conversation participant, time in video, and specific word conveyed. Human extraction of this information is time consuming and limits the amount of content that may be reviewed. LabGym (Hu et al. 2023) is a free open-source software tool that utilizes artificial intelligence (AI) to identify and quantify animal behavioral phenotypes. LabGym was employed and trained to detect button presses in the YouTube videos, producing output identifying timestamps in video where button pressing occurred. LabGym was not capable of providing information on the emotional content or topics of conversation. To overcome this, AI (ChatGPT 5) was used to perform a form of sentiment analysis that focused on emotional states as a function of valence and arousal. Interspecies and intraspecies comparisons of emotional valence were performed using chi-squared analyses and odds-ratio comparisons to assess similarity and differences between individuals.
Discussion: Interspecies conversations offer an unprecedented opportunity to assess the internal state of animals. One of those states is emotion and psychological well-being. This project explored computational and AI methods to identify emotional phenotypes and determine emotional state in companion animals.
Clinical Significance: Some companion animals demonstrate undesirable behavioral phenotypes (behavioral problems) and exhibit self-destructive and/or property destructive behaviors which can cause owners to relinquish or even euthanize their pets. The results of this research offer the potential for early detection of psychological issues in companion animals for which early intervention can resolve the issue in time to prevent any trauma or harm to the pet or owner.
Conclusion: Preliminary results of this project suggest that it is possible to detect distinct differences in emotional state between different animals engaged in interspecies communication using augmented button pressing combined with computational and AI tools. Identifying and understanding the internal emotional state of animals presents new ways to diagnose and potentially treat behavioral problems, enhancing quality of life and strengthening the human-animal bond.
Cited Papers:
Bastos APM, Houghton ZN, Naranjo L, Rossano F. Soundboard-trained dogs produce non-accidental, non-random and non-imitative two-button combinations. Sci Rep. 2024 Dec 9;14(1):28771.
Hu Y, Ferrario CR, Maitland AD, Ionides RB, Ghimire A, Watson B, Iwasaki K, White H, Xi Y, Zhou J, Ye B. LabGym: Quantification of user-defined animal behaviors using learning-based holistic assessment. Cell Rep Methods. 2023 Feb 24;3(3):100415.

Presenter: Jeselle-Ann Laxa

TITLE OF TALK: "Histological comparison of the immune response between BQ and B19 chickens after coccidiosis inoculation "

Presenting Author: Jeselle-Ann Laxa
Email: jeselleann.laxa@westernu.edu
DVM Class: 2027
Research Advisor: Dr. Theros Ng

HISTOLOGICAL COMPARISON OF THE IMMUNE RESPONSE BETWEEN BQ AND B19 CHICKENS AFTER COCCIDIOSIS INOCULATION

Authors - Jeselle-Ann Laxa, Lisa Griggs, Brandi A. Sparling, Robert L. Taylor, Jr., Yvonne Drechsler, Theros T. Ng

Affiliations -College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA 91766, USA; Davis College of Agriculture and Natural Resources, West Virginia University, Morgantown, WV-26506-6108, USA

Mentor - Dr. Theros Ng, PhD, Western University of Health Sciences College of Veterinary Medicine, therosng@westernu.edu

Abstract Content -
Coccidiosis is an enteric infection in chickens that causes substantial economic losses and animal welfare concerns in the poultry industry. Coccidiosis is caused by pathogenic protozoans of the Eimeria species, which infect intestinal cells, impair nutrient absorption, and lead to mortality in severe cases. This study investigated the genetic basis of susceptibility by comparing two chicken lines: BQ (resistant) and B19 (susceptible). We hypothesized that BQ chickens exhibit greater villi-to-crypt ratios, fewer parasite loads in tissue, upregulated immune markers (TLR4 and NF-κB), and increased T-cell activation post-infection. Using a 2 x 2 factorial design, we assigned female birds to each of four groups (n = 9 each): BQ control, BQ infected, B19 control, and B19 infected. On day 28 of age, we inoculated infected groups with 10 times the regular dose of COCCIVAC-D2, which consists of a mixture of Eimeria maxima, tenella, mivati, acervulina, brunatti, and necatrix. At 35 days of age (7 days post-infection), we performed necropsies and collected jejunal samples for single-cell transcriptomic analysis and spatial sequencing analysis. To validate the sequencing data, we histologically prepared and stained the jejunal samples. We used H&E staining to assess villus morphology and quantify parasite load. In addition, we used immunofluorescence (IF) staining to localize the expression of TLR4, NF-κB, CD3, CD4, and CD8 proteins and evaluate immune activation and T-cell localization. With these findings, we aim to enhance our understanding of immune responses and intestinal pathology in genetically divergent chickens, thus supporting breeding strategies that improve disease resistance to coccidiosis in poultry

Presenter: Samantha Marecek

TITLE OF TALK: "Developing Chemical Inhibitors that Selectively Target FOP-ALK2 Mutants Without Disrupting Wild-Type ALK2 Physiological Signaling"

Developing Chemical Inhibitors that Selectively Target FOP-ALK2 Mutants Without Disrupting Wild-Type ALK2 Physiological Signaling

Samantha Marecek1, Chen Xie1, Ivan Revilla2, Yun Luo2, Jijun Hao1

1 College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA 91766
2 College of Pharmacy, Western University of Health Sciences, Pomona, CA 91766

Fibrodysplasia ossificans progressiva (FOP) is a rare genetic disorder marked by progressive heterotopic ossification in extraskeletal sites. It affects approximately 1 in 2 million individuals, with no ethnic or geographic predilection. FOP is caused by a heterozygous mutation in the intracellular glycine-serine-rich (GS) domain and cytoplasmic domain of the ACVR1/ALK2 gene, which encodes a type I bone morphogenetic protein (BMP) receptor. The most common mutation, R206H, disrupts a key inhibitory salt bridge between Arg375 and Asp354, resulting in constitutive ALK2 activation and enhanced BMP signaling, even in the absence of ligand.

This gain-of-function mutation forms a unique ATP-binding pocket, allowing inhibitors to target the mutant form without interacting with the wildtype receptor. Our study aims to identify chemical compounds that selectively target the ALK2R206H mutation while minimizing physiological effects on the wildtype receptor.

98 compounds, which show more than 3-fold higher binding affinity to the ALK2R206H mutant compared to the wildtype ALK2, were identified through virtual screening of a multi-million compound library in collaboration with the WesternU Molecular Computing Core (WMCC). Using a NanoBRET™ Target Engagement Intracellular Kinase Assay, we verified the activity of these compounds in cultured HEK-293 cells transfected with ALK2R206H. We treated the cells with the 98 candidate compounds, assessed their inhibitory effects on ALK2 mutant cells by measuring BRET signals, and calculated the BRET ratio for half-maximal inhibitory concentrations (IC_{50}). Initial assays identified seven promising compounds, which we then verified in wildtype ALK2-transfected HEK293 cells.

