



New Mexico

INBRE

IDeA Networks of Biomedical Research Excellence



Annual Symposium

July 27 - 29, 2026

Hotel Encanto

Las Cruces, NM

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A message from the director...

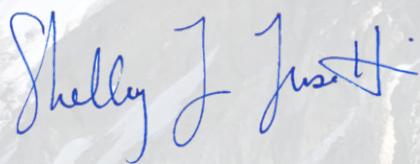
I welcome everyone to the 2026 NM-INBRE annual symposium. I am excited to see all of the faculty, students, and administrators that have participated in our program over the last year. The NIH-funded INBRE program in New Mexico, now in its 26th year, has provided opportunities to expand biomedical research infrastructure through a network of ten institutions of higher learning in the state.

NM-INBRE strives to provide a base for research faculty to build their careers and a brace when wanting to expand their research into new areas. In addition to professional development opportunities, we have supported 165 research projects through the DRP Program and 164 data science pilots through our Data Science Core. Faculty supported by NM-INBRE have gone on in their careers to secure \$157M in additional NIH funding to support independent research.

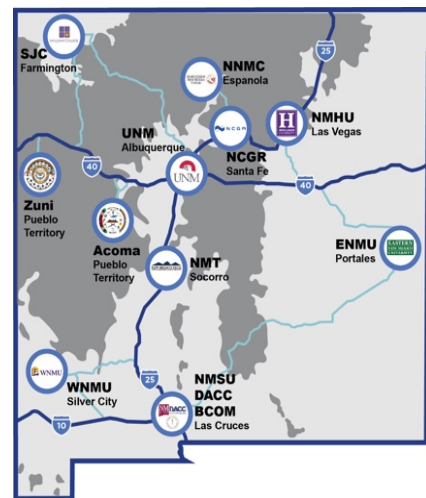
Student training is a major priority for NM-INBRE. Over the years, we have provided research training and professional development activities to more than 1,650 participants. Undergraduate and graduate students receive mentored training through DRPP-funded labs. In 2019, we established a formal training program known as the New Mexico INBRE Student Experience (NISE). Nearly 500 students have participated in either research bootcamps or internships and 96% of the 195 student participants that have graduated since 2019 have remained in STEM fields.

I am exceedingly proud of the accomplishments of the NM-INBRE program. We remain committed to building on our successes. As usual, we will continue to adapt to the needs of our various stakeholders. However, we are facing new barriers and unforeseen difficulties as we traverse the changing priorities of the federal government. NM-INBRE and scientists, in general, are working in extraordinary times and under extraordinary conditions. It is imperative that we remain attentive to the forces that are driving these changes, both as scientists and as citizens of this great country. There is a need for all of us to work harder to communicate the benefits of scientific research, even in its most basic forms. A theme at this year's symposium is communicating "big picture" ideas that are the driving force for our research projects. Many times it is an unanswered question that propels increments of discovery and the large breakthroughs that result (sometimes decades later) were unimaginable. The non-scientific community needs to understand our "*Everest*", that seemingly impossible summit we are striving to reach... the purpose, the struggle, and the prize!

With the very best wishes,



Shelley Lusetti, NM-INBRE Director and Principle Investigator





Monday, July 27, 2026

2:00 pm-5:30 pm	Registration check-in Poster set-up	Lobby San Andres
3:30 pm-4:30 pm	Kevin Houston, NMSU: Student research committee meeting <i>by invitation only</i>	Socorro
3:30 pm-5:00 pm	Faculty professional development workshop, required of DRPP and NIRF Awardees, open to all faculty	San Andres
5:30 pm-7:30 pm	Welcome Address - hors d'oeuvres & cash Bar	San Andres/Avenida

Tuesday, July 28, 2026

7:00 am-8:15 am	Breakfast	San Andres
8:15 am-8:45 am	Shelley Lusetti, NM-INBRE PI: Welcome remarks, introductions, and overview of INBRE	San Andres
8:45 am-9:15 am	Charlotte Gard, NMSU Amy Wagler, NMSU Joann Mudge, NCGR: INBRE Data Science Core	San Andres
9:15 am-10:15 am	Institutional Liaisons: Research landscape at partner institutions	San Andres
10:15 am-10:45 am	Break	Avenida
10:45 am-11:30 am	Research presentations: session 1	San Andres
	David Donley, NMHU: I've got iron on my mind: exploring factors that shape the neuroinflammatory response of microglia	
	Huixin Zhan, NMT: Personalized AI from the operating rom to recovery for rural New Mexico	
	Jacob Jaszczak, NMSU: Dissection somatosensory development in a multicellular context	
11:30 am-11:35 am	Matthew Campen, UNM: Perspective #1: the <i>Everest</i> of unanswered health questions	
11:35 am-12:15 pm	Carolyn Hovde Bohach Univ of Idaho: Etiquette, scientific decorum: guidelines, expectations, and unwritten rules	San Andres
12:15 pm-1:30 pm	Lunch and Key Note Address Kathryn Hanley, NMSU: What doesn't kill you mutates and tries again: Current research on and control of emerging infectious diseases	San Andres
1:30 pm-2:30 pm	Poster session: odd-numbered posters	San Andres
2:30 pm-3:30 pm	Poster session: even-numbered posters	San Andres
3:30 pm-3:35 pm	Jeffrey Arterburn, NMSU: Perspective #2: the <i>Everest</i> of unanswered health questions	San Andres
3:35 pm-4:20 pm	Research presentations: session 2	San Andres
	Michaelann Tartis, NMT: Optimizing fabrication strategies to enable transcriptomic analysis of mechanically loaded neural tissue constructs	
	Daniel Chadborn, NMHU: Student well-being, identity, and inspiration: longitudinal and comparison research in New Mexico, across the U.S., and abroad	
	Ryan Ashley, NMSU: CXCL12/CXCR4 Signaling coordinates early placental development: Insights from a translational sheep model	
4:20 pm-4:25 pm	Raj Shah, UNM: Perspective #3: the <i>Everest</i> of unanswered health questions	San Andres
4:25 am-4:55 pm	Undergraduate research short talks: session 1	San Andres
	Alicia Tirado, UNM (Virtual Bioinformatics): Global transcriptomic comparison of Alzheimer's disease	
	Devyn Erickson, ENMU (NMSU Internship): Toxicity assessment of treated produced water from thermal and membrane processes and post treatment organic extract on human cell lines	
	Matthew Bacho, Univ of Hawaii at Manoa (UNM Internship): Switching protein translation mechanisms affects hippocampal CA1 pyramidal cell activity	
5:15 pm-7:00 pm	2026 DRPP applicant working session (hors d'oeuvres provided) <i>by invitation only</i>	San Andres

Symposium Agenda



Symposium Agenda

Wednesday, July 29, 2026

7:00 am-8:00 am	Breakfast	San Andres
8:15 am-8:30 am	Announcements	San Andres
8:30 am-9:15 am	Research presentations: session 3	San Andres
	Matthew Guberman-Pfeffer, NMSU: Two sides to every enzyme: how electrostatics couple active sites to interaction surfaces	
	Corey Green, ENMU: Mechanisms of contaminant resistance and their physiological consequences	
	Rhiannon West, NMMC: Evolutionary genomics of immune variation: building a framework to link the major histocompatibility complex, microbiomes, and chemical communication	
9:15 am - 9:20 am	Erik Yuki, NMSU: Perspective #4: the <i>Everest</i> of unanswered health questions	
9:20 am-9:50 am	Undergraduate research short talks: session 2	San Andres
	Braden Holden Silvis, NMSU (Virtual Bioinformatics): Investigating the molecular basis of sickle cell nephropathy through comparative bioinformatics.B45:B47	
	Jose Hernandez, NMT (Home Internship): Development and characterization of a hydroxyapatite-based composite scaffold loaded with natural medicine for bone tissue engineering	
	Finn McManus, DACC (Bootcamp): Physiological attributes and antimicrobial activity of bacillus atrophaeus	
9:55 am - 10:00 am	Brad Shuster, NMSU: Perspective #5: the <i>Everest</i> of unanswered health questions	
10:00 am-10:30 am	Break	Avendia
10:30 am-12:00 pm	Student-centered panel discussion	San Andres
	Charlotte Gard, NMSU Amy Wagler, NMSU Joann Mudge, NCGR: Working in Data Science	
	Michele Shuster, NMSU Sally Pias, NMT Juchao Yan, ENMU: Research mentors	
10:30 am-12:00 pm	Faculty-centered panel discussion	San Rafael
	Shelley Lusetti, Kathryn Hanley, Jeff Arterburn, Raj Shah, Erik Yuki, and Brad Shuster: Research career challenges and strategies to survive and win	
12:00 pm-12:30 pm	Shelley Lusetti, NM-INBRE PI: Wrap up and awards	San Andres
12:30 pm	Depart with sack lunches available	Avendia
1:00 pm-2:00 pm	Amy Wagler, NMSU: NMSU INBRE high performance computing, <i>registration required</i>	San Andres

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Data Science Core

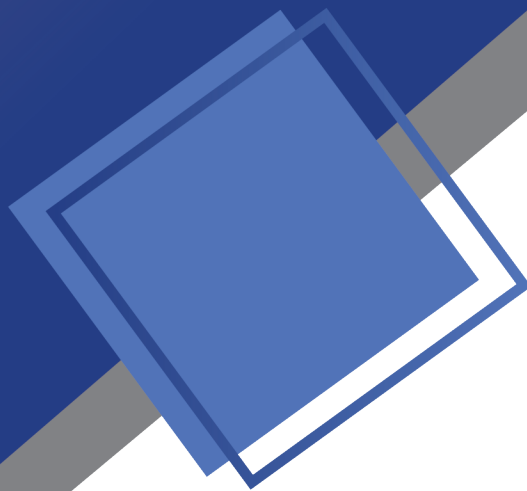
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Investigator	Project Title	Project Type
Ashley, R.	From Ewe to You: Advancing Understanding of Preeclampsia with a Translational Sheep Model	Pilot (PPE)
Baker	Physiochemical characterization of breast milk fat composition and its correlation to factors of maternal	RAIN
Chadborn	Social Identity and inspiration on social and psychological outcomes in students	Research Project
Donley	Iron modifies the neuroinflammatory response to AD: exploring mechanistic targets	Research Project
Green	Genetic mechanisms of contaminant resistance and their physiological consequences	Pilot (PPN)
Guberman-Pfeffer	Electrostatics couple Active Sites to Interaction Surfaces in Electron Transfer	Research Project
Jaszczak	Dissection of multi-sensory development in Drosophila	Research Project
Nandy	The Role of Serum Amyloid A in Hyperglycemia-mediated effects on Breast CSCs	Pilot (PPN)
Tartis	Linear Fusion of Cerebral Organoids for Enhanced TBI Modeling	Pilot (PPE)
West	The role of major histocompatibility complex in maintaining species diversity in pupfishes	Research Project
Zhan	REACT - Rehabilitation through Embodied Agentic Clinical Transfer	Pilot (PPN)

Updated May 27, 2026



New Mexico

INBRE

Data Science Core

In need of statistical, bioinformatics, or high performance computing support? Use the QR code to learn more about our services and to reach out. We are here to help!

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Keynote Speaker



Dr. Kathryn A. Hanley

Regents Professor of Biology, NMSU

What doesn't kill you mutates and tries again: Current research on and control of emerging infectious diseases

Factors such as climate change, land use change and human mobility all accelerate the emergence of novel pathogens and resurgence of established pathogens. At the same time, recent changes in US priorities for and funding of infectious disease research have diminished surveillance, suppressed epidemiological data, and undermined or halted progress on diagnostics, vaccines and therapeutics. Additionally, mis/disinformation has led to backsliding on childhood vaccination and the re-appearance of preventable diseases; indeed the US stands on the precipice of losing its measles elimination status. As the co-PI of one of the ten NIH-funded Centers for Research on Emerging Infectious Diseases, Dr. Kathryn Hanley has had a “front row seat” to the recent havoc in infectious disease research and control. In this seminar, she will describe the process of pathogen emergence and the factors that facilitate it, provide an overview of the countermeasures that can be used to prevent or mitigate pathogen emergence, summarize some of the major obstacles to effectively deploying these countermeasures, and conclude on a hopeful note by emphasizing recent breakthroughs in the field.



External Advisory Committee



Dr. Ann Bertagnolli

Dr. Bertagnolli recently retired as Associate Director and Program Coordinator of the Montana INBRE program, which distributed over \$60 million in biomedical research funds statewide and built a network of 15 academic institutions, including seven tribal colleges. She coordinated more than 200 faculty and 2,000 student research projects, including eight Native American graduate fellowships, and gained extensive experience mentoring faculty and students in research design and execution. She has served as a reviewer for NIHMD program grants and an External Evaluator for the Wyoming INBRE program. Currently, she is collaborating with two other IDeA programs at Montana State University to develop a Community Engagement Core that trains investigators to build research partnerships with tribal and rural communities, drawing on expertise from INBRE, CAIRHE, and the CTR program. We are pleased to welcome Dr. Bertagnolli, the heart and soul of the Montana INBRE network, as the newest member of our New Mexico INBRE External Advisory Committee.



Dr. Carolyn Hovde Bohach

Carolyn Hovde Bohach, Ph.D. is a University Distinguished Professor and Director of the Idaho INBRE Program at the University of Idaho. A microbiologist with postdoctoral training from Harvard Medical School, her research focuses on *E. coli* O157 and other foodborne pathogens, with an emphasis on developing interventions such as bovine vaccination, bacteriophage therapy, and improved on-farm management practices. She has authored more than 100 scientific publications, received numerous national and university awards for excellence in research and teaching, is a Fellow of the American Association for the Advancement of Science (AAAS), and serves as the PD/PI of the statewide Idaho INBRE Program.



Dr. Joe Konopelski

Dr. Konopelski has been a member of the faculty at the University of California, Santa Cruz since July 1984, where he retired in 2022. Dr. Konopelski has served as the Associate Dean of Research and the Chair of the Department of Chemistry and Biochemistry. More recently, he has served as Vice-Chair, and then Chair, of the Santa Cruz Division of the UC Academic Senate. In 2014 he was appointed interim Dean of the Baskin School of Engineering. His research interests include total synthesis and methodology development, and heterocyclic chemistry.



Dr. Jean Patterson

Dr. Patterson served as Chair of Virology and Immunology at the Texas Biomedical Research Institute from 1996-2015. She is a member of the design team that completed construction of a 36,000 square foot laboratory building that holds 12 Biosafety Level 2 labs, three Biosafety Level 3 labs, and one Biosafety Level 4 lab. Dr. Patterson's main research interest is medical countermeasures for hemorrhagic fevers and animal models of Zika virus and she serves as Chair of National Primate Centers Working Group on Zika Virus. Dr. Patterson is a member of the Microbiology and Infectious Diseases Research Committee of the National Institute of Allergy and Infectious Diseases and a member of the National Scientific Advisory Board for Biosecurity.



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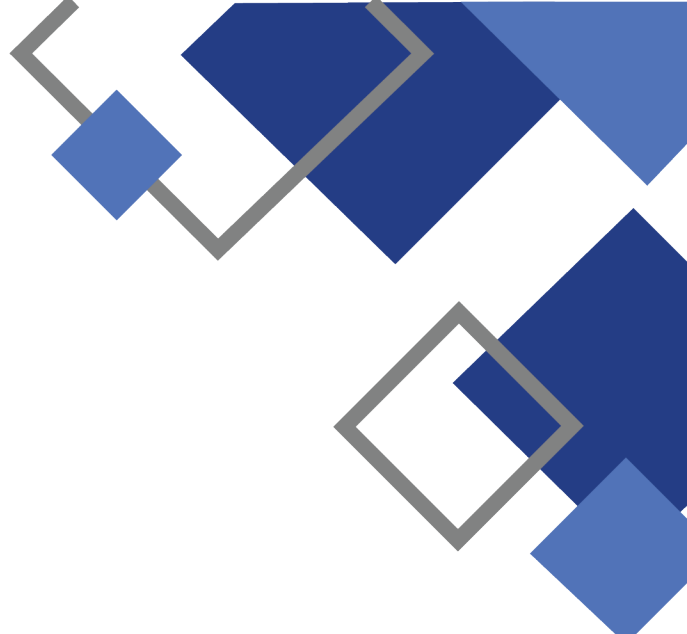
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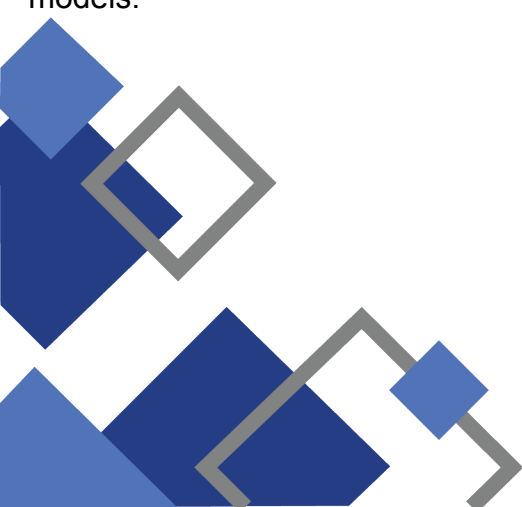
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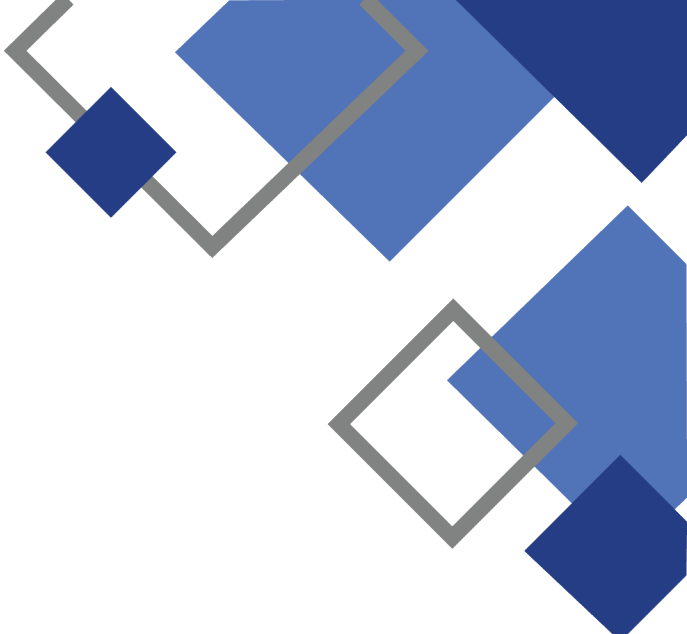
David Donley

New Mexico Highlands University

I've Got Iron On My Mind: exploring factors that shape the neuroinflammatory response of microglia

Iron accumulates in the brain early in Alzheimer's disease, but how this affects microglia, the brain-resident immune cells, is not well understood. Using a cell culture model, we exposed microglia to iron before activating them with amyloid-beta, the protein that forms plaques in Alzheimer's disease (AD). Iron pushes these cells into an energy-production pattern associated with a poorly controlled inflammatory response, and this effect is blocked by drugs that limit iron-related toxicity. A broad screen of proteins in these cells showed that iron suppresses several proteins that normally act as an inflammatory brake, including one called NMES1. These data suggest that iron disables the mechanisms microglia use to keep inflammation in check. To test this iron-inflammation relationship in AD patients, we utilized the Allen Institute SEA-AD dataset, which contains molecular data from human Alzheimer's brains. This effort identified tiers of candidate genes that sit at the crossroads of iron handling, inflammation, and Alzheimer's disease, based on factors like genetic risk and severity of brain pathology. These gene tiers will guide our development of interactive, code-free tools that will allow us to interrogate the SEA-AD dataset for other under appreciated targets such as NMES1. Together, this work supports a model where excess iron disables the natural inflammatory safeguards in the brain, and lays the groundwork for testing these iron-linked targets in an Alzheimer's mouse model and other translational models.

