Wyoming IDeA Networks for Biomedical Research Excellence Spring Research Conference

April 18th-19th, 2024

University of Wyoming, UW Conference Center (UWCC), Laramie, WY

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Wyoming IDeA Networks for Biomedical Research Excellence (INBRE)

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Wyoming INBRE Spring Research Conference (April 18-19, 2024): **SCHEDULE**

THURSDAY APRIL 18 TH, 2024

*All oral presentations are scheduled in the **University of Wyoming Conference Center (UWCC), Salon E** (West end of Hilton Garden Inn Hotel); Alternate locations for specific meetings and poster sessions are indicated in the schedule table below.*

Morning Sessions:

Time	***DRPP Project Type***	***Presenter*** *(University of Wyoming department)*	***Title***
9:15-9:40 am	Welcome & Introduction	Wyoming INBRE Program Director: Dr. Scott Seville	
9:40-10:00 am	Thematic 1	Christina McDonnell (Department of Psychology)	Efficacy of a PTSD Intervention for Autistic Adults on Biobehavioral Health
10:00-10:20 am	Thematic 2	Grace Shearrer (Department of Family and Consumer Sciences)	Growth, Insulin Resistance, and Reinforcement Learning (GIRRL) study
10:20-10:40 am	*Break*		
10:40-11:00 am	Collaborative 1	Danielle Bruns (Division of Kinesiology and Health)	Myocardial Protein Citrullination in Sex-Specific Cardiac Aging
11:00-11:20 am	Thematic 3	Katelyn Kotlarek (Division of Communication Disorders)	Quantifying the Impact of Muscle Overlap in Primary Palatoplasty
11:20-11:40am	Thematic 4	Elizabeth Case (Department of Veterinary Sciences)	Uncovering the Contribution of *C. burnetii* Developmental Stage to Intracellular Pathogenesis
11:40-1 pm	*Lunch on your own*		

Afternoon sessions:

Time	***DRPP Project Category***	***Presenter*** *(University of Wyoming department)*	***Title***
1:00-1:20 pm	Thematic 5	Nicole Bedford (Department of Zoology and Physiology)	The Neurodevelopment of Voluntary Urination in Mice

1:20-1:40 pm	Pilot 1	Jason Gigley (Department of Molecular Biology)	Theft of Host Iron Machinery to Acquire Iron by *Toxoplasma gondii*
1:40-2:00 pm	Pilot 2	Jennifer Stephens (School of Nursing)	The Experience of Cancer for Rural and Frontier Wyoming Adult Oncology Patients: A Two-Phase Mixed Methods Study
2:00-2:20pm	Collaborative 2	Grant Bowman (Department of Molecular Biology)	High-Resolution Genetic Analysis of Connectivity in a Membraneless Compartment
2:20-2:40 pm	*Break*		
2:40-3:00 pm	Collaborative 3	Elliott Hulley (Department of Chemistry)	Structural Characterization of the Hemoglobin of Wyoming Fauna
3:00-3:20 pm	Pilot 3	Jay Gatlin (Department of Molecular Biology)	Characterizing Cell Cycle Dependent Changes in the Dynein Interactome
3:20-3:40 pm	Pilot 4	Jerod Merkle (Department of Zoology and Physiology)	Integrating Sociality and Migration to Inform Disease Spread
3:40-5:00pm	*Break*		
12:00-4:30pm	*Graduate Poster Set Up* (UW Conference Center Salon C/D)		
5:00-7:00 pm	Graduate Poster Presentations/ Reception (UW Conference Center Salon C/D)		

FRIDAY APRIL 19TH, 2024

*All oral presentations are scheduled in the **University of Wyoming Conference Center (UWCC), Salon E** (West end of Hilton Garden Inn Hotel); Alternate locations for specific meetings and poster sessions are indicated in the schedule table below.*

Morning sessions:

Time	***DRPP Project or CC PL report***	**Presenters** *(University of Wyoming and/or Wyoming Community College)*	**Title**
9:00- 9:20 am	Welcome & Introduction	Wyoming INBRE Program Director: Dr. Scott Seville	
9:20-9:40 am	NWC INBRE Activity Report	Eric Atkinson (Northwest College)	Bioinformatics and Basic Research in the Big Horn Basin: Opportunities for Project-Based Inquiry while Building Laboratory Skills and Knowledge of Theory: the Whole Kit and Caboodle.

9:40-10:00 am	Collaborative 4	Riley Bernard (Department of Zoology and Biology)	Examination of *Pseudogymnoascus destructans* Viability at Seasonal Bat Roost Sites
10:00-10:20 am	Collaborative 5	John Oakey (Department of Chemical & Biomedical Engineering)	"Soil on a Chip" Platform to Directly Study Inter-Organismal Interactions
10:20-10:40 am	*Break*		
10:40-11:00 am	UWC and CC INBRE Activity Report	Dagmara Motriuk-Smith (University of Wyoming at Casper, and Casper College)	Undergraduate Research at Casper College and the University of Wyoming at Casper Supported by INBRE
11:00-11:20 am	CWC INBRE Activity Report	Bill Finney (Central Wyoming College)	Spring 2024 Central Wyoming College INBRE Report
11:20-11:40 am	EWC INBRE Activity Report	Christopher Wenzel (Eastern Wyoming College)	Eastern Wyoming College (EWC) INBRE Progress Report: Microbial Ecology
12:00-1:30 pm	**Statewide Steering Committee working lunch meeting** (Marian H Rochelle Gateway Center/MHRGC, Boyd Room, level 2): SSC, EAC members and Wyoming INBRE Executive Committee only (lunch provided)		
11:40-1:30 pm:	*Lunch on your own for other attendees*		

Afternoon sessions:

Time	***DRPP Project or CC PL report***	**Presenters** *(University of Wyoming and/or Wyoming Community College)*	**Title**
1:30-1:50 pm	Collaborative 6	Cody Gifford (Department of Animal Sciences)	Effects of Diet on Indicators of Metabolic Health Using a Biomedical Swine Model
1:50-2:10 pm	NWCCD INBRE Activity Report	Ami Erickson (Northern Wyoming Community College District- Sheridan and Gillette Colleges)	Northern Wyoming Community College INBRE-Supported Research Activities
2:10-2:30 pm	WWCC INBRE Activity Report	David Tanner (Western Wyoming Community College)	INBRE Research at Western Wyoming College
2:30-2:50 pm	*Break*		
2:50-3:10 pm	LCCC INBRE Activity Report	Ami Wangeline / Zachary Roehrs (Laramie County Community College)	Forging Ahead on the Path of Research Experiences for All – LCCC Annual Research Report
3:10-3:20 pm	Closing remarks (Dr. Scott Seville)		

3:20-4:30 pm	*Break*
All day until 4:15pm	*Undergraduate poster set up* (UW Conference Center Salon C/D)
4:30-6:30 pm	Undergraduate Poster Presentations/ Reception (UW Conference Center Salon C/D)
6:30 pm	Conference adjourns

DETAILED SCHEDULE AND ABSTRACTS

FACULTY ORAL PRESENTATIONS

All faculty oral presentations (DRPP Thematic, Pilot, and Collaborative Projects, and Community College Project Lead updates) are held on Thursday April 18th and Friday April 19th, 2024, ***at the UW Conference Center*** *(UWCC; West end of Hilton Garden Inn),* **Salon E**.

THURSDAY, APRIL 18TH, 2024
UWCC Salon E

9:15-9:40 am: Welcome and Introductions by R. Scott Seville (Wyoming INBRE program Director/PI)

9:40-10:00 am: *Thematic Project 1*: **Efficacy of a PTSD Intervention for Autistic Adults on Biobehavioral Health**. Christina G. McDonnell

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ABSTRACT. Posttraumatic stress disorder (PTSD) is highly prevalent and characterized by a set of symptoms (intrusions, avoidance, hyperarousal, and negative mood and thoughts) that occur after a traumatic event. When untreated, chronic PTSD symptoms can lead to biomedical consequences, including reduced physical activity, disrupted sleep, cardiovascular health risk, chronic diseases, and early mortality. PTSD risk is particularly high among autistic adults. Autism is a neurodevelopmental diagnosis defined by social communication differences and restricted/repetitive behaviors, now diagnosed among 1 in 45 adults (2.26% of all adults in Wyoming). Pilot data shows that autistic adults experience a high number of traumatic events and symptoms, yet little research has evaluated evidence-based PTSD interventions for autistic adults. Thus, untreated chronic PTSD may exacerbate disparities in chronic diseases and behavioral health outcomes for autistic adults. The aims of this project are to (1) examine the initial feasibility and efficacy of a telehealth based, brief evidence-based intervention for PTSD among autistic adults, (2) pilot the use of wearable technology to evaluate whether the intervention is associated with changes in biobehavioral health metrics (activity, sleep, resting heart rate), and (3) obtain feedback from autistic adults on ways to modify and enhance the program, consistent with community engaged, participatory research methods. If experiencing significant PTSD symptoms, 30 autistic adults will receive a telehealth delivered 5-week program: Written Exposure Therapy (WET). Each week and 1- and 6-months post treatment completion, they will complete re assessment of their PTSD and mental health symptoms and physical health outcomes to evaluate (1) changes over the course of the 5-week program, and (2) whether changes are maintained over time. This presentation will provide an overview of these methods, and preliminary outcomes from year 1 of this project. Implications for future research will be discussed.

10:00-10:20 am: *Thematic Project 2*: **Growth, insulin resistance, and reinforcement learning (GIRRL) study.** Grace E. Shearrer[1,2], Muzayyana Akhmadjonova[2], Charles Palmer[3], Matthew Herr[3]

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ABSTRACT. Girls have a 60% higher prevalence rate of youth onset type 2 diabetes (yoT2D), and rural youth have 3 times higher odds of developing yoT2D. Research has shown that the frontline treatment for T2D is less effective in yoT2D. The brain is an emerging treatment target for insulin resistance (IR). Dopamine signaling at striatal dopamine 2 receptors (D2R) is negatively correlated with IR, which has led to D2R agonists approval for treatment of T2D in adults. Furthermore, striatal dopamine and D2R signaling is reflected in reinforcement learning (RL), with low D2R signaling related to negative RL (avoiding choices that lead to negative outcomes). Further, low spontaneous eye blink rate (sEBR), a marker of striatal dopaminergic activity, predicts negative RL. Understanding the relationship between D2R function (*via* RL and sEBR) and IR may provide preliminary evidence for dopamine based yoT2D treatments. The present study uses puberty as a naturalist model of insulin resistance in girls (n=60, body mass index percentile [BMI%] > 85%, 8-15y). We are actively collecting data to assess the following aims. Aim 1 tests the relationship between IR (*via* oral glucose tolerance test), sEBR (*via* resting state eye tracking), and RL (via probabilistic reward task) at baseline using a repeated measures linear model. Overall, we hypothesize that IR is related to low dopamine availability (negative RL and low sERB). Aim 2 predicts change (stable, worsening, or improving) in glycemia, *via* hemoglobin A1c (HbA1c), after 1-year based on baseline RL (positive or negative) and sEBR using multinomial logistic regression. We hypothesize that low dopamine availability (negative RL and low sERB) will be related to 20% higher odds of worsening glycemia after 1-year (similar to genetic risk factors). The present study is the first to examine a brain-based risk factor for IR.

10:20-10:40 am: ***Break***

10:40-11:00 am: *Collaborative Project 1:* **Myocardial protein citrullination in the aging heart.** Samantha K. Shorthill[1], Finley R. Klinger[1], Aykhan F. Yusifov[1], Joshua P. Thornburg[1], Florence Teulé-Finley[2], Brian D. Cherrington[3], Danielle R. Bruns[1,3]

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ABSTRACT. Advanced age is the primary risk factor for heart failure, an enormous public health burden. Cardiac aging is sexually dimorphic, with women more likely to develop diastolic dysfunction for which no therapies exist. Despite this well-established sex difference, underlying molecular mechanisms of sex differences in cardiac aging are unknown. Citrullination, a post-translational modification catalyzed by the peptidylarginine deiminases (PAD) enzyme family, is positively regulated by the sex hormone estrogen (E2). This suggests a potential novel mechanism of age-related cardiac function changes in women that has not yet been previously studied in the aging heart. We hypothesized that PAD expression and citrullination are sexually dimorphic with aging such that as E2 levels decline, so too does citrullination, thus contributing to diastolic dysfunction. We quantified expression of PAD2, the primary cardiac isoform, in male and female reproductively competent young (3 months) and aged (21 months) C57BL6 mice. We found PAD2 expression decreased with age in the female heart, concomitant with decreases in myocardial protein citrullination. To identify potential mechanisms of differential citrullination by age, we performed cit-mass spectrometry. Citrullination of sarcomeric, metabolic, and mitochondrial proteins was detected in the heart, with overall lower levels of citrullinated proteins in aged females compared to young. To confirm direct regulation of PAD2 by E2, a cohort of young and aged mice underwent ovariectomy (OVX) with or without E2 replacement, provided orally in the water (0.5µM E2) for three weeks. Although E2 post-OVX increased uterine weight consistent with estrogen action, no changes of PAD2 expression were observed in young females. Contrary to our hypothesis, PAD2 expression increased with OVX and OVX+E2 in aged females, indicating additional PAD2 regulators in the heart beyond E2. Consistent with PAD2 regulation of diastolic dysfunction with aging, global deletion of PAD2 exacerbated the HFpEF phenotype in aging females. Together, we collectively establish the presence of citrullination in the heart that changes with age. Elucidation of the mechanisms underlying PAD2 expression and citrullination remains to be determined to identify therapies for the aging female heart.