We identify compound 28 as the most promising candidate to selectively inhibit the mutant gene with minimal inhibition of the wildtype gene at 250 nM. We will be modifying the compound to increase affinity for the mutant gene over the wildtype gene.

Cited Papers

1. Botello-Smith, W.M., et al., Polymodal allosteric regulation of Type 1 Serine/Threonine Kinase Receptors via a conserved electrostatic lock. PLoS Comput Biol, 2017. 13(8): p. E1005711.
2. Chaikuad, Apirat, et al. "Structure of the bone morphogenetic protein receptor ALK2 and implications for fibrodysplasia ossificans progressiva." Journal of Biological Chemistry 287.44 (2012): 36990-36998.
3. Davis, Alison J., et al. "An ALK2 inhibitor, BLU-782, prevents heterotopic ossification in a mouse model of fibrodysplasia ossificans progressiva." Science Translational Medicine 16.749 (2024): eabp8334.
4. Pignolo, Robert J., Eileen M. Shore, and Frederick S. Kaplan. "Fibrodysplasia ossificans progressiva: clinical and genetic aspects." Orphanet journal of rare diseases 6.1 (2011): 80.

Presenter: Anita Onedera

TITLE OF TALK: "Comparative In Vitro Study on Selective Effects of Honeybee (Apis Mellifera) Venom on Canine Cancer Cells"

Title: COMPARATIVE *IN* VITRO STUDY ON SELECTIVE EFFECTS OF HONEYBEE (*APIS MELLIFERA) VENOM ON CANINE CANCER CELLS*

Author: Anita M. Onedera, anita.onedera@westernu.edu, DVM 2028

Other authors: Boris Baer (University of California Riverside, Department of Entomology, Riverside, CA), and Yvonne Drechsler (Western University of Health Sciences, College of Veterinary Medicine, Pomona, CA)

Research Advisor: Yvonne Drechsler

Honeybee venom is recognized since ancient times for its therapeutic properties. The key bioactive component of bee venom is a peptide, *melittin*, a 26-amino acid oligopeptide, which makes up for about 50% of the venom's dry weight. While bee venom has been known for its association with pain and inflammation from stinging, it is recently spiking increasing interest amongst scientist for its potential for alternative therapeutic applications, specifically in holistic anticancer therapy. In previous studies, *melittin* was found to disrupt and target whole-cell membrane structures in comparison to chemotherapeutic drugs. Its mechanism of anti-cancer effect depends largely upon the type of the cancer cell, and it ranges from disruption of metastasis, proliferation, angiogenesis, cell cycle to the apoptosis of cancer cells.

The aim for this study is to collect honeybee venom and conduct an *in vitro* study to comparatively test the effect of the bee venom on several cancer cell lines: 1. A72, canine melanoma cells; 2. HAS canine hemangiosarcoma cancer cells. A noncancerous cell line, MDCK Madin-Darby canine kidney cells, was used as the control. Honeybee venom was collected and prepared following a protocol used at the Center for Integrative Bee Research at UCR. Microscopic evaluation of cells and flowcytometry were used to measure stages of apoptosis (Annexin V/PI Staining) and venom concentration curves were performed to identify selective therapeutic doses.

This study demonstrated that treatment type, apoptosis stage (early vs. late), and cell line all had significant effects on apoptosis induction, with notable interactions observed among these factors. Specifically, the effectiveness of treatments was not uniform across cell lines and was further influenced by the stage of apoptosis measured. These findings highlight the complexity of cellular response to apoptotic stimuli and underscore the importance of considering both biological and technical variables in in vitro cancer studies.

The A72 canine cancer fibroblast cell line, despite its unknown origin and prior well-documented resistance to apoptosis, was intentionally included in this study. This cell line provided a valuable model for optimizing assay conditions and establishing reproducibility across difficult- to-treat cancer cells. All experimental conditions were performed in triplicates and multiple independent assays were conducted following the same protocol, and resulting data consistently reflected similar trends to those presented.

A three-way ANOVA revealed significant main effects of treatment ($F(6,56) = 163.006$, $p < .001$, $\eta^2_p = 0.946$), Stage of Apoptosis ($F(1,56) = 1799.971$, $p < .001$, $\eta^2_p = 0.970$), and Cell Line ($F(1,56) = 56.110$, $< .001$, $\eta^2_p = 0.500$) on apoptosis %. Significant two-way interactions were observed for Treatment × Stage ($F(6,56) = 118.113$, $p < .001$, $\eta^2_p = 0.927$), Treatment × Cell Line ($F(6,56) = 5.542$, $p < .001$, $\eta^2_p = 0.373$), and Stage × Cell Line ($F(1,56) = 42.569$, $p < .001$, $\eta^2_p = 0.432$). Additionally, a significant three-way interaction was found ($F(6,56) = 8.050$, $p < .001$, $\eta^2_p = 0.463$), indicating that the effect of treatment on apoptosis % varies depending on both stage and cell line. Bar graph analysis indicated that late apoptosis predominated over early apoptosis across both cell lines and treatment conditions. Notably, control cells exhibited a substantial level of late apoptosis, which may reflect methodological limitations, as restricted plate size likely limited cell growth and induced apoptosis.

Future studies will extend this methodology to other cancer cell lines, such as canine hemangiosarcoma, murine T-cell lymphoma, and canine squamous cell carcinoma, to further evaluate treatment effects across diverse tumor models. Given the complexity of the apoptotic pathways and many interacting components, future efforts will also focus on standardizing protocols and refining treatment conditions. Streamlining these methods will be critical in reducing variability, improving comparability across experiments, and enhancing the translational relevance of findings to clinical oncology.

Presenter: Devin Sanders

TITLE OF TALK: "Novel Drug Combinations for Addressing Polymicrobial Biofilms In Vitro"

Devin Sanders1,2, Maya Svidensky1,2, Mariann Chang1,2, Riley Capton1,2, Dr. Ayman Mostafa1, Dr. Paramita Basu3, Dr. Priyank Kumar1,2
1College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA, 2STRIDE LAB, 3New York College of Podiatric Medicine, NY

Mentor: Priyank Kumar M.S. Ph.D; Western University of Health Sciences College of Veterinary Medicine, pkumar@westernu.edu

Drug tolerance and resistance is a growing issue in human and veterinary medicine that leads to worse treatment outcomes, increased treatment cost, and welfare concerns. A key mediator of both tolerance and resistance is the formation of biofilms. Biofilms are extracellular matrices that create an ideal microenvironment for microbial survival and block both drug and immune cell activity on microbes. Clinically, biofilms are often polymicrobial instead of monomicrobial, meaning that they are composed of multiple species instead of one. There is evidence that polymicrobial biofilms are more resistant than monomicrobial ones, and this is likely contributing to clinical recalcitrance.
Dermatophytosis is a fungal disease of the skin (cutis) that affects humans and animals, causing pain, alopecia, and further complications such as nail-bed infections (onychomycosis). There is now evidence that dermatophytosis infections are polymicrobial, involving both bacteria and fungi.2 This makes dermatophytosis a promising disease model for studying potential therapies for polymicrobial biofilms. Our aim is to potentiate the efficacy of clinically-relevant antimicrobials against multi-species biofilms *in vitro* by using them in synergistic combinations. A systematic review (done according to PRISMA 2020 guidelines) identified microbial species and antimicrobials for use in our experiments. Seven drugs were selected and their MICs were established via MIC assay. The most promising drugs were used in combination against *E. coli-E. faecalis* biofilms. Vancomycin with Gentamycin was the most promising combination for use in novel antibiofilm drug formulations. Our future aim is to produce bacterial-fungal co-cultures and evaluate combinations with antibiotics with antifungals against them.