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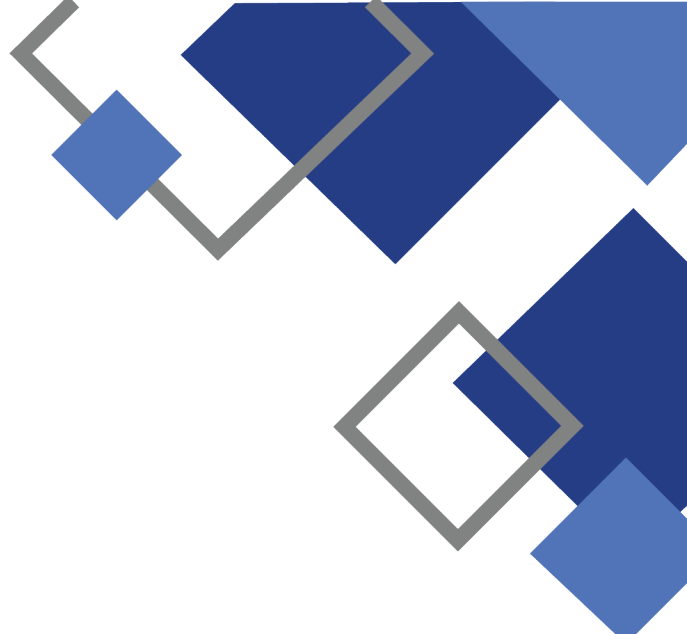
Huixin Zhan

New Mexico Tech

Personalized AI from the Operating Room to Recovery for Rural New Mexico

In rural New Mexico, a patient who needs surgery often travels hours to reach it — and returns home to recover with little specialized support. Across our state, 24.7% of residents live in rural areas and many counties have too few surgeons and therapists, leaving aging and veteran patients with slower, lonelier recoveries and, in the operating room, exposure to rare but catastrophic mistakes. The most feared, a bile duct injury during gallbladder surgery, almost always begins with a single misperception: the surgeon believes the anatomy is safe to cut when it is not. Why has AI not solved this? Because today's surgical robots and assist tools are built one task at a time and ignore who the patient or clinician is — and because most models confidently answer even when they should not. No one has connected the operating room to the recovery room, or taught a model to know the limits of its own judgment. REACT changes that. Our objective is one personalized model that follows a patient across care. In Aim 1 we taught it the fingerprint of each surgeon's movements; on open surgical data it reached 84.96% accuracy, beating standard training. In Aim 2 we carry that knowledge into stroke rehabilitation. Building on this, our proposed continuation gives the model the wisdom to stay silent when surgery is safe and warn when it is not — a vigilant second set of eyes, proven safe before it ever reaches a New Mexico operating room.

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Jacob Jaszczak

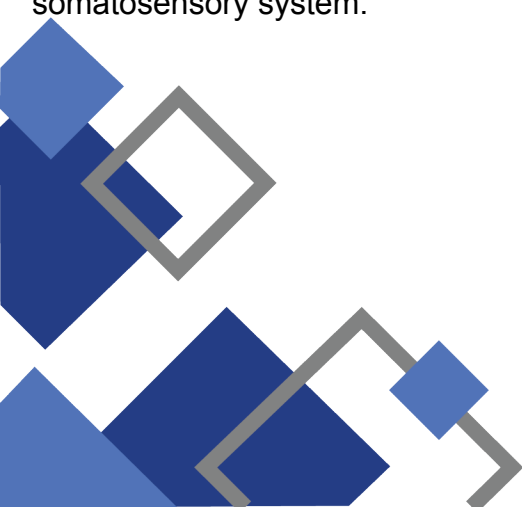
New Mexico State University

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Dissection somatosensory development in a multicellular context

Dysfunction of the somatosensory system profoundly impacts many conditions across development, including chronic pain, the tactile-sensitivity of autism spectrum disorders in children, and the hot-flushes of perimenopause in adults. A functional somatosensory system requires not only sensory neurons, but also epidermal, glial, and immune cells. All of these cells function together to build the multicellular context of a functional somatosensory system. For example, recent research has revealed unexpected roles for skin cells in detecting stimuli and modulating neuron function. Past research has tracked the transcriptional profiles of sensory neurons during development in humans and mice. Due to experimental constraints that arise from the anatomy of the mammalian somatosensory system, these transcriptomes are missing the important tissue context of the somatosensory system. The anatomy of the *Drosophila* somatosensory system allows us to address this gap by allowing for collection of both sensory neurons and context cells at the same time. Furthermore, my lab's previous work demonstrates that *Drosophila* can illuminate important events in sensory function development. We are currently conducting single nucleus RNA sequencing (snRNA-seq) on the *Drosophila* somatosensory system to measure transcriptomes of neurons and their associated context cells during development. With this snRNA-seq transcriptome, we will determine which signaling events orchestrate sensory development, as well as map these events back to mammalian transcriptomes. By revealing novel developmental molecular targets, and uncovering transferable principles of somatosensory development, we will identify targets that can be modulated to treat chronic pain and sensory dysfunction in the multicellular somatosensory system.

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Michaelann Tartis

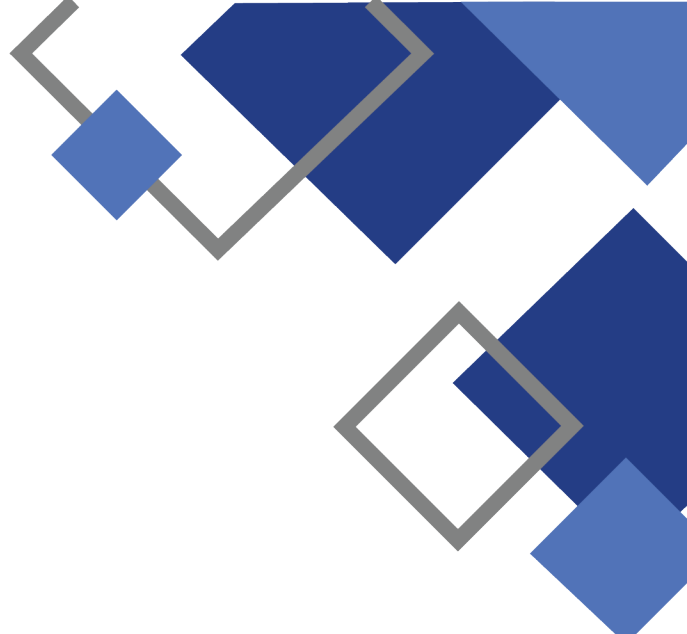
New Mexico Tech

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Michael Kerns,

Optimizing Fabrication Strategies to Enable Transcriptomic Analysis of Mechanically Loaded Neural Tissue Constructs

Traumatic brain injury (TBI) affects over 2.8 million Americans annually, yet mechanistic understanding remains limited by inadequate experimental models. Cerebral organoids recapitulate the complex cellular environment of brain tissue, but their small size (1–2 mm) necessitates embedding in a larger tissue-mimicking platform for exposure to high-rate shear deformation. Following deformation, the limited number of harvested cells yields insufficient RNA for robust transcriptomic analysis of mechanical injury responses. To overcome this constraint, we are developing and comparing multiple fabrication strategies to generate larger three-dimensional neural constructs with sufficient tissue mass for downstream molecular analysis. Three approaches are evaluated: (1) embedding and linear fusion of intact organoids, (2) bioprinting of pre-formed spheroids, and (3) extrusion printing of cell suspensions. Each is fabricated across three matrices—Matrigel, GelMA, and a custom bio-ink—to identify the formulation that best supports construct integrity, viability, and RNA yield. Both cerebral organoids and U87 glioblastoma spheroids are used; the rapidly proliferating U87 line enables efficient optimization of printing and embedding parameters before translation to slower-growing cerebral organoids. Constructs will be embedded in brain-matched polyacrylamide hydrogels and subjected to TBI-relevant shear deformation (strains $\geq 20\%$, strain rates $10\text{--}100\text{ s}^{-1}$) with strain fields mapped by digital image correlation. By identifying the fabrication and matrix combination that maximizes RNA yield while preserving mechanical testability, this work will establish a scalable platform linking quantified tissue deformation to transcriptomic injury signature. Ultimately, these results will contribute to evidence-based safety standards across sports, occupational, and military settings and aid the development and testing of therapeutics.

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Daniel Chadborn

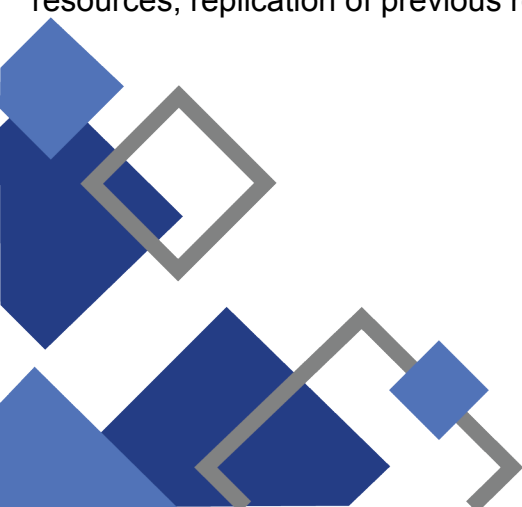
New Mexico Highlands University

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Tamara Vyncke,
Katie Bowmaster,
Andromeda Day,
Julienne Rirsimmah
Amelia Clark

Student Well-Being, Identity, and Inspiration: Longitudinal and Comparison Research in New Mexico, Across the U.S., and Abroad

Incoming Freshman students grapple with a multitude of new experiences when joining a college campus which may impact their psychological wellbeing (Pascarella et al. (2004). Previous research shows that identity development both assists in enhancing wellbeing and boosts relevant factors such as inspiration and motivation as well (Haslam et al., 2009). Because individuals hold numerous identities that are made salient throughout their day-to-day life, these identities can change the way that they engage with others and feel about themselves, which in the context of students could result in positive social, educational, and mental health outcomes (Turner, 1985). While higher education institutions often work to build resources, facilitate community, and improve student outcomes, data on effectiveness outside of usage is not always collected, leading to questions on how effective some of these resources and the policies governing them are. This project, concluding a 4 month pilot study, 10 month longitudinal study with NMHU students, and numerous U.S., international, and broader New Mexico Comparisons seeks to examine the impact of well being on a number of factors. Beginning with a discussion on the impacts of learning communities and campus identity, my presentation will also highlight the issues students face, how identity impacts well-being outcomes, and how New Mexico Students compare to their peers at home and abroad. Furthermore, I will discuss the work we are concluding and our goals for wrapping up the project, including findings on access to campus resources, replication of previous research on inspiration and agency, and more.

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Ryan Ashley

New Mexico State University

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Ema Alvarez,
Monet Hunt
Niklas Kronlein

CXCL12/CXCR4 Signaling Coordinates Early Placental Development: Insights from a Translational Sheep Model

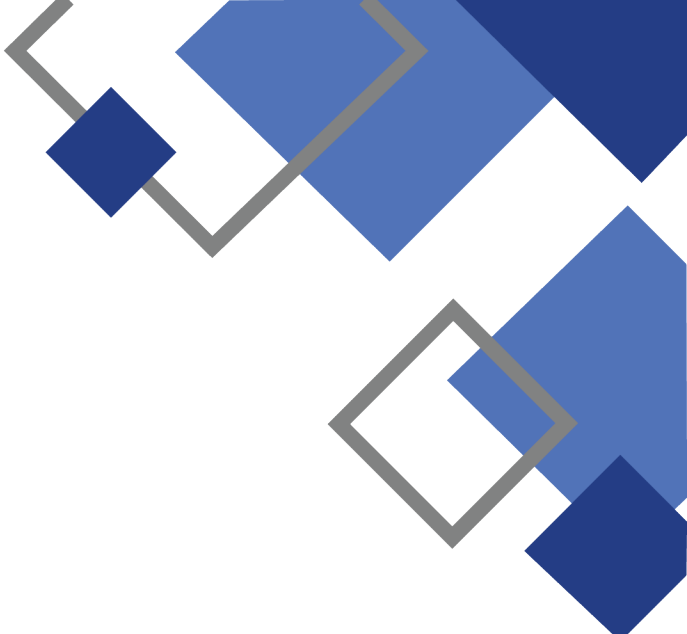
Successful placentation requires coordinated trophoblast differentiation, maternal immune adaptation, and vascular remodeling during the peri-implantation period. Disruptions in these processes contribute to pregnancy disorders including placental insufficiency, fetal growth restriction, and preeclampsia. The chemokine CXCL12 and its receptor CXCR4 are expressed at the fetal-maternal interface, and regulate trophoblast migration, immune function, and angiogenesis. Dysregulation of this signaling axis is implicated in preeclampsia, fetal growth restriction, and recurrent pregnancy loss. However, the in vivo mechanisms by which CXCL12/CXCR4 signaling regulates early placental development remain poorly understood. Sheep exhibit remarkable anatomical, physiological, and developmental similarities to human pregnancy, providing a highly translational large-animal model for investigating mechanisms governing placental establishment. To address this knowledge gap, we tested the hypothesis that inhibiting CXCL12/CXCR4 signaling during implantation disrupts early placental programming. Pregnant ewes received intrauterine infusion of AMD3100 (CXCR4 antagonist) from gestational Day 12 to Day 19, and fetal membrane and endometrial tissues collected on Day 20. Pregnancy establishment was unaffected by treatment; however, AMD3100 increased pregnancy-associated glycoprotein abundance, reduced expression of key angiogenic mediators (VEGFA, PLGF, FLT1, and ANGPT1), shifted immune signaling toward a pro-inflammatory phenotype, altered glucose and amino acid transporter expression, and increased LC3B-II abundance, consistent with metabolic stress. Collectively, these findings suggest CXCL12/CXCR4 signaling coordinates vascular, immune, and metabolic pathways essential for functional placental development. Using a translational sheep model provides new mechanistic insight into the early origins of placental insufficiency and identifies CXCL12/CXCR4 signaling as a potential therapeutic target for improving pregnancy outcomes in both women and livestock.



**Matthew
Guberman-Pfeffer**
New Mexico State University

Two Sides to Every Enzyme: How electrostatics couple active sites to interaction surfaces

Life depends on enzymes that couple, in ways not fully understood, active site reactions with surface interactions. As an interface, how does a protein coordinate enzymatic activity within adaptive biomolecular networks? Virtually all biomolecules are charged, and those charges steer association while modulating enzymatic activity within and critically across domain boundaries, creating 'wireless' networks of integrated processes. Their multi-purposed nature requires suboptimal but sufficient tradeoffs that could serve as regulatory handles. We envision that a distributed, interconnected structure-function map gives a protein the adaptability to integrate into a biomolecular network and render it robust, within limits, to environmental stresses. Using molecular dynamics and quantum mechanics/molecular mechanics, we explore both intra- and interdomain mechanisms of functional coupling through electrostatics. Intramolecularly, we ask when, how, and to what extent active site reactivity is modulated by the number, composition, distribution, and buffering capacity of protonatable residues. We study an orthologous series of topologically conserved proteins (cytochromes c/c2 and high potential iron sulfur proteins) that perform the same function while varying across evolution and engaging different partners. Intermolecularly, we ask how isoform-specific electrostatics modulate interdomain docking and electron transfer rates through electric field effects in nitric oxide synthases (NOSs), paradigmatic examples of the multi-domain proteins that make up more than 80% of eukaryotic proteins and play critical roles in neurological, cardiovascular, and immune function. These investigations will connect molecular events to phenotypic outcomes, reveal how biological systems respond to environmental cues, and ultimately help design therapeutic biomolecular 'prosthetics' that seamlessly integrate into cellular processes.

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Corey Green

Eastern New Mexico University

Mechanisms of contaminant resistance and their physiological consequences

Organic legacy contaminants such as dioxin and dioxin-like compounds remain environmentally ubiquitous and pose a significant risk to both human and environmental health. A possible solution for the survival of a population is through evolutionary rescue mitigated through molecular pathways such as the arylhydrocarbon receptor pathway. We hypothesized that genetic or epigenetic variation with the AhR pathway will be responsible for PCB 126 resistance within zebrafish populations and individuals resistant to PCB 126 will display a reduced ability to cope with common environmental stressors. A parental F0 hybrid wildtype line of zebrafish was created to increase genetic diversity. An LC50 for PCB 126 was determined for F1 fish and a secondary set of F1 was grown out after exposure to the LC50 concentration. Surviving F1 fish produced an F2 generation for which a second LC50 was determined and a second set of F2 are currently being grown out after exposure at LC50 concentration. Samples of F2 fish were collected for genetic, epigenetic, and transcriptomic analysis. Metabolic scope was determined in F2 fish using aquatic respirometry techniques. All data from resistant fish was compared back to concurrently grown out controls. This study aims to establish a new vertebrate model of contaminant resistance and provide a novel insight into molecular mechanisms of contaminant resistance and the evolutionary trade off resulting in physiological consequences.