11:00-11:20 am: *Thematic Project 3*: **Quantifying the Impact of Muscle Overlap in Primary Palatoplasty: A Descriptive Analysis at Rest and During Speech.** Katelyn J. Kotlarek[1], Ilana Neuberger[2,3], and Gregory C. Allen[4,5]

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[2]Department of Radiology, Children's Hospital Colorado, Aurora, CO 80045

[3]Department of Radiology, University of Colorado Anschutz Medical Campus, Aurora, CO, 80045

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ABSTRACT. Children born with a cleft palate typically undergo primary reconstruction of the palate around one year of age. Two common approaches to surgical repair, the intra-velar veloplasty (IVV) and Furlow double-opposing Z-plasty, both aim to restore the levator veli palatini (LVP) muscle, which lifts and retracts the soft palate during speech production. Genuine uncertainty exists regarding the ideal surgical approach.

The purpose of this study is to determine the long-term impact imposed by the surgical procedure to the velopharynx and LVP muscle in children with repaired cleft palate and to ascertain whether lack of LVP overlap during palatoplasty yields a functional difference during speech production. To date, 6 children with repaired cleft palate who previously received an IVV have completed the study protocol. All participants underwent a speech sample and magnetic resonance imaging using a non-sedated, child-friendly protocol. MRI scans included a T2-weighted 3D scan at rest and 2, T2-weighted scans during sustained /i/ and /s/. Published normative datasets were used for preliminary comparison (Kollara & Perry, 2014; Perry et al., 2018; Tian et al., 2010). Participants demonstrated an asymmetrical LVP muscle sling with a thin midline. At least one participant with an IVV demonstrated dimensions beyond 2 standard deviations of the normative mean for LVP origin-origin distance, velar length, and effective velar length, while velar thickness and LVP angle of origin remained similar to age and race-matched peers. Effective velopharyngeal ratio ranged from 0.36-1.00. During phonation, one participant demonstrated LVP diastasis. Compared to published normative data, participants with an IVV demonstrated similar angles of origin but a longer LVP muscle during phonation. Percent contraction of the LVP muscle ranged from 9.02-13.29%. Effective velar length was greater during phonation yet resulted in less velar stretch (0.45-2.18 mm) compared to similar-aged children.

11:20-11:40 am: *Thematic Project 4*: **Dissecting the Role of *C. burnetii* Developmental Stage in Intracellular Pathogenesis.** Leslie A. Sims and Elizabeth D. Case

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ABSTRACT. *Coxiella burnetii* is the agent of Q fever, a highly infectious respiratory zoonosis transmitted to humans from domestic ruminants. This obligate intracellular bacterium has a biphasic developmental cycle in which it alternates between 2 disparate morphologies. The extracellular small cell variant (SCV) is highly durable, environmentally stable, and metabolically inert. The large cell variant (LCV) is the bacterium's fragile, intracellular, replicative form. While both cells have been described as infectious, this has only been observed during *in vitro* studies with cellular infection models that are irrelevant *in vivo*. We hypothesize that the ability to generate an environmentally resistant SCV is a requirement for infectivity and development of Q fever. During natural infection, the inhaled bacteria are phagocytosed by alveolar macrophages, and then traffic to a pathogen-tailored compartment which resembles a terminal phagolysosome. It is within this acidic, degradative, *Coxiella* containing vacuole that the bacteria begin their transition to LCV and replicate for 7 days prior to returning to the SCV form. We have some evidence that the developmental cell types of *C. burnetii* have a differential potential for successful infection of the bacterium's primary pathogenic niche in humans- macrophages. Inocula which are enriched for either developmental cell type show differential growth kinetics that are dependent on the infected host cell type. While *Coxiella* stocks replicate similarly in fibroblast cells lines irrespective of their developmental stage, we have found that stocks enriched for LCV cell types replicate faster in primary macrophages than those which primarily contain SCVs. Our study aims to extend these findings by comparing the macrophage's innate

immune response to infection with each cell type. Once the pathogenic potential of these two cell types is resolved, we can understand other fundamental aspects of disease progression, and the development of Q fever sequelae.

11:40 am-1:00 pm: Lunch on your own

1:00-1:20 pm: *Thematic Project 5:* **Sex-specific expression of social dominance hierarchy in laboratory mice.** Ryan S. Pitesky*[1], McKinzie L. Wade*[1], Samantha C. Patterson[2], Rachel E. Fanelli[1], Nicole L. Bedford[1]

(*Co-first author)

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ABSTRACT. Social dominance hierarchy is a key organizing principle of many animal societies, including humans. Notably, social rank has important consequences for evolutionary fitness as well as physiological and emotional health. In male laboratory mice, social rank is communicated via urinary scent marks. However, whether scent marking correlates with other metrics of social dominance, and whether scent marking is used by female mice to advertise rank, remains poorly understood. Here, we compare the developmental trajectories of urination behavior in male and female mice and show that both sexes can express territorial scent marking as early as four weeks of age, although this behavior is more common in males. We next explore the relationship between scent marking and social rank in two classical dominance tests: the tube test and warm spot assay. We found that male scent markers showed no consistent correlation with performance in either the tube test or the warm spot assay. By contrast, female scent markers tended to win the tube test but lose the warm spot assay. Last, we compared neuronal activation during urination behavior in scent markers and non-scent markers using immediate early gene expression. We found differential *cFos* expression in the medial preoptic area of the hypothalamus according to both sex and social rank. This brain region is associated with diverse sex-specific and rank-specific behaviors and projects to lower urinary tract-controlling neurons of the pontine micturition center. Altogether, our results indicate the existence of sex-specific neural mechanisms of social hierarchy expression in laboratory mice.

1:20-1:40 pm: *Pilot Project 1:* **Theft of Host Iron Machinery to Acquire Iron by *Toxoplasma gondii.*** Stephen L. Denton[1], Alexa Mejia[1], Lindsay L. Nevarez[1], Tathagato Roy[1], Miguel P. Soares[2], Barbara A. Fox[3], David J. Bzik[3], and Jason P. Gigley[1]

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ABSTRACT. Chronic *Toxoplasma gondii* (*T. gondii*) heart and brain infections have severe health impacts, however, there are no effective approaches to eliminate the

parasite from these tissues. *T. gondii* relies on acquiring from the host several nutrients essential for successful infection. One of those nutrients is iron. The *long-term goal* is to define mechanisms by which *T. gondii* acquires nutritional iron from the host to design better therapies to cure chronic infection. The *overall objectives* of this project are to dissect the mechanism(s) by which *T. gondii* acquires iron from the host. The *rationale* is elucidating how host iron is being stolen by the parasite could offer a strong scientific framework to develop new therapies to eliminate this infection. Iron is essential for *T. gondii* growth and replication. How iron is acquired by *T. gondii* is unclear. We discovered the genome of *Toxoplasma gondii* lacks conserved genes for iron transport and storage and show these host cell proteins including the transferrin receptor 1(TfR1), and cargo transferrin (Tf) are robustly taken up and incorporated into growing tachyzoites. Acquisition of these host cell proteins was conserved across host cell species and parasite virulence type. Host cell TfR1 and Tf uptake was required for parasite infection. Increased trafficking of host cell transferrin receptor 1 and transferrin to endolysosomes boosted tachyzoite acquisition of host proteins and growth rate. Whether this theft is the mechanism by which the parasite acquires iron is still not clear. This study provides insight into essential functions associated with *T. gondii* theft of host iron transport proteins. Our results also uncover a novel host-parasite interaction potentially conserved across the phylum Apicomplexa.

1:40-2:00 pm: *Pilot Project 2:* **The Experience of Cancer for Rural and Frontier Wyoming Adult Oncology Patients: A Two-Phase Mixed Methods Study.** Jennifer M.L. Stephens, Sherrill J. Smith, and Chenoa K. Williams

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ABSTRACT. *Background*: Scant inquiry has been done to understand the rural Wyoming oncology patient journey. Most research includes neighboring states and lumps Wyoming residents into an amorphous “rural” population. However, empirical information indicates that Wyomingites *are* unique, and their healthcare needs are complex due to being in this rural state. When a patient is diagnosed with cancer in Wyoming, their survival journey may include out-of-state referrals for diagnostics, treatments, and follow-up care. A lack of oncology specialists and palliative care in Wyoming, combined with challenges including transportation, small cancer-cohorts, weather, finances, and housing to name a few, can be daunting for those facing cancer. *Method:* This Wyoming INBRE 2-year grant (2023-2025) project supports a mixed method study exploring the first-hand experiences of adult oncology cancer patients who are Wyoming residents. A two-phased methodology includes gathering both patient and oncology healthcare provider perspectives. Data collection includes demographic survey information along with transcriptions from in-depth qualitative one-on-one interviews done either in-person or through a virtual platform (ZOOM). *Results:* Recruitment into this study started in the Fall 2023. Currently, over 40 interviews have been completed (patients, n=24; healthcare providers, n=16) and several more are scheduled. Recruitment will continue through the Summer 2024. Several gaps in care have been identified and regularly arise in interviews. *Next Steps:* The results of this study will be utilized to inform provider decisions around healthcare access and health

disparities present within the current oncology care environment in Wyoming. Additionally, healthcare providers and administrators will find this knowledge useful in care planning, case management, telehealth administration, resource allocation, and as a foundation for improving psychosocial factors that impact the client cancer journey. The foundational information gathered from this study will inform several new projects including an NIH R01 application for a palliative care pilot project that is Wyoming-specific.

2:00-2:20 pm: *Collaborative Project 2:* **Identifying amino acid sequence features of a protein hub that organizes bacterial cytoplasm.** Tanner Roberts[1] Breelyn Semon[1], Hannah Shuler[1], Carter Wiberg[1] Brooke Johnson[2], Hannah Swan[2], Samantha Patterson[3], Rachel Kaiser[3], Maddie Sites[3], Ellie Groves[3], Tess Palen[3], Ainsley Hokanson[3], Rachel Heffley[3], Cody McClarnon[3], Joshua Holmes[1], Dagmara Motriuk-Smith[1], and Grant Bowman[3]

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ABSTRACT. Despite being the simplest known forms of life, bacterial cells are highly organized. Many species segregate the cytoplasm into biochemically distinct zones through the formation of membraneless microcompartments. In *Caulobacter crescentus*, a protein called PopZ self-assembles into large structures that span the width of the cell poles, forming microcompartments that selectively partition dozens of different client proteins apart from the main cytoplasm. At least ten client proteins gain selective entry by interacting directly with a highly conserved, partially helical 26 amino acid domain in PopZ's N-terminus. Here, we describe a genetic screen for identifying amino acid sequence features within PopZ that are responsible for these interactions. We built a comprehensive mutant library that includes all possible point mutations across PopZ's N-terminal hub domain. Three teams of undergraduate students at Western Wyoming, UW Casper, and UW Laramie institutions have thus far screened over 392 library entries and identified more than 60 loss-of-function mutants. The data is providing information on the structural and biochemical nature of the binding interface, and whether different client proteins utilize unique, partially overlapping, or the same set of binding sites on PopZ. As we continue the screen, additional sequence information will reveal increasingly rich views of the structure and function of this molecular hub and how it contributes to complex subcellular organization in bacteria.

2:20-2:40 pm: Break

2:40-3:00 pm: *Collaborative Project 3*: **Efforts Towards Building a Protein Crystallography Lab.** Elliott B. Hulley[1] and Eric C. Atkinson[2]

[1]Department of Chemistry, University of Wyoming, 1000 E University Avenue, Laramie WY 82071
[2]Department of Biology, Northwest College, 231 W. 6th Street, Powell, WY 82435

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ABSTRACT. Modern structural biology depends on molecular-level understanding of the tertiary structures that nucleic acids, proteins, and other biological molecules attain in vivo. Of the techniques available, single-crystal X-Ray Diffraction (sc-XRD) is one of the most successful and least ambiguous technologies, and hundreds of thousands of structures have been determined using sc-XRD. The Department of Chemistry at the University of Wyoming, with funding from Wyoming INBRE, recently acquired a new sc-XRD instrument that has the capability to solve structures of small-to-medium sized proteins. Although the new instrumentation is rated for studies of small-to-medium sized proteins, formally adding that capability to its operation requires (1) assessing the instrument's capabilities for protein work using experimental protein crystals, (2) developing a knowledge base of protein crystallization conditions and requirements, (3) building the infrastructure for shipping and handling of crystalline protein samples, and (4) training students and faculty in the use of crystallographic solution software designed specifically for biomolecules. This talk will be an introduction to the challenges involved and an update on the progress made towards building this capability.