CVM Year and Email: DVM 2027; devin.sanders@westernu.edu

Poster presentation

References:

1Anju, V. T., Busi, S., Imchen, M., Kumavath, R., Mohan, M. S., Salim, S. A., Subhaswaraj, P., & Dyavaiah, M. (2022). Polymicrobial infections and biofilms: Clinical significance and eradication strategies. *Antibiotics*, *11*(12), 1731. https://doi.org/10.3390/antibiotics11121731
2Costa-Orlandi, C., Sardi, J., Pitangui, N., De Oliveira, H., Scorzoni, L., Galeane, M., Medina-Alarcón, K., Melo, W., Marcelino, M., Braz, J., Fusco-Almeida, A., & Mendes-Giannini, M. (2017). Fungal biofilms and polymicrobial diseases. *Journal of Fungi*, *3*(2), 22. https://doi.org/10.3390/jof3020022

Presenter: Lyly Truong

TITLE OF TALK: "Comparative Bioinformatics Study of Genomic Traits for Language and Memory in Humans, Dogs, and Cetaceans"

Presenting author: Lyly Truong (Lyly.truong@westernu.edu), DVM 2028

Research Advisor: Kristopher Irizarry

Title: COMPARATIVE BIOINFORMATICS STUDY OF GENOMIC TRAITS FOR LANGUAGE AND MEMORY IN HUMANS, DOGS, AND CETACEANS

Authors: Lyly Truong, Kristopher Irizarry

Abstract:
The use of language has been seen as something that is only specific to humans. However, the ability to learn and process language, along with working memory capacity have evolved in other diverse species as well. The evolution of language learning and working memory involves a complex interplay of genetic, neurological, and cognitive adaptation, which presents multiple avenues for exploration. This research study aims to conduct a comparative investigation into the genomic phenotypes associated with language learning and working memory across humans, dogs, and cetaceans. Humans and cetaceans exhibit significant genomic convergence in cognitive-related pathways, and dogs have been artificially selected for communication traits linked to their domestication and social learning. These species exhibit distinct yet comparable cognitive capabilities, suggesting shared genetic and neurobiological foundations. Selected from previous published literature on PubMed, we have chosen 5 genes for our list of interest: FOXP2, COMT, DRD4, SHANK3, and GRIN2A. The genes were selected due to their association with language learning in humans (FOXP2), working memory (COMT), cognitive abilities (DRD4), synaptic and neuron development (SHANK3), and neurodevelopmental disorders (GRIN2A). Using the Ensembl Genetics Repository and the NCBI genetic database, we were able to acquire amino acid sequences for the species of interest. Then the amino acid sequences were aligned and phylogram were created using CLC Genomics Workbench 25, and the area of differences were reviewed and analyzed with previous published works for any significance. Some significant findings we found were that dolphins and orcas have perfectly conserved orthologs of FOXP2 with one another & are the most similar to humans compared to the other 3 species with a 98.22% similarity. The Great White sharks have the biggest difference to the rest of the species due to having the shortest amino acid sequence for FOXP2. In COMT, we saw that at the evolutionarily conserved sites position 211, the dog had an amino acid change that was different to the rest of the species of interest. Changing from an Arginine to Glutamine leads to a loss of charge and size differences, which can affect the interactions of atoms and affect protein stability and function. All these areas of interest we found would require further research to investigate to confirm their significance. Although the data is not concrete, it has allowed us to gain insights into the genetic basis of cognitive abilities and the evolutionary adaptations underlying communication and memory retention of non-mammals.

Presenter: Reese Turner

TITLE OF TALK: "Barcoded magnetic Beads: Advancing Tick Borne Disease Molecular diagnostics and surveillance in canines"

Presenting Author: Reese Turner
Email: reese.turner@westernu.edu
DVM Class: 2028
Research Advisor: Dr. Sheema Mir

Title: BARCODED MAGNETIC BEADS: ADVANCING TICK-BORNE DISEASE MOLECULAR DIAGNOSTICS AND SURVEILLANCE IN CANINES

Authors: Reese Turner, Noelle Jue, Mariann Chang, Dr. Sheema Mir
Western University of Health Sciences, College of Veterinary Medicine

Ticks serve as vectors for a multitude of bacteria, protozoa, helminths, and viruses, many of which are transmissible to humans and their animal counterparts. As pathogen-carrying tick species expand their geographic range into non-endemic areas, we anticipate an increase in serious tick-borne illnesses like Lyme disease, Anaplasmosis, Babesiosis, and Tick-borne Encephalitis. Our goal is to develop a cost-effective, high-throughput diagnostic test to improve early detection of disease and to support preventive measures. Using barcoded magnetic bead technology, we created a multiplex assay that aims to provide a streamlined diagnostic for veterinarians. We analyzed 40 retrospectively collected canine whole blood samples, each undergoing DNA extraction, PCR amplification, and multiplex analysis. All positive and negative controls yielded expected results, further validating the accuracy of our diagnostic platform. The use of retrospective clinical samples emphasizes the potential for our assay to be used in both routine diagnostics and broader tick-borne disease surveillance, aligning with the principles of One Health.

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Presenter: Samantha Wasielewski

TITLE OF TALK: “This study aims to evaluate the efficacy of acupuncture in stimulating luteolysis in jennies undergoing early pregnancy termination”

Presenting Author: Samantha Wasielewski
Email:
DVM Year: 2028
Research Advisor: Dr. Segabinazzi

This study aims to evaluate the efficacy of acupuncture in stimulating luteolysis in jennies undergoing early pregnancy termination. Specifically, it will assess whether selected acupoints alone can induce luteolysis or if targeted administration of a microdose of dinoprost tromethamine (a prostaglandin F2α analogue) into these acupoints can achieve this. Researchers use prostaglandins to manipulate the estrous cycle and terminate pregnancies in equids. Still, they often apply protocols established for horses to donkeys due to limited availability of species-specific data. In this study, 12 pregnant jennies will be randomly assigned to one of five treatment groups to evaluate the efficacy of acupuncture and acupuncture-assisted PGF2α administration in inducing luteolysis. Group 1 will receive the standard systemic dose of dinoprost (5 mg), commonly used in mares. Group 2 will receive a microsystemic dose (0.125 mg), previously shown to be insufficient for termination. Group 3 will receive a microdose injected into the Bai-Hai acupoint. Group 4 will receive 1 mL of saline into the Bai-Hai acupoint as a control. Group 5 will receive 1 mL of saline into the GB21 acupoint. The primary outcome will be pregnancy termination, evaluated via ultrasonography and hormone analysis, including progesterone and PGFM, to monitor luteal regression and embryonic vesicle disappearance. Additionally, we will compare side effects such as cramping, sweating, tachycardia, and tachypnea across treatments during the first 90 minutes post-treatment. This study aims to refine PGF2α-based protocols for donkeys, providing insight into more efficient and less invasive methods than traditional systemic treatments.

