The Department of Biology

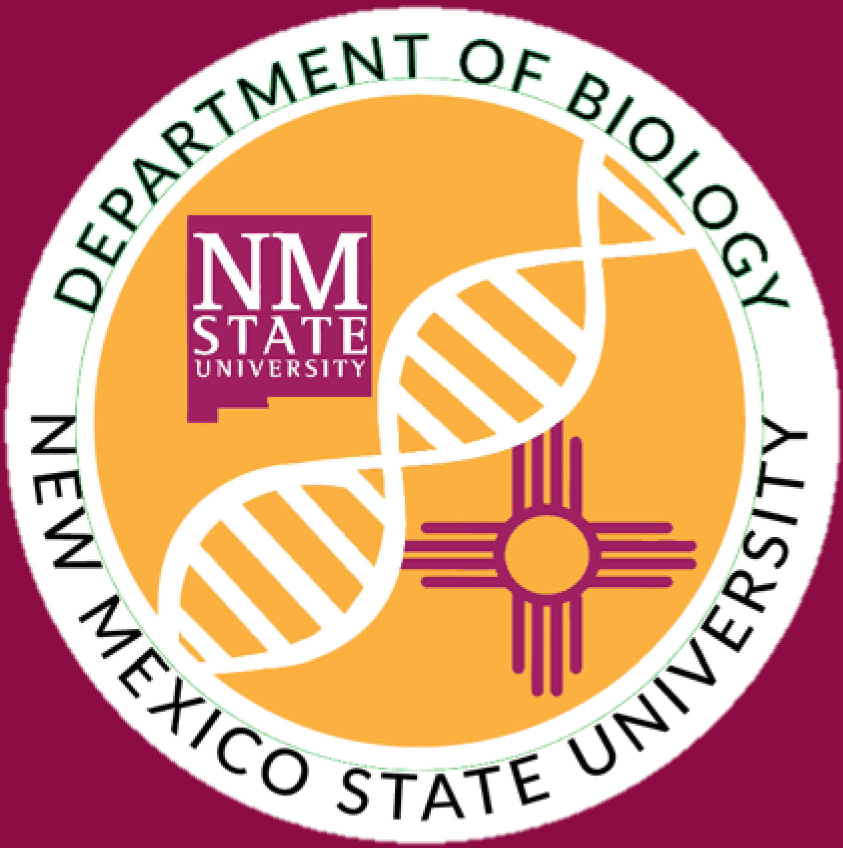
at

New Mexico State University

presents the

Annual Biosymposium

Saturday, March 28th, 2026
Domenici Hall
Lecture Hall 102
Las Cruces, NM



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Domenici Hall
Lobby and 102
Saturday, March 28th, 2026

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8:55 AM - Welcome

9:00-10:15 AM - Oral Presentations Session 1

Talk #	Presenter	Title
1	John Agbetsi	Gravid Anopheles stephensi Detects Indole for Oviposition Despite Ablation of Antennae and Maxillary Palps
2	Eriberto Osorio	In response to urban noise, gray catbirds are immediately flexible in song frequency and amplitude
3	Jade Collins	Investigating the evolutionary history of mimosine production in mimosoid legumes
4	Crisandra Diaz	Understanding the Enemy: Bacterial pathogenesis of novel bacterium FD111 in Nannochloropsis oceanica cultures
5	Priscila Fourzan	Developing novel reporters to explore cellular mechanics in living cells

10:15-10:30 AM – Coffee Break

10:30-11:45 AM - Oral Presentations Session 2

Talk #	Presenter	Title
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7	Jaime Arroyo	Buoyancy increases sensitivity to chemical nociception
8	Jonathon Valencia	The effect of repeated low-dose endotoxin injections on circulating steroid hormones in nulliparous Rambouillet ewes
9	William Grooms	Habitat selection by an endangered chipmunk is altered by competition and non-stationarity
10	Osher Ostroff	Algal Consortia and Monocultures of Chlorella sorokiniana and Micractinium sp. Exhibit Comparable Productivity in Revolving Algal Bioreactors

Domenici Hall
Lobby and 102
Saturday, March 28th, 2026

Afternoon Session

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12	Gabriel Borg	Sterile-Insect-Technique: Hormetic Ethanol Feeding results in Up-regulation of Antimicrobial Peptide Genes in X-ray-irradiated Aedes aegypti males.
13	Vanessa Pando	DEG/ENaC channel ppk1 and TMEM16 channel subdued are required for wound-induce chemical-allodynia
14	Caleb Fyock	Effects of Stormflow Events on Water Quality in the New Mexico Rio Grande River Basin
15	Negin Jazi	Corticosterone Receptor Expression Varies Across Tissues in Chronically Stressed Budgerigars