3:00-3:20 pm: *Pilot Project 3*: **Characterizing Cell Cycle Dependent Changes in the Dynein Interactome**. Zainab Almazadeh[1], Miroslav Tomschik[1], Martin Wuhr[2], and Jesse Gatlin[1]

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ABSTRACT. Cytoplasmic dynein (dynein) is a ubiquitous microtubule motor protein found in all metazoan cells. The motor is responsible for most of the retrograde vesicular transport (from the outside of the cell toward the nucleus) that occurs during interphase as well as for spatially organizing microtubules during mitosis. The myriad of different dynein functions is facilitated by many known dynein adaptors and activators. We hypothesize that dynein's mitotic functions result from the motor's interactions with specific regulatory proteins during this stage of the cell cycle. To characterize cell cycle dependent changes in the dynein interactome, we are adopting an approach that uses CRISPR-engineered cells containing a component of dynein fused to APEX2, an enzyme that facilitates proximal biotinylation of dynein-interacting proteins and their subsequent identification via mass spectrometry. By comparing the interphase dynein interactome with the mitotic dynein interactome, we hope to identify potential targets for therapeutic interventions of diseases the mechanistically rely on cell division, namely a subset of autoimmune disorders and cancers.

3:20-3:40 pm: *Pilot Project 4*: **How habitat availability and sociality interact to influence the potential for disease spread in wildlife**. Jerod Merkle

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ABSTRACT. The configuration of food availability plays a fundamental role in shaping the movement decisions of wild animals. When food hotspots are present on the

landscape, it can influence how individuals encounter and interact with each other. Encounters and interactions provide the building blocks for disease transfer among wild animals, ultimately influencing the potential for disease spillover to humans and livestock. In this talk, I will first outline how sociality is an ecological scale of inference that is often missing from wildlife research. Then, I will discuss research on how habitat availability and configuration influence contact rates and disease prevalence in mule deer in Wyoming. Finally, I will discuss the implications of this work relative to Chronic Wasting Disease, a fatal prion disease that affects deer species in Wyoming and beyond. Enhancing our understanding of habitat-contact relationships is essential to make predictions about when and where pathogen transmission might occur, which is key to understanding disease dynamics and spread, as well as prioritize management actions in time (e.g., among years) and space (e.g., among herd units).

3:40-5:00 pm: Break

12:00-4:30 pm: *Graduate Poster Set up (UWCC, Salon C/D).*

5:00-7:00 pm: *Graduate Poster Presentations/Reception (UWCC,* ***Salon C/D****)*

FRIDAY, APRIL 19TH, 2024
UWCC Salon E

9:00-9:20 am: Welcome and Introductions by R. Scott Seville (Wyoming INBRE program Director/PI)

9:20-9:40 am: *NWC Project Lead Report:* **Bioinformatics and Basic Research in the Big Horn Basin: Opportunities for project-based inquiry while building laboratory skills and knowledge of theory: the whole kit and caboodle.** Eric C. Atkinson[1], Allan Childs[2], Uko Udodong[2], and Austin Conklin[1]
[1]Biology Department, Northwest College, 231 W. 6th Street, Powell, WY 82435
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ABSTRACT. NWC INBRE supports undergraduate research, exploration, and mentoring spanning topics from a) novel antibiotic research, b) characterization and modification of bactericidal compounds in spices, c) water quality within the Big Horn Basin, d) avian disease, e) metabarcoding hymenopterans, rodent droppings, and cave systems, to f) curriculum development meeting the following program goals: 1) enhance opportunities for WY community college undergraduates to better understand (and ultimately participate in) the field of biomedical research; and 2) develop a pipeline of students with an interest in biomedical science who would then go on to complete their baccalaureate degrees and/or graduate degrees at UW. Collaborated with Drs. Merkle and Hulley addressing disease transmission in migrating cervids and haemoglobin description in Wyoming wildlife, respectively, with WGF. Our new faculty member initiated a weekly journal club “SPARK.” Transitioning back to face-to-face gatherings in 2021, and rather than concentrating on our major research projects we emphasize exposure to basic laboratory, research, and professional skills over this year. With pre

and post Knowledge Surveys via COI barcoding. we substantially increased the skill level of students while maintaining intellectual growth in the fields of genomics, bioinformatics, evolution, disease ecology, scientific professional development, and ethics. Since 2020, 66 students participated in our program: 31 students graduating with AS degrees; two have entered nursing school, 15 transferring to UW (10 awarded INBRE Transition support). Two REUs were gained. Professional development for faculty was provided via MDIBL/UNH T3, NIH-RTP2, graduate course enrollment (e.g., SMSC Conservation Genomics), and continued analysis and sample development via avian disease research in which students gained skills important to field-based biomedical research. This year's research group of 16 included six international students. We recently occupied new research space with an additional 260 ft^2 of cabinetted lab space to our existing 350 ft^2.

9:40-10:00 am: *Collaborative Project 4*: **Evaluation of growth and viability of *Pseudogymnoascus destructans*, the causal agent of White Nose Syndrome in bats.** Braden D. Mays[1,2], Riley F. Bernard[3], Steven L. Miller[2], Ami L. Wangeline[1].

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ABSTRACT. One of the primary conservation concerns for bats in the Great Plains, Inter- and Rocky Mountain West, is the emergence of white-nose syndrome (WNS). The causative agent of WNS is *Pseudogymnoascus destructans* (Pd), a psychrophilic filamentous opportunistic pathogen. This non-native fungus is decimating populations of bats, including recently moving through populations in Wyoming. The focus of the current study is to create new procedures for the isolation, culture, maintenance and evaluation of the pathogen to aid in management decisions to minimize pathogen transmission and increase persistence of bat populations. The first goal is a full growth parameter analysis including determining the ideals of temperature, light, media and humidity while also gaining insight into culture based morphological changes and the culture conditions that can cause dormancy and fungal death which was completed in spring of 2024. These developed methods will be used in spring and fall of 2024 to examine viability of Pd collected from roost sites at bridges via swabbing roost surfaces. Viability analysis will be done in combination with nucleic acid detection methods used to determine presence/absence. We anticipate that these collections will yield Wyoming specific variants of Pd, which can then be further analyzed to estimate bat susceptibility allowing us to better understand the disease etiology in our region, and potentially throughout the Intermountain West.

10:00-10:20 am: *Collaborative Project 5:* **"Soil on a Chip" Platform to Directly Study Inter-Organismal Interactions.** Simon Rachou[1], Chris Wenzel[2], and John Oakey[1]

[1]Department of Chemical and Biomedical Engineering, 1000E University Avenue, Laramie, WY 82071

[2]Department of Science and Mathematics, Eastern Wyoming College, Torrington, WY 82240
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ABSTRACT. Soil is a complex, multiscale system of solid, aqueous, and gaseous phases that contain an enormous diversity of prokaryote and eukaryote life. Its importance to agriculture, carbon cycling, and food chains make it one of the most critical components of the terrestrial ecosystem, yet also one of the most challenging to study. Aside from the extreme physical, chemical and biological diversity found in soil, soil is optically opaque, which presents intractable barriers to imaging and directly studying long-term events such as root development and interactions between the myriad of species present. To overcome these difficulties, we have developed a "soil on a chip" – a structured, controlled soil-like milieu that can be used to structure and directly observe interactions between soil organisms and between soil organisms and growing plant roots. This platform will be applied to the study of symbiotic root-fungal interactions in osmotically challenged soil conditions. Understanding how dynamic conditions affect these interactions in real time will provide a framework to study and understand implications for fertilizer use and drought tolerance. We focus upon understanding the function of arbuscular mycorrhizae (AM), obligate fungal symbionats that interact with the root systems of more than 80% of land plant species and provide water and inorganic nutrients such as phosphate and nitrogen in return for more than 20% of plant fixed carbon. AM acts as an extension of the root system and greatly increases plants' ability to access nutrients and moisture. In this project, we have developed a microfluidic soil on a chip platform to visualize co-cultures of fluorescently encoded *N. benthanmiana* roots with *Rhizophagus irregularis* spores. This talk will focus upon technological developments that improve root integration and the control of the artificial soil milieu.

10:20-10:40 am: Break

10:40-11:00 am: *UWC and CC Project Lead Report:* **Undergraduate research at Casper College and the University of Wyoming at Casper supported by INBRE.**
Dagmara Motriuk-Smith
University of Wyoming at Casper, 125 College Drive, Casper, WY 82601
Email: motriuk@uwyo.edu
ABSTRACT. The objective of the INBRE-supported research is to integrate research experience and enhance learning experience for students interested in pursuing careers in biomedicine. Last year, twelve students were awarded INBRE Internships and were mentored by five faculty members. These students participated in a variety of research projects including topics such as: digitization and identification of the herbarium specimens, investigation of amino acid sequence features of a polar organizing protein, gender-specific heart aging, and wing damage caused by the effects of the white nose syndrome. Additionally four faculty members engaged in collaborative research and three of them received Wyoming INBRE STEM seed grants. An equipment grant was awarded to purchase a new fluorescence microscope.

11:00-11:20 am: *CWC Project Lead Report:* **Spring 2024 Central Wyoming College INBRE Report.** William F. Finney[1], M. Gans[1], Lucy Graham[1], Matt Herr[2], Kirsten Kapp[1], Jacki Klancher[1], Charles Palmer[2], Claudia Troxel[1], and Tara Womack-Shultz[1]

[1]Arts and Sciences Division, Central Wyoming College, Riverton, WY 82501

[2]Business, Technology, Health, & Safety Division, Central Wyoming College, Riverton, WY 82501

Email: bill@cwc.edu

ABSTRACT. INBRE-supported faculty at Central Wyoming College continue to engage undergraduate students in research and develop broadly applicable skills in wide-ranging projects. **Professors Charles Palmer and Matt Herr** are working with University of Wyoming professor Grace Shearrer on her "Girls Insulin Resistance and Reinforcement Learning" (GIRRL) study. **Professor Lucy Graham** is investigating the effects of wildfire smoke on oncogenic changes to protein and RNA expression in cell culture and is working with **Dr. Claudia Troxel** to examine the effects on compounds in plants used in traditional Native medicine on these cultures. **Professor Kirsten Kapp** continues her work investigating the sources of microplastic pollution in natural waters. **Professor Jacki Klancher** HIKES, BIKES, and literally takes students to the highest peaks to understand the connections between the health of our environment and human health. **Professor Tara Womack-Shultz** has and continues to be open to participate in collaborative projects with faculty at the University of Wyoming and throughout the INBRE network.

11:20-11:40 am: *EWC Project Lead Report:* **Eastern Wyoming College (EWC) INBRE Progress Report: Microbial Ecology.** Christopher R. Wenzel

Department of Science and Mathematics, Eastern Wyoming College, Torrington, WY 82240

Email: cwenzel@ewc.wy.edu

ABSTRACT. The INBRE program at Eastern Wyoming College (EWC) has involved 26 undergraduate students since it began in 2009. At least 15 students have gone on to pursue or are planning to pursue higher degrees in Biology or Biomedical related fields. Research at the EWC-INBRE Laboratory focuses on three major areas including 1) the role of microbes in biogeochemical cycles; 2) environmental tolerances of soil microbes; and 3) collaborative development of a microfluidic platform for observing fungal-plant interactions. Student tasks have included 1) microbial DNA extraction and quantification; 2) polymerase chain reaction (PCR) to determine the presence or absence of microbial genes; and 3) determination of variation in microbial environments. Additional support has been provided by supplemental equipment purchases using INBRE funds including 1) Nano-Drop UV-vis for DNA quantification; 2) Bio-Rad T100 Thermal Cycler for gene detection; 3) So Low -40 freezer for nucleic acid preservation; 4) Stirling Ultra-cold -86 freezer; and 5) Chai-Bio quantitative PCR (qPCR) unit, and 6) GelDoc Go Gel Imaging System with Image Lab Touch Software. EWC has provided 414 square feet of laboratory space dedicated to faculty-student research; computer and laboratory resources; transportation support to and from faculty-student statewide and regional meetings and conferences, graduate-level courses for faculty, and laboratory training

sessions for both students and faculty. The INBRE program has been an invaluable addition to the Pre-Health Science and Biology-based programs on our campus. It has provided state-of-the-art equipment for biomedical research, hands-on experiences and scholarship opportunities for students, and enhanced the caliber of our science faculty, thereby attracting better-prepared students to our campus.

12:00-1:30 pm: Statewide Steering Committee working lunch meeting (MHRGC, Boyd Room; SSC, EAC members and Wyoming INBRE Executive Committee only)

11:40-1:30 pm: *Lunch on your own for other attendees*

1:30-1:50 pm: *Collaborative Project 6:* **Effects of diet on indicators of metabolic health using a biomedical swine model.** K. A. Gallegos[1], H. C. Cunningham-Hollinger[1], J. L. Burkett[2], and C. L. Gifford[1]

[1]Department of Animal Science, University of Wyoming, 1000E University Avenue, Laramie, WY 82071

[2]Agriculture Department, Casper College, 125 College Drive, Casper, WY 82601

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ABSTRACT. Increased levels of total and saturated fat, sodium and refined carbohydrates are generally associated with the human western style dietary (WSD) pattern. Numerous epidemiology studies have reported positive associations between WSD and chronic disease risk. The current collaborative project uses modification of diet ingredients to assess the macronutrient impact of feeding a WSD or higher protein (HP) healthy style eating pattern over the rapid postnatal growing phases of a swine biomedical model. Swine are assigned to the WSD or HP in a parallel (only received one dietary treatment) or crossover arrangement (switched to the other diet halfway through the feeding phase) to evaluate the impact of diet quality on intestinal morphology, systemic markers of inflammation, fecal microbiota, and skeletal muscle changes during postnatal growth phases. The overall aim of this collaborative project is to evaluate if the composition of diet during specific phases of growth in this biomedical swine trial provides further physiological insights to the risk of developing chronic disease among young adults. Data collection is ongoing as part of this two-year collaborative study between Casper College and the University of Wyoming. In addition, undergraduate students from both institutions are an essential part of this study. Future research based off this collaborative data will focus on comparison of ingredients, such as animal or plant food sources, that contribute to both macronutrient and micronutrient levels reported in NHANES (National Health and Nutrition Examination Survey) human dietary intake data.