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Rhiannon West

Northern New Mexico State College

Co-Authors:

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Hope Lopez,
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Evolutionary Genomics of Immune Variation: Building a Framework to Link the Major Histocompatibility Complex, Microbiomes, and Chemical Communication

How variation in immune genes influences host–microbe interactions, behavior, and health remains one of the unanswered questions in biology. The major histocompatibility complex (MHC), a highly polymorphic family of immune genes responsible for antigen presentation, has been linked to disease resistance, microbiome composition, social recognition, and mate choice across vertebrates. However, mechanisms connecting immune genetic variation to behavioral divergence and health remain poorly understood. To address this challenge, we developed genomic resources for three sympatric Bahamian pupfish sister-species (*Cyprinodon variegatus*, *C. desquamator*, and *C. brontotheroides*). Comparative genomic analyses identified predicted major histocompatibility complex class II (MHCII) syntenic regions, revealing conserved and divergent immune gene architecture, including classical and non-classical MHCII genes and putative pseudogenes. Genome-wide dN/dS analyses identified over 11,400 ortholog pairs per comparison, with approximately 1,100 genes showing evidence of positive selection ($dN/dS > 1$). A bimodal distribution revealed a subset of genes evolving under strong selection, including 761 and 744 genes with $dN/dS \geq 30$ and 223 genes shared between comparisons. Together, these findings establish a genomic framework for investigating how immune variation influences host–microbe interactions and complex phenotypes. Future studies will integrate MHC variation with gut and skin microbiome composition, GC-MS characterization of chemical signatures in skin mucus and conditioned water, and behavioral assays to test whether immune genetic variation shapes social recognition through microbiome-derived chemical signals, microbiome-independent MHC-associated cues, or both. This research begins to address a biomedical challenge: understanding how immune genetic variation regulates host–microbe interactions and influences health across vertebrates, including humans.



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Coralie Ahrenskeaff

St. Johns College

Co-Authors:

Dr. Ryan J. Marcheschi,
Diana C. Bautista Tovar,

An Investigation of *Priestia endophytica*

Bacterial resistance to antibiotics is a concerning problem in hospital settings. Specifically, the microorganisms known as the ESKAPE pathogens pose a real concern in healthcare due to their resistance to antimicrobial treatments. This short eight-week research project seeks to find antimicrobial compounds extracted from a soil sample that can inhibit the growth of organisms closely related to these ESKAPE pathogens. Using many of the methods in the Tiny Earth Research Guide, soil was extracted near Mesilla Valley Bosque State Park by the Rio Grande River. Bacteria were diluted using serial dilution and were grown on various growth media in order to observe their behavior in diverse environments. One microorganism was chosen for further investigation due its notable ability to prevent the growth of *Staphylococcus epidermidis*. DNA analysis suggests that this organism is *Priestia endophytica*. Future analysis of the antimicrobial molecules produced by this organism could lead to the development of new antibiotics.



Emily Arias

Eastern New Mexico University

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Estimating the rates of haemosporidian (Apicomplexa: Haemosporida) infection and turnover in birds of northwest New Mexico

Although commonly thought of as uniquely infecting humans in the tropics and causing the disease malaria, haemosporidians in fact parasitize a diversity of vertebrate hosts other than humans. Indeed, over 5,000 species of haemosporidians are known to infect birds, while 95% of human malaria cases are caused by only two species. Preliminary studies of haemosporidians infecting birds have demonstrated important impacts on the fitness, range limits, and community structure of birds; yet malaria parasites remain unsurveyed in most bird species and communities. Indeed, malaria infections in birds appear to be common, including here in New Mexico. I conducted a survey of haemosporidian parasites infecting birds in the Chuska mountains, a previously unstudied region of northwest New Mexico. Specifically, I screened 47 avian host individuals, representing 10 species. Within the Chuska mountains, I discovered a combined infection rate of 117%, which is higher than reported in any previous study of haemosporidians in New Mexico. At the host species level, I discovered that infection rates were also higher than previously reported for the avian species screened. I am currently in the process of screening a larger sample of host individuals and comparing patterns of community turnover, or change in haemosporidian species composition, between the Chuska mountains and other mountain ranges in New Mexico. In conclusion, my research is generating a novel dataset and insights that will deepen our understanding of these important biotic interactions in New Mexico.



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Switching protein translation mechanisms affects hippocampal CA1 pyramidal cell activity

Principal cells in hippocampal CA1 demonstrate increased firing at a specific location known as a place field. To maintain the stability of newly formed place fields, synaptic consolidation is required, which involves new protein synthesis. Experimentally induced disruption of protein synthesis via intraperitoneal injection of anisomycin inhibits synaptic consolidation and destabilizes newly forming place fields. Moreover, the classic pharmacological experiments cannot isolate the synaptic locus of consolidation for place field stabilization as the systemically delivered agents affect all cells. We hypothesize that the CA1 place cells themselves must undergo synaptic consolidation involving cap-dependent translation to maintain place field stability. To test this hypothesis, we have used the chemogenetically-inducible iPKR mouse line to suppress cap-dependent translation by activating the integrated stress response (ISR) in principal neurons (labeled with AAV-CaMKII α -Cre). Mice were implanted with electrodes for awake, behaving electrophysiological recordings while exposed to a familiar and novel context over 24 hours. In a separate cohort of mice, we measured protein translation of key targets relevant to ISR. Our preliminary results show increased population firing hours after drug infusion to activate ISR. Immunohistochemistry validated Cre expression in hippocampal CA1 based on expression of eGFP included in the construct. Western Blot results aim to show the time course for ISR activation and cap-dependent translation suppression. We anticipate our proteomic results will help elucidate the unexpected increase in neuronal activity that should have been stable or suppressed following reduction of cap-dependent translation.



Johnathan Bacon

Eastern New Mexico University

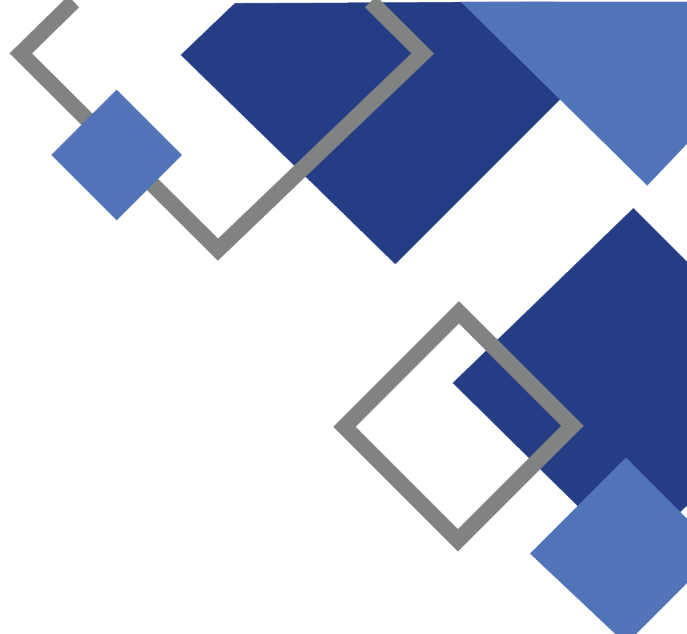
Co-Authors:

Dr. Ryan J. Marcheschi,

Soil Microbes and their Antibiotic Capabilities Against ESKAPE Pathogens

As deadly bacteria continue to spread, they develop resistances to the various antibiotics used in their treatment. This behavior is especially a concern in relation to ESKAPE pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter spp.), a title given to pathogens commonly found in healthcare environments which exhibit an already high resistance to antimicrobial treatments. Research into identifying new compounds which can be used to inhibit the growth of ESKAPE pathogens can help to act against their growing resistances. The research presented was performed to identify the antimicrobial capabilities of various soil microorganisms, especially in their ability to prevent the spread of microbes closely related to that of the ESKAPE organisms.

Microbes from a soil sample from Las Cruces were collected based on their abilities in preventing the growth of other microbes from the same environment. These organisms then had their physical microbial characteristics identified under light microscopy, their metabolic characteristics identified under a wide variety of tests, and their resistance to currently used antibiotics identified. Additionally, the 16S rRNA gene was amplified via Polymerase Chain Reaction such that their DNA could be sequenced and compared to that of the NCBI database, allowing for the identification of the microbes. Ultimately, it was discovered that the organism identified as *Pseudomonas asiatica* prevented the growth of *Staphylococcus epidermidis*, a close relative to *Staphylococcus aureus*. *P. asiatica* was a gram negative bacillus. For future research, the antibiotics it produces are being isolated for further experimentation against ESKAPE organism relatives.

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Turna Basak

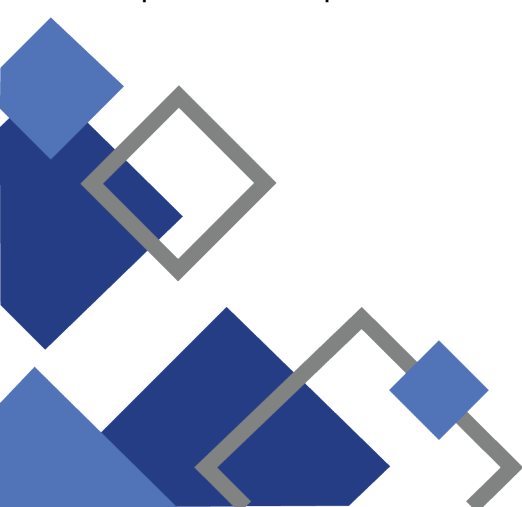
New Mexico Tech

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Anthony Baker,
Michaelann Tartis

Design and Validation of a Custom Syringe-Pump Bioprinting System for Anisotropic Cell Constructs to Model Traumatic Brain Injury

Traumatic brain injury (TBI) occurs when mechanical forces damage tissue and disrupt normal neurological function. Tissue injury can depend on the direction of strain relative to fiber orientation, as fiber alignment causes tissue to deform more readily in one direction than another. Therefore, predictive in vitro TBI models must incorporate directional properties to better replicate native brain mechanics and evaluate injury as a function of fiber orientation. To model this directional response in vitro, a customized bioprinter was adapted onto a Creality Ender 3 V2 platform. The original filament extruder system was replaced with volumetric syringe-pump extrusion using an open-source design (Replistruder 4) capable of printing living cerebral cells suspended in bioink for biological injury assessments. Modifications included replacing the original Creality 4.2.2 mainboard with a BIGTREETECH SKR Mini E3 V3.0 to drive a high-torque stepper motor, and flashing custom Marlin firmware. System calibration included tuning the stepper driver current to the extrusion motor's rated current, extruder step calibration, and optimizing extrusion parameters to achieve high-resolution printing with channel widths of approximately 300 μm . Using this platform, anisotropic structures will be subjected to shear loading with the applied load oriented either parallel, 45° or perpendicular to the printed fiber direction. Digital Image Correlation will be used to quantify local strain fields and determine how strain magnitude and distribution vary with fiber orientation. Overall, preliminary results are expected to establish a reproducible fabrication pipeline to measure differences in shear response between anisotropic and isotropic cell constructs.

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Karla Benitez

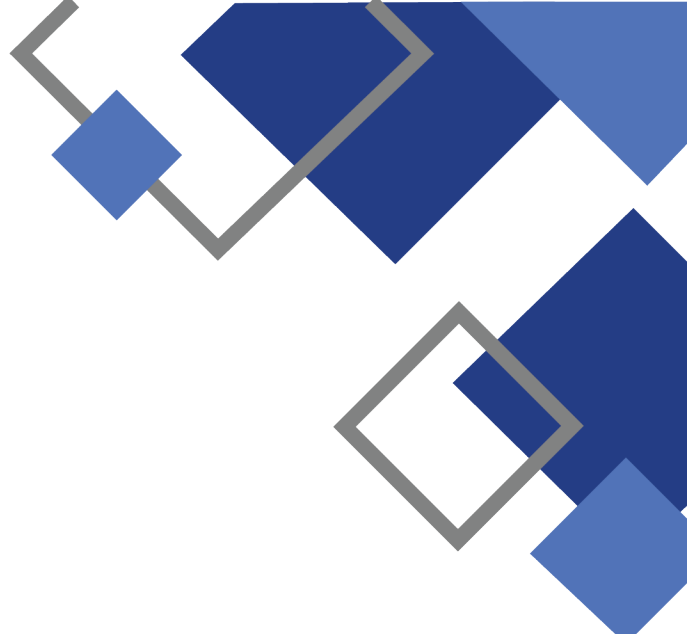
Eastern New Mexico University

Co-Authors:

Dr. Ryan J. Marcheschi,

Isolation and Characterization of a Soil Bacterium with Antimicrobial Activity Against *Enterococcus raffinosus* and *Bacillus subtilis*

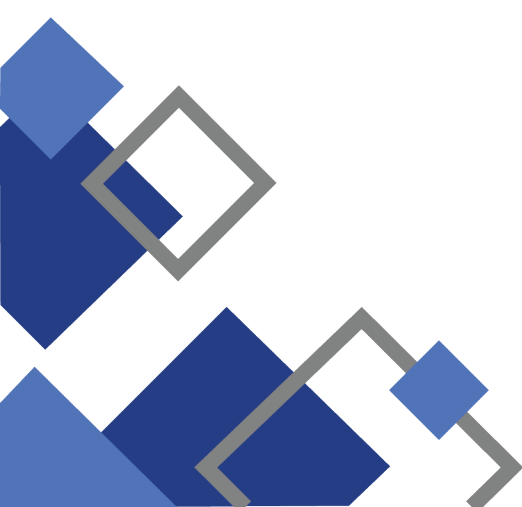
The increasing ability of bacteria to become resistant to antibiotics, especially in hospital settings, is a growing concern. As more bacterial species develop resistance to commonly used antibacterial treatments, there is a greater need to discover new compounds that can effectively prevent bacterial growth. The research presented here was conducted to help identify potential new antimicrobial compounds that are effective against bacterial species closely related to important ESKAPE pathogens, including *Enterococcus raffinosus*, *Staphylococcus epidermidis*, *Escherichia coli*, *Acinetobacter baylyi*, *Pseudomonas putida*, *Bacillus subtilis*, and *Enterobacter aerogenes*. In this study, we isolated bacteria from soil samples to determine whether they could inhibit the growth of other microorganisms in their surrounding environment. After isolating the bacteria, we used several physiological and metabolic tests to help identify their characteristics and determine which antibiotics they were naturally resistant or susceptible to. We also examined the shape, structure, and arrangement of the bacterial cells using light microscopy. Finally, we used PCR to amplify a portion of the 16S ribosomal RNA gene, and we analyzed its DNA sequence to identify the bacterial isolates. Overall, the research presented here shows that organism 2B, which was isolated from soil obtained from Las Cruces, NM, can prevent the growth of *E. raffinosus* and *B. subtilis*. Organism 2B is Gram-positive, is non-motile, and is resistant to penicillin, kanamycin, novobiocin, neomycin, streptomycin, tetracycline, and chloramphenicol. The metabolic capabilities of Organism 2B include nitrate reduction, sorbitol fermentation, fructose fermentation, mannitol fermentation, and glucose fermentation.

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Alan Blair
New Mexico Tech

Interactions between Dectin-1 and Glucans

The Interactions Between Dectin-1 and Glucans The goal of this summer was to study the effects of glucans on myeloma cells rich with Dectin-1. This area of study is important as it could be used to help treat myeloma cancer and could reveal what kind of glucans increase proliferation of myeloma cells. The question at hand is what glucans cause proliferation of myeloma cells to increase or decrease; this needs to be known because glucans are present in many things including things such as the cell wall of *C. Albicans*. This means that the presence of *C. Albicans* could possibly increase/decrease the proliferation of myeloma cells. To determine what effects different glucans, have on myeloma cells, cells were grown from a frozen stock and cultured until an adequate amount were present to use for experiments. The main experiments being run were to be XTT assays to measure metabolic activity of the cells and viability staining and cell counting to determine whether the glucans had any effect on the cells. Unfortunately, the cell cultures developed sudden contamination that caused a shift in the experimental question as there was not enough time to culture new cells before the end of the program. Because of this the question was shifted to, what are the effects of Dectin-1 on *C. Albicans*. Since yeast contains glucans in their cell wall theoretically Dectin-1 could bind to the glucans and reduce the proliferation of the yeast cells.

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Kathryn Bowmaster

New Mexico Highlands University

Co-Authors:

Dr. Daniel Chadborn,

The Efficacy of Campus Counseling: Examining the Relationship Between Service Engagement and Student Well-Being

Student well-being is a critical predictor of academic success, persistence, and overall quality of life, yet increasing rates of stress, anxiety, and depression continue to challenge colleges and universities. As higher education institutions notice a growing mental health crisis, counseling services have emerged as one of the primary interventions used to support students' psychological health. However, questions remain regarding the extent to which engagement with these services is associated with measurable improvements in student well-being, particularly across diverse demographic groups. This study examines the relationship between students' participation in counseling services and their self-reported well-being using a longitudinal survey design. By analyzing data from a diverse sample size, this study investigates whether the frequency and duration of counseling sessions correlate with higher levels of resilience and psychological well-being. Additionally, the research evaluates the gap between resource visibility and resource utilization, questioning if knowing about services is as impactful as participating in them. The findings aim to provide university administrators and mental health practitioners with evidence-based insights to optimize campus support systems. Ultimately, this research highlights the necessity of moving beyond the availability of services and toward ensuring that counseling interventions effectively foster lasting psychological health and academic achievement.



Noah Bronder-Major

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Rhiannon West

Sequence and Analysis of Cyprinodontidae MHCII for Potential Correlation of Sympatric Mating Preference Across Pupfish

The Major Histocompatibility Class II (MHCII) is a complex set of genes which, in addition to activating the adaptive immune response, has been shown in some species to take part in mate choice. Here we explore the potential for MHCII to serve as a component of sympatric preference across pupfish (Cyprinodontidae). Mating trials were performed on 278 Bahamian specimens representing 3 species (*C. brontotheroides*, *C. desquamator*, *C. variegatus*) to determine correlation between behavioral patterns and MHCII. To date, DNA from 94 fin clips sampled from the fish used in the mating trials has been extracted, the β subunit of MHCII has been amplified using PCR, and amplicons have been sent for Sanger sequencing using both forward and reverse primers to optimize sequence length. Alignments were generated in ClustelW from sequence data from successful runs, concatenated, and compiled to construct a bootstrapped Maximum Likelihood Tree. Phylogenetic frameworks were compiled to evaluate association of fish allele preference. Processing sequences included coding sites for heterozygous indication and ensuring phylogenetic analysis used all sites to ensure inclusion of ambiguous bases. Phylogenetic structure showed clear links between species, grouping MHCII from *C. brontotheroides* into its own cluster. Further work will expand pupfish datasets and MHC II compatibility studies across these species to verify these preliminary findings.