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3:30-4:00 PM - Remove posters

***GF & V:** gluten free and vegan meal options will be available.

Speakers by alphabetical surname

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Diaz, Crisandra	4	Understanding the Enemy: Bacterial pathogenesis of novel bacterium FD111 in *Nannochloropsis oceanica* cultures
Fourzan, Priscila	5	Developing novel reporters to explore cellular mechanics in living cells
Fyock, Caleb	14	Effects of Stormflow Events on Water Quality in the New Mexico Rio Grande River Basin
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Valencia, Jonathon	8	The effect of repeated low-dose endotoxin injections on circulating steroid hormones in nulliparous Rambouillet ewes

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Aktar, Mst Tasrin	2	Using Differential Gene Expression Analysis to Investigate *Heteropsylla cubana* Herbivory Responses in the Genus *Leucaena*.
Araiza, Alan	3	Involvement of anillin and septins in atypical cleavages
Awaogu, Chinyere	4	Role of Notch-Delta signaling during muscle development in the sea star
Baca, Gabrielle	5	Characterizing immune genes in *Triatoma rubida*, a possible vector of Chagas Disease in the Southwestern United States.
Biehler, Lindsey	6	Impact of RNA interference, the front-line antiviral defense of mosquito vectors, on the outcomes of within-cell competition between sylvatic and human-endemic strains of dengue virus
Brazil, Samantha	7	Determining the role of the small GTPase Rap1 in morphogenesis during *Drosophila melanogaster* eye development
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Abstract Highlights

Oral Presentations

By Order of Presentation

Talk 1:

Gravid *Anopheles stephensi* Detects Indole for Oviposition Despite Ablation of Antennae and Maxillary Palps

John Agbetsi [1], Jiannong Xu[2]

Department of Biology, New Mexico State University.

Oviposition site selection is critical for mosquito population dynamics. Gravid mosquitoes rely on chemical cues to identify suitable breeding habitats. However, the sensory mechanisms governing this behavior in this species remain poorly understood. We examined the role of indole, a microbial volatile associated with aquatic environments, in oviposition site choice and assessed the involvement of sensory organs in its detection. In two-choice oviposition assays, water conditioned with first-instar larvae attracted gravid females (OAI = 0.56), whereas water from fourth-instar larvae was repellent (OAI = -0.20). Indole elicited strong oviposition attraction across a broad concentration range (0.1-50 μM), with no clear dose-response relationship. Surgical ablation of antennae and maxillary palps did not abolish indole-mediated preference but significantly reduced behavioral variability, suggesting that these structures modulate, rather than solely mediate, indole detection. Reanalysis of transcriptomes of antennae, maxillary palps, and legs in An. gambiae and An. coluzzi, along with quantitative RT-PCR in An. stephensi, revealed the expression of chemosensory genes (including Obp1, Obp13, Obp25, Obp71, Or2, and Or10) in the legs, indicating a potential role for leg chemosensation in oviposition decisions. Conversely, exposure of gravid females to 1 μM indole increased transcript levels of AhR, Obp1, Or2, and Or10 compared with water-treated controls, suggesting that indole induces transcriptional changes in these genes, consistent with the persistent detection of indole despite the ablation of the antennae and maxillary palps. Following RNAi-mediated knockdown of AhR, our data suggest that AhR may function as a transcription factor that regulates indole-responsive olfactory genes.

Talk 2:

In response to urban noise, gray catbirds are immediately flexible in song frequency and amplitude

Eriberto Osorio[1,2], Anna E. Williams[2], Juliane A. Calvert[2], Erin M. Naman[2], Ethan M. Dray[2], Jackson R. Vickers[2], Shannon K. Eppert[2], and Dana L. Moseley[2]

[1]Department of Biology, New Mexico State University, Las Cruces, New Mexico
[2]Department of Biology, James Madison University, Harrisonburg, Virginia