1:50-2:10 pm: *NWCCD Project Lead Report:* **Northern Wyoming Community College INBRE-Supported Research Activities**. Ami Erickson[1,2], Scott Newbold[2], Rob Milne[2], and Stephanie Servetas[2,3]

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[2]Natural Sciences, Sheridan College, Sheridan, WY 82801

[3]Biosystems and Biomaterials Division, National Institute of Standards and Technology, Gaithersburg, MD 20899
Email: amie@sheridan.edu
ABSTRACT. Faculty and students at Sheridan College, Northern Wyoming Community College District, have been actively engaged in research and educational endeavors associated with biomedical and scientific inquiry and supported by Wyoming INBRE. A team of students, supervised by Dr. Stephanie Servetas and Dr. Ami Erickson, have investigated various topics while gaining skills in DNA isolation, purification and sequencing, bacteria isolation and culture, aseptic technique, experimental design, microscopy, and plant propagation. Research topics include identifying soil bacteria and fungi associated with different plant communities, extracting and sequencing fossilized plant DNA, developing a technique to identify heritage Wyoming apples with SSR targeting primers and apple genomic BLAST inquiries, and characterizing the microbial profile of different sourdough starters. Sheridan College students taking Natural Science and Agricultural Science classes are exposed to research techniques important to the biomedical fields, and the students have the opportunity to develop laboratory and field research skills. General Biology faculty are developing a lab exercise that will use yeast DNA and restriction enzymes to expose students to DNA extraction, PCR, gel electrophoresis, and genotyping. Many science classes incorporate independent, inquiry-based research projects, during which students develop a scientific hypothesis. Students use equipment and materials associated with biomedical research to test their hypotheses. Detailed examples will be shared during our presentation.

2:10-2:30 pm: *WWCC Project Lead Report:* **INBRE Research at Western Wyoming College.** David A. Tanner
Western Wyoming Community College, 2500 College Drive, Rock Springs, WY 82901
Email: datanner@westernwyoming.edu
ABSTRACT. The purpose of INBRE research at Western Wyoming Community College is intended to introduce freshman and sophomore students to research, provide them the opportunity to apply the scientific method, encourage students to pursue consider careers in the sciences, and to expand our current understanding of the natural world through presentation and publication of research work. Six students at WWCC participated in INBRE funded research. Topics of research included microbiology, protein-protein interactions, evolution, and bioinformatics. We currently have two faculty participating in INBRE research programs. One student from WWCC was award a UW Transfer Award, one student has received a nursing residency in Cheyenne, one student transferred to West Minster College, and one student was admitted to medical school. Research as currently practiced at WWCC would not be possible without INBRE funding, which has allowed us to retain quality faculty and facilitated the development of our students into capable and responsible scientists.
2:30-2:50 pm: *Break*

2:50-3:10 pm: *LCCC Project Lead Report:* **Forging ahead on the path of research experiences for all – LCCC annual research report.** Gavin J. Martin, Zachary P. Roehrs, and Ami L. Wangeline

Laramie County Community College, 1400 E. College Drive, Cheyenne, WY, 82007
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ABSTRACT. The mission of the Laramie County Community College (LCCC) IDeA Network for Biomedical Research Excellence (INBRE) research group is to improve access to authentic research experiences for our students. This year has been eventful, with a forward leap into new projects, bringing in new students, two new faculty, expanding opportunities and making plans for the coming year. This year has seen the expansion of the bioinformatics-based model for our Scientific Research class, with three projects currently underway, two on beetle group systematics and one on eDNA. For the insect projects, students are presented with a large Anchored Hybrid dataset and receive a mix of training, related both to the scientific method, as well as how to use bioinformatic tools available through the Wild Iris cluster. The eDNA project is focused on pond sediments and is part of our ongoing development of a CURE for BIOL1010 to be implemented in Fall 2024. Our hope is to have an all-encompassing research experience for all biology students at LCCC through use of our microscopes (SEM and Confocal fluorescence), DNA extraction, 16s amplification and nanopore sequencing, all of which has been funded through INBRE over the years. Through these new directions we feel we will be able to keep supporting the Wyoming INBRE pipeline.

3:10-3:20 pm: Closing Remarks (Scott Seville)

3:20-4:30 pm: *Break*

All day until 4:15 pm: *Undergraduate Poster Set up (UWCC,* ***Salon C/D****)*

4:30-6:30 pm: *Undergraduate Poster Presentations/Reception (UWCC,* ***Salon C/D****)*

6:30 pm: *Conference Adjourns*

UW GRADUATE STUDENT POSTER PRESENTATION ABSTRACTS

Resting-State Connectivity between the Salience Network and Left Thalamus in Adolescents Predicts Sugar-Sweetened Beverage Intake a Year Later. Muzayyana Akhmadjonova[1,2] and Grace Elisabeth Shearrer[1,2,3]

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ABSTRACT. Sugar sweetened beverage (SSB) consumption is associated with increased adiposity in childhood. We aimed to predict SSB intake at year-2 from year-1 resting-state functional magnetic resonance (rsfMRI) connectivity in children. We used baseline demographic and rsfMRI data and year-2 SSB intake data (Block Kids Food Survey) from the Adolescent Brain Cognitive Development study. Participants were included if they had complete baseline rsfMRI correlation data (subcortical 19 regions of interest [ROI] to Gordon cortical 12-network ROIs and cortical to cortical), height and weight, household income, sex, age; and year-2 SSB intake data. We defined SSB intake groups as low (<8 foz/day) and high (>16 foz/day). Groups were matched on sex, age, body mass index percentile (BMI%) and household income using nearest neighbor (n/SSBgroup=1854, age=9.95y±0.63, BMI%=63.1±0.02, sexF=1467). We used a grid search linear support vector classifier (n_{train}=2085, n_{test}=927) with univariate feature selection to determine how many and which ROIs to include in our model out of 416 baseline ROIs. Selected features were used in a binary logistic regression (bootstrapping=1000) to predict high SSB intake at year-two (n_{train}=741, n_{test}=186). All training and testing groups were exclusive. All modeling was performed in Python using SciKit Learn. Stronger connectivity between the salience network and left thalamus (OR=0.57, CI=-1.65:0, p=0.05) was related to lower odds of high SSB consumption at year-2. Previous research shows connectivity between the salience network (insula, anterior cingulate, and ventral striatum) and the thalamus is related to balancing homeostatic demands. Our work suggests that weakening this homeostatic connectivity predisposes children to higher SSB intake.

Anxiety on the Rocks: College Students' Anticipatory and Compensatory Urges to Drink in Response to a Laboratory-Based Social Stressor Task. Katherine A. Berry and Alison Looby

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ABSTRACT. Stressful social and evaluative situations may increase alcohol use among undergraduates as a means of coping in anticipation of the stressful event or to modulate negative affect post-event. This study examined anticipatory and compensatory urge to drink using a modified Trier Social Stressor Task (TSST) among college student drinkers (N =129, M_{age} = 19.49, 81.4% white non-Hispanic, 62.8% female), based on baseline social anxiety, alcohol coping motives, and type of nonverbal feedback provided during the task. Participants were informed they would give a video-recorded speech that would be evaluated in real-time by two researchers

and were randomized to receive positive or negative nonverbal feedback during their speech. Participants reported urge to drink and completed an alcohol pour task both in anticipation of and following completion of the TSST. All participants reported significantly increased urge to drink from baseline both in anticipation of and following the stressor task. Coping motives and social anxiety predicted stronger anticipatory urge to drink, though there were no significant interactive effects. Conversely, there were no significant predictors on the anticipatory pour task. For compensatory urge to drink and amount poured, there were significant three-way interactions between condition, coping motives, and social anxiety, such that students who received negative feedback and endorsed high coping motives and social anxiety reported the strongest urge and poured the most alcohol after the TSST. Results highlight targets of intervention to reduce problematic alcohol use, including finding alternative ways to manage negative emotion, and indicate the need to attend to anticipatory *and* compensatory drinking.

Discovering the Role of Maternal Choline Supplementation on Epigenetic Programming and Behavioral Outcomes. Naomi Boldon[1], Bo Shui[2], Jen Grenier[3], Jill Keith[4], Brian Cherrington[5], Barbara Strupp[6], and Paul Soloway[7]

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ABSTRACT. Choline plays integral roles in neurodevelopment through production of acetylcholine (neuronal signaling) and formation of phosphatidyl choline (neuronal cell membrane properties) and is the primary dietary methyl donor (gene expression). Despite the increased need for choline during pregnancy, 90% of women do not consume the Adequate Intake (AI) level, and choline is not currently included in standard prenatal vitamins. While there is growing evidence maternal choline supplementation (MCS) during pregnancy lessens offspring cognitive dysfunction in the Ts65Dn mouse model of Down syndrome (DS) and exerts lifelong cognitive benefits for typically developing offspring in both humans and rodent models, we know very little about possible mechanisms. This research is designed to elucidate epigenetic changes produced by MCS that correlate with improved performance in attention tasks in trisomic (DS) mice and/or neurotypical (2N) mice. Our hypotheses are that MCS during pregnancy and lactation leads to chromatin accessibility in specific cell types of offspring. **1.** MCS normalizes epigenetic states in certain trisomic cell types, bringing them closer to 2N states, which manifests as improved cognitive functioning. **2.** MCS imparts epigenetic changes in disomic (2N) mice with a concomitant improvement in cognitive functioning. By identifying alterations in genotypes affected by MCS, we will identify key genes, loci, and pathways that lead to cognitive and attention deficits, and mechanisms of action of MCS. The results of our study will inform efforts to improve

cognitive functioning in DS, as well as provide widespread neuroprotection and improved cognitive functioning in the population at large. Our study is the first to apply single cell methods to characterize complex, nutritionally modified behavioral traits, which enables correlations among molecular features found in single cell types with measured behaviors. Our research supports the foundational work necessary to understand the molecular mechanisms underlying behavioral traits and through which MCS confers its benefits.

Emotion Regulation Among Gender Diverse Autistic Adults. Kaitlyn Breitenfeldt, Alison Tassone, Theresa Andrzejewski, Saily Gomez Batista, and Christina McDonnell
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ABSTRACT. Emotion regulation (ER) difficulties can significantly negatively impact an individual's mental and physical well-being (Aldao et al., 2016). Although ER difficulties have been increasingly recognized as highly prevalent and related to mental health in autistic individuals, little research has examined sex or gender differences within autistic adults. In non-autistic individuals, sex differences in ER are thought to be associated with the higher prevalence of some types of mental health symptoms in females (Nolen-Hoeksema, 2012). Preliminary research supports this in autistic females (Weiner et al., 2023). A growing body of research suggests there is an overlap between autism and gender diversity and that understanding the mental health of autistic individuals who are gender diverse is a critical priority (Warrier et al., 2020). In non-autistic populations, gender-diverse individuals have been shown to have more ER difficulties (Hatzenbuehler et al., 2008). 276 Autistic adults, including 93 cisgender women (CW), 128 cisgender men (CM), and 55 gender-diverse individuals (GD), completed self-report measures, including the Difficulties in Emotion Regulation Scale (DERS-16), Patient Health Questionnaire (PHQ-4), Posttraumatic Symptom Checklist (PCL-5), and Satisfaction with Life Scale (SWLS). The three groups differed on three of the five DERS-16 subscales, with the GD group reporting significantly more difficulties when compared to CM. Each of the gender groups demonstrated moderate positive correlations between the DERS-16 total score and the PHQ-4 (r =.412-.553) and the PCL-5 (r =.447-.512) and weak negative correlations with the SWLS (r =.283-.349). These correlations did not differ significantly across groups. Further, GD adults report significantly less life satisfaction than CW, and GD adults and CW both reported significantly more trauma symptoms than CM. The results indicate that gender-diverse autistic adults may be experiencing more difficulties in the ER, resulting in poorer mental and physical health, emphasizing the need to ensure that ER supports are inclusive and affirming for gender-diverse autistic adults.