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The Efficacy of Campus Counseling: Examining the Relationship Between Service Engagement and Student Well-Being

Student well-being is a critical predictor of academic success, persistence, and overall quality of life, yet increasing rates of stress, anxiety, and depression continue to challenge colleges and universities. As higher education institutions notice a growing mental health crisis, counseling services have emerged as one of the primary interventions used to support students' psychological health. However, questions remain regarding the extent to which engagement with these services is associated with measurable improvements in student well-being, particularly across diverse demographic groups. This study examines the relationship between students' participation in counseling services and their self-reported well-being using a longitudinal survey design. By analyzing data from a diverse sample size, this study investigates whether the frequency and duration of counseling sessions correlate with higher levels of resilience and psychological well-being. Additionally, the research evaluates the gap between resource visibility and resource utilization, questioning if knowing about services is as impactful as participating in them. The findings aim to provide university administrators and mental health practitioners with evidence-based insights to optimize campus support systems. Ultimately, this research highlights the necessity of moving beyond the availability of services and toward ensuring that counseling interventions effectively foster lasting psychological health and academic achievement.



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The Effect of Perceived Ease of Access to Campus Mental Health Services on Student Well-Being

University students face considerable challenges throughout their studies that can have a substantial impact on their mental health. Students' knowledge of campus resources allocated to support their mental health is mediated by many factors: gender, off or on-campus residence status, or current mental health (Yorgason et al., 2008). Following up on a broader longitudinal study at NMHU examining issues and use of campus resources, this series of comparison surveys aims to explore the relationship between perceived ease of access to mental health resources on campus and student wellbeing. We hypothesize that students who report greater perceived ease of access to mental health resources (regardless of actual use) will report a more positive sense of wellbeing than students reporting a perceived difficulty accessing mental health resources (regardless of actual use), and that students who report a higher degree of perceived ease of access to mental health resources utilize the resources more frequently than students who report a higher degree of perceived difficulty accessing resources. Data from New Mexico students ($n = 120$) and the rest of the United States ($n = 400$) was collected related to knowledge of campus resources, perception of ease of accessibility, and other related factors and examined alongside wellbeing using Supranowicz & Paz's physical, mental, and social well-being scale (PMSW-21). Poster will discuss the initial findings and broader implications for campus resource access, use of resources, and how campus size may impact these factors.



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Social behavior in the Jamaican fruit-eating bat (*Artibeus jamaicensis*)

Animal behavior influences and interacts with an organism's physiology and ecology. For example, intraspecific interactions (those within a species) influence how an individual or population uses space and other resources. In species that form large social groups, these intraspecific interactions are highly observable during reproductive seasons. Here we examine the social behaviors of one such social species, *Artibeus jamaicensis*. This species has a harem style mating system, but little is known about the formation of or what behaviors are occurring within these groups. To observe and categorize these behaviors during a breeding trial, we used continuously monitoring video cameras paired with antennas that track animal identity using Passive Integrated Transponder tags [TO1.1]. Following ten female bats over seven nights, here we present data from the first 11% of data collected as well as an ethogram developed from these [TO2.1] observations. Preliminary analyses reveal trends in the frequency of behaviors, types of behaviors most and least observed, and the correlation between light-dark cycles and activity-levels. Our findings provide a stable foundation for further research on the social behaviors of *Artibeus jamaicensis*.



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From Exposure to Organismal Response: Interpreting Sublethal Vanadium Toxicity in Adult Zebrafish

Vanadium is an environmentally relevant contaminant entering freshwater ecosystems through mining, fossil fuel combustion, industrial activities, and the redistribution of metals following wildfires. As environmental exposure becomes more common, predicting how contaminants alter organismal function has become an increasingly important goal of aquatic toxicology. Behavioral, physiological, and tissue-level endpoints each provide unique insight into organismal response to vanadium exposure. Here, we examined whether evaluating these complementary responses together provides a more complete understanding of whole-organism toxicity following sublethal vanadium exposure. Using adult zebrafish (*Danio rerio*) as a vertebrate model, physiological and behavioral endpoints were evaluated following seven-day aqueous exposure to sodium metavanadate (NaVO_3). Respiratory function was characterized through aquatic surface respiration, opercular beat rate, and closed-system respirometry, providing complementary measures of behavioral compensation, ventilatory effort, and metabolic performance. Vanadium accumulation was quantified using inductively coupled plasma mass spectrometry (ICP-MS) to determine tissue-specific accumulation in gill and liver tissues and whole-body vanadium burden in residual body tissues. Hepatosomatic index was measured as an indicator of metabolic condition and organismal energy allocation. Each endpoint was selected to characterize a distinct aspect of organismal function, allowing physiological responses to be interpreted collectively rather than as isolated indicators of toxicity. By relating internal vanadium burden to coordinated changes in respiration, metabolism, and behavior, we evaluated how complementary measures contribute to a more complete interpretation of sublethal vanadium toxicity and the physiological state of the organism.



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Micro and Nano-plastic (MNPs) Exposure Leads to Altered Immune Response in Mice

As global MNPs contamination has grown exponentially, a parallel rise has been observed in the incidence and prevalence of autoimmune disorders. Microplastics leech into everyday life, as particles are broken down from plastic products that can immediately enter our body. Emerging research suggests that no human population remains unexposed to microplastics. We hypothesize that MNPs in the body dysregulate immune responses; the effects of MNPs on CD4 T-cell responses such as cytokine production are unknown. To examine this in smaller detail we will look specifically at CD4 T-cells; they are one type of immune cell that drives autoimmune responses. Therefore, the goal of this study is to examine how Ocean plastic-derived MNPs affect CD4 T-cells. In this study, we used ocean plastic-derived MNPs that are environmentally relevant, particles that are 20 microns across and comprised primarily of polyethylene plastic. The novelty of the MNPs that we are using reflects a real-world scenario and are of the same size detected in human bodies. For the CD4 T-cells, they were isolated from the spleen of C57Bl/6 mice, some activated with CD28/CD3 and some treated with microplastics over a 1- and 2-day period to act as controls. The different time intervals show how MNPs affect CD4s at different activation states. From this treatment, the RNA was extracted and reverse transcribed into complimentary DNA (cDNA) followed by qPCR to measure cytokine production. The current results of this study have suggested that MNP may alter CD4 cell responses, specifically higher cytokine production.



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More than Membership: How Student Organizations Affect Campus Identity, Community, and Well-Being

University culture is directly connected to Student engagement, as students are the community members who shape campus culture. There are many types of student organizations. Involvement in these student organizations has been shown to enhance students' college success and well-being. We sought to examine differences between students in student organizations and those who are not. We hypothesized that students would develop higher levels of campus identity and that their inclusion in student orgs would boost other variables, such as well-being. Across five studies, we evaluated the impact of student organizational membership and several other factors. Participants were collected from NMHU ($n = 139$), an international sample ($n = 314$), a Canadian student sample ($n = 301$), and two broader U.S. studies ($n = 403$, $n = 400$). Surveys examined various student organizations and their connections to identity, campus community, and well-being. Preliminary results show that the U.S. and international samples were significant at salient levels for university student identity and most aspects of sense of belonging and well-being. The final analysis will also include information from the official summer 2026 U.S. and New Mexico comparison studies. Results indicate that being part of campus organizations comes with benefits, not only a heightened sense of community but also boosts in well-being. However, university size may decrease these effects, with smaller universities seeing benefits regardless of organizational memberships.



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Engineering Antibacterial Functionality in Ti–Cu Alloys through Controlled Dewetting

Titanium and its alloys are widely used for orthopedic and dental implants because of their excellent biocompatibility and mechanical properties. However, the growing incidence of orthopedic implant infections and peri-implantitis has increased interest in Ti–Cu alloys as promising materials for biomedical and clinical applications. Recent studies have explored nanoparticle-based surface coatings on Ti–Cu alloys as an effective approach to simultaneously improve antibacterial activity and mechanical stability by modifying the surface chemistry. Nevertheless, nanoparticle-coated implants often experience limitations such as excessive coating thickness, poor interfacial adhesion, coating delamination, cytotoxicity, and reduced cell viability. To address these challenges, pure Ti and Ti–Cu alloy implants were fabricated using arc melting and subsequently modified through the controlled dewetting of Pt nanoparticles to enhance their antibacterial efficacy and mechanical performance. The novelty of this study lies in the use of controlled dewetting as a nondestructive post-processing method to biofunctionalize inorganic implant surfaces while promoting strong nanoparticle adhesion to the substrate. Pure Ti and Ti–xCu alloys containing 2 and 5 wt.% Cu were produced by arc melting and then surface-modified through controlled nanoparticle dewetting. Their antibacterial activity was evaluated against *Staphylococcus aureus* and *Pseudomonas aeruginosa*. In addition, cytocompatibility was assessed using NIH3T3 fibroblast cells. The findings demonstrate that controlled nanoparticle dewetting is a robust surface-engineering strategy for enhancing the antibacterial functionality and mechanical performance of Ti-based implants for biomedical applications.



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Characterization of Ethanol Sensitivity in *Slc39a8* Heterozygous Knockout Mice

Alcohol is a commonly used addictive substance worldwide, and alcohol use disorder (AUD) has a substantial genetic component. Genome-wide association studies have identified a potential role for the *Slc39a8* gene in risk for problematic alcohol use and alcohol consumption. *Slc39a8* encodes the metal ion transporter ZIP8, which transports zinc, manganese, and other metal ions across cellular membranes that could influence an individual's susceptibility to AUD, including metal ion homeostasis, cellular metabolism, and dopamine signaling. Here, we sought to explore the role of *Slc39a8* in two measures of alcohol (ethanol) sensitivity using *Slc39a8* heterozygous knockout mice and wild-type littermates. Sensitivity to ethanol-induced ataxia was assessed using the Balance Beam test, in which mice received a low dose (1.4 g/kg) of ethanol and traversed a narrow beam while the number of foot slips was recorded. To measure sensitivity to the sedative-hypnotic effects of ethanol, mice were tested one week later for ethanol-induced Loss of Righting Reflex. Mice received a 3.75 g/kg dose of ethanol, and the time required to regain the ability to right themselves was recorded. Blood samples were collected at the time of recovery to determine blood ethanol concentrations. Ultimately, understanding how biological and genetic factors such as variations in *Slc39a8* function contribute to traits like alcohol sensitivity and excessive alcohol consumption may help in the development of more effective treatments and prevention for AUD.



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The Effects of Climate Change on Soil Bacterial Abundance

Microbial communities inhabiting soils are essential to human, animal, and environmental health. They perform ecosystem functions such as decomposition, nutrient cycling, and can suppress pathogens. While climate change has been known to impact soil microbial communities, its effects on the activity and abundance of human pathogenic bacteria in our region remain understudied. The purpose of this study was to quantify the effects of increased temperature and decreased precipitation on bacterial abundance across the Merriam Powell Elevation Gradient in Arizona. Established in 2002 and spanning four ecosystems, this experimental array includes intact plant soil cores that were transplanted downslope to simulate future warmer and drier conditions. We hypothesized that the amount of bacteria would decrease due to the environmental changes. To test how changes in temperature and precipitation affect the soil bacterial abundances, soil samples were collected from each core and frozen to preserve the microbes and DNA in the soil. DNA was extracted from 40 soil samples per ecosystem. Then, the bacterial abundance analysis was achieved through quantitative PCR (qPCR) with primers targeting the bacterial 16S rRNA gene. Our results showed generally negative responses of bacterial abundances to transplantation across the elevational gradient, which is consistent with the long term impacts of reduced precipitation and warming observed in other soils. Future work will pair qPCR with amplicon sequencing, metagenomic sequencing, and pathogen assays to identify soil borne human pathogens, assess changes in soil virulence potential, and evaluate the long term effects on the plant rhizosphere pathogen communities.



Taylor Emerson

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Examining the Microbiota-Gut-Brain Axis in *Drosophila Melanogaster* Using Associative Learning and Memory Assays

Drosophila melanogaster is an optimal model for studying the gut-brain axis due to its simple microbiome and ability to develop numerous mutants, allowing researchers to examine their underlying biological mechanisms. Immune communication and neurotransmitters influence learning, memory, development, and social behavior. These have also been linked to depression, Parkinson's disease, and Alzheimer's. Our research evaluates how the default states of gut bacterial microbes affect neurological functions. We compared conventionally reared flies with axenic flies and gnotobiotic flies containing a defined microbiome. My contribution utilized an olfactory T-maze assay to examine associative learning and memory. In this assay, flies are trained to associate a specific odor with an electric shock. They are then placed in a testing chamber, where we observe if they avoid the preconditioned odor. This experiment will help determine whether the absence of microbiomes, which carry gut bacteria, alters olfactory learning and memory between conventionally reared flies and axenic flies. Ultimately, the long-term goal of this research is to understand the biological processes that cause microbiome-dependent behavioral changes. To assess if reducing activity in redundant neurotransmitter systems reveals small behavior changes caused by the microbiome, we use dopamine and octopamine deficient flies. Our research will also apply mutants, antibiotic treatments, and neurotransmitter-targeting drugs to see if gut bacteria affect behavior through development or changes in brain chemistry while entering adulthood. Our research will test whether restoring the microbiome or altering neurotransmitters with drugs can reverse behavioral defects.



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Toxicity Assessment of Treated Produced Water from Thermal and Membrane Processes and Post Treatment Organic Extract on Human Cell Lines

The production of crude oil is a large part of the economy in the Permian Basin, but the produced water (PW) that comes from the extraction process is highly toxic. Because of this, the topic of purifying the PW so it is fit to be re-released into the environment is a concern, and the effects that it'll have on human health have become a large question. The PW from four different oil and gas corporations using thermal and membrane processes was studied. The samples used were raw PW, distillates from each purification process, the post-treatment product, and organic extract from the post-treated water. Various assays were conducted to assess toxicological effects on cell viability, gene expression, and aryl hydrocarbon receptor (AhR) activation of liver cells (Hep-G2) after exposure. What can be expected is that the treated PW will show minimal cytotoxicity and that the organic extract produced from the post-treatment water from all the samples will show fewer contaminants activating the AhR and less impact on the cells' viability, highlighting the need for the post-treatment following the respected purification processes. Further assays will be done using the organic extracts in addition to all the tests being done on other human cell lines to understand how the PW affects all parts of the human body and is safe for discharge and reuse in our environment. Keywords: Produced water, thermal and membrane purification, cell viability, gene expression, activation of aryl hydrocarbon receptors



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Paenibacillus lautus as a soil-based Inhibitor of ESKAPE Relatives

Antibiotic resistance in bacterial pathogens is a growing problem, and it's especially serious in hospital settings. Nearly 20 years ago, researchers identified a group of organisms now known as the ESKAPE pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp.) as a major concern, since many of them resist standard antimicrobial compounds that can stop the growth of organisms closely related to them. For this study, we isolated microorganisms from soil and tested whether they could stop other nearby microbes from growing. Once we had our isolates, we ran a series of tests to characterize their physiological and metabolic traits, and we checked which antibiotics they were naturally resistant or susceptible to. We used light microscopy to look at their cell shape, structure, and organization, and we used PCR to amplify a region of the 16S ribosomal RNA gene so we could sequence it and identify the microbes. Overall, this research shows that *Paenibacillus lautus*, isolated from soil collected from South Las Cruces, can inhibit the growth of *E. raffinosus*, *S. epidermidis*, and *B. subtilis*, which are "safe relatives" of the ESKAPE pathogens. *P. lautus* is Gram-positive, it produces endospores, it is motile and it is resistant to Streptomycin, Erythromycin, Tetracycline, Chloramphenicol, Penicillin, and Kanamycin. This organism also tested positive for Catalase, Oxidase, Nitrate reduction, and it fermented Xylose, Fructose, Galactose, Lactose, Sucrose and Raffinose. In the future, further investigation of the antimicrobial molecules produced by *P. lautus* may lead to development of new antibiotics.



Koda Fister

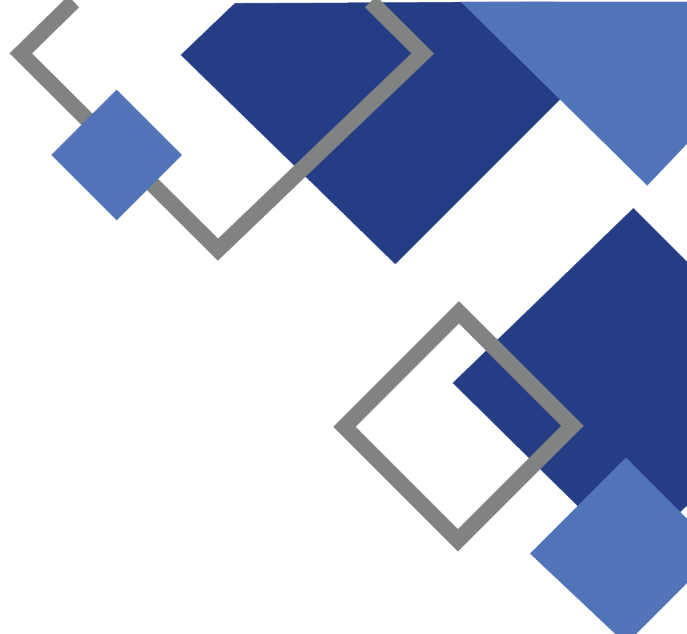
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Cytobacillus firmus: Metabolic Characteristics and Antimicrobial-Producing Potential

Antibiotic resistance is a growing global health concern, especially among bacteria related to the ESKAPE (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp.) pathogens. As many bacteria become resistant to common antibiotics, discovering new antibiotic compounds from microorganisms has become very important. In this study, soil bacteria were isolated and tested for their ability to inhibit the growth of bacteria related to the ESKAPE pathogens. The isolate was identified as *Cytobacillus firmus* using 16S rRNA sequencing and characterized through microscopy, Gram staining, and metabolic testing. *Cytobacillus firmus* showed antimicrobial activity against *Staphylococcus epidermidis*. The organism is Gram-variable, rod-shaped to slightly curved, forms clusters, produces endospores, and is motile. It tested positive for oxidase and amylase activity. It tested negative for the fermentation of glucose, xylose, galactose, sorbitol, lactose, sucrose, and raffinose, as well as for salt tolerance, catalase, urease, and lipase activity.