Immediate flexibility is the ability in which a bird shifts its song frequency or amplitude in response to noise fluctuations in the environment. This ability has been observed in many urban residing species in response to the loud and low-frequency urban noise within cities. Within species population differences for this ability have been found when comparing rural populations and urban populations. The Gray Catbird, Dumetella carolinensis, is a migratory songbird found in habitats spanning a rural to urban gradient. Recently, it was found that catbirds increased minimum, maximum, and peak frequency in noisier habitats such as cities. We conducted an observational study and an experiment broadcasting noise across an urban noise gradient to find evidence for a potential mechanism catbirds may use in response to levels of increasing urban noise. A parabolic microphone and a Larson Davis Sound Advisor 831c were used simultaneously to record singing males to detect changes in frequency and amplitude in response to experimental noise. We found catbirds sing with immediate flexibility in both frequency and amplitude. Catbirds raise their minimum frequency in response to low-frequency noise and lower their maximum frequency in response to high-frequency noise. Overall, Catbirds sang louder by 2dB in response to low-frequency noise playback.

Talk 3:

Investigating the evolutionary history of mimosine production in mimosoid legumes

Jade Collins[1] and Donovan Bailey[1]

[1] Department of Biology, New Mexico State University

Mimosine is an amino acid-like molecule, a tyrosine analog, produced by plants classified into the mimosoid clade of the legume plant family. The anabolic process that produces mimosine, which is toxic to most animals, is thought to have evolved from the gene for cystathionine β-lyase (CBL) as a defense mechanism against insects and other herbivores. Mimosoid legumes are important plants due to their geographic range, ecological and agricultural significance, and scientific contributions. They are scientifically significant as a model for genetic studies due to their multiple whole genome duplications (WGDs). WGDs along with other classes of gene duplications, create extra copies of genes on which evolution can act, facilitating adaptation and divergence. However, the evolution of mimosine production in legumes remains unclear. The objective of this project is to explore the evolutionary history of the genes involved in mimosine production and degradation by collecting relevant genomes, determining orthologous gene groups, and analysing the evolutionary history for the species and gene trees through the lens of gene duplications. The progress to date includes the collection of 14 mimosoid genomes, 2 outgroups, and 7 reference sequences known to be involved in mimosine production/degradation. The preliminary results from an orthofinder analysis identify gene family expansions in the mimosine-producing plants for all three reference sequence ortholog groups. Future directions include characterizing the duplications into specific classes of events that have contributed to the evolution of mimosine to develop a better understanding of the process behind its novel evolution.

Talk 4:

Understanding the Enemy: Bacterial pathogenesis of novel bacterium FD111 in *Nannochloropsis oceanica* cultures

Crisandra Jade Diaz[1], Alina A. Corcoran[1]

Biology Department, New Mexico State University[1]

Current agricultural and environmental changes require adaptive strategies to address shortages in food, feed, and even fuel production. Microalgal cultivation addresses these needs while providing a sustainable alternative to traditional crops due to its ability to be grown on non-arable land and ability to sequester CO_2. However, just like any other crop, algae are susceptible to predation by environmental pests. Our lab focuses on large-scale growth of *Nannochloropsis oceanica*, a microalgal culture known for its high-value lipids and proteins. Recently within this system, a novel bacterial pathogen known as FD111 has emerged that can decimate these large-scale cultures overnight. FD111 is a rod-shaped, motile bacterium of the *Oligoflexus* genus that exhibits predatory behavior similar to *Bdellovibrio*-and-like-organisms (BALOs). FD111 uses its flagella to attach to the cell wall of *N. oceanica* before creating a pore through which it enters the cell. Once inside, FD111 replicates until the cell lyses, releasing numerous individual bacteria into the culture. FD111 has yet to be isolated. My work aims to isolate FD111 to further understand mechanisms of infection as well as test chemical methodologies that prevent algal cultures from crashing. My attempts to isolate FD111 from crashed cultures have included filtration, centrifugation, and plating on R2a media which had been used in the isolation of other *Oligoflexus* species. Previous studies conducted by members of our team at ASU have had some success with using individual cell sorting to isolate similar bacterial species. We are currently implementing their strategy to isolate FD111 from infected microalgal cells.