Impact of Obesity on Sleep and Prefrontal Cortex Function in Mice. Haifa Chargui[1], Whitney Walker[1], Prince Peter Wormenor[2], Nathan C. Cupertino[1,4], Brandon L. Roberts[1,2,3,4]
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[2]Program in Neuroscience, University of Wyoming, Laramie, WY 82071
[3]Department of Animal Science, University of Wyoming, Laramie, WY 82071,

[4]Department of Psychological and Brain Science, University of Massachusetts, Amherst, MA 01073
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ABSTRACT: Obesity leads to numerous pathologies, such as type 2 diabetes, metabolic disorders, cardiovascular disease, and psychiatric disorders. The prefrontal cortex (PFC) is a brain region highly involved in governing stress, fear responses, cognition, and memory. Notably, exposure to high-fat diet (HFD) disrupts neural function in the PFC. Here we address how exposure to high-fat diet impacts sleep and PFC function in adult mice. We used a mouse model of diet-induced obesity (65% kcal from fat). In adulthood, CTR male mice were placed into a non-invasive sleep recording system. We measured baseline sleep, and after one week, mice were split into two groups, either continuing on standard chow or receiving a HFD. After our sleep measurements, brains were collected for *ex vivo* patch-clamp electrophysiology. We recorded from neurons in the prelimbic (pl) PFC at zeitgeber time (ZT) bins 6-10 or 18-20. We then measured the endogenous function of plPFC pyramidal neurons. The first goal of this study is to understand how circadian disruption develops after exposure to HFD. The second goal is to determine how high-fat diet impacts PFC neural function in mice. Here, we answer these questions by combining *in vivo* sleep monitoring with *ex vivo* patch-clamp electrophysiology. This work forms the foundation for future studies focused on the lifelong neurobehavioral impact of HFD exposure and how it influences emotional and cognitive function.

Acute Effects of Physical Exercise in College Students with and without ADHD.
Meisa M. Khaireddin[1], E. A. Miller[1], J. M. Vasko[1], J. W. Serrano[1], D. K. Smith[2], and C. M. Hartung[1]
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[2]Department of Kinesiology & Health, University of Wyoming, Laramie, WY 82071
Email: mkhaired@uwyo.edu
ABSTRACT: There are limitations to psychosocial and pharmacological interventions for ADHD despite their effectiveness. For example, stimulant medications are ineffective or intolerable for 20-50% of individuals with ADHD. Research has suggested that physical exercise (PE) has effects beyond improving physical health. A review of PE effects in youth with ADHD suggests PE can yield medium-to-large effects on ADHD symptoms and executive functioning (EF). In adults, however, there has been little research on the effects of PE on these outcomes. Thus, the goal of the current study is to examine the acute effects of PE on EF task performance. Participants were UW students (*N* = 29). EF tasks were completed at two sessions. For one session, high intensity interval training (HIIT) was completed before EF tasks. Participants were grouped by ADHD status and sex. A power analyses indicated 9 participants were needed in each group (36 total). So far, we have collected data from 26 participants. We hypothesized that EF would improve regardless of ADHD status after a HIIT session. Also, we hypothesized that EF would improve more for individuals with ADHD. We continue to collect and enter data and have not yet conducted analyses. We will analyze the data and present it on 04-18-24. We will conduct repeated measures 2 (ADHD vs. Non-ADHD) x 2 (non-HIIT vs. HIIT) ANOVAs. We expect two main effects and an interaction. If our hypotheses are confirmed, this would justify additional research

examining exercise as a treatment option for individuals with ADHD (*e.g*., chronic effects studies). Exercise may be a substitute for individuals with ADHD who do not want to take medication or who cannot tolerate its side effects. Furthermore, PE may also serve to prevent the broad-ranging poor health outcomes associated with ADHD (*e.g*., obesity, cardiovascular disease).

A Comprehensive Evaluation of the Growth Preferences for the Causative Agent of White-Nose Syndrome, *Pseudogymnoascus destructans.* Braden Mays[1], Ami L. Wangeline[1], Riley F. Bernard [2], and Steven Miller[3]

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ABSTRACT. *Pseudogymnoascus destructans* (*Pd*) is a psychrophilic fungus whose genus is commonly found in soils in colder environments, including caves and mines. *Pseudogymnoascus destructans* causes the epizootic disease white-nose syndrome, which is responsible for the deaths of millions of bats in North America; as the fungus disrupts the hibernation cycle as well as gas/water exchange processes that take place across wing membranes. Bats are keystone species, providing pollination and seed dispersal services for specific plants. Bats also provide agricultural crop pest management that saves farmers an estimated 3-50 billion dollars a year in pesticide use. Previous research on the fungus has mainly been approached with a basic understanding of mycology and microbiology; as well as an emphasis on nucleic acid-based detection methods which can be used to identify presence, but not viability of the fungus. To improve our understanding of *Pd*, we are testing a pure culture from the American Type Culture Collection on a wide array of media types at different concentrations, seeking media that results in efficient and fast fungal growth with conidia development. Further, we also aim to discover what leads to inefficient and/or stressed growth. This developed preferred media method will be used for the refined identification and evaluation of viability of *Pd* during different seasons and locations; from the collection via swabs from roost and hibernaculum sites from around Wyoming. By doing these experiments we hope to move to a more encompassing understanding of *Pd* than previous studies; including the ecology, transmission, and impact on bat species in North America.

Constructing a Self-Assembled Heat Chamber Suitable for Thermoregulatory Research and Heat Acclimation Training. Kevin E. Miller[1], Jenna A. Beckley[1], Dillon Nye[1], Bailee R. Smith[1], Jimmy G. Bautista[1], Timothy J. Robinson[1], Emily E. Schmitt[1], Danielle R. Bruns[1], Zachary J. Schlader[2], Christopher Bell[3], and Evan C. Johnson[1]

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ABSTRACT. Environmental chambers (HEC) are crucial for thermoregulation and heat acclimation research, but cost burdens drive the creation of cost-effective makeshift heat chambers (MHC). While MHC's offer affordability, doubts persist about a MHC's

ability to maintain stable TEMP and %RH, potentially confounding physiological responses in human thermoregulation. Purpose: Build a MHC to maintain temperature and humidity suitable (±1.1-1.7 °C and ± 2-3 %) for thermoregulatory research and heat acclimation protocols. Methods**:** A 10'x10'x8' PVC frame with plastic sheeting, and 5 heaters and 3 humidifiers, was set to maintain 40°C and 40% RH. 6 young adults, across BMI categories, underwent 4 exercise protocols (Resting, $\dot{V}O_{2max}$, Cycling, Heat Tolerance) in the MHC, recording TEMP and %RH every 3 minutes. The $\dot{V}O_{2max}$, cycling, and heat tolerance protocols were repeated for repeatability analysis. The heat tolerance protocol was performed a third time in a HEC for comparison. Descriptive statistics analyzed deviations from hypothetical means of 40°C and 40%, while approximate F-tests and 95% confidence intervals assessed COV differences between trials and MHC-HEC. A linear mixed model explored factors (metabolic heat, outside temperature, equipment heat, BMI) affecting the deviation from the hypothetical mean TEMP (40°C). Correlation analyses investigated links between independent factors and TEMP/%RH variations. Results: Mean TEMP was consistently below the hypothetical 40°C (39.90±0.32°C), while %RH was consistently higher than 40% (40.86±0.59). TEMP COV range was 1.56-1.77%, and %RH COV was 4.66-5.62%. Repeated trials showed no differences in TEMP, %RH, and COV (95% CI, TEMP [39.81-39.98], %RH [40.44-41.15]; all $p > 0.05$). In heat tolerance, MHC displayed different TEMP (39.86-40.03°C) and %RH (40.63-41.15%) compared to HEC (39.39-39.57°C; 42.48-43.01%; $p < 0.001$). However, the MHC was closer to the hypothetical 40°C and 40% than the HEC. The linear mixed model revealed no significant influence of factors on TEMP variation (All $R^2 < 0.50$; $p > 0.05$). Correlation analyses showed weak non-significant correlations between independent factors and TEMP/%RH variations ($r = -0.16$-0.13; all $p > 0.05$). Conclusion: The constructed MHC, priced under $2,000, is suitable for thermoregulation research at 40°C and 40% RH

Assessment of Mood, Emotion Regulation, and Substance Use Across Days.

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ABSTRACT. Emotional regulation refers to attempts to control one's emotions via adaptive (accepting situations) and maladaptive (blaming others for one's emotions) strategies. Additionally, some individuals may exhibit harmful patterns of substance use as a maladaptive regulation strategy, and a history of mood symptoms (e.g., hypomanic symptoms) often co-occurs with a substance use history. This study aimed to examine frequencies of emotional regulation strategies, mood symptoms, and substance use across a 7-day period in adults recruited online (N = 229; 1243 observations across days; *M*age = 37.17, 19-86 years). Majority identified as cisgender (n = 213, 93.01%), female (n = 124, 56.62%), and white (n = 186, 84.93%). Using diagnostic cutoffs suggesting a likely presence of alcohol use disorder (AUD) and cannabis use disorder (CUD), 58 and 45 participants met AUD and CUD criteria, respectively. Individuals reported 102 (10.06%) and 107 (10.55%) days where they used alcohol or cannabis, respectively, for the purpose of regulating mood. Additionally, multiple regression analyses were used to assess relations between reported mood disorder symptoms and likely alcohol or cannabis use disorder symptoms. For individuals reporting alcohol or

cannabis use respectively, substance use criteria scores accounted for a total of 10.22% and 17.45% of total variability in mood disorder experiences ($\beta = .320$, $R^2 = .102$, $p = <.001$; $\beta = .418$, $R^2 = .175$, $p = <.001$). Thus, as mood symptoms increased, so did AUD/CUD ratings. Regarding use of emotion regulation strategies, majority of individuals reported using acceptance strategies across days (adaptive; score > 1: n = 803, 79.19%; n = 884, 87.18%). Most also reported using rumination across days (maladaptive; score > 1: n = 708, 69.82%; n = 702, 69.23%). These findings inform understanding of mood, emotion regulation, and substance use assessment across days, providing a starting point towards informing more precise intervention efforts.

Microbial Stem Cells: Using Asymmetric Division to Enhance Bioreactor Productivity. Steven Poyer

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ABSTRACT. Bioreactors have become an increasingly attractive method for the production of renewable fuels, pharmaceuticals, food additives, and the management of agricultural waste. While the underlying technology continues to improve efficiency and yield, a significant hurdle to the use of bioreactors remains that product synthesis and cell proliferation are often mutually antagonistic activities, leading production to be self-limiting. An elegant solution to this problem is to control cell differentiation within a culture, allowing the roles of cell growth and product synthesis to be assigned to two different cell types. The first cell population, factory cells, would sustain constant production, utilizing all cell machinery to that end. While a second population, stem cells, would focus solely on asymmetric cell division, leading to constant replenishment of the factory cells. As many diverse organisms are used in bioreactors, our research focuses on disparate methods of leveraging asymmetric differentiation to achieve these goals.

Role of VRK1 in Nuclear Size Regulation and Morphology in *Xenopus* Extracts. Haritha Prabha[1], Utkarsh Kapoor[2] and Daniel L. Levy[1]

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ABSTRACT. Understanding the mechanisms controlling the size and shape of the nucleus is crucial in cell biology, particularly due to the observed changes in nuclear characteristics in cancer. Vaccinia-Related Protein Kinase1 (VRK1) is a serine-threonine kinase that belongs to the casein kinase-1 family and plays multiple roles in cell division, proliferation, and nuclear envelope assembly. However, the explicit role of VRK1 in regulating nuclear size has not been extensively studied. A recent screen identified VRK1 as a potential regulator of nuclear size. We use *Xenopus laevis* egg extract system, which allows de novo nuclear assembly and growth for our experiments. Immunofluorescence confirmed VRK1's presence in the extracts, displaying a punctate pattern within the nucleus. By employing various approaches, such as small-molecule inhibitors and immunodepletion of VRK1, we find that inhibiting or depleting VRK1 results in a significant reduction in nuclear size and the emergence of nuclear

membrane invaginations. Live imaging of nuclear assembly using GFP-NLS in the presence of VRK1 inhibitor shows us that inhibition of VRK1 results in nuclear envelope rupture as well as changes in nuclear growth and import rates. Chromatin distribution was also affected by VRK1 inhibition. One of the substrates of VRK1, Barrier-To-Autointegration Factor 1's distribution was affected by VRK1's inhibition. Moreover, we study if VRK1 is capable of liquid-liquid phase separation due to the presence of disordered regions at its N- and C- terminals using the Phase Co-Existence Slab method. Future research will focus on identifying the specific VRK1 substrates involved in nuclear size regulation.

Mass Spectrometry Reveals Citrullinated Proteins in Gonadotrope Cells. Elizabeth B. Quigley[1], Stanley B. DeVore[2], Shaihla A. Khan[3], Zachary M. Geisterfer[4], Heather M. Rothfuss[1], Ari O. Sequoia[1], Paul R. Thompson[5], Jesse C. Gatlin[6], Brian D. Cherrington[1], and Amy M. Navratil[1]

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ABSTRACT. Peptidylarginine deiminases (PADs or PADIs) catalyze the conversion of positively charged arginine to neutral citrulline, which alters target protein structure and function. Our previous work established that gonadotropin releasing hormone agonist (GnRHa) stimulates PAD2-catalyzed histone citrullination to epigenetically regulate gonadotropin gene expression in the gonadotrope derived LβT2 cell line. However, PADs are also found in the cytoplasm. Given this, we used mass spectrometry (MS) to identify additional non-histone proteins that are citrullinated following GnRHa stimulation and characterized the temporal dynamics of this modification. Our preliminary data reveal temporally citrullinated proteins associated with distinct cellular pathways following 10 and 30 minutes of GnRHa stimulation. We found citrullinated proteins associated in cell proliferation, transcriptional activation, mitogenesis, and RAS/RAF/MEK/ERK signaling cascades, all of which are vital to gonadotrope function. Not only do we see signaling cascades as targets of GnRHa induced citrullination, our preliminary data also reveal citrullination of proteins facilitating vesicle release from LβT2 cells within 10 minutes of GnRHa stimulation. Additionally, our *in vitro* work has identified a number of cytoplasmic cytoskeletal proteins as targets of citrullination. To determine if this event is PAD specific, we utilized the pan-PAD inhibitor biphenyl-benzimidazole-Cl-amidine (BB-ClA), which results in decreased levels of citrullination in our identified protein targets. Taken together, our data suggests that GnRHa induced citrullination is an important post-translational modification of gonadotrope derived cells.