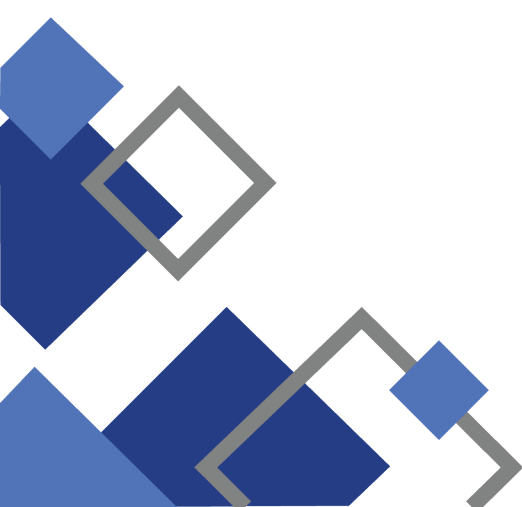
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Joel Flores

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Biophysical Characterization of the SARS-CoV-2 ORF3a and Human VPS39 Proteins

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) accessory protein ORF3a has been implicated in disrupting the fusion of autophagosomes with lysosomes, thereby impairing autophagic flux and promoting viral replication. ORF3a is a transmembrane viroporin that facilitates ion transport across cellular membranes, alters host cell physiology, and contributes to virus release. One of its host binding partners is the human vacuolar protein sorting 39 (VPS39), a subunit of the homotypic fusion and vacuole protein sorting (HOPS) complex. The HOPS complex plays a critical role in endosomal trafficking and lysosomal biogenesis by mediating the tethering and fusion of late endosomes and lysosomes. Interaction between ORF3a and VPS39 disrupts HOPS-mediated membrane fusion, leading to defective autophagy and enhanced viral replication. This study aims to characterize the biophysical interaction between ORF3a and VPS39 through quantitative binding analysis. Recombinant VPS39 was expressed in *Escherichia coli* using a pET expression system with IPTG induction, whereas recombinant ORF3a was produced in ExpiSf9 insect cells using a baculovirus expression system generated with pFastBac and DH10Bac. Both proteins were purified by immobilized metal affinity chromatography (IMAC) followed by size-exclusion chromatography (SEC). The interaction between ORF3a and VPS39 will be quantitatively characterized using isothermal titration calorimetry (ITC), which measures the heat released or absorbed during binding to determine the equilibrium dissociation constant (K_D), binding stoichiometry, and thermodynamic parameters of the interaction. These studies will provide mechanistic insight into how ORF3a hijacks the host autophagy machinery and may facilitate the development of antiviral strategies targeting the ORF3a–VPS39 interaction.

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Serum Amyloid A: An Upstream Regulator of Hyperglycemia-Induced Mitochondrial ROS in Triple Negative Breast Cancer

Triple-negative breast cancer (TNBC) is the most aggressive breast cancer subtype, with high rates of recurrence, metastasis, and poor clinical outcomes. Breast cancer patients with preexisting diabetes have a 28% shorter disease-free survival than nondiabetic patients, highlighting the clinical significance of hyperglycemia in breast cancer progression. Our preliminary studies identified the pro-inflammatory protein Serum Amyloid A (SAA) to be elevated in TNBC tumorspheres under hyperglycemic conditions and demonstrated that SAA regulates the cancer stem cell (CSC) population. We hypothesized that hyperglycemia promotes CSC maintenance through SAA-dependent mitochondrial reactive oxygen species (mtROS) signaling. TNBC cell lines MDA-MB-231 and BT-549 were cultured under hyperglycemic (25 mM glucose) conditions. SAA expression was transiently inhibited using siRNA, and mtROS levels were quantified by flow cytometric analysis of MitoSOX fluorescence (1 μ M; n = 3–6 biological replicates with triplicates per group). Appropriate siRNA and flow cytometry controls were included, and statistical significance was assessed using Student's t-test. SAA inhibition under hyperglycemic conditions reduced the proportion of MitoSOXhi cells compared with controls, although the response varied between cell lines. These findings suggest that SAA is an upstream positive regulator of mtROS in TNBC under hyperglycemic conditions. Future rescue studies restoring mtROS levels in SAA-inhibited cells are needed to determine whether mtROS mediates the effects of SAA on CSC maintenance and plasticity.



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Dr. Judy Cannon

Metabolic Regulation of T cell Motility by Chemokines

In Dr. Cannon's lab, we are investigating a type of immune system cell known as T cells. T cells are considered naive until they detect an infection. Once T cells detect an infection, they become activated to defend the body by clearing the infection. The focus of this study is on the chemokine receptors to observe how chemokine receptors help T cells move around tissue and clear an infection. At the moment, we are observing T cell immune responses and examining chemokine receptors such as CXCR3 and CXCR4, and how CXCR3 and CXCR4 help T cells move by ATP production through processes such as glycolysis, which burns sugar, and oxidative phosphorylation, which uses the mitochondria to generate ATP. The main question we will be addressing is: How do chemokine receptors signal T cells to use glycolysis or oxidative phosphorylation for movement? For our experiments, we isolate and activate T cells to perform Transwell migration assays to measure T cell migration in response to chemokines such as CXCL10 (CXCR3 ligand) and CXCL12 (CXCR4 ligand). We have done Transwell experiments and found that the CXCL10 signal induces more T-cell migration than the CXCL12 signal. To further this project, we plan to include inhibitors of glycolysis and oxidative phosphorylation to see whether they change or block cell movement in response to CXCL10 and CXCL12. This will eventually help us understand the metabolic pathways T cells use to move and clear infection.



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Isolation and Characterization of *Bacillus mojavensis* with Antimicrobial Activity Against Gram-Positive Bacteria

The increasing prevalence of antibiotic-resistant bacterial pathogens, particularly the ESKAPE pathogens, poses a significant global public health challenge due to their ability to evade many conventional antimicrobial therapies. This study aimed to identify soil bacteria capable of producing antimicrobial compounds effective against bacteria related to these clinically important pathogens. Soil microorganisms were isolated and screened for antimicrobial activity against neighboring bacteria. Physiological and biochemical assays were performed to characterize metabolic capabilities and antibiotic resistance. Cellular morphology was examined using light microscopy. Molecular identification was achieved by amplifying and sequencing a portion of the 16S ribosomal RNA (16S rRNA) gene, followed by comparison with known bacterial sequences. One of these microorganisms, which was isolated from soil in Las Cruces, NM, was identified as *Bacillus mojavensis*. This microorganism inhibited the growth of *Enterococcus raffinosus* and *Staphylococcus epidermidis*. It was Gram-positive, non-motile, and resistant to streptomycin. Biochemical testing demonstrated that the organism was salt tolerant, reduced nitrate, hydrolyzed starch, produced acetoin through glucose fermentation, fermented mannitol, sucrose, and glucose, and produced catalase. The antimicrobial activity of *Bacillus mojavensis* against Gram-positive bacteria highlights its potential as a source of novel antimicrobial compounds. These findings support continued investigation of soil microorganisms as promising candidates for the discovery of new treatments to combat antibiotic-resistant bacterial infections.



Jose Hernandez

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Dr. Manish Jain

Development and Characterization of a Hydroxyapatite-Based Composite Scaffold Loaded with Natural Medicine for Bone Tissue Engineering

Interest in bone tissue engineering has increased due to the growing demand for effective treatments for dental and craniofacial defects, musculoskeletal disorders, and bone-related cancers. Conventional therapies, such as autologous bone grafts, are limited by donor-site morbidity, restricted bone availability, and the need for additional surgery. This study aims to develop and characterize a multifunctional hydroxyapatite (HA)-based composite scaffold that combines the favorable biological and mechanical properties of multiple materials for bone tissue regeneration. HA is widely used in bone tissue engineering because of its structural similarity to human bone. However, its lack of antimicrobial activity and poor mechanical properties require modification before use as a scaffold. Previous studies have shown that incorporating magnesium oxide (MgO) into HA enhances alkaline phosphatase activity, promoting osteogenic differentiation, while yttria-stabilized zirconia (YSZ) improves chemical stability, fracture toughness, and hardness without compromising biological properties. The novelty of this study is the incorporation of ginger extract and tannic acid for their therapeutic effects. It is hypothesized that loading an HA composite scaffold with these natural compounds will produce a material with improved mechanical strength, biocompatibility, and antibacterial activity for bone tissue regeneration. Physicochemical characterization was performed using FTIR, XRD, and SEM, and antibacterial activity against *Staphylococcus aureus* was evaluated.



Tawnee Hicks

San Juan College

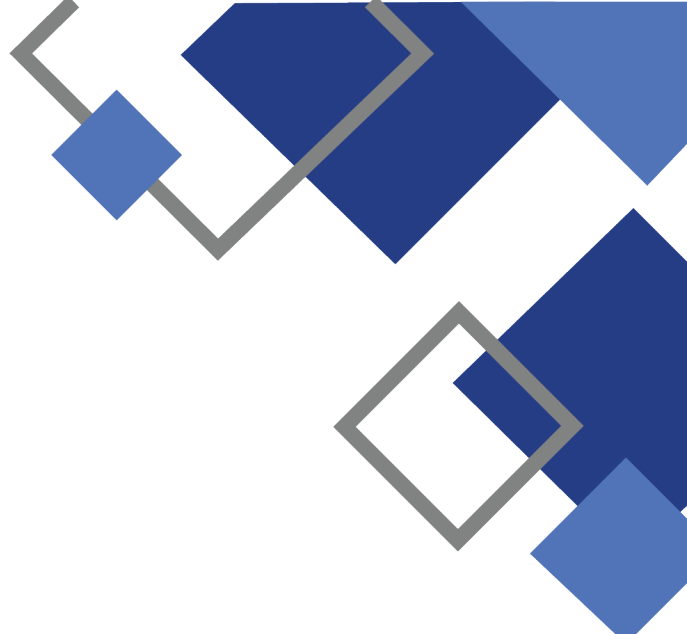
Co-Authors:

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The Role of the Gut-Brain Axis in Aggression and Courtship Behaviors of *Drosophila melanogaster*

Although the gut-brain axis has been recognized since the nineteenth century, much remains unknown about its influence on social behavior. Our model organism, *Drosophila melanogaster*, is well suited to investigate these interactions because of its well-characterized genetics, conserved neurobiological pathways, and relatively simple gut microbiome. Given these advantages, this study aims to investigate the role of the gut-brain axis in modulating social behaviors such as aggression and courtship. We hypothesize that *D. melanogaster* reared under axenic conditions will exhibit reduced aggression and courtship behaviors compared to conventionally reared (CR) individuals with unaltered gut microbiota. To test this hypothesis, two behavioral assays will be performed.

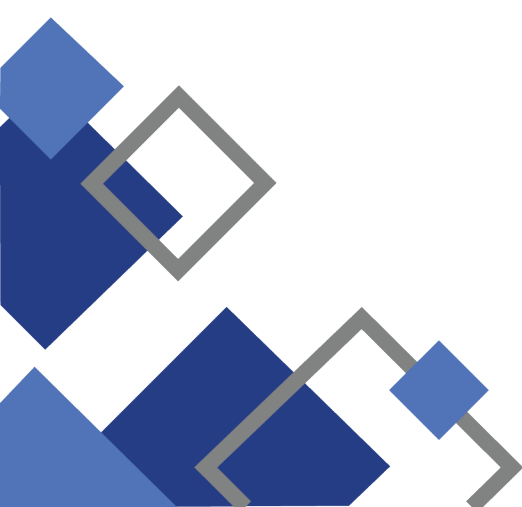
Aggressive behavior will be quantified by placing pairs of males from each rearing condition in arenas containing a food resource and recording the latency and frequency of aggressive interactions during 20-minute observation periods. Courtship behavior will be evaluated by recording mating pairs from each rearing condition and quantifying courtship behaviors as well as latency to copulation. Findings from this study may provide insight into the role of the gut-brain axis in regulating social behaviors and contribute to a broader understanding of microbiota-mediated behavioral mechanisms.

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Braden Holden-Silvis
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Investigating the Molecular Basis of Sickel Cell Nephropathy Through Comparative Bioinformatics.

Chronic Kidney Disease (CKD), caused by Sickel Cell Disease (SCD), also known as Sickel Cell nephropathy, affects around 30% of the nearly 8 million people worldwide with SCD. The specific sickle mutations in the gene coding for beta-hemoglobin (HBB) can lead to organ damage, blindness, and death. Specifically in the kidneys, sickle-shaped cells can cause abnormalities to tubular and glomerular function; sickle-shaped cells also result in less oxygen being carried to the kidneys, which can lead to deregulation due to the death of kidney cells. This research examines the overlap of molecular pathways between Sickel Cell Disease and Chronic Kidney Disease and how Sickel Cell links to kidney damage and the onset of Sickel Cell nephropathy. Sickel Cell Disease is a chronic disease that is heavily stigmatized and deemed a "Black disease," and millions of people from a myriad of races can be carriers or victims of the erratic pain crises, misadvocation, and false information surrounding Sickel Cell Disease. Sickel Cell nephropathy is another potential complication for those with Sickel Cell Disease and is often only recognized by those affected by, or studying the disease. With the help of bioinformatic tools such as ShinyGO, ReviGO, and GEO2R, I am comparing molecular pathways and GO biological processes, with aims to determine differences and similarities in those with SCD, CKD, or controls.

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Sexual Dimorphism in *Drosophila* Gut lipid homeostasis.

Abstract: Lipid homeostasis is fundamental to organismal health, energy production, membrane integrity, and cellular signaling. Its dysregulation drives obesity, diabetes, and cardiovascular disease. Sexual dimorphism profoundly influences metabolic physiology—females and males differ in fat distribution, storage capacity, and disease susceptibility. However, the molecular mechanisms driving these sex-specific programs, particularly within the gut—the primary site of dietary lipid processing—remain incompletely understood. We leverage *Drosophila melanogaster*, a powerful genetic model sharing ~75% of human disease-related genes and possessing functionally analogous metabolic organs: the gut for digestion and endocrine signaling, and the fat body for combined hepatic and adipose functions. In this study, we investigate the combined effects of sex and age on LD dynamics in adult *Drosophila*. Flies of both sexes at various ages were dissected, stained with BODIPY (neutral lipids) and DAPI (nuclei), and examined via fluorescence microscopy. Our imaging revealed three key findings: first, lipid droplet content progressively deteriorates with advancing age, accompanied by a marked decline in lipid accumulation; and second, females consistently store significantly more lipid droplets throughout the gut compared to males, which exhibit a leaner phenotype with reduced LD storage and third, males and females process dietary fats differently at the cellular level. These observations establish that lipid metabolism in *Drosophila* exhibits sexually dimorphic, age-dependent trajectories that mirror mammalian sex differences in obesity and diabetes risk. Future studies will focus on elucidating the genetic and hormonal regulators enforcing these gut-intrinsic sexual programs, with the goal of informing sex-specific therapeutic strategies.



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New Mexico Tech

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Huixin Zhan

Decoding Reservoir- and Human-Associated Orthohantavirus Protein Signatures with Protein Language Models

Orthohantavirus is a genus of zoonotic RNA viruses maintained in animal reservoirs that can cause severe human disease after spillover. Identifying sequence features associated with pathogenicity is important for understanding viral evolution, spillover risk, and disease surveillance. In this study, we evaluated whether PLMs can distinguish reservoir-associated from pathogenicity-proxy Orthohantavirus protein sequences. A curated dataset of 452 protein windows representing S, M, and L genome segments from NCBI Protein/GenBank records was used to compare a majority baseline, TF-IDF logistic regression, ProtBERT, ProstT5, and multiple ESM2 variants. Models were evaluated using repeated stratified cross-validation, and prediction errors were analyzed across genome segments, host groups, and sequence accessions. Results show that protein windows contain measurable signal for distinguishing reservoir-associated and pathogenicity-proxy labels, although performance varied across models. The strongest biological finding was that errors were not randomly distributed, but concentrated in specific genome segments, host lineages, and recurrent sequence windows. Pathogenicity-proxy windows from *Homo sapiens*, particularly from M-segment, were often classified as reservoir-like, suggesting that some glycoprotein-region windows may be conserved or sequence-ambiguous between human-associated and reservoir-associated viruses. Conversely, reservoir windows from hosts such as *Reithrodontomys sumichrasti*, *Oligoryzomys costaricensis*, and *Abrothrix longipilis* were repeatedly assigned pathogenic-like probabilities, indicating similarity to human-associated pathogenicity-proxy patterns. These findings suggest that the models capture biologically meaningful sequence patterns associated with host lineage, segment-specific conservation, and pathogenicity-proxy labels. However, given the limited dataset size and proxy labeling strategy, these models should be viewed as prioritization tools for further biological investigation rather than definitive predictors of pathogenicity.



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Kisspeptin Regulation and the Correlation with Vascular Reactivity in LBMI Young Women

Kisspeptin is a neuropeptide that works upstream to gonadotropin releasing hormone (GnRH) and plays a crucial role in the female reproductive hormonal cycle. Kisspeptin binds to the KISS1R receptor and stimulates the release of GnRH to the anterior pituitary. The release of this hormone causes the LH and FSH to release from the anterior pituitary and has positive and negative feedback with Estrogen. Studies of women with low and high BMIs can have significant fluctuation in kisspeptin production which has been linked to infertility. In this study, we focused on females with low BMI (16-21), and their kisspeptin levels with the potential correlation to lowered Estrogen and the effects on the vasodilation to conduit arteries during exercise. Leptin and adiponectin are hormones produced from adipocytes which when elevated to normal levels is a trigger of both the start of puberty as well as regulating normal menstrual cycles. LBMI and low-fat mass cause decreased secretion of leptin and adiponectin suppressing the hormonal cycle. We hypothesized that low BMI women with lower fat mass could have disrupted production of kisspeptin and Estrogen which is linked to the attenuated vascular dilation during exercise. In this study, we measured the vascular blood flow response to graded limb exercise and measured plasma levels of Estrogen and Kisspeptin during the menses and proliferative phase of the menstrual cycle in young women (18-25 year).