Talk 5:

Developing novel reporters to explore cellular mechanics in living cells

Priscila Fourzan, Yasmin Khodary, Taylor Landfair, Maria Visconti, Abdul Al-Nouman, Jennifer Curtiss and Charles B Shuster

Department of Biology, New Mexico State University

The actin cytoskeleton is the primary determinant of cell shape and driver of shape change in animal cells. Understanding how alterations in the cytoskeleton translate into changes in cell mechanics not only requires direct biophysical measurements but also intracellular biosensors that can detect forces on the cytoskeleton with high spatiotemporal resolution. Towards these ends, we have developed candidate reporters based on the THATCH domain of Talin and the LIM domains of Zyxin, two actin-binding domains that form “catch” bonds, where actin binding is stronger when tension is applied to the filament. To validate these candidates, we are expressing each in different cellular contexts. In mammalian tissue culture cells, the Talin reporter bound to all actin structures when expressed at high levels, whereas the Zyxin-LIM domain bound to focal adhesions and cell-cell contacts, suggestive of mechanosensitivity. Additionally, the Zyxin/Talin reporters showed reduced actin co-localization when contractility was inhibited with myosin II activity modulators. Preliminary studies in sea star oocytes demonstrated that the Talin reporter was recruited to the cortex during a Rho and myosin II-dependent contractile wave during meiosis I. Finally, expression in the Drosophila imaginal disc (where the forces acting on cells during morphogenesis are well-characterized) suggests that the Zyxin reporter associates with the apical cytoskeleton in both the morphogenetic furrow and forming ommatidia. Current efforts are focused on further validating these constructs to identify a probe that most accurately reports the transient changes in cellular mechanics that occur at the subcellular level and at second time scales.

Talk 6:

Lower sugar supply affects mosquito fecundity and *Plasmodium berghei* development in *Anopheles stephensi* mosquitoes.

[1]Poorni De Silva and [1]Jiannong Xu

[1]Department of Biology, New Mexico State University

Mosquito-borne diseases impose major public health and economic burdens, with malaria, caused by Plasmodium parasites, being among the most significant. Because mosquitoes primarily rely on plant-derived sugars for energy, understanding sugar metabolism is crucial for assessing vector competence. This study investigates how sugar availability influences survival, reproduction, and Plasmodium development in *Anopheles stephensi*. Females maintained on a low-sugar diet (0.5% sucrose) exhibited over 80% survival for at least seven days under humid conditions sufficient to complete a gonotrophic cycle with normal fecundity. Notably, low-sugar-fed mosquitoes showed higher P*lasmodium berghei* infection intensities than those fed 10% sucrose. Furthermore, we utilized a 0.5% sucrose diet to select low-sugar-tolerant mosquitoes over generations. Initially, these mosquitoes had higher parasite loads, but by the fifth generation displayed reduced infections compared to wild-type, suggesting an adaptive shift possibly governed by genetic factors that affect carbohydrate metabolism. Comparative fecundity analysis revealed that the low-sugar-selected group produced more eggs than both the 0.5% sucrose-fed and the 10% sucrose-fed wild-type mosquitoes, indicating that the low-sugar scheme has selected mosquitoes with sufficient reproductive capacity and tolerance to low-sugar conditions. Quantitative RT-PCR revealed that expression of trehalase, Cabut, and acetyl-CoA carboxylase was repressed after a normal blood meal but less so in *P. berghei*-infected mosquitoes, suggesting a role in immunometabolic regulation during infection. Overall, our findings indicate that *An. stephensi* can adapt to low-sugar conditions, with implications for parasite development and vector competence. These findings warrant further investigation into the genetic and epigenetic regulation of immunometabolism in malaria vector mosquitoes.

Talk 7:

Buoyancy increases sensitivity to chemical nociception

Jaime Arroyo, Vanessa Pando, Raul Chavez, Mica Roacho, Kaitlin Victorian, Jacob Jaszczak

Department of Biology at New Mexico State University

Spaceflight poses a major challenge in proprioceptive adaptation, the body's ability to sense its position and coordinate movements. In microgravity, altered sensory feedback leads to motor impairments that can alter mission tasks (Weber et al. 2017) and heighten pain experiences (Sauer et al. 2023). While astronauts train in pools to simulate weightlessness, the neural mechanisms linking proprioception and nociception in these environments remain poorly understood. To investigate, we developed an experimental system using *Drosophila* larvae. While high concentrations of hydrochloric acid typically induce nociceptive behaviors in freely crawling larvae (Lopez-Bellido et al. 2019), we discovered that larvae also show these responses when suspended in buoyant conditions. We find that larvae will also exhibit acid induced nociceptive behaviors when suspended in liquid. We have begun comparing how larvae respond to acid stimuli if they are crawling (terrestrial) or suspended (buoyant). We find that when larvae experience acid damage, they lose terrestrial nociceptive sensitivity to acid stimuli (hypoalgesia). In contrast, larvae that experience acid damage and are tested in the buoyant condition do not lose nociceptive sensitivity to acid. We hypothesize that the increase in sensitivity in the buoyant condition arises from a change in proprioceptive sensation. Our ongoing work aims to determine whether inhibition or activation of proprioceptive circuits can decrease the nociceptive hypersensitivity of buoyant larvae. This system could be an effective model for understanding how the neurological process of proprioception modulates nociceptive sensitivity.