Sexually Dimorphic Immunity to *Toxoplasma gondii* Infection. Tathagato Roy, Kaatje Fisk, Keagan Keplinger, Sai Kit Ng, Erica Ashley Farris, and Jason Gigley
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ABSTRACT. *Toxoplasma gondii* infection outcomes are sexually dimorphic with females exhibiting higher morbidity and mortality than males during HIV/AIDS. Natural Killer (NK) cells are a major early controller *Toxoplasma* infection. Since CD4+ T cells are absent during HIV/AIDS and females are more susceptible to Toxoplasmic encephalitis (TE), we investigated how CD4 T cells impacted mouse survival and NK cell responses in mice. Female CD4KO mice succumbed to *T. gondii* earlier than male CD4KO mice. Wild type (WT) mice similarly increased IFNg+ NK cell numbers regardless of sex and NK cell responses were intact in male CD4KO mice after infection. However, infected CD4KO female mice had 50% fewer IFNg+ NK cells than infected WT female mice and CD4KO male mice. To confirm our results, we next tested survival and NK cell responses in female and male MHCII deficient (MHCIIKO) animals. To our surprise survival, and IFNg+ NK cells were not significantly different between WT or MHCIIKO female and male mice. Additionally, the lack of T and B cells do not co-relate with differential survival outcomes and NK cell responses in female and male mice. These results suggest only in female mice and not in male mice CD4 co-receptor expression is required for survival and correlates with optimal NK cell responses during acute *T. gondii* infection. Our findings reveal an unappreciated sexual dimorphic role of CD4 co-receptor expression in regulation of NK cell responses to acute infection including *T. gondii* infection.

On-Tissue Derivatization for Enhanced Carbohydrates and Sterols Detection in Bee and Rat Brain *via* MALDI/MALDESI Mass Spectrometry. Nilay Saha[1], Andrew Goodenough[1], Taylor Hatcher[2], Michael Dillon[2], and Franco Basile[1]
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ABSTRACT:
The utilization of mass imaging techniques, such as MALDI-MS imaging, has proven to be an invaluable tool in obtaining spatiotemporal dynamics of various compounds. Through this method, the distribution of a wide range of compounds can be obtained. However, certain molecules, such as sterols and carbohydrates, present a significant challenge in terms of ionization, rendering it difficult to attain spatial information through MALDI-MS imaging alone. To overcome this limitation, on-tissue derivatization of sterols and carbohydrates can be a powerful technique for identifying the spatial distribution of these molecules. In the first step of method development, bee sections were extracted with MTBE/MeOH/H2O solvent, and the aqueous layer was taken for carbohydrate derivatization and mixed with Girard P reagent. For sterol derivatization, the organic layer was treated with cholesterol oxidase followed by Girard P at a 1:1:1 ratio. MALDI-MS analysis was performed using DHB matrix and a MALDI-ToF/ToF-MS system (5800; Sciex). Similarly, on tissue derivatization was performed by spraying cholesterol oxidase and Girard P reagent with HTX-TM sprayer. Enhanced signals of carbohydrates in bee aqueous extracts (from head, thorax, and abdomen sections) were achieved

upon derivatization. Strikingly different spectra of the bee extract were obtained when derivatized with the GP as compared to underivatized samples. A strong signal was detected corresponding to a monosaccharide of the form [M + GP]+ ion at m/z 314.1, where M corresponds to a carbohydrate with the molecular formula $C^6H^{12}O^6$. In the case of sterol detection, successful derivatization was achieved in bee and rat brain. The two-step reaction, oxidation of the hydroxyl group to a carbonyl group by cholesterol oxidase followed by reaction with GP reagent, yielded a strong signal at m/z 530.4 in bee, likely corresponding to 24-methylenecholesterol and at m/z 518.4 likely corresponding to 5-CHOLESTEN-3β-OL.

Exercise Alters the Metabolome of Circadian Disrupted Mice in a Sex Dependent Manner. Sharanya Satyanarayana[1], Hope D. Welhaven[2,3], Nicholas A. Marcello[4], Elijah McCoy[4], Evan T. Scholten[5], Danielle R. Bruns[4,5,6], William D. Todd[6], and Emily E. Schmitt[4,5*]

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ABSTRACT. Circadian rhythms are critical for all biological processes, with misalignment of rhythms causally implicated in age-related disease like metabolic disease. One of the primary lifestyle interventions that aid in healthy aging for all physiological functions is exercise, and exercise has been shown to be able to phase shift and/or entrain circadian rhythms. As such, the purpose of our study was to characterize alterations of the metabolome in circadian disrupted male and female C57BL/6J mice randomly assigned to timed exercise on a treadmill compared to those that remained sedentary (no exercise). We quantified circadian gene expression in the skeletal muscle and liver as well as global metabolic profiles. Serum metabolites were extracted and an untargeted analysis via LC-MS/MS was performed. Analyses included hierarchical cluster analysis (HCA), principal component analysis (PCA), and partial least squares-discriminate analysis (PLS-DA) presenting a significant difference between the two group (exercise vs no exercise) in a sex-dependent manner. A total of 3,197 metabolite features were detected across all experimental groups. Our metabolomics data reveals sex differences in animals that did or did not exercise specifically in metabolites related to amino acid, drug, lipid, and energy metabolism. Taken together, our results demonstrate that exercise changes the metabolome in circadian disrupted mice. This data provides insight into the metabolomic response to exercising during circadian disruption.

The Aging Mouse as a Model for Nocturia. Sushumna Satyanarayana[1], Danielle S. Taylor[2], Adam C. Nelson[2], Danielle R. Bruns[1,2], Nicole L. Bedford[2], and Emily E. Schmitt[1]

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ABSTRACT. Waking at night to urinate (nocturia) is a highly prevalent and morbid problem in older adults and is associated with cardiovascular disease, increased risk of falls, depression, and poor quality of life. Therapeutic interventions are limited, in large part due to poor mechanistic understanding of pathophysiology and lack of an animal model that recapitulates phenotypic characteristics of the disorder. To date, models of nocturia have not addressed two major contributing factors- advanced age and circadian disruption. We aimed to fill this gap and validate the aged (19–21-month-old) mouse as a novel model of nocturia that recapitulates impaired circadian control of urination. As expected, circadian rhythms (amplitude) were blunted with age in both sexes. While young males urinated significantly more during their respective day, this effect was blunted in aged males. Expression of clock genes and regulators of volume status in the kidney were also blunted with age. Expression of the mechanosensor Piezo1 was differentially expressed by day-night in the bladder of young mice and this day-night expression was completely reversed with aging. identify chronotherapy for this unmet need.

Investigating the Female Reproductive Tract Mucosa as a Sex Specific Site for Anti-Citrullinated Protein Antibody Formation. Ari O. Sequoia[1], Rachael Horne[1], Kali Franckowiak[1], Heather M. Rothfuss[1]; M. Kristen Demoruelle[2]; and Brian D. Cherrington[1]

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ABSTRACT. Rheumatoid Arthritis (RA) is an autoimmune disease characterized by the inflammation and subsequent degradation of synovial joints. While both men and women develop this disease, there is a three-fold higher rate of women suffering from RA. Women often develop the disease earlier and experience worse clinical outcomes compared to men. Years of research has been unable to explain the clear sex disparity seen in RA, despite several known reproductive factors that affect risk in women, including age of menarche, parity, and the post-partum period. Previous studies show that RA autoimmunity develops when citrullinated (cit) proteins are generated at a mucosal surface by peptidylarginine deiminase (PAD) enzymes, which post-translationally covert arginine to a non-coded citrulline residue in target proteins. Auto-antibodies to cit-proteins termed anti-citrullinated protein antibodies (ACPAs) are produced in the mucosa, but can become systemic and lead to joint inflammation. Shared mucosal sites (ie. lung, gingiva, and gastrointestinal tract) have yet to explain the sex disparity, leading us to hypothesize that the female reproductive tract (FRT) mucosa is a female specific site of ACPA formation. Specifically, we are investigating whether PAD enzymes and cit-proteins are present in FRT fluid (FRT-F) and serum across the menstrual cycle in women and estrous cycle in mice. Our results

demonstrate that PAD enzymes and cit proteins fluctuate in women's FRT-F across the menstrual cycle and in wild type mouse FRT-F during the estrous cycle. Interestingly, PAD enzymes are not detectable in wild type mouse serum but are abundant in FRT-F across the estrous cycle. The FRT has a unique immune system, prompting us to next examine if total immunoglobulin G (IgG), ACPAs, and the cytokines IL-6, IL-8, and TNFα are also present in FRT-F and serum in wild type mice. Our results show that they not only fluctuate across the estrous cycle, but their respective levels differ between FRT-F and serum. Our current studies are using mass spectrometry to identify the mouse FRT citrullinome across the estrous cycle. Ultimately, our objective is to identify possible targets for sex-specific diagnostic tests or treatments to improve clinical outcomes for women suffering from RA.

The Contribution of *C. burnetii* Developmental Stage to Intracellular Pathogenesis. Leslie Sims and Elizabeth Case
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ABSTRACT. *Coxiella burnetii* is a Gram-negative, obligate, intracellular bacterium and the causative agent of the zoonosis Q fever, a highly infectious respiratory disease. This bacterium has a biphasic cell morphology. The small cell variant (SCV) is the inert, extracellular form. This form is believed to be the cause of natural infection due to its environmental stability. The large cell variant (LCV) is intracellular and fragile. During infection, *Coxiella* is inhaled into the lungs and phagocytosed by alveolar macrophages, where it is trafficked to a pathogen-tailored compartment called the *Coxiella* containing vacuole (CCV), which resembles a terminal lysosome. While in this CCV, the SCV transitions into an LCV and begins to replicate. Both forms have been described as infectious using *in vitro* models of infection in immortalized cell lines. However, these cellular infection models are largely irrelevant to pathogenesis *in vivo* due to traditional cell lines used. We have developed a primary macrophage infection model that better replicates the effects of Q fever at the cellular level. These bone marrow derived macrophages (BMDM) retain the bactericidal activity that is not conserved in traditional cell lines. We hypothesize that the SCV's extraordinary environmental stability imparts an enhanced ability to survive the BMDM phagolysosome relative to the LCV form. Our plan to test this hypothesis is to separate the SCV and LCV populations and test their ability to infect and replicate in BMDMs. We have grown different ages of *Coxiella burnetii* in an effort to get a more pure population of SCVs and LCVs. Each of those stocks were then used to infect both an epithelial cell line and primary macrophages in which we saw differences of growth curves in the different cell types. Next, we will generate pure populations of each cell type through density gradient centrifugation. We will also move to mouse models after the *in vitro* testing. By resolving the infectious potential of these two cell types, we will better understand Q fever infection dynamics and disease progression.