Kylie Jenkins

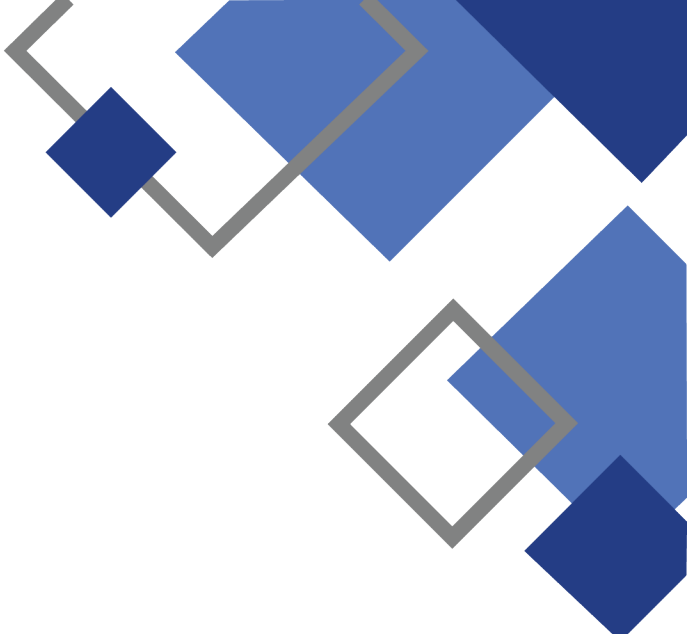
New Mexico Tech

Co-Authors:

Dr. Ryan J. Marcheschi,

Antibiotic Properties of a strain of *Priestia endophytica* isolated from soil in Las Cruces

Bacterial pathogens with antibiotic resistance capabilities have become an increasing issue, especially in hospital settings, namely several microorganisms known as ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp.) which were identified nearly 20 years ago. As current and traditional antimicrobial treatments are not very effective therefore, this research was conducted to aid in the identification of new antimicrobial compounds capable of inhibiting the growth of microorganisms closely related to these ESKAPE pathogens. In this study we isolated soil microbes to determine if they could inhibit the growth of other microbes in their nearby environment. After isolating microbes with these capabilities, we then characterized both their physiological and metabolic capabilities with a variety of tests and determined which antibiotics they were naturally resistant, or susceptible, to. Additionally, the cellular shape, structure, and organization of these microbes were observed with light microscopy, and the Polymerase Chain Reaction technique was used to amplify a region of the 16S ribosomal RNA gene and the DNA sequence of that gene region was used to identify the isolated microbes. Overall, the research presented here shows that a strain of *Priestia endophytica*, which was isolated from soil obtained from Las Cruces, NM can prevent the growth of *E. raffinosus* and *B. subtilis*. This Gram-negative, non-motile organism is resistant to penicillin. The metabolic capabilities of this organism include the fermentation of mannitol, mixed acid fermentation, and the fermentation of fructose.

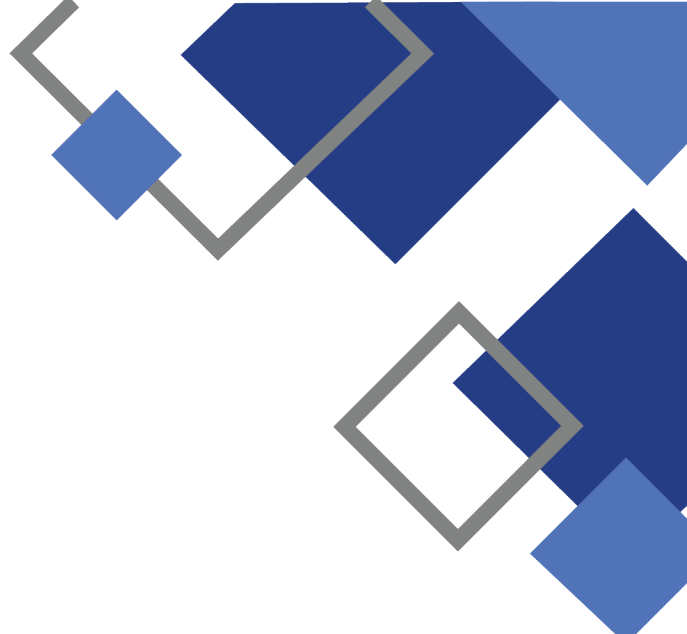
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Michael Kerns
New Mexico Tech

Tracking of Shear waves in ANGUS Phantoms via Nonlinear Cross Correlation

During impacts to the skull, the brain can receive a traumatic brain injury (TBI), sustaining long term damage. Previously our group designed, fabricated, and tested an anthropomorphic gyrencephalic unified standard (ANGUS) phantom, a model of the human brain used for testing blunt and blast TBIs. The ANGUS phantom is composed of polyacrylamide hydrogel that is tuned to mimic brain tissue to replicate tissue mechanics. One of the primary methods used to track the deformation of the tissue phantom within a skull is digital image correlation (DIC). This method relies on using a random speckle pattern embedded in a transparent phantom, tracked with a high speed camera. This cannot be done in vivo, as cameras cannot be used with intact skulls. However, non-invasive transcranial ultrasound is regularly used in the clinic to visualize hemodynamics. Similar to DIC, high frame rate ultrasound can quantify tissue deformation using a process called nonlinear cross correlation (NCC). By embedding ~50 micron glass spheres in the ANGUS phantom, a random yet consistent set of echos are received and tracked over time. The Verasonics Vantage 64 ultrasound research system with a L11-5v transducer is used to create and receive these echos, which are then processed in MATLAB using the MUST Toolbox. The result of this processing is a strain map of the tissue during impact. Using this technique it may be possible to quantitatively investigate brain deformation in vivo during high rate events, which is otherwise impossible, currently.

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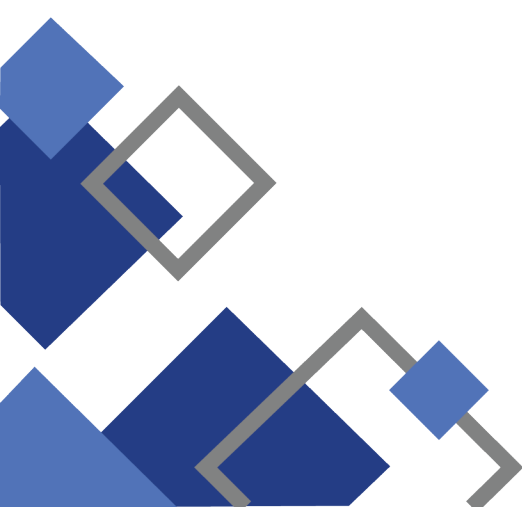
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James kurui

New Mexico Highlands University

QUANTUM MECHANICAL STUDIES on PER- and POLY-FLUROALKYL SUBSTANCES

PFAS (Per- and polyfluoroalkyl substances) are synthetic compounds with C–F bonds of varying chain lengths and functional groups. As emerging pollutants, PFAS cause environmental concern due to their persistence and health risks like cancer, decreased fertility, hormone disruption, and reduced immune function. In New Mexico, contamination across water reservoirs, private wells, and public systems exposes an estimated 92,521 people above regulatory PFAS levels. Despite regulatory efforts, significant gaps remain in understanding their behavior in drinking water systems. This study investigates how PFAS structural features (chain length, functional groups) influence electronic properties to provide a framework predicting environmental persistence, transport, and biological interactions, supporting remediation strategies. We hypothesize that increasing chain length modulates electronic and optical descriptors non-linearly (including HOMO–LUMO gap and polarizability), correlating with biological persistence and intermolecular interactions. Perfluoro carboxylic acids were selected for this phase as leading contaminants. Density Functional Theory (DFT) calculations using B3LYP and M06-2X functionals with 6-31G(d,p) and 6-31+G(d,p) basis sets in the gas phase and implicit solvent phase analyzed these electronic properties. While early to fully confirm, results indicate that the HOMO–LUMO gap, dipole moment, electronic chemical potential (μ), average local ionization energy (ALIE_{min}), and molecular electrostatic potential (ESP_{min}) exhibit minimal systematic dependence on perfluoroalkyl chain length. Instead, these electronic properties appear governed primarily by local structural and electronic effects associated with the functional headgroup and molecular conformation.

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Taylor Landfair

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Charles B. Shuster

Drivers of cell fate in mitotically delayed cancer cells

Cancer develops through the dysregulation of one or more cellular processes, including mitosis. Drugs that interfere with microtubule dynamics have been employed in the treatment of cancer for decades without a clear understanding of how cancer cells respond when they cannot complete mitosis and cytokinesis. Indeed, cancer cells exhibit variable cell fate responses when undergoing mitotic arrest, both between cell lines and within individual cells, and this heterogeneity may contribute to the limited efficacy of anti-mitotic drugs. Indeed, cells may undergo cell death during mitosis or slip back into interphase, at which point cells may then undergo cell cycle arrest, die, or continue to cycle. Our lab recently conducted RNA-SEQ on three cervical cell lines that exhibit differential cell fate responses to mitotic delay in an effort to identify genes whose differential expression may affect cell fate. From these efforts, we identified several candidate genes associated with mitotic cell death (c-Myc) or survival (Bcl-2 and Bcl-xL). To test whether these differentially expressed genes influenced cell fates between the cancerous (HeLa, SiHa) and noncancerous (CX16) cell lines, we conducted RNA interference of the death (c-Myc) and survival (Bcl-xL) -associated genes in our three cervical cell lines. Preliminary results from siRNA knockdown, Western blotting, and high-throughput imaging suggest that c-Myc and Bcl-xL function as potential determinants of cell fate, and current efforts are now focused on over-expression of these genes using a Tet-inducible system to alter cell fates in mitotically arrested cells.



Aubrey Lasiloo

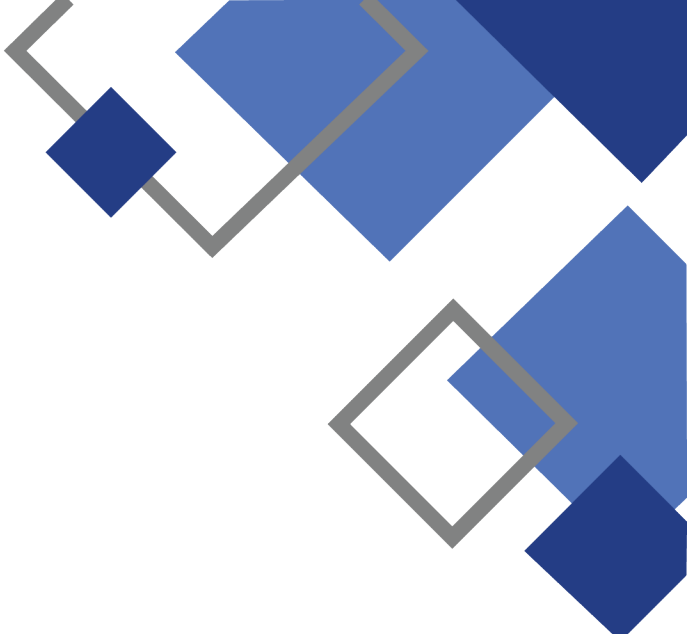
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Testing lifespan-extending tRNA synthetase inhibitors in a *C. elegans* model of Huntington's disease

Huntington's disease is an inherited neurodegenerative disorder that affects 50,000 people annually in the United States and leads to progressive movement disorders, cognitive decline, and ultimately death. There is currently no cure for this condition. Symptoms typically begin between the ages of 30 and 50, with disease severity worsening over time. Huntington's disease is caused by the aggregation of mutant huntingtin protein containing expanded polyglutamine (polyQ) repeats. Our laboratory studies the basic biology of aging to better understand the mechanisms underlying age-related diseases. We have identified a class of novel compounds that significantly extend lifespan in multiple laboratory models, including the budding yeast *Saccharomyces cerevisiae* and the nematode *Caenorhabditis elegans*. These compounds also activate cellular stress-response pathways, including the ATF-4-mediated integrated stress response, which may enhance cellular protein quality-control mechanisms such as autophagy and proteasomal degradation of damaged proteins. Preliminary studies have also demonstrated delayed protein aggregation in an amyloid- β *C. elegans* model, supporting the rationale for evaluating these compounds in Huntington's disease. My project asks whether these lifespan-extending compounds can delay the onset of disease symptoms in a *C. elegans* model of Huntington's disease expressing the disease-associated polyglutamine repeat Q40. These worms develop movement defects as Q40 proteins aggregate with age. By comparing movement and survival between treated and untreated animals, we can determine whether activation of ATF-4 mediated stress-response pathways by tRNA synthetase inhibitors delays disease progression, which could lead to potential therapeutic strategies for Huntington's disease.

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Ashley Lindsey

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Transcriptomic signatures of substance use disorder and their implications for evidence-based harm reduction programs

Substance use disorder is a highly stigmatized disease affecting roughly 64 million people globally. A culmination of genetics, lifestyle, socioeconomic factors, and trauma, addiction claims over 3 million lives per year. Although the biological mechanisms that drive addiction are still being discovered, harm reduction programs are already impacting how addiction is treated as well as reducing the stigma many people have. This study will evaluate how harm reduction programs from Canada, the United States, and South Korea differ and, using publicly available datasets, compare differential gene expression, pathways, and biological processes in brain tissue among those suffering with substance use disorder. This research aims to further our understanding of the genetics behind addiction and guide future harm prevention programs towards more effective treatments.

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Hemanth Madduri

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Unified Generative Multimodal Framework for Surgical AI and Stroke Rehabilitation

Reliable assessment of surgical performance and post-stroke rehabilitation movement is critical for patient safety, clinical training, and recovery monitoring, but current evaluation often depends on expert review of complex video data, which is time-consuming, subjective, and difficult to scale. A key scientific challenge is to determine whether fine-grained human action patterns can serve as reusable markers of procedural quality and functional performance across clinical domains. This project first studies surgical gesture prediction as a foundation for modeling structured clinical actions, then transfers the learned representation to surgical phase prediction and skill assessment. We propose a multimodal generative framework that integrates visual, linguistic, and action features to capture temporal dependencies among gestures, phases, and performance scores. On the JIGSAWS surgical dataset, the model achieves strong performance across gesture recognition, phase prediction, and Global Rating Scale skill assessment, with transfer learning improving phase-prediction training efficiency by at least 35 percent. We further extend this idea to stroke rehabilitation, where limited labeled data and costly clinician annotation restrict automated movement assessment. By adapting surgical action representations to rehabilitation action prediction, this work explores whether shared structure in human motor sequences can support scalable, data-efficient clinical evaluation.



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Investigating Behavioral Mate Choice in *Cyprinodon*: The Role of MHCII Immune Gene Similarity

Mate choice is a fundamental component of sexual selection and can influence reproductive behavior and reproductive isolation. The Major Histocompatibility Complex class II (MHCII) has been proposed as one factor that may contribute to mate choice by influencing behavioral preferences between potential mates. This study focused on two species of fish, *Cyprinodon variegatus* and *Cyprinodon brontotheroides*, as a model for examining mate choice. The primary question addressed is whether behavioral preferences in *Cyprinodon* is associated with similarities in MHCII immune gene profiles. To answer this question mate choice-related behavioral data were extracted and quantified from previously recorded video footage. Video recordings were analyzed to document the amount of time focal fish spent associating with potential mates, along with other courtship-related behaviors, using standardized scoring criteria. This study did not involve experimental manipulation and instead emphasized accurate behavioral observation and data collection to generate a reliable behavioral dataset. Preliminary analyses from our top-performing statistical model demonstrated a positive relationship between behavioral preference and MHCII compatibility. When fish were presented with a clear genetic choice they spent more time interacting with potential mates that shared a MHCII gene profile. These findings suggest that immune-related genetic characteristics may influence social and reproductive behavior in *Cyprinodon*. Future work will expand behavioral observations and genetic information to better understand the mechanisms underlying mate choice and reproductive isolation in this species. The resulting dataset will contribute to future ecological and evolutionary studies while providing a foundation for continued investigation of behavioral preferences in *Cyprinodon*.



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Metabolic Adaptation of *Klebsiella pneumoniae* and *Klebsiella aerogenes* Under Nutrient Deprivation and Oxidative Stress

Klebsiella pneumoniae and *aerogenes* are opportunistic pathogens commonly associated with hospital-acquired infections and development of antibiotic resistance. They are facultative anaerobes that alter their respiratory strategies in response to environmental conditions. This study investigates how *K. pneumoniae* and *K. aerogenes* adapt in environments that mimic microbial competition. Conditioned media was generated by growing each species to plateau phase then removing live cells, leaving behind depleted nutrients and metabolic byproducts. Growth and metabolic analysis revealed that exposure to conditioned media altered bacterial physiology, reducing oxidative phosphorylation-based ATP production while maintaining glycolytic ATP production. Growth analysis demonstrated reduced growth rates in conditioned media, suggesting that *Klebsiella* species transition into a low growth state under stressful conditions. To investigate the factors contributing to this shift, glucose was added back to conditioned media to determine whether restoring a primary carbon source could improve growth. Ascorbic acid and hydrogen peroxide treatments were introduced to examine bacterial responses to oxidative stress and identify changes in stress tolerance. Growth responses under these conditions showed that glucose is responsible for determining the growth rate while the redox state of the environment is responsible for setting the carrying capacity of the system. These findings demonstrate that *Klebsiella* species undergo metabolic switches in response to environmental stress and the population level growth kinetics are determined by both resource availability and signals in the immediate environment. These data provide insight into how pathogenic *Klebsiella* species persist under stress and may contribute to developing new approaches for targeting other bacterial survival mechanisms.



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Physiological Attributes and Antimicrobial Activity of *Bacillus Atrophaeus*

The rise in cases of antibiotic resistance in bacterial pathogens has been an ongoing and steadily increasing problem, especially in medical settings. Nearly twenty years ago, a group of microorganisms collectively known as ESKAPE pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp.) that exhibited concerning levels of resistance to traditional antimicrobial treatments were identified. The research presented here was conducted to contribute to the ongoing identification of new antimicrobial compounds that are effective at inhibiting the growth of microorganisms that are closely related to the ESKAPE pathogens. In this study, we isolated microbes from soil samples in New Mexico and determined if they could prevent the growth of other microbes near them in their environment. Then, we characterized their physiological and metabolic properties using a variety of tests. We also determined which antibiotics these isolated microorganisms were naturally resistant and/or susceptible to. We observed the cellular shapes, structures, and organization of these microbes using light microscopy, then used the Polymerase Chain Reaction technique to amplify a specific region of the 16S RNA gene to identify them. Overall, the research presented here shows that *Bacillus atrophaeus*, which was isolated from soil from just outside of Cloudcroft, can prevent the growth of *B. subtilis*, *E. raffinosis*, *S. epidermis*, and *A. baylyi*. This organism is non-motile and is resistant to none of the tested antibiotics.