Talk 8:

The effect of repeated low-dose endotoxin injections on circulating steroid hormones in nulliparous Rambouillet ewes

J.A. Valencia, S.C. Gurule, and J.A. Hernandez Gifford

Department of Animal and Range Sciences, New Mexico State University, Las Cruces, NM

Unprecedented declines in female fertility highlight emerging challenges in reproductive biology across populations. Lipopolysaccharide (LPS) is derived from the outer membrane of gram-negative bacteria and promotes the release of proinflammatory cytokines ultimately decreasing estradiol (E_2) concentrations. How long these effects of LPS persist when given in a low-dose is less understood. The aim of this study is to evaluate the consequence of multiple injections of low-dose LPS on circulating E_2 and progesterone (P_4) concentrations throughout two consecutive estrous cycles. Fourteen Rambouillet ewes (age 19 mo; 56.4 ± 1.5 kg) were stratified by body weight (BW) and assigned to receive subcutaneous injections of saline (CON, n = 4), 1.5 µg/kg BW LPS (LOW, n = 5), or 3.0 µg/kg BW LPS (HIGH, n = 5) on d 5, 10, and 15 of a synchronized estrous cycle. Serum was collected to be analyzed using radioimmunoassay on d 0, 5, 10, 15, 16, and every other day following until d 34 relative to LPS challenge. On d 0 prior to LPS injection, E_2 and P_4 concentrations were similar among treatments confirming synchronization. However, by d 10 HIGH had lower P_4 concentrations compared with CON ($P < 0.05$). Similarly, LPS-treated groups on d 16 demonstrated decreased E_2 compared to CON ($P < 0.01$). By d 2 of the second cycle, E_2 concentrations remained lower in LPS-treated ewes compared with CON ($P = 0.06$). These data demonstrate repeated endotoxin exposure delays P_4 and diminishes E_2 concentrations across multiple cycles, indicating sustained disruption of female fertility.

Talk 9:

Habitat selection by an endangered chipmunk is altered by competition and non-stationarity

William E. Grooms[1], Fiona McKibben[2], Jennifer K. Frey[1]

[1]Department of Fish Wildlife and Conservation Ecology, New Mexico State University; [2]Department of Fish and Wildlife Sciences, University of Idaho

Habitat selection is a behavioral process resulting in the use of resources disproportionately to their availability in the environment that can be influenced by interactions with other species or can vary spatially across the landscape. The Peñasco least chipmunk *(Neotamias minimus atristriatus*; PLC) is an endangered taxon endemic to the Sacramento Mountains complex in southcentral New Mexico, USA. The taxon only persists in two populations, occurring in radically different vegetation communities. Our objectives were to determine whether habitat selection by the PLC was altered by the presence of a competitor, the gray-footed chipmunk (*N. canipes*; GFC), and to determine whether habitat selection by PLC was consistent across different environments. We assessed the influence of GFC on habitat selection by PLC at the landscape scale using multispecies occupancy models. We found strong evidence that PLC alter their habitat selection in the presence of GFC by selecting areas with high visual obstruction, suggesting that the functional role of visual obstruction is to reduce competition between the species. We compared the habitat preferences of the PLC at two locations and found strong evidence that Peñasco least chipmunks selected for similar vegetation structure across different vegetation communities, consisting of a mix of shrubs and herbaceous cover. Our results provide a better understanding of the role visual obstruction plays in the coexistence of chipmunks and describe a fundamental habitat requirement of this imperiled species.

Talk 10:

Algal Consortia and Monocultures of *Chlorella sorokiniana* and *Micractinium* sp. Exhibit Comparable Productivity in Revolving Algal Bioreactors

Ostroff Osher[1], Corcoran Alina[1]