An Essential Role for Casein Kinase 1 Delta and Epsilon in Endometrial Development and Pregnancy. Dania Sinzu-Prieto[1], Cindy A. Pru[1], John P. Lydon[2], Emily E. Schmitt[1], and James K Pru[1]

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ABSTRACT. Casein kinase 1 δ and ε (CK1δ/ε) are serine/threonine kinases that coordinate the circadian rhythm, DNA damage responses, mitosis/meiosis, cytoskeletal functions and development. Abnormally elevated expression of CK1δ/ε is commonly associated with neural, renal and reproductive cancers. Given that the female reproductive system undergoes complex cycles of proliferation and differentiation during early postnatal development, the estrous cycle and pregnancy, it is hypothesized that Csnk1δ/ε are essential for female fertility. In order to assess this, the expression of CK1δ/ε mRNA and protein in the female reproductive tract (FRT) was evaluated by qPCR and IHC, respectively, during postnatal days (pnd) 5-21, the estrous cycle, and the early pregnancy (DOP 1-9). Conditional ablation of Csnk1δ/ε using Pgr-Cre mice was used to assess gene function in the FRT. CK1δ/ε were dynamically regulated in tissues of the FRT in response to sex steroids and early pregnancy. During postnatal uterine development, CK1δ/ε was abundantly expressed throughout the uterus with a decrease in the stroma starting on pnd 9. CK1δ/ε were prominently expressed in adult endometrial luminal and glandular epithelia on DOP 1 (elevated estradiol), but then transitioned to the subluminal stroma just prior to implantation and decidualization (rising progesterone). Dual ablation of Csnk1δ/ε resulted in complete infertility stemming from abnormal endometrial development including reduced tissue expansion and lack of endometrial glands, as well as diminished cervical and vaginal expansion. Initial assessment of Csnk1δ/ε ablation from periovulatory follicles suggested no impact on ovulation or formation of corpora lutea. Based on these data, Csnk1δ/ε are robustly expressed throughout the FRT and are required for uterine adenogenesis and expansion of the endometrium, cervix and vagina during early postnatal life. Ongoing studies using alternative Cre drivers will determine if CK1δ/ε are required in adult uterine function during early pregnancy and maintenance of the glandular epithelium. Additionally, the mechanism of action by which these two kinases coordinate endometrial development and decidualization will be assessed using spatial transcriptomic and proteomic approaches. *Supported by NIH HD102386 and the Curtis and Marian Rochelle Endowment.*

The Functional Requirement for PGRMC Proteins in Uterine Decidualization and their Role in Lipid Metabolism and RNA Biology. Nikhil Srivastava[1,2], Nicole C Kelp[3], Todd S. Paisley[1], Cindy A. Pru[1], John P Lydon[4], and James K. Pru[1]
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ABSTRACT. Progesterone receptor membrane component (PGRMC) 1 and PGRMC2 are required for female fertility. Their *in vivo* mechanisms of action remain poorly understood. The objective was to use conditional mutagenesis in mice to begin understanding PGRMC functions using a multi-omics approach. **Methods:** Intact and ovx+steroid hormone treated female *Pgrmc1/2*$^{fl/fl}$ and double conditional knockout (dcKO, *Pgrmc1/2*$^{d/d}$) mice were used in artificial decidualization experiments and for evaluating the decidual metabolome on day of pregnancy (DOP) 7.5. We developed a *Cag-loxP-STOP-loxP-Pgrmc2-3XFlag* (*Pgrmc2-OE*) mouse line for assessing the impact of PGRMC2 over-expression on fertility and in immunoprecipitation experiments to identify PGRMC2-interacting proteins (DOP 7.5). **Results:** Conditional knockout of *Pgrmc1/2* with *Pgr-Cre* mice caused a significant decidualization impairment in response to artificial stimulation in both intact and ovx+steroid treated female mice. Paraffin-embedded decidual tissue sections from dcKO mice contained intracellular spaces consistent with lipid droplets. An unbiased metabolomics profiling study revealed that *Pgrmc1/2* ablation disrupted decidual metabolism of several classes of membrane lipids including phosphatidylcholine/ethanolamine/serine/inositol, lysophospholipids and plasmalogens. *Pgr-Cre*-driven over-expression of PGRMC2-3XFLAG caused a decline in fecundity. This mouse was used in an immunoprecipitation study coupled with proteomic analysis to identify PGRMC2-interacting proteins in DOP 7.5 decidual tissue. Among several classes of proteins that were found to interact with PGRMC2, proteins involved in RNA binding/export (CSE1L, XPO1, BZW1, SRSF2, DDX39b), lipid metabolism (ABHD12/16b, PAFAH1B1) and peroxisome function (PEX3/6/11B/13, ABCD1/3) were detected. The peroxisome is a principal organelle that coordinates membrane lipid synthesis and processing. Western blot validation studies were completed for candidate interacting proteins and their expression was confirmed in decidual tissue by IHC. **Conclusion:** PGRMC proteins are essential for uterine decidualization and likely function to regulate membrane lipid metabolism, RNA biology, and peroxisome function. *Supported by NIH HD102386, GM103432, and the Curtis and Marian Rochelle Endowment.*

Engineering Listerial Bactodrones for Cancer Immunotherapy. Kiet N. Tran, Huong Giang Pham, Larissa Gomelsky, Jason P. Gigley, and Mark Gomelsky
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ABSTRACT. Alongside chemotherapy and radiotherapy, immunotherapy has become essential in the management of cancer. A promising avenue within immunotherapy lies in using bacteria to trigger the immune system against cancer and to deliver antitumor agents. Attenuated strains of the intracellular pathogen *Listeria monocytogenes* (*Lm*) are attractive as vectors for cancer immunotherapy because *Lm* can colonize tumor microenvironments, where it propagates and spread within the tumors until infected cells are eliminated by the immune system. *Lm* has been harnessed for the delivery of tumor antigens and demonstrated remarkable safety and moderate efficacy in clinical trials. To further enhance safety and improve efficacy of the *Lm*-based cancer immunotherapy, we are empowering *Lm* with a remote-control system and enhancing its antitumor payload capacity, thus turning *Lm* into bacterial drones (bactodrones). The remote-control system is expected to enable the release of the antitumor payloads by

Lm within tumors when most bacteria are cleared from the healthy tissues. To enhance bactodrone payload capacity, we are engineering and comparing efficiencies of DNA, RNA and protein-based delivery systems. Here, we present an engineered anhydrotetracycline-inducible remote-control system that tightly regulates gene expression in *Lm in vitro* and *in vivo*. We also compare performance of the *Lm* bactodrones engineered to deliver DNA, RNA and protein payloads into the cytosol of tumor cells. Our results show that *Lm* can deliver diverse payloads into tumors and release them in response to a remote signal, which is expected to enhance safety and efficacy of the *Lm*-based cancer immunotherapies.

Small Molecules Vary in their Ability to Protect Labile Biomolecules during Desiccation. Chaitra Shree U S Udugere Shivakumnara Swamy, Kenny Nguyen, Tyler Gonzalez, Vincent Nicholson, and Thomas C. Boothby

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ABSTRACT. Desiccation, the loss of intracellular water, is extremely detrimental to living cells, damaging the cell's labile components like proteins, nucleic acids, and membranes. Despite this, there are desiccation-tolerant organisms, such as tardigrades, which have evolved to survive the loss of nearly 95% of their intercellular water. A major strategy through which desiccation-tolerant organisms mitigate damage is the enrichment of small molecules. However, there are hundreds of different metabolites implicated in desiccation tolerance and their exact functions are poorly understood. Here, we screen several small molecules spanning various categories, including excipients, osmolytes, sugars, polymers, and polyamines, to assess their ability to prevent four different types of desiccation-induced damage: protein unfolding, protein aggregation, membrane leakage, and RNA degradation. Our results demonstrate that small molecules vary significantly in their protective capacity. Known desiccation tolerance mediators such as trehalose, sucrose, maltose, and polyamines exhibited notable efficacy in preventing various types of damage. Several small molecules were only able to prevent one type of desiccation-induced damage, highlighting the specificity of their mechanisms. Overall, this research underscores the multifaceted nature of desiccation stress, as well as the need for organisms to enrich themselves with multiple diverse protectants. Ultimately, understanding the mechanisms of these protectant molecules could offer potential avenues for developing novel strategies for the transportation and long-term storage of pharmaceuticals in arid conditions, eliminating the need for reliance on the cold chain. These advancements hold promise for addressing challenges within the pharmaceutical industry while promoting sustainability and efficiency.

Friends or Food. Sheila Walsh[1], Cole Stevens[2], and Dan Wall[3]

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ABSTRACT. Myxobacteria are a group of Gram-negative bacteria that live in the soil where they feed on organic materials including other bacteria. These bacteria are not only known for their predation of other microbes but also for their social behavior and

ability to form multicellular fruiting bodies wherein cells differentiate into environmentally resistant spores. Recently, several myxobacteria were isolated and found to be in symbiotic relationships with one or more other bacterial species. Symbiotic relationships can be parasitic, commensal, or mutualistic depending on if one or more organisms involved are benefiting from the relationship. Mutualistic relationships are hypothesized to be a fundamental step toward the evolution of complex multicellular life on our planet; the endosymbiotic theory. Understanding bacterial symbiosis will help shed light on the past as well as shape the future of our understanding of complex biological interactions. Using molecular techniques, we seek to elucidate how these mutualistic organisms grow, move, share nutrients, and develop into fruiting bodies. Moreover, using bioinformatics we are investigating their genomes to identify prophage, secondary metabolite (SM) biosynthetic gene clusters, and toxin/antitoxin systems. Thus far we have located many phage-like genes in both of the *Archangium* genomes as well as more than 40 SM gene clusters and greater than 10 toxin/antitoxin systems being produced by both organisms. Additionally, we have selected several excellent candidates for future fluorescent microscopy which allow us to differentially stain and track cell-cell interactions, gliding motility, and other social behaviors.

Learning from Yourself: Self-Similar Avatars for Foreign Language Learning.

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ABSTRACT. Previous studies investigate the use of virtual humans in language learning, and of self-similar virtual humans, or doppelgängers, in virtual reality (VR) for feedforward learning in physical memorization tasks, but the use of doppelgängers in foreign language learning remains an underexplored area in VR research. We investigate the role of doppelgängers in vocabulary retention tasks and the impacts of doppelgänger use on foreign language anxiety, a critical factor in determining language learning proficiency and outcomes. Participants (n = 14) completed three Spanish language lessons presented by a doppelgänger, a generic virtual human, or a disembodied voice in VR. Participants completed a modified version of the Foreign Language Anxiety Classroom Scale to assess foreign language anxiety and were asked to recall vocabulary terms after lesson completion. We observed no statistically significant differences between vocabulary retention or foreign language anxiety between the lesson delivery types, but differences existed in feelings of learning inadequacy (p = 0.0408) between the generic and self-similar virtual human conditions.

UNDERGRADUATE POSTER PRESENTATIONS

Dhruv **Ahuja**, and Sean Harrington. **Genetic Variations and Adaptations amongst different Kingsnake Populations.** Department of Molecular Biology, University of Wyoming (Laramie, WY); **Email:** dahuja1@uwyo.edu

Rebecca **Ash**[1], Jessie Carbert[2], Amie Erickson[1], and Stephanie Servetas[1,3]. **Improved DNA Extraction for Heritage Apples.** [1]Department of Agriculture, Sheridan College (Sheridan, WY); [2]Department of Biology, Northern Wyoming Community College District- Sheridan College (Sheridan WY); Biosystems and Biomaterials Division, National Institute of Standards and Technology (Gaithersburg, MD); **Email:** rebeccaash@sheridan.edu

Tara **Baer**, Kinley Bollinger, Anna Knight, Tamara Rozmetova, Anna Rozmetova, Sahra Jumaberdiyeva, Mekan Esenov, and Joey Andrade. **Investigating Antimicrobial Activity of *Artemisia spp.* Extracts against *Staphylococcus aureus, Escherichia coli, and Pseudomonas aeruginosa*.** Biology Department, Northwest College (Powell, WY); **Email:** tara.baer@nwc.edu

Jordan J. **Barth**[1], Jason G. Landen[1], Adam C. Nelson[1], Morgane Vandendoren[1], Glenn Tattersall[2]. **Thermoregulatory Preference in Mutated Mice.** [1]Department of Zoology Physiology, University of Wyoming (Laramie, WY); [2]Department of Biological Sciences, Brock University (Ontario, Canada); **Email:** jbarth1@uwyo.edu

Taylor **Berg**[1], Brooke Johnson[1], and Riley F. Bernard[1,2]. **Using Three Survey Methods to Inventory Mammal Species Presence at Rimrock Historic & Recreation Area (BLM).** [1]University of Wyoming - Casper (Casper, WY); [2]Department of Zoology & Physiology, University of Wyoming (Laramie, WY); **Email:** Tberg1@uwyo.edu

Nathan **Butz**, Sheila Walsh, and Dan Wall. **Auxotrophic Cross Feeding: A Closer Look.** Department of Molecular Biology, University of Wyoming (Laramie, WY); **Email:** nbutz@uwyo.edu

Jessie **Carbert**[1], Rebecca Ash[2], Ami Erickson[2], and Stephanie Servetas[2,3]. **The Diversity of Local Sourdough Starters.** [1]Department of Biology, Sheridan College (Sheridan, WY); [2]Department of Agriculture, Northern Wyoming Community College District- Sheridan College (Sheridan, WY); [3]Biosystems and Biomaterials Division, National Institute of Standards and Technology (Gaithersburg, MD); **Email:** jessiecarbert@sheridan.edu

Kellyn B. **Chandler**[1], Sean Harrington[2], Eric Quallen[3], Merav Ben David[1]. **On Obesity and Genetics: Exploring the Role of Relatedness in Body Mass of Captive Least Chipmunks.** [1]Department of Zoology and Physiology, University of Wyoming (Laramie, WY); [2]Wyoming INBRE Data Science Core, University of Wyoming (Laramie, WY); [3]Raystown Field Station, Juniata College (Huntingdon, PA); **Email:** kchandl5@uwyo.edu

Chavely **Cruz Cárdenas**[1], Mason H Agor[1], Trevor Hible[1], Madison Olson[1], Abby Boatman[1], Brian Cherrington[2], Danielle Bruns[3], and Florence Teulé-Finley[1]. **Investigating Cardiac Function through the study of Myocardial Citrullination Patterns in Mice: Effects of Age and Gender on Cardiac Peptidyl Arginine Deiminase/PAD Expression.** [1]University of Wyoming at Casper, 125 College Drive, Casper WY 82601; [2]Department of Zoology and Physiology, University of Wyoming (Laramie, WY); [3]Division of Kinesiology and Health, University of Wyoming (Laramie, WY); **Email:** ccruzcar@uwyo.edu