POSTER
PRESENTATIONS

POSTER
PRESENTERS

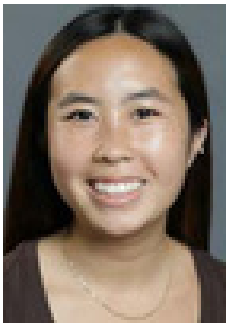
Bridgette Bloss

Jasmine Diaz

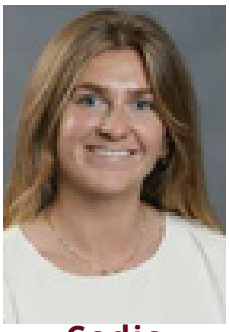
Chenelle Domecillo

Jessica Flores

Sara Gonzalez



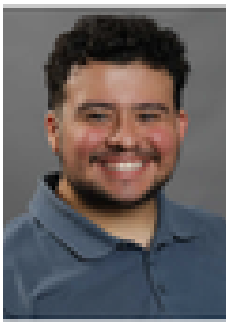
Noelle Jue



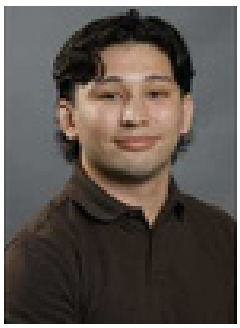
Codie Konrad

Lyssabeth Lorico

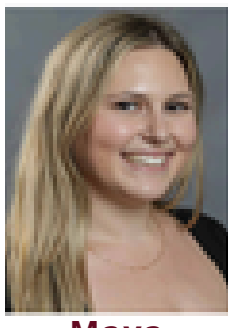
Yimeng Lu



Isaac Mejia



Eric Santana



Maya Svidensky

Clarisse Yen

Presenter: Bridgette Bloss

ABSTRACT TITLE: "Spatial Analysis of Infammatory Fibroblast and Key Signaling Molecules Involved in Canine Atpoic Dermatitis"

Poster – Bridgette Bloss and Yvonne Drechsler
Bridgette Bloss
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DVM 2028
Research advisor: Yvonne Drechsler

SPATIAL ANALYSIS OF INFLAMMATORY FIBROBLASTS AND KEY SIGNALING MOLECULES INVOLVED IN CANINE ATOPIC DERMATITIS

Yvonne Drechlser , Dipl. Biol, PhD, Associated Dean of Research, Professor of Immunology and Bridgette Bloss Western University of Health Sciences DVM 2028

Atopic dermatitis (AD) is a chronic inflammatory skin disease marked by intense pruritus, barrier dysfunction, and immune dysregulation. In both humans and dogs, AD involves complex interactions between epithelial and immune cells—including fibroblasts, keratinocytes, and T cells—driven primarily by Th2 and Th17 cytokine signaling. These pathways contribute to persistent inflammation and tissue remodeling. This study aims to characterize cytokine expression in canine skin by comparing control, lesional (inguinal), and non-lesional (shoulder) sites using RNAscope in situ hybridization. By spatially localizing and quantifying inflammatory mRNAs, we aim to clarify the role of fibroblast-associated signaling in the progression of canine AD.

Material and Methods: Tissue Collection and Preparation: A total of 10 skin samples were collected from: 5 healthy canines (non-atopic) and 5 canines clinically diagnosed with atopic dermatitis. Samples were taken from the shoulder region (non-lesional) and from the inguinal region (lesional). The samples were preserved as FFPE (Formalin-Fixed Paraffin-Embedded) and each wax block contained 3–4 tissue samples. Tissue Sectioning of FFPE blocks were sectioned at 5 µm using a microtome at the Health Education Center (HEC), Western University of Health Sciences (Pomona, CA). Two blocks, 7–8 tissue tissue sections, were mounted on Superfrost Plus GOLD slides. RNAscope Pretreatment and In Situ Hybridization using RNAscope™ Multiplex Fluorescent Reagent Kit v2 (Advanced Cell Diagnostics) was used for mRNA detection, following the Sample Preparation and Pretreatment protocol for FFPE tissues. All hybridization and pretreatment steps were performed at the Rodney Weinberg Center (RWC), Western University (Pomona, CA). HybEZ Oven II was used to complete ACD incubation and Major Sciences Oven Innovative Life Sciences Tool was used for baking slides with the addition of a 30 minute baking step added after deparaffinization to prevent detachment. Coverslips were placed onto slides using Fluoromount G. Evaluate the samples with fluorescent images were acquired using the Leica Microscope CMS GmbH (Ernst-Leitz-Str. 17-37, K8 model) in the HEC. Each slide was imaged across four immunofluorescence channels corresponding to specific mRNA targets using Leica LAS X Navigator Software: Blue (DAPI): nuclear stain - Exposure: 3.0 and FIM 55%, Green (GFP filter): IL17F - Exposure: 8.0 and FIM 55%, Red (TXR filter): DCN (decorin) - Exposure: 8.0 and FIM 55%, and Magenta (Cy5 filter): IL26 - Exposure: 12.0 and FIM 55%.

The fluorescent images show control, lesional, and non-lesional skin from dogs with atopic dermatitis (AD), highlighting mRNA localization using four fluorescence channels: DAPI (nuclei), GFP (IL17F), TXR (DCN), and Cy5 (IL26). Ongoing analysis aims to quantify and compare mRNA expression levels across skin types, providing insight into differential cytokine signaling and fibroblast-associated pathways involved in AD progression.

This study demonstrates the feasibility of using RNAscope to visualize inflammatory mRNA transcripts (DCN, IL17F, and IL26) in canine skin tissues affected by atopic dermatitis. Fluorescent imaging revealed differential expression patterns across the three diferent samples, supporting the role of fibroblast-associated cytokine signaling in disease progression. However, variability in tissue adhesion and occasional imaging artifacts, including partial tissue loss and background staining in controls, limited consistent visualization in some samples. Further quantitative analysis is needed to confirm observed trends and more accurately distinguish subtle differences between lesional and non-lesional expression profiles. Continued protocol optimization—including improved tissue preparation and imaging consistency—will be important to ensure accurate and reliable data in future analyses.

Presenter: Jasmine Diaz

ABSTRACT TITLE: "A Pilot Study: Bee Venom Anticancer Treatment Efficiency on Superficial Malignant Tumors in Dogs."