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Optimizing High-Speed Data Acquisition Systems to Increase Fluorescence Lifetime Data Resolution in Time-Resolved Flow Cytometers

Flow cytometry is a high-throughput analytical technique used to characterize cells and small particles by measuring fluorescence and light scatter as individual cells pass through a focused laser beam. These measurements are used in a variety of biomedical research applications to distinguish cell populations, evaluate therapeutic responses, and investigate disease pathways. Conventional flow cytometers can be adapted to also acquire fluorescence lifetime (FLT) measurements of cells or particles. FLT, defined as the amount of time it takes for an excited fluorophore to return from its excited state to its ground state, is a useful parameter in flow cytometry because it is independent of fluorescence intensity, and it is sensitive to the local biochemical environment, including changes in pH, protein interactions, and cellular metabolism. In this study, a custom-built frequency-domain flow cytometer was optimized by adjusting the modulation frequency of the system's excitation laser and the sampling rate of a Teledyne 14-bit, 2 GSPS ADQ data acquisition system, with the goal of increasing FLT data resolution. Signals collected by the high-speed acquisition system were processed using custom MATLAB signal analysis algorithms to determine FLT values. Our findings show that adjusting the laser modulation frequency alone was not as effective as increasing the sampling rate of the ADQ in order to produce more precise FLT measurements. The results of this work will allow for increased resolution of shorter fluorescence lifetimes via the adaptation of conventional flow cytometers, enabling precise monitoring of cellular metabolism and therapeutic response without requiring specialized flow cytometry instrumentation.



Long Nguyen

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Predicting Alzheimer's Disease Neuropathology from Single-Nucleus Gene Expression Using Machine Learning

Alzheimer's disease is marked by progressive neuropathological changes, including amyloid- β plaques, tau tangles, neuronal loss, and gliosis, but standard pathology labels such as ADNC, Braak, CERAD, and Thal are costly and labor-intensive to measure directly. This project investigates whether single-nucleus gene expression from human brain tissue can be used to predict these Alzheimer's disease pathology stages. Using the SEA-AD DREAM Challenge dataset, which includes over 1.2 million nuclei, 36,601 genes, two brain regions, and 84 donors, I developed a machine-learning pipeline that normalizes gene expression data, reduces dimensionality with PCA, trains neural-network models with class-balanced loss and regularization, and aggregates cell-level predictions to the donor level. The resulting pipeline achieved strong performance on categorical neuropathology staging and ranked first on the SEA-AD Agent Track Task 1 leaderboard. This work shows that transcriptomic profiles contain useful signals for estimating Alzheimer's disease severity and supporting biomarker discovery.



Padraic Nielsen

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Studies into the Regulatory Dynamics of a Key Effector of Immune Defense

Large-scale conformational motions gate the multi-step, multi-electron transfer from NADPH through FAD and FMN to the catalytic heme of the opposite protomer in homodimeric inducible nitric oxide synthase (iNOS), a principal effector of innate host defense. Two 2026 cryo-electron microscopy studies have provided the first structural views of the FMN subdomain both shielded against FAD and de-shielded, docked on the oxygenase domain of the partner protomer. Because these static snapshots alone cannot reveal the conformational regulatory dynamics and kinetics that govern iNOS activity, we apply enhanced-sampling molecular dynamics to elucidate (1) how the set-point and kinetics of the shielded/de-shielded reductase domain equilibrium depend on cofactor redox state, calmodulin, and bound NADP(H); (2) the dynamics and energetics of the linker-mediated association of the reductase with the oxygenase of the partner protomer; (3) whether FMN is recharged by sliding between the FAD-proximal and heme-proximal poses while the reductase stays docked, or by undocking, rotating back to the shielded state, and re-docking to deliver the next electron; (4) if allostery communicated through the oxygenase dimer coordinates the docking of reductase arms in an alternating-site mechanism; and (5) the molecular interactions at the reductase–calmodulin–oxygenase interface that drive calmodulin's conformational-state selection upon binding the interdomain iNOs linker. Taken together, these studies will yield a model of the regulatory dynamics of iNOS that can be leveraged for isoform-specific therapies and generalized to the >80% of eukaryotic proteins that are also multi-domain assemblies.



Reya Padilla

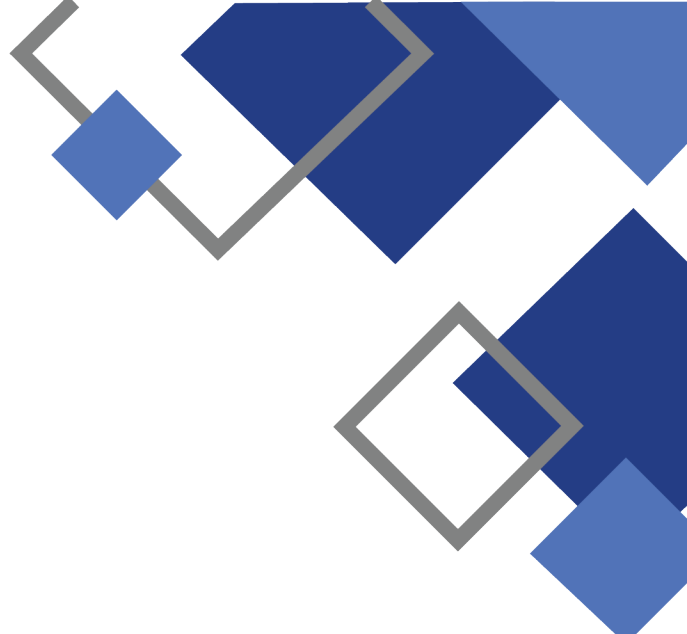
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Dr. Charles B. Shuster

Dissection of Anillin nuclear localization and function in sea stars

The contractile ring is a transient assemblage of actin and myosin II filaments that constricts to partition two daughter cells. A central organizer of contractile ring assembly is Anillin (ANLN), a multidomain protein that links the contractile ring to the plasma membrane and integrates signals from the mitotic spindle to facilitate ring assembly and constriction. In yeast and humans, ANLN is targeted to the nucleus during interphase and recruited to the cell equator during ring assembly. However, recent studies suggest that ANLN may function during interphase at cytoskeletal domains under stress or tension. Sea star ANLN contains the conserved, N-terminal bipartite Nuclear Localization Signal (NLS) as well as an atypical motif, the PV-NLS. It is through such motifs that Importin proteins bind and transport ANLN into the nucleus. To further explore the roles of ANLN during sea star meiosis, we mutagenized residues within the bipartite NLS as well as the atypical PY-NLS either alone or in combination and then performed transient expression studies in cultured human cells. Fluorescently-tagged sea star ANLN localized strongly to the nucleus, but single or double mutations of the bipartite NLS had minimal effects on nuclear targeting. Current efforts are focused on determining whether the atypical PV-NLS sequence is required for nuclear localization. Once a nuclear targeting sequence is identified, control and NLS-mutants will then be followed through oocyte activation and meiotic progression to determine whether precocious recruitment of ANLN during interphase interferes with the normal cytoskeletal dynamics that accompany meiotic re-entry.

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Katelyn Powers

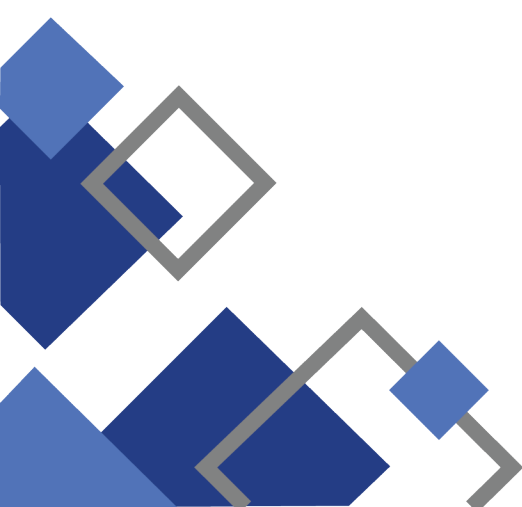
Nevada State University

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Dr. Ryan J. Marcheschi,

Antimicrobial Potential of *Bacillus Velezensis* Strain Against ESKAPE Pathogens

Bacterial pathogens increasing their resistance to antibiotics is a chronic issue, particularly in medicinal settings. A handful of microorganisms known as the ESKAPE pathogens are of special interest in relation to this topic due to their strong resistance to antibacterial medication. To address this issue, this research was conducted to contribute to the identification of new antimicrobial compounds that can obstruct the growth of these pathogens. In this study, we separated soil microbes and tested them against ESKAPE relatives to determine if the microbes are able to prevent their growth. The biochemical processes of these microbes were tested and their susceptibility or resistance to antibiotics was examined. We inspected the cellular forms and structures of these microorganisms using light microscopy. PCR was then used to amplify a section of the 16S ribosomal RNA gene and the DNA sequence was used to identify the microbes. Overall, the research presented here shows that *Bacillus velezensis*, which was isolated from soil obtained from a rest area west of Mesilla, can prevent the growth of *E. raffinosus*. *B. velezensis* is gram stain positive and motile. The metabolic capabilities of this organism include: gelatin hydrolysis, starch hydrolysis, lipid hydrolysis, and acetoin production from glucose fermentation. *B. velezensis* can also ferment fructose, mannitol, and sorbitol.

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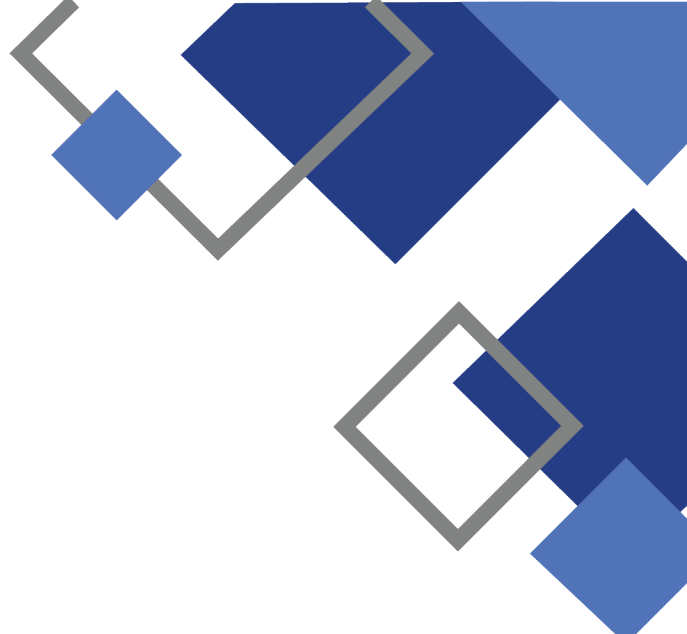
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Jessica Pulgarin
New Mexico State University

Sparse Studies to Rapid Expansion: Tracking Research on Reproductive

Bacterial pathogens increasing their resistance to antibiotics is a chronic issue, particularly in medicinal settings. A handful of microorganisms known as the ESKAPE pathogens are of special interest in relation to this topic due to their strong resistance to antibacterial medication. To address this issue, this research was conducted to contribute to the identification of new antimicrobial compounds that can obstruct the growth of these pathogens. In this study, we separated soil microbes and tested them against ESKAPE relatives to determine if the microbes are able to prevent their growth. The biochemical processes of these microbes were tested and their susceptibility or resistance to antibiotics was examined. We inspected the cellular forms and structures of these microorganisms using light microscopy. PCR was then used to amplify a section of the 16S ribosomal RNA gene and the DNA sequence was used to identify the microbes. Overall, the research presented here shows that *Bacillus velezensis*, which was isolated from soil obtained from a rest area west of Mesilla, can prevent the growth of *E. raffinosus*. *B. velezensis* is gram stain positive and motile. The metabolic capabilities of this organism include: gelatin hydrolysis, starch hydrolysis, lipid hydrolysis, and acetoin production from glucose fermentation. *B. velezensis* can also ferment fructose, mannitol, and sorbitol.

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Isabella Quay

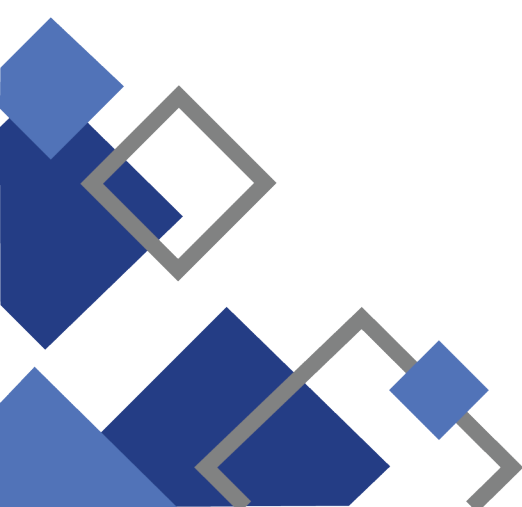
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Dr. Ryan J. Marcheschi,

Antibiotic Resistance Research Study Using Soil Samples

As the world evolves around us, microbes evolve to become more antibiotic resistant. Antibiotics that are used and have delivered efficient results are now becoming less efficient, to the point of having no effect on microbes. The major concern is with the microorganisms that are found in hospital settings and cause life-threatening infections, known as the ESKAPE pathogens. The focus of this study was to isolate microbes collected from soil samples and to determine if those microbes could prevent the growth of bacteria closely related to the ESKAPE pathogens. The soil was collected from Oasis State Park (34.25987 N, 103.35014 W) and microbes were isolated. After they were isolated, various tests were performed to identify and determine their physiological and metabolic capabilities. We also tested the natural antibiotic resistance and susceptibility of these microbes. The shapes, organization, and cellular structures of the microbes were investigated using Gram staining and light microscopy. Furthermore, PCR was used to amplify a portion of the 16S rRNA gene, then DNA sequencing of the product and bioinformatics tools were used to genetically identify the isolated microbes. Overall, the results of this research show that the microbe YA3, genetically identified as *Bacillus proteolyticus*, can prevent the growth of *E. raffinosus*. This organism is Gram-positive, mono- and diplo- bacillus, and is motile. It is catalase-, oxidase-, nitrate reductase-, and amylase-positive and it ferments xylose and produces acetoin from glucose fermentation.

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Joar Rabago

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Dr. Corey Green

The Effects of Polychlorinated Biphenyls on the Symbiosis of Sea Anemones

PCBs are a class of persistent contaminants found in aquatic ecosystems which have the ability to interfere with symbiotic relationships between aquatic organisms and associated microflora. In this experiment, the impacts of Aroclor 1254, a mixture of PCBs, on symbiosis and bacterial associations of sea anemones is investigated. The sea anemones will be subjected to acclimatization under laboratory conditions where they will be fed brine shrimp daily and placed in artificial seawater of 35g/L. Daily monitoring will be done for water quality variables such as temperature (70-72°F), salinity and pH (8.4-8.8) throughout the acclimatization process. Following this, the sea anemones will be exposed to one of five treatments; H₂O control, DMSO control, Aroclor 1254 of 0.5mg/L, 1.0mg/L, and 4.0 mg/L with 6 sea anemones in each treatment in the first trial. These trials being conducted for a 96-Hour exposure. After the treatment period, the tissues will be homogenized, serially diluted and the bacteria grown on LB agar, nutrient agar, and seawater agar. DNA extraction will be done on homogenized samples and tested for quality using agarose gel electrophoresis and bacterial culturing. These results will contribute to an understanding of ecological impacts of PCB contamination on marine symbiotic systems.



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Quantifying the Impact of Oxygen Deprivation on SARS-CoV-2 Viral Uptake in Cells

Nearly 20% of people who have COVID-19 develop post-acute sequelae of SARS-CoV-2 infection (PASC), commonly known as Long COVID-19. PASC is characterized by persistent symptoms such as blood vessel dysfunction, fatigue, and brain fog. In many cells the integrin $\alpha 5 \beta 1$ serves as a co-receptor alongside the ACE2 receptor to facilitate SARS-CoV-2 entry into the cell. Because both $\alpha 5 \beta 1$ and ACE2 contribute to viral entry, $\alpha 5 \beta 1$ may be a promising therapeutic target for reducing the chronic inflammation and vascular and neurological complications associated with Long COVID-19. Our previous studies prove that hypoxic (low oxygen) conditions increase the production of $\alpha 5 \beta 1$ expression in cells. Increased $\alpha 5 \beta 1$ expression has been linked to hastened viral entry and disrupted cell barrier function. As a result, individuals with reduced tissue perfusion or vascular disease may be more susceptible to infection. To determine whether the upregulation of $\alpha 5 \beta 1$ expression increases the potential risk of SARS-CoV-2 infection due to hypoxia, we study whether hypoxic cells display an increase in susceptibility of infection compared to normoxic (normal oxygen) cells, when exposed to low viral loads of SARS-CoV-2. Using fluorescently labeled SARS-CoV-2(R18) we compared the viral uptake in cells when exposed to low viral loads under normoxic and hypoxic conditions. Differences in viral uptake between normoxic and hypoxic cells provide a measurement of infection-likelihood under each condition. This comparison allows us to assess how hypoxia affects susceptibility of low-level exposure of SARS-CoV-2 and may help explain how oxygen deprivation influences viral infection risk.



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Isolation of an antimicrobial-producing strain of *Bacillus halotolerans* obtained from local soil with the potential of inhibiting the growth of two ESKAPE relatives

The increasing antibiotic resistance among many bacterial pathogens, particularly those most commonly found in hospital settings, has been an increasing problem. To be more specific, the microorganisms known as the ESKAPE pathogens, which were identified nearly 20 years ago, have resistance to many traditional antimicrobial treatments. To address this issue, this research was conducted to contribute to the identification of new antimicrobial compounds that are effective at inhibiting the growth of the pathogens. We isolated microbes from the soil and initially determined if they could inhibit the growth of ESKAPE relatives. After isolating a few selected microbes, we then did a series of tests to characterize their physiological and metabolic capabilities. We tested their resistance and/or susceptibility to several common antibiotics and we determined their cellular shapes using light microscopy. We also used the PCR technique to amplify the 16S rRNA gene region and used its DNA sequence to genetically identify each selected microbe. Overall, the research presented here shows that a strain of *Bacillus halotolerans*, which was isolated from soil obtained south of the Chemistry & Biochemistry building at NMSU, can prevent the growth of *S. epidermidis* and *E. coli*. This strain of *B. halotolerans* is Gram-positive, is motile, and is sensitive to all commercial antibiotics tested. The metabolic capabilities of this strain include: salt tolerance, producing acetoin from glucose fermentation, decomposing hydrogen peroxide into water and oxygen, oxidizing molecules via cytochrome c oxidase, reducing nitrate, fermenting mannitol and sucrose, and hydrolyzing urea, starch, gelatin, casein, and lipids.