[1]Department of Biology, New Mexico State University

Algae play an increasingly important role in sustainable wastewater treatment systems for their ability to remove nutrients while generating harvestable biomass. Algal biomass can be repurposed for secondary applications like fertilizer enrichment and biofuel production, enhancing both the economic and environmental value of these systems. Among cultivation strategies, revolving algal bioreactors (RABs) are particularly useful for attached biofilm growth. RABs simplify harvesting, reduce operational cost, and improve light exposure by rotating biofilms through air and nutrient-rich media, mitigating light limitations. This study utilized RABs to evaluate performance differences between a naturally occurring algal consortium and monocultures cultivated under greenhouse conditions using anaerobic digestate effluent as the wastewater nutrient source. Two comparative experimental runs were conducted: first using *Chlorella sorokiniana*, and the second using *Micractinium sp.*, to assess strain-dependent monoculture performance relative to the consortium. Biomass productivity, photosynthetic yield (Fv/Fm), and nutrient concentrations (NO_3-N, NH_3-N, PO_4^{3-}) were monitored throughout each trial, and 16S and 18S sequencing was performed at multiple time points to evaluate community composition and stability. In the *C. sorokiniana* experiment, median productivity was similar between monoculture (0.31 g m^{-2} d^{-1}) and consortium treatments (0.35 g m^{-2} d^{-1}; $p = 0.33$). In the *Micractinium sp.* experiment, monocultures exhibited higher median productivity (0.35 g m^{-2} d^{-1}) than consortia (0.27 g m^{-2} d^{-1}), though this difference was not statistically significant ($p = 0.07$). Overall, productivity was comparable across systems, with evidence of strain-dependent trends. Future work will assess whether synthetic algal–bacterial co-cultures can enhance monoculture performance through engineered mutualistic interactions.

Talk 11:

Characterizing Patterns of DNA Methylation and Homologous Gene Expression in the Context of Gene Duplication Type for the Tetraploid *Leucaena trichandra*

Noelle Molina[1], Mike Lopez[1], and C. Donovan Bailey[1]

[1]Department of Biology, New Mexico State University

Gene duplication is a major evolutionary force in plants, influencing gene retention, divergence, and expression. Duplicated genes can arise through whole-genome duplication (WGD) or more limited tandem, proximal, transposed, or dispersed events, each of which may shape evolutionary trajectories differently. This study investigates variation in DNA methylation patterns among duplication types and evaluates the association between DNA methylation states and homologous gene expression divergence in *Leucaena trichandra*. *L. trichandra* is a non-model species that underwent ancestral WGD ca. 16 mya. Bisulfite sequencing from leaf tissue was used to generate genome-wide DNA methylation data. In plants, DNA methylation is classified as gene body methylation (gbM), transposable element methylation (teM), or unmethylated (uM). We analyzed and compared methylation patterns across all duplication events exhibiting differential gene expression. Preliminary results suggest that teM is associated with gene silencing, whereas gbM and uM are associated with transcriptional activity. Results further indicate that methylation patterns differ among duplication types. Ongoing analyses aim to determine how DNA methylation varies with gene age.

Talk 12:

Sterile-Insect-Technique: Hormetic Ethanol Feeding results in Up-regulation of Antimicrobial Peptide Genes in X-ray-irradiated *Aedes aegypti* males.

Gabriel Borg[1], Dr. Immo A. Hansen[1]

[1]Department of Biology, New Mexico State University

The Sterile Insect Technique (SIT) has emerged as a promising new control strategy for reducing mosquito populations and controlling mosquito-borne diseases. Radiation treatments that are part of the SIT protocol can decrease male mosquito fitness and curb the effectiveness of SIT. The incorporation of hormetic ethanol into the adult *Aedes aegypti* diet, prior to irradiation, has been shown to increase male longevity compared to mosquitoes fed on a standard sugar-water diet. Here, we investigate the behavioral and gene expression changes that arise from feeding adult male A. aegypti a 5% ethanol diet over a seven-day period followed by X-ray irradiation at 50 Gy. The ethanol-treated group showed higher locomotor activity and life span than the control group. Whole body transcriptomics analyses at one, two-, and three hours post-irradiation revealed hundreds of rapidly up- and down-regulated genes. Notably, a group of anti-microbial peptides is up-regulated two hours post-irradiation. Our results suggest that anti-microbial peptides, primed by ethanol feeding, may serve as radioprotectant genes. Our findings will help improve mosquito SIT protocols.

Talk 13:

DEG/ENaC channel ppk1 and TMEM16 channel subdued are required for wound-induce chemical-allodynia

Vanessa Pando, Jaime Arroyo, Mica Roacho, Kaitlin Victorian, Janet Gomez, Raul Chavez, Jacob Jaszczak

Department of Biology at New Mexico State University

Many organisms rely on nociceptive sensory systems to detect and respond to stimuli in their environment. Although there have been studies that suggest that physical or UV irradiation damages the epidermis