Presentation: Poster
Presenter: Jasmine Diaz, DVM class of 2028
Advisor: Dr Clark and Dr. Drechsler

A Pilot Study: Bee Venom Anticancer Treatment Efficacy on Superficial Malignant Tumors in Dogs

Honeybee venom (BV) has become of increasing interest as an alternative anticancer therapy. Most studies found BV effective in treating multiple human cancer cell lines in vitro. The molecular composition of BV is well characterized, and melittin, apamin, and phospholipase A2 are identified as the major active components of bee venom, reported to be involved in the observed anti-cancer effects. The biological effect of these bioactive peptides are various degrees of membrane-disrupting properties as a first step to trigger cell apoptosis, in addition to its anti-inflammatory and anti-angiogenic properties. Studies in mice/rats have shown BV to have selective anticancer effect on human colorectal, ovarian, lung, and cervical cancers. Pre-clinical in vivo studies have only included laboratory animals (mice/rats) thus far. Based on the knowledge available at this point, this project will test bee venom efficacy in animal cancer patients' biopsy samples. The bee venom will be provided through CIBER (Center for Innovative Bee Research, University of California Riverside) and used as a treatment on cultured cells. Melittin efficacy will be tested on the biopsy samples as well. If proven effective, an in vivo project will follow to determine the use of bee venom as an affordable alternative holistic anticancer treatment modality in small animals.

Background

Multiple in vitro studies have determined selective anticancer effectiveness of the bee venom. These were predominantly carried out on cancer cell lines and mice in human medical research. In this in-vivo pilot veterinary clinical study we will be testing the efficacy and safety of the experimental localized (intratumor) bee venom application for the treatment of malignant subcutaneous tumors in dogs- patients will include privately owned dogs presented with easily accessible subcutaneous tumors. The aim of this project is to conduct a limited scale clinical study of bee venom as a potential veterinary anticancer treatment that can lead histologically to cellular apoptosis and observable visual regression of cutaneous and subcutaneous malignant tumors in dogs. The hypothesis is that the bee venom will lead to tumor regression over the course of 2-month treatment. If proven effective, a larger scale clinical study project will follow and open the potential of use bee venom as alternative and affordable anticancer treatment modality in pet animals and potentially open the possibility of its use in human holistic medicine. Venom extraction will take place at University of California, Riverside. Bees will be anesthetized in humidified CO2. Bee body and forceps will be sprayed with 80% alcohol. Body is held in place with one forceps, and the stinger is then forcefully pulled out of the abdomen of the bee. This results in the removal of the entire sting apparatus. The sting apparatus is washed in 100 ul of ice-cold sterile Hayes saline. The venom gland and reservoir are briefly washed in 50 ul of cold Hayes before being transferred to an Eppendorf tube containing 100 ul of sterile saline. A total of 20 venom glands is collected per sample and pooled into a single Eppendorf tube. The sample is then transferred to a Thermo Miero 21R centrifuge and spun at 15'000 rpm at 4 °C for 15 minutes. The supernatant is removed using a Gilson pipette without disturbing the pellet and transferred into a cooled Eppendorf tube. The sample is then centrifugated a second time at 15'000 rom for 10 minutes The supernatant is mixed with 0.9% NaCl (sterile saline) and transferred to a final Eppendorf tube and immediately frozen at -80 Celsius

Presenter: Chenelle Domecillo

ABSTRACT TITLE: "Effects on Different Diets on Inflammation, Biological Aging, Microbiome, and Body Conditions in Dogs"

Student: Chenelle Domecillo, chenelle.domecillo@westernu.edu, Class of 2027
Research Advisor: John Tegzes
Poster Presentation

Effects of different diets on inflammation, biological aging, microbiome, and body condition in dogs

John Tegzes[1], Vincent Michels[2], Chenelle Domecillo[3]
Author Affiliations:
[1]John Tegzes, MA, VMD, Dipl. ABVT, Dean of Western University of Health Sciences College of Veterinary Medicine, Pomona, CA
[2]Vincent Michels, DVM, Residency Trained in Nutrition, Just Food for Dogs
[3]Chenelle Domecillo, CVM Student at Western University of Health Sciences, Pomona, CA

In humans, current epigenetic studies show significant differences following an omnivorous diet compared to those following a plant-based diet (Landry et al., 2023). Surveys have shown canine guardians reported very good health, increased longevity, fewer health disorders, and ideal body condition in their dogs fed plant based diets (Domínguez-Oliva et al., 2023). Additionally, there is evidence that nutrition plays a role in reducing inflammation, biological aging, and microbiome composition (Alexander et al., 2017, Liversidge et al., 2024). The overall goal of this snapshot study is to examine diet's effect on inflammation, DNA methylation associated with biological aging, ear and gut microbiome, and body condition score in dogs who have been maintained on one of the following diet types for at least one year: meat-based kibble, meat-based fresh whole food, plant-based kibble, or plant-based fresh whole food.

Research Grant: National Institutes of Health (NIH; T35AI170483)
Student Support: National Institutes of Health (NIH)

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Presenter: Jessica Flores

ABSTRACT TITLE: "Passive And Active Tick Survillence IN SOUTHERN CALIFORNIA"

Presenting Author: Jessica Flores
Authors: Jessica Flores, Amy Lee, Janel Ortiz, and Rhea Hanselmann
Name/Email/Class: Jessica Flores/ jessica.dulguime@westernu.edu/ DVM Class: 2028
Research Advisor: Dr. Rhea Hanselmann Format: Poster

PASSIVE AND ACTIVE TICK SURVEILLANCE IN SOUTHERN CALIFORNIA

Introduction: Ticks are vectors of zoonotic diseases that can cause significant morbidity in both animals and humans.1Tick populations are expanding their geographic ranges due to factors such as climate change, habitat modification, and increased movement of wildlife and domestic animals, raising concerns for emergence of tick-borne diseases in new regions.2Despite these risks, systematic, regional tick surveillance in Southern California remains limited. The objective of this study is to characterize tick species distribution, abundance, and host associations in the region through passive collection from animal hosts and active sampling from the environment. Understanding tick host preferences, geographic, and temporal distributions will inform prevention strategies and provide a baseline for future studies on tick-borne disease risk in Southern California.

Materials and Methods: From 2023 to 2025, animal shelters, wildlife rehabilitation centers, veterinary facilities, and farms located in Los Angeles, San Bernardino, Riverside, Orange, San Diego, and Imperial counties were asked to submit ticks collected opportunistically from small and large domestic animals and wildlife. Participants submitted ticks to Western University of Health Sciences, College of Veterinary Medicine for identification to genus, species (when possible), life stage, and sex based on morphological characteristics using stereomicroscopy.3,4 Starting in 2025, ticks were also actively collected from the environment on a 20-site grid located on the Voorhis Ecological Reserve at California State Polytechnic University Pomona (CPP), in Los Angeles county. At each site, a 100-m2 area was surveyed for questing ticks using a 1-m2 cotton flag.5 All sites were sampled once per season (March/April, June/July, August/September) and collected ticks were identified by at least two observers at CPP. All ticks were stored in 90% alcohol for future pathogen diagnostics. Seasonal and geographic distribution of tick abundance, species distribution, and host associations were examined and, for Los Angeles County, ticks collected via passive and active surveillance in 2025 were compared.