Joshua P. **Duckwitz**, Brett A. Ralston, Stanley B. Devore, and Brian D. Cherrington. **Altering DGCR8 Expression Modulates Biogenesis of PTTG1 Targeting miRNAs 300 and 329 in Lactotrope Cells.** Department of Zoology and Physiology, University of Wyoming (Laramie, WY); **Email:** Jduckwit@uwyo.edu

Kassidy **Dunagan**, Alivia Fansler, Kira Welch, Gavin Martin, and Ami Wangeline. **Edna: The Fashionista of Freshwater Microbes.** Department of Biology, Laramie County Community College, (Cheyenne, WY); **Email:** aliviafansler@student.lccc.wy.edu

Ansley **Else[1]**, Ami Erickson[1], Audrey Hirschman[1], and Stephanie L Servetas[2]. **Identifying Active Mycorrhizae in Soil Sampled from Domestic and Native Sunflower Rhizospheres.** [1]Department of Agriculture, Sheridan College (Sheridan, WY); [2]Biosystems and Biomaterials Division, National Institute of Standards and Technology, (Gaithersburg, MD); **Email:** ansleyelse@sheridan.edu

Erica A. **Farris**, Tathagato Roy, Lauren Lynde, and Jason Gigley. ***Toxoplasma gondii* Effects on Infection Behavior and Dissemination in Mice with Myeloid Cells Lacking Transferrin 1 Receptor.** Department of Molecular Biology, University of Wyoming (Laramie, WY); **Email:** efarris1@uwyo.edu

Abigail **Flesvig**, Josef Culver, Kaleigh Gunderson, and Christopher Wenzel. **Soil Fungi Predominate under Warming and Drying Conditions.** Department of Science and Mathematics, Eastern Wyoming College (Torrington, WY); **Email:** cwenzel@ewc.wy.edu

Kevin **Fontana**, Benjamin Mcnair Elizabeth Straight, Danielle R. Bruns. **Deletion of Cardiac AMPK Distinctly Affects the Right and Left Ventricle.** Division of Kinesiology & Health, University of Wyoming (Laramie, WY); **Email:** Kfontan1@uwyo.edu

Lili **Fox**[1], Ami Erickson[1], and Stephanie Servetas[2]. **A Study of the Changing Garden Soil Microbiome throughout the Seasons.** [1]Department of Agriculture, Northern Wyoming Community College District- Sheridan College (Sheridan, WY); [2]Department of Microbiology, NIST (Gaithersburg, MD); **Email:** lilifox@sheridan.edu

Josey S. **Frazier**[1], Amanda L Parsons[2], Alan T Stenquist[3], John D Kisiday[2], and John S Oakey[2]. **Dynamic Multimodal Mechanical Stimulation of Chondrocytes: A**

Microfluidic Approach. [1]Department of Molecular Biology, University of Wyoming, (Laramie, WY); [2]Department of Chemical and Biomedical Engineering, University of Wyoming (Laramie, WY); [3]Molecular and Cellular Life Sciences, University of Wyoming (Laramie, WY); **Email:** jsfrazi14@uwyo.edu

Kadriya **Gaydutdinova**, Joey Andrade, Tara Baer, Russel Baer, Kinley Bollinger, Aiur Erov, Mekan Esenov, Adisyn Gamble, Riley Heindl, Joshua Jameson, Sahra Jumaberdiyeva, Anna Knight, Max Myradov, Anna Rozmetova, and Tamara Rozmetova. **Wasps, Bees, and Ants, Oh My!: Metabarcoding the Hymenoptera Microbiome of the Big Horn Basin, The Sequel.** Biology Department, Northwest College (Powell, WY); **Email:** kadriya.gaynutdinova@nwc.edu

Tracy **Goheen**, Thomas Baker, Michael Lance, John Dickinson, Petru Baraghin, Abraham Bailey, Eduardo Garcia, Matt Herr, Charles Palmer. **Supporting Growth Insulin Resistance and Reinforcement Learning through Electromechanical Software Development.** Central Wyoming College (Riverton WY); **Email:** TMG0819@cwc.edu

Caroline **Hansen**, Julia Yearout, and Riley F. Bernard. **Feasting in the Night: A Dietary Investigation of Wyoming Bats.** Zoology and Physiology Department, University of Wyoming (Laramie, WY); **Email:** chanse34@uwyo.edu

Riley D. **Heindl**, and Eric C. Atkinson. **Dancing in the Dark: Mesocarnivores of the Bighorn Basin.** Department of Biology, Northwest College (Powell, WY); **Email:** heindlriley@gmail.com

Gabriel V. **Heuer**[1], Kiet N. Tran[2], Justus M. Nelson[2], Mark Gomelsky[2]. **Safe Listeria for Treatment: An Obligate Intracellular Auxotroph**. [1]Department of Zoology & Physiology, University of Wyoming (Laramie, WY); [2]Department of Molecular Biology, University of Wyoming (Laramie, WY); **Email:** gheuer1@uwyo.edu

Dylan **Hicks,** and Charlotte Snoberger. **Exploring Spatial Distribution and Habitat of Spadefoots near Casper, Wyoming.** Department of Biology, Casper College (Casper, WY); **Email:** dylan.hicks2@mycc.caspercollege.edu

Sam **James**, JuliAnne Allgood, and Jared Bushman. **Electrode Configurations for Sensitive and Specific Detection of Compound Muscle Action Potentials to the Tibialis Anterior Muscle after Peroneal Nerve Injury in Rats.** Department of Pharmacy, University of Wyoming (Laramie, WY); **Email:** sjames8@uwyo.edu

Brooke **Johnson**[1], Hannah Swan[1], Britney Force[1], Chelby Frandsen[1], Joshua Holmes[2], Dagmara Motriuk-Smith[1], Grant Bowman[3]. **Investigation of the Binding Regions of the Polar Organizing Protein PopZ.** [1]University of Wyoming-Casper (Casper, WY); [2]Western Wyoming Community College (Rock Springs, WY); [3]University of Wyoming-Laramie (Laramie, WY); **Email:** brookej024@gmail.com

Brooke **Johnson**[1], Taylor Berg[1], and Riley F. Bernard[1,2]. **Determining Bat Community Composition over a Limited Elevational Gradient in Casper, WY.** [1]University of Wyoming- Casper; [2]Department of Zoology and Physiology, University of Wyoming (Laramie, WY); **Email:** brookej024@gmail.com

Lachlan **Johnson**, Suengmee Jung, Jongchan Woo, and Eunsook Park. **Building a Database for Fungal Structure and Function for Food Security.** Department of Molecular Biology, University of Wyoming (Laramie, Wyoming); **Email:** ljohn130@uwyo.edu

Anna **Knight**, Aiur Erov, Mekan Esenov., Adisyn Gamble, Kadriya Gaynudtinova, and Riley Heindl. **Investigating Antimicrobial Activity of *Juniperus spp.* Extracts against *Staphylococcus aureus*, *Escherichia coli*, and *Pseudomonas aeruginosa*.** Biology Department, Northwest College (Powell, WY); **Email:** anna.knight@nwc.edu

Willow **Larson**[1], Ilana Neuberger[2,3], Krystle Barhaghi[2,3], and Katelyn J. Kotlarek[1]. **Growth of the Tensor Veli Palatini Muscle Under Two Year of Age.** [1]Division of Communication Disorders, University of Wyoming (Laramie, WY); [2]Department of Radiology, Children's Hospital Colorado (Aurora, CO); [3]Department of Radiology, University of Colorado Anschutz Medical Campus (Aurora, CO); **Email:** wlarson4@uwyo.edu

Sara **Leach**[1,2], Matthew Walter[2], and Luis Alza[2]. **Casper College Entomology Collection**. [1]University of Wyoming at Casper (Casper, Wyoming); [2]Casper College (Casper, WY); **Email:** sara.leach@mycc.caspercollege.edu

Elizabeth **Lungren**[1], Cindy A. Pru[1], Jacob M. Pru[1], Aydin Guzeloglu[2], Thomas R. Hansen[2], and James K. Pru[1]. **Establishing the Uterine Function of ISG15 in Mammalian Pregnancy.** [1]Program in Reproductive Biology, Department of Animal Science, University of Wyoming (Laramie, WY); [2]Animal Reproduction and Biotechnology Laboratory, Department of Biomedical Sciences, Colorado State University (Fort Collins, CO); **Email:** elungren@uwyo.edu

Aspen **Malkuch**, and Grant Bowman. **A Novel Switch for Genetically Programming Bacterial Stem Cells.** Department of Molecular Biology, University of Wyoming (Laramie, WY); **Email:** amalkuch@uwyo.edu

Landry **May**[1], Ami Erickson[1], Stephanie Servetas[1,2] and Brett Hale[3]. **The Effects of AgriGro Product Application on Field Peas and the Soil Microbiome.** [1]Department of Agriculture, Northern Wyoming Community College District- Sheridan College (Sheridan, WY); [2]Biosystems and Biomaterials Division, National Institute of Standards and Technology, (Gaithersburg, MD); [3]Research and Development, Agrigro (Doniphan, MO); **Email:** landrymay@sheridan.edu

Kendall L. **Moyte**, Pooja Gupta, William D. Todd, Brian D. Cherrington. **Peptidylarginine Deiminase (PAD) Expression in the Female Hippocampus During**

the Estrous Cycle. Department of Zoology and Physiology, University of Wyoming (Laramie, WY); **Email:** kmoyte@uwyo.edu

Ryan S. **Pitesky**, Rachel E. Fanelli, McKinzie L. Wade, and Nicole L. Bedford. **Social Dominance is Disrupted in the Shank3b Mouse Model of Autism Spectrum Disorder.** Department of Zoology & Physiology, University of Wyoming (Laramie, WY); **Email:** rpitesky@uwyo.edu

Emily **Polson**, Grace Shearrer and Lola Acres. **Mobile regulation of cravings training: usability study.** Department of Family and Consumer Sciences, College of Agriculture, Life Sciences & Natural Resources, University of Wyoming (Laramie, WY) Email: epolson1@uwyo.edu

Rishab M. **Ranjitkar**[1], Kate Bunton[2], Brad H. Story[2], and Katelyn J. Kotlarek[1]. **Identification of Stop-Nasal Consonants in 2-Year-Old Synthesized Speech Based on Velopharyngeal Coupling Area.** [1]Division of Communication Disorders, University of Wyoming (Laramie, WY); [2]Department Speech, Language, and Hearing Sciences, University of Arizona (Tucson, AZ); **Email:** rranjit1@uwyo.edu

Joel **Sorensen**[1], and Riley F. Bernard[1,2]. **Quantifying Wing Damage Observed on Bats Captured During the Active Season in Western South Dakota and Eastern Wyoming.** [1]University of Wyoming–Casper (Casper, WY); [2]Department of Zoology & Physiology, University of Wyoming (Laramie, WY); **Email:** jsoren20@uwyo.edu

Mary **Teague**[1,2], Lynn Moore[3], Caroline Hansen[1], Stacey Scott[3], and Luis Alza-Leon[2]. **Herbarium Horizons: Exploring New Places, Plants, and Historical Plant Community Shifts in Wyoming.** [1]Department of Biology, University of Wyoming (Laramie, WY); [2]Department of Biology, Casper College (Casper, WY); [3]Independent Researcher (Casper, WY); **Email:** Mary.teague@mycc.caspercollege.edu

A. Lucas **Wall,** and Daniel M. Wall. **The use of *Streptococcus mutans* Bacteriophage to Isolate and Identify Cell Surface Proteins.** Department of Molecular Biology, University of Wyoming (Laramie, WY); **Email:** lwall2@uwyo.edu

Alexandra J. **Walters**. **Brooding Birds? Not with this Dammed Food: an Examination of the Effects on Trophic Structure from Arthropods to Passerines.** Department of Biology, Casper College (Casper WY); Email: alexjwalters01@gmail.com

Josephine **Walton**[1], Stephanie Servetas[2], Erickson Ami[1], and Mike Bloodsworth[3]. **Unearthing Ancient Secrets: Exploring Fossilized Plant DNA**. [1]Department of Agriculture, Northern Wyoming Community College District- Sheridan College (Sheridan WY); [2]Biosystems and Biomaterials Division, National Institute of Standards and Technology, (Gaithersburg, MD); [3]Sheridan College Museum of Discovery (Sheridan, WY); **Email:** josephinewalton@sheridan.edu

R. Cole **Wyatt**[1], Cole F. Nelson[1], William D. Todd[2], Emily E. Schmitt[1]. **Circadian Disruption and the Effect of Exercise in Mice.** [1]Department of Kinesiology and Health, University of Wyoming (Laramie, WY); [2]Department of Zoology and Physiology University of Wyoming (Laramie, WY); **Email:** cwyatt5@uwyo.edu

Kai M. **Yeager**, Jim Mildenberger. Taylor Fearson, Chayse Rowley, Dr. Robert A. Petit III, and Joseph Reed. **Antimicrobial Resistance Genes in Wyoming: Clinical Isolates 2013-2015.** Wyoming Public Health Lab (Cheyenne, WY); **Email:** kyeager1@uwyo.edu