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Dr. Erik Yukl

Characterizing the Pyruvate Dehydrogenase Complex from *Caulobacter Crescentus*

Pyruvate dehydrogenase (PDH) is a central metabolic enzyme complex linking glycolysis to the tricarboxylic acid (TCA) cycle by converting pyruvate into acetyl-CoA. Comprised of 3 catalytic enzymes (E1-E3), it is highly conserved in all domains of life although there are differences between PDH from eukaryotes and gram-negative bacteria. We have identified an E1 enzyme from the gram-negative bacterium *Caulobacter crescentus* that is unusual in that it is more closely related to homologues from eukaryotes than other bacteria. Further, the E1 β subunit contains an N-terminal lipoyl domain that is typically only observed on E2. In this project, we investigate the function of this domain by generating a deletion mutant ($\Delta 1-100$) using site-directed mutagenesis. The resulting protein will be expressed, purified by Ni-NTA affinity chromatography, and steady-state kinetics measured and compared to the WT. Because the lipoyl domain is connected to the E1 β by a flexible swinging-arm region, deletion may improve the likelihood of obtaining high-quality crystals of this unusual E1 enzyme. In parallel, efforts are underway to purify the entire PDH complex of *C. crescentus*. By assembling the three core components, E1, E2, and E3, we aim to reconstitute a functional complex that can be studied as a whole by heterologous expression in *E. coli* or by purification of native PDH from the source organism, *C. crescentus*. Together, these two approaches aim to clarify how the lipoyl domain contributes to PDH complex structure and activity, and to shed light on whether bacterial PDH regulation shares mechanistic features with its eukaryotic counterparts.

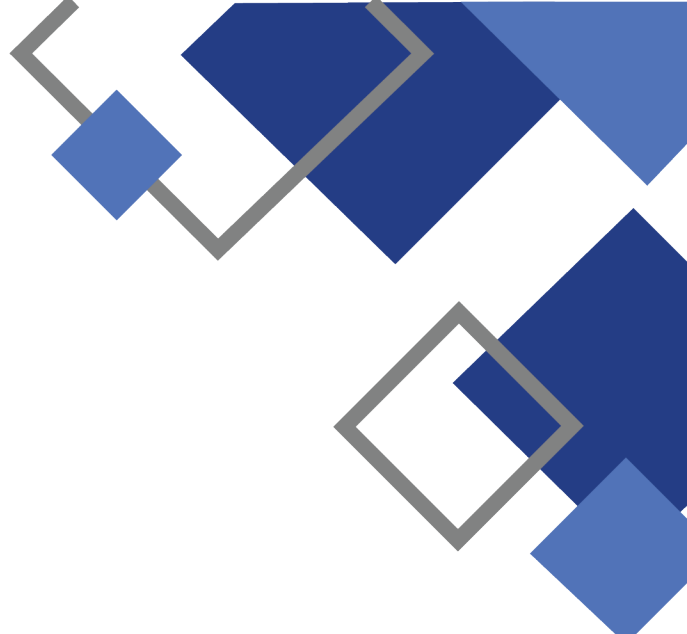


Nariyus Silas

San Juan College

The Impact of Alcohol Exposure on Gastrointestinal Alcohol Dehydrogenase Expression in Dopamine- and Octopamine-Deficient Fruit Flies

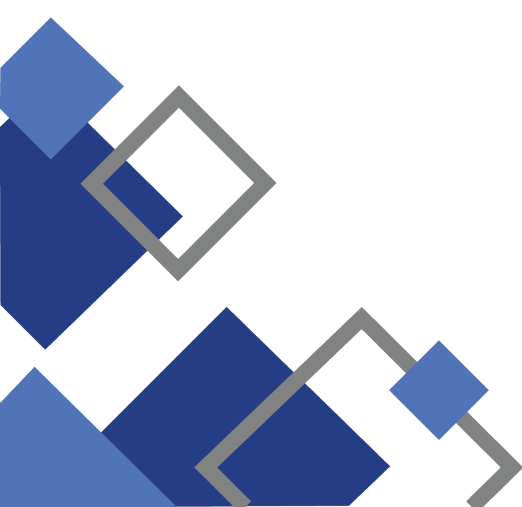
The brain-gut axis is a bidirectional connection between the gastrointestinal tract, commensal gut microbes, and the nervous system. *Drosophila melanogaster* is an established model organism for studying metabolic and neurological pathways because of its similarity to human metabolism. In *Drosophila*, ethanol is primarily metabolized by alcohol dehydrogenase (ADH), which is highly expressed in the midgut and reduces the concentration of ethanol that crosses the blood-brain barrier. The concentration of ethanol that reaches the brain can be qualitatively estimated by behavior and quantitatively estimated by the expression levels of ADH. This study investigated the effects of chronic ethanol exposure on gastrointestinal ADH gene expression in dopamine-deficient, octopamine-deficient, and wild-type *D. melanogaster* maintained under either commensal or axenic conditions. Flies were chronically exposed to ethanol-containing diets for approximately three weeks before the midgut was dissected for quantitative polymerase chain reaction (qPCR) analysis. Expression of the ADH gene was standardized to the housekeeping gene ribosomal protein L32 (RpL32). Alcohol-associated behaviors were also qualitatively assessed to examine potential relationships between gene expression and behavioral responses. Preliminary findings suggest that chronic ethanol exposure alters ADH gene expression and that both catecholamine deficiency and the absence of commensal gut microbiota may influence ethanol metabolism and alcohol-associated behaviors. These observations are consistent with altered gastrointestinal ethanol metabolism that could increase ethanol exposure to the brain. This study contributes to understanding how interactions between neurotransmitter signaling and the gut microbiome influence ethanol metabolism and behavior.

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Alicia Tirado
University of New Mexico

Characterizing the Pyruvate Dehydrogenase Complex from *Caulobacter Crescentus*

Pyruvate dehydrogenase (PDH) is a central metabolic enzyme complex linking glycolysis to the tricarboxylic acid (TCA) cycle by converting pyruvate into acetyl-CoA. Comprised of 3 catalytic enzymes (E1-E3), it is highly conserved in all domains of life although there are differences between PDH from eukaryotes and gram-negative bacteria. We have identified an E1 enzyme from the gram-negative bacterium *Caulobacter crescentus* that is unusual in that it is more closely related to homologues from eukaryotes than other bacteria. Further, the E1 β subunit contains an N-terminal lipoyl domain that is typically only observed on E2. In this project, we investigate the function of this domain by generating a deletion mutant ($\Delta 1-100$) using site-directed mutagenesis. The resulting protein will be expressed, purified by Ni-NTA affinity chromatography, and steady-state kinetics measured and compared to the WT. Because the lipoyl domain is connected to the E1 β by a flexible swinging-arm region, deletion may improve the likelihood of obtaining high-quality crystals of this unusual E1 enzyme. In parallel, efforts are underway to purify the entire PDH complex of *C. crescentus*. By assembling the three core components, E1, E2, and E3, we aim to reconstitute a functional complex that can be studied as a whole by heterologous expression in *E. coli* or by purification of native PDH from the source organism, *C. crescentus*. Together, these two approaches aim to clarify how the lipoyl domain contributes to PDH complex structure and activity, and to shed light on whether bacterial PDH regulation shares mechanistic features with its eukaryotic counterparts.

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Cayla Totten

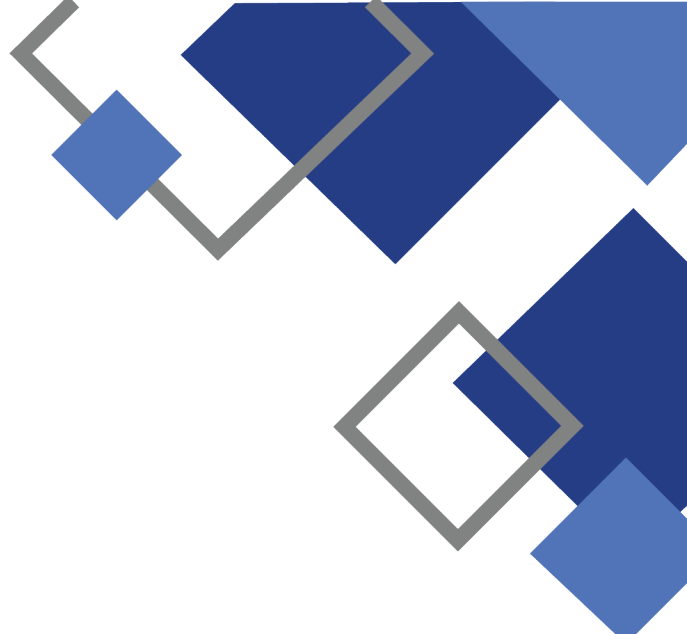
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Effects of Generational Exposure to PCB 126 on Zebra Fish

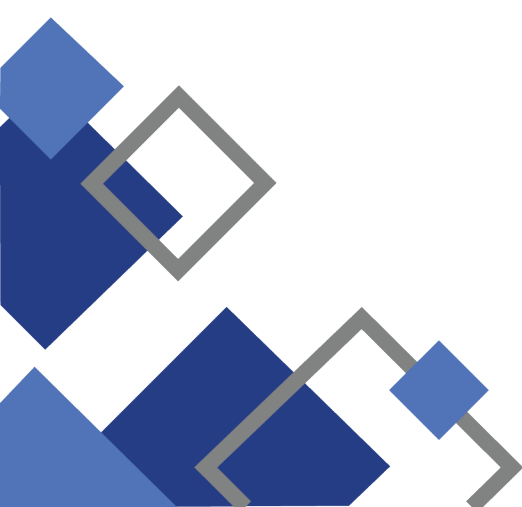
Pyruvate dehydrogenase (PDH) is a central metabolic enzyme complex linking glycolysis to the tricarboxylic acid (TCA) cycle by converting pyruvate into acetyl-CoA. Comprised of 3 catalytic enzymes (E1-E3), it is highly conserved in all domains of life although there are differences between PDH from eukaryotes and gram-negative bacteria. We have identified an E1 enzyme from the gram-negative bacterium *Caulobacter crescentus* that is unusual in that it is more closely related to homologues from eukaryotes than other bacteria. Further, the E1 β subunit contains an N-terminal lipoyl domain that is typically only observed on E2. In this project, we investigate the function of this domain by generating a deletion mutant (Δ 1-100) using site-directed mutagenesis. The resulting protein will be expressed, purified by Ni-NTA affinity chromatography, and steady-state kinetics measured and compared to the WT. Because the lipoyl domain is connected to the E1 β by a flexible swinging-arm region, deletion may improve the likelihood of obtaining high-quality crystals of this unusual E1 enzyme. In parallel, efforts are underway to purify the entire PDH complex of *C. crescentus*. By assembling the three core components, E1, E2, and E3, we aim to reconstitute a functional complex that can be studied as a whole by heterologous expression in *E. coli* or by purification of native PDH from the source organism, *C. crescentus*. Together, these two approaches aim to clarify how the lipoyl domain contributes to PDH complex structure and activity, and to shed light on whether bacterial PDH regulation shares mechanistic features with its eukaryotic counterparts.

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Marisa Valdez
New Mexico Tech

Using soil-based microbial enzymatic activity to bridge the gap between genomics and ecosystem data

Depleted uranium (DU) contamination is a severe threat in soil ecosystems due to its high toxicity. However, microbes can utilize uranium for redox-reactions involved in their metabolic pathways or immobilize uranium by phosphate solubilization, providing the possibility of a microbe-based soil remediation strategy. Although metagenomics can reveal potential microbial functions and monitoring the ecosystem can track geochemical activity, a critical gap remains in connecting genomic data to ecosystem dynamics. This study aims to bridge that gap by using enzymatic assays to quantify DU's (plus DU and additional nutrients) impact on enzymatic activities in soil and the correlation with genomic potential and ecosystem processes. Soil samples were collected across the EMRTC DU gradient located in Socorro, New Mexico. Soil samples from each site received four different treatments; a carbon source (juniper litter), a phosphorus source (tripotassium phosphate), a mixture of both carbon and phosphorus, and a control group containing no additions, resulting in a total of sixteen observed samples. For each sample, we measured the activity of extracellular hydrolytic enzymes that are important drivers of nutrient cycling: beta-glucosidase (carbon), beta-N-acetylglucosaminidase (nitrogen) leucine amino peptidase (nitrogen), and alkaline phosphatase (phosphorous). By bridging the gap between genomics and ecosystem dynamics, soil extracellular enzymatic activity establishes a solid framework for future targeted bioremediation efforts toward DU contamination.

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Audree Vigil

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Do Older Adults Benefit from Offloading Memory? Examining the Saving-Enhanced Memory Effect in Older Adults

The saving-enhanced memory effect is observed when saving information externally facilitates subsequent learning of new information. A recent study found no evidence of saving-enhanced memory in older adults, but this study used word lists and required participants to decide when to save. We investigated whether the saving enhanced memory effect emerges in older adults when a more naturalistic task with lower decision-making demands is employed. The study used design with 3 factors. Age was manipulated quasi-experimentally, matching participants based on gender and level of education. Participants learned pairs of lists (List A, then List B), half of which were word lists and half of which were lists of trivia facts. For some pairs, List A was saved, and for others, it was not saved. We were primarily interested in recall performance for the unsaved lists. Enhanced performance on List B when participants believed List A has been saved, compared to when they believed it had been deleted, would indicate a saving-enhanced memory effect. We expect that, at least for the trivia facts, older adults will show saving-enhanced memory, though the magnitude of this effect may be smaller than observed in younger adults. This study will enhance our understanding of how older adults may benefit from offloading memory onto external stores. Ultimately, this work may inform strategies older adults might use to narrow or even close the recollection gap between younger and older adults.



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Development of a novel machine-learning tool to track cancer cell fates from low-resolution data sets

Machine learning tools and Generative AI have vastly improved the ability to track movements from subcellular structures to whole tissues in living organisms. For high-resolution imaging applications such as confocal microscopy, open-source (CellPose) and commercial (Imaris) packages afford efficient tracking and quantification of fluorescent structures within 4D data sets. However, these packages are not useful for analyzing transmitted light images. Our lab seeks to understand the variability of cancer cell responses to mitotic arrest when cells are unable to complete mitosis. Cancer cells display a high degree of heterogeneity in response to mitotic arrest, where some cells die by apoptosis while others slip out of mitosis to die later or attempt another cell cycle. The Sartorius Incucyte high-throughput imaging system monitors cells over time and can quantify apoptosis with a fluorescent reporter. However, the system also generates a phase contrast image for each time point, enabling us to quantify all possible cell fates manually. To automate the identification of different cell fates from these low-resolution image stacks, we developed a Python-based computer-vision workflow to label and track cells over time. This pipeline consists of multiple Python libraries including matplotlib, scikit-image, trackpy, and a RandomForestClassifier machine learning model. Our tool currently labels and categorizes cells undergoing mitosis, measuring parameters including size, shape, movement, and fate prediction data for each cell in a tiff image stack. Current efforts are focused on improving the mitosis timing feature as well as training our machine learning model to more precisely predict complex cell fates.



Tamara Vyncke

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A Comparison of International and Domestic Students on Belonging and Wellbeing

The transition to university presents academic and social challenges that can influence students' well-being, motivation, and sense of belonging. Previous research has demonstrated that developing meaningful social identities is associated with greater inspiration, engagement, and psychological well-being. Building on Chadborn and Reysen's (2016) model of social identity and inspiration, the present study examines whether the relationship between social identity and inspiration differs between domestic and international students attending Canadian universities. In addition, this study investigates whether the proportion of international students at an institution influences this relationship by examining the size of the international student population as a potential contextual moderator. Participants ($N = 301$) from multiple Canadian universities completed measures of social identity, inspiration, well-being, and sense of community. Analyses include group comparisons, correlational analyses, and moderation models to examine whether institutional context influences the association between social identity and inspiration. Findings will contribute to a better understanding of how university environments shape students' experiences of belonging and inspiration. Results may inform institutional policies and programs aimed at fostering inclusive campus communities and promoting the academic success and psychological well-being of both domestic and international students.



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Matthew Guberman-Pfeffer

ProPrep: An Accessible Approach to Molecular Dynamics of Aqueous and Membranous (metallo) Proteins

As the CryoEM and AI structural revolution outstrips the pace of biochemical functional characterization, molecular dynamics (MD) and quantum mechanical/molecular mechanical (QM/MM) simulations are growing in importance as analytical techniques. That potential, however, is currently impeded by the substantial expertise and effort required for their proper setup. Feature-rich preparation programs tend to offer customization at the expense of extensive training and manual effort, while simplified tools provide usability in exchange for hidden or unchangeable defaults. Worse still, several tools with different input syntaxes and file formats need to be daisy-chained to address a given research question. To make the use of MD and QM/MM methods more widely available and efficient, we present ProPrep, a workflow manager that helps users ACE IT by providing access to a cohesive set of educationally annotated interactive tools with traceable output. ProPrep orchestrates structure retrieval, assembly, alignment, curation, repair, simulation, and analysis for both aqueous and membrane-embedded proteins by interfacing to 15 programs in AmberTools, 4 bioinformatics online databases, and 2 quantum chemistry packages. An extensible framework detects, parameterizes, and transforms specialized residues such as metal sites, modified amino acids, and organic cofactors into force field-compatible forms. At every step, ProPrep makes the underlying reasoning visible rather than automating it away, and preserves each action in a session log that can be shared for reproducibility, replayed to regenerate results, or adapted as templates for batch work. In doing so, ProPrep serves both the newcomer learning the field and the expert working at scale.



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Subcellular compartmentalization of the Methionine adenosyl-transferase complex MAT2A and MAT2B

Methionine adenosyl-transferase 2A (MAT2A) is an enzyme from the methionine cycle that catalyzes the conversion of methionine and ATP into S-adenosylmethionine (SAM) in most tissues. Methylation is a widespread reaction across the cell and SAM is the primary methyl donor for DNA, RNA, lipids, and protein methylation. Recent studies have reported that nuclear localization of MAT2A in hepatocarcinoma and other types of cancer correlates with poor prognosis. However, this is not true for breast cancer. Although these discrepancies are expected due to the heterogeneity in cancer, the MAT2A nuclear localization might be related to hypermethylation status of histones and DNA, a relevant process for some cancer types. However, the mechanisms that promote MAT2A nuclear localization and whether this could be related to hypermethylation are yet unknown. The objective of this summer's research project was to determine whether MAT2A localizes to the cytoplasm or nucleus in HeLa and HEK293 cell lines. To answer this question, we fractionated cells and obtained nuclear and cytoplasmic fractions. The purity of these fractions and the localization of MAT2A was tested by western blot analysis. Additionally, we analyzed the nuclear and cytoplasmic localization of MAT2A using confocal microscopy. Western blotting showed that MAT2A levels were lower in the nuclear fraction of HeLa and HEK293 cells. Interestingly, immunofluorescence showed that MAT2A had greater nuclear localization. Ongoing analysis of the fluorescence signal is underway. These findings may inform future studies in MAT2A's role in viral replication, virus-host interactions, and cancer treatments.