Results: Between July 2023-August 2025, 1,159 ticks were submitted by 25 facilities (15 veterinary practices; 9 animal shelters; 1 wildlife center) and 5 individuals. Most ticks were collected in spring (22.7%) and summer (63.7%) seasons. Ticks were collected from 5 counties with most originating from San Bernardino (39.9%) and Los Angeles (39.1%) counties. Rhipicephalus sanguineus (83.8%) was the most common species identified with most collected from domestic dogs. Dermacentor spp. (6.2%), Haemaphysalis leporispalustris (1.4%), and Ixodes pacificus (0.3%) were the other hard ticks collected from animal hosts. The soft tick Otobius megnini (n=57; 5% of all ticks) was collected from llamas at a facility in Los Angeles County and from a cat in San Bernardino County. Environmental sampling in the spring and summer yielded Dermacentor spp. (n=24), Ixodes pacificus (n=1), and Haemaphysalis leporistalustris (n=1). However, small sample sizes of these tick species collected from host animals in 2025 precluded host-environment comparisons.

Discussion & Conclusion: Continued systematic passive tick surveillance complements ongoing active surveillance efforts and will improve understanding of spatial, temporal, and host-specific tick distributions in Southern California. Long-term monitoring of tick distributions is essential to establish accurate baseline patterns and inform exposure prevention strategies.6

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Presenter: Sara Gonzalez

ABSTRACT TITLE: "Decoding Communication: Analyzing Genetic and Behavioral Evidence for Language evolution Across Species"

Title: DECODING COMMUNICATION: ANALYZING GENETIC AND BEHAVIORAL EVIDDENCE FOR LANGUAGE EVOLUTION ACROSS SPECIES

Presenting Author: Sara Gonzalez (sara.gonzalez@westernu.edu), DVM 2028
Research Advisor: Kristopher Irizarry PhD (kirizarry@westernu.edu)
Authors: Sara Gonzalez, Kristopher Irizarry B.S, PhD

Abstract:
The use of spoken and written language is a remarkable and unique human characteristic, shaped by genetic, neuroanatomical, and cognitive factors. While this ability is uniquely developed in humans, components of language such as vocal learning, recognition of language, and working memory can also be observed in other species. Amongst these components, vocal production learning- the ability to hear novel sounds, imitate them, and reproduce them is especially significant. This trait is supported by specialized brain circuits in both human and songbird species, despite their distant evolutionary history. In contrast, non-human primates, despite their close genetic relationship to humans lack this ability (Jarvis, 2019).The purpose of this research is to investigate the basis of language as a phenotype by analyzing and comparing genes that contribute to brain circuitry, communication, speech, and cognition in humans, neanderthals, gorillas, chimpanzees, bonobos, dogs, and zebra finches. This project will offer new insights into the genetic factors that influence language and communication and potentially emphasize genetic conservatism or non-conservatism. Five candidate genes were selected from existing literature- FOXP2, ROBO1, SLIT1, CNTNAP2, DCHS1. They were selected because of their association with language development, axon guidance, cognition, and working memory. Basic functions of selected genes were confirmed using the Gene bank database. The amino acid sequences of candidate genes were obtained from Ensembl genomics repository database. The longest isoforms were selected for best comparison. Alignments and phylogenetic trees were created using Qiagen CLC. Protein annotations and domains were obtained by using the UniProt database. Domains were used to identify areas of high importance. Alignments were analyzed for degree of variability or similarity and cross referenced with existing literature. Since neanderthal protein sequences were unavailable, existing literature was used to identify fixed amino acid changes or variability (FOXP2, DCHS1, CNTNAP2). Those not mentioned in literature were assumed to be identical to human (ROBO1 and SLIT1). Video examples of these species were conducted to observe behaviors like vocalizations/call types, facial expressions, gestures/sign language, vocal imitation/learning, body language, eye contact, and signaling. Edits to images made on PowerPoint. Some significant findings we found regarding FOXP2 were that humans and neanderthals share a highly conserved amino acid at position 347, all other species analyzed in the study had different amino acids in this position. Also, there were regions in the FOXP2 in the chimp, bonobo, gorilla, dog, and zebra finch all lacked amino acids which could highly affect the phenotype of language. Lastly, we were able to identify a polyQ stretch which is critical for FOXP2 function. Interestingly, the ROBO1 protein had a region stretching from position 5-45 where only the chimp and bonobo had amino acids. The protein sequence of SLIT1 highlights an interesting variation at position 459 where the zebra finch has an Alanine (non-polar) whereas the remaining species have a Threonine (polar). The difference in polarity could potentially affect the protein's structure, stability, and function. The DCHS1 protein sequence revealed a unique human substitution that disrupts a conserved Asparagine at position 938. Lastly, the protein sequence for CNTNAP2 revealed humans having an Asparagine at position 215 where all other species have a Lysine. In conclusion, areas of variability and conservation were found when analyzing the amino acid sequences of the candidate genes. The purpose of this study was to collect, analyze, and identify areas of interest. These regions of interest require further research to confirm their significance. This data provided insights into the genetic factors that influence language and communication.

Presenter: Noelle Jue

ABSTRACT TITLE: "Multiplex Diagnositic Assay for Surveillance of Tick-Borne Diseases in Turkey Vultures (Cathartes Aura) from Southern California"

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Presenting Author: Noelle Jue, noelle.jue@westernu.edu, DVM Class 2028
Research Advisor(s): Dr. Sheema Mir, Dr. Miguel Saggese

MULTIPLEX DIAGNOSTIC ASSAY FOR SURVEILLANCE OF TICK-BORNE DISEASES IN TURKEY VULTURES (CATHARTES AURA) FROM SOUTHERN CALIFORNIA

Noelle Jue1, Elizabeth Crown1, Leslie Buntyn,1 Mariann Chang1, Peter H. Bloom2, EmaLee Blumhagen1, Miguel D. Saggese1, and Sheema Mir1

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Due to climate change, the United States of America has observed a significant rise in the risk of tick-borne infection for humans and animals, intensifying the need for cost- and time-efficient diagnostic methods. While there are no current studies about the presence of tick-borne pathogens in Turkey Vultures *(Cathartes aura)* of Southern California, investigation into tick-borne diseases (TBDs) in this species remains of interest in wildlife health because of their possible role in the ecoepidemiology of TBDs. Using 37 archival turkey vulture blood samples from 2016 and 2017 processed through DNA extraction and PCR amplification, this study uses the lab's previously developed high-throughput multiplex diagnostic assay utilizing Barcoded Magnetic Bead (BMB) technology to detect two targeted tick-borne pathogens, *Anaplasma phagocytophilum* and *Borrelia burgdorferi*. The resulting data showed 2 of the 37 samples being positive for *Anaplasma phagocytophilum*, and 1 additional sample being positive for both *Anaplasma phagocytophilum* and *Borrelia burgdorferi*. The positive controls for the target pathogens displayed positive detections as expected, validating the assay's sensitivity. This study is part of an ongoing investigation and development of a multiplex assay for TBDs. Our assay is poised to be an impactful tool in the One Health triad, as it can be utilized in future surveillance studies and clinical diagnostics.

Presenter: Codie Konrad

ABSTRACT TITLE: "Fibroblasts' Potential Role as Immune Regulators of T-Cells of T-Cells in Canine Atopic Dermatitis"

Codie Konrad
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FIBROBLASTS' POTENTIAL ROLE AS IMMUNE REGUALTORS OF T CELLS IN CANINE ATOPIC DERMATITIS

Codie Konrad and Yvonne Drechsler

College of Veterinary Medicine, Western University of Health Sciences, Pomona, CA

Atopic Dermatitis (AD) is initially an immune mediated pruritic inflammatory response to allergens on the skin. In chronic conditions, AD presents with clinical signs such as lesions, alopecia, erythema. Unfortunately, underlying mechanisms of the immune response in chronic conditions is not fully understood. Therefore, pharmacological treatments target either pruritic or general immune pathways but are not curative.

Recent studies have demonstrated the atopic immune response to involve many different immune cells, fibroblasts, and keratinocytes. Keratinocytes within the epidermis activate and induce cytokines upon contact or damage to an allergen. Their activation initiates the inflammatory response, recruiting immune cells to the epidermis and possibly activating fibroblasts in the dermis. Associated effects are the clinical signs seen such as the intense itching and redness of the skin. A major immune cell group involved are T lymphocytes which contribute to cytokine production and cell signaling. A specific type of Th response, Th17, produces cytokine IL-26 and represents a very pro-inflammatory state that might contribute to the deleterious cycle leading to chronic inflammation. An important cytokine of this response, IL-17, has been proved to contribute to cell signaling and inflammation in the atopic skin. Our previous single-cell sequencing study suggests fibroblasts might play an important role in this process and need to be further investigated. We have used CRISPRa technology, co-culturing fibroblasts expressing IL-26 with primary canine T cells. RNA from these cells was analyzed with PCR to investigate cytokine expression of Th17 responses. We expect to characterize immune signaling between fibroblasts and other cells in the atopic skin.

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Presenter: Lyssabeth Lorico

ABSTRACT TITLE: "Effects of Colostrum and Housing on Health and Welfare of Calves in Conventional and Organic Diary Farms"

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DVM 2027

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EFFECTS OF COLOSTRUM AND HOUSING ON HEALTH AND WELFARE OF CALVES IN CONVENTIONAL AND ORGANIC DAIRY FARMS

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This project is part of a larger study to examine how dairy husbandry influences neonatal calf welfare, nutrition, and development of the gastrointestinal microbiota, and how these factors contribute to the growth of healthy, active, and emotionally developed calves that later become productive dairy cows. This portion of the project focused on characterizing the welfare and microbiome of developing dairy calves. We took colostrum, fecal, and hair samples from calves on a conventional farm in California (n=44) and an organic farm in Colorado (n=40). Brix refractometers measured colostrum. Aerobic plate counts and quantitative-PCR determined microbial load using fecal samples collected at birth, 3, 7, 14, 30, and 60 days. We measured cortisol levels from hair samples collected at birth and 14 days. For each calf, we also recorded health and welfare parameters through respiratory scores, fecal scores, milk consumption, serum total protein, weights and behavior videos. We hypothesized that group-housed calves and those fed higher quality colostrum would have lower cortisol levels, improved health parameters and than those that were individually-housed and fed lower quality colostrum. Initial results generally supported our hypotheses with a positive correlation between colostrum quality and serum total protein, decreased cortisol from birth to 14 days for all calves with group-housed calves having a larger magnitude of difference, higher quality colostrum associated with organic husbandry practices, and non-significant effects of freezing on colostrum quality and microbiome. This study is ongoing and serves as a starting point for further research into factors affecting developing dairy calves.

Presenter: Yimeng Lu

ABSTRACT TITLE: "The Fate of Low Pathogenic Avian Influenza Virus in the Presence of Bovine Lactoferrin or Ovotransferrin: A Comparative Study"

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THE FATE OF LOW PATHOGENIC AVIAN INFLUENZA VIRUS IN THE PRESENCE OF BOVINE LACTOFERRIN OR OVOTRANSFERRIN: A COMPARATIVE STUDY

Abstract

In January 2025, the USDA detected for the first time a new variant of highly pathogenic Avian Influenza A virus (H5N1 AIV) in dairy cows. Guided by recent studies, we intend to use an in vitro low pathogenic Avian Influenza model to examine and compare the ability of two naturally occurring iron-binding proteins - bovine lactoferrin (bLF) and ovotransferrin (Otrf) – to address this emerging threat. Solid-phase direct binding and colorimetric caspase-3 assays will be used to determine their impact on H5N9 attachment and virus -induced apoptosis on cell lines commonly used in AIV studies. Inhibitory bLF effects against human adapted influenza A subtypes have been reported, and Otrf which shares more than 50% of its sequence identity also exhibits antiviral activity. In our preliminary work the potential cytotoxic effect of two-fold serial dilutions of bLF was assessed in Madin Darby Canine Kidney (MDCK) cells. Cells were initially grown to 70% to 80% confluency in T-75 culture flasks. Following viability testing, 2 x 10^6 cells were cultured in triplicate in RPMI containing either 25, 12.5, 6.25, 3.12 or 1.56 µM of bLF in a 96-well plate. Control wells were devoid of bLF. At 24 hours, cell morphology was examined using brightfield microscopy. No cytotoxic effects were observed. Interestingly, wells with higher concentrations of bLF were more stellate, more confluent and more difficult to trypsinize. Future experiments will evaluate cell viability and the molecular basis for the observed concentration-effect relationships.

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Presenter: Isaac Mejia

ABSTRACT TITLE: “Developing a Fret-Based Assay to Monitor Hantavirus RDRP Endonuclease Activity”

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Project Title: DEVELOPING A FRET-BASED ASSAY TO MONITOR HANTAVIRUS RDRP ENDONUCLEASE ACTIVITY
Authors: Isaac Mejia, Saima Ali, Hoangvi Le, Sheema Mir, Mohammad Mir*
Abstract: Hantaviruses, members of the Bunyavirales order, are emerging, negative-strand RNA viruses classified as category A pathogens due to their potential to cause severe disease with high mortality rates in humans. Transmission typically occurs through inhalation of aerosolized excreta from infected rodents. Currently, there is no approved cure for hantavirus infection. The hantavirus genome consists of three negative-sense RNA segments, S, M, and L encoding the nucleocapsid protein (N protein), glycoprotein precursor (GPC), and RNA-dependent RNA polymerase (RdRp), respectively. The RdRp is a large 420 kDa enzyme responsible for both viral mRNA transcription and genome replication in the host cell cytoplasm. Hantaviruses initiate these processes through a "cap-snatching" mechanism, wherein the N-terminal endonuclease domain of the RdRp cleaves host mRNA preferentially at a guanosine (G) residue located 14 nucleotides downstream of the 5′ cap. The resulting capped RNA fragment serves as a primer for transcription and replication of the viral genome. More than 300 viruses within the Bunyavirales order, including many of medical relevance, utilize this cap-snatching mechanism. Inhibiting the endonuclease activity of RdRp represents a promising strategy to disrupt cap snatching and block viral replication. The endonuclease domain of segmented negative-strand RNA viruses is structurally conserved, making it an attractive target for broad-spectrum antiviral development. The pET30a(+) plasmid harboring the gene encoding the N-terminal endonuclease domain of the hantavirus RdRp was amplified in E.coli. The resulting plasmid was transformed into Rosetta (DE3)pLacI competent E.coli cells for protein expression. The protein was purified using NiNTA chromatography on AKTA purification system. To test the endonuclease activity of the purified endonuclease domain, the protein was incubated with a 30 nucleotide long RNA containing a 6-FAM fluorophore at the 5’ terminus and an Iowa black quencher at the 3’ terminus. The protein cleaved the RNA generating a dequenched fluorescence signal, verifying the activity of the purified endonuclease domain. This assay will enable high-throughput screening of chemical libraries to identify potential inhibitors of the hantavirus cap-snatching endonuclease.

Presenter: Eric Santana

ABSTRACT TITLE: "Evaluation of epigenetic mutations by T. gondii in brains of people with HIV and its link to glial formation"

Title:

110 Character limit

Evaluation of epigenetic mutations by T. gondii in brains of people with HIV and its link to glial formation

Abstract:

1,750 Character Limit

Toxoplasma gondii (T. gondii) is an apicomplexan parasite infecting 10–40% of people in the US. While felines are its definitive host, transmission to intermediate hosts, such as humans, occurs through consuming undercooked meat or contact with feline feces. In humans, the parasite remains dormant as bradyzoites, however, in immunocompromised hosts, reactivation of trophozoites can cause neurological disease. Toxoplasmosis is a common HIV-associated infection, yet the broader impact of zoonotic parasites on the central nervous system in people with HIV (PWH) remains unclear. Recent evidence from brains of PWH with T. gondii infection shows DNA methylation changes to enhancers and gene bodies, consistent with literature studying rodents infected with the parasite. Genes in PWH had an overrepresented association with glioma and glioblastoma development. This study investigates whether T. gondii modulates host epigenetic mechanisms to drive tumorigenesis.

Using brain samples from the California NeuroAIDS Tissue Network and the UC San Diego Last Gift cohort, we are evaluating the expression of EZH2, a histone methyltransferase linked to common brain neoplasia, and its dysregulation in PWH infected with T. gondii. To better understand the role of EZH2 in glioblastoma formation, we sought to identify differential DNA methylation patterns associated with EZH2 inhibition in a U-251 glioblastoma cell line. By identifying overlapping epigenetic changes between in vivo T. gondii infection in PWH and U-251 cells treated with an EZH2 inhibitor, we aim to identify potential epigenetic mechanisms linking T. gondii infection to brain tumorigenesis, advancing our understanding of the broader impacts of this common zoonotic parasite.

Presenter: Maya Svidensky

ABSTRACT TITLE: "Biofilm-mediated antifungal resistance in dermatophyte species affecting humans and animals"

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BIOFILM-MEDIATED ANTIFUNGAL RESISTANCE IN DERMATOPHYTE SPECIES AFFECTING HUMAN AND ANIMALS

Dermatophytosis is a superficial fungal infection that a5ects both humans and animals each year. It is caused by dermatophytes—filamentous fungi adapted to invade and utilize keratin-rich tissues such as the skin and nails for growth and reproduction. In veterinary patients, dermatophytosis is among the most common skin disorders, significantly impacting animal health and welfare. It is particularly prevalent in species such as horses, dogs, and cats, where it causes ring-shaped patches of hair loss, scaling, and inflammation, leading to discomfort and secondary complications if left untreated. The primary treatment for dermatophytosis involves antifungal medications that target the ergosterol biosynthesis pathway—the main sterol component of the fungal cell membrane. Itraconazole is among the most e5ective agents used. However, the emergence of antifungal resistance, driven in part by biofilm formation, has complicated the treatment of dermatophytosis in veterinary medicine. Biofilms are complex microbial communities encased in an extracellular matrix that enhances microbial survival by protecting pathogens from antifungal agents and host immune defenses. These biofilms often consist of polymicrobial communities, increasing their resilience to standard treatments like Itraconazole and necessitating the development of innovative therapeutic approaches. E5ectively addressing the challenges of antifungal-resistant dermatomycoses is essential—not only to improve outcomes in veterinary patients but also to reduce the risk of zoonotic transmission and protect public health.

Presenter: Clarisse Yen

ABSTRACT TITLE: "IBD therapeutic candidate: Adenosine Receptor Signaling as a Metabolic Regulator of T effector cell activation"

IBD therapeutic candidate: Adenosine Receptor Signaling as a Metabolic Regulator of T effector cell activation

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Background: Inflammatory Bowel Disease (IBD) is triggered by an excessive Th1 effector cell response to commensal bacteria, leading to intestinal damage. Anti-inflammatory treatments fail to prevent relapsing episodes, making the development of novel therapy crucial. Previous studies demonstrated the protective role of adenosine in mouse colitis models. It acts as an anti-inflammatory mediator by regulating neighboring cells through the adenosine receptor (A2AAR). Cell metabolism reprogramming towards glycolysis is a hallmark of inflammatory responses and T cell proliferation. This research project aims to understand how A2AAR signaling regulates T cell metabolism to mitigate T cell-dependent inflammation.

Methods and Results: Isolated naive CD4+ T cells from splenocytes of wildtype mice were differentiated *in vitro* into Th1 cells and reactivated in the presence or absence of A2AAR agonists. Cells were collected at 2 or 18 hrs. post-stimulation to evaluate T cell receptor activation **(**mTOR phosphorylation) by flow cytometry, perform a glucose uptake assay using 2-NBDG, and by qPCR of the gene expression of glycolytic-related molecules (i.e transcriptional factors HIF-1α and Myc, glucose transporter GLUT-1, glycolysis enzyme hexokinase 1). Th1 cells were also analyzed in real-time using the Seahorse Agilent technology to evaluate their glycolysis rate. We hypothesize that A2AAR engagement inhibits mTOR phosphorylation leading to glycolytic gene downregulation and therefore suppression of glycolytic capacity to limit Th1 cell activation.

Conclusion: A2AAR is an appealing new anti-inflammatory therapeutic for patients with IBD due to its potential to regulate T cell activation through limitation of glucose metabolism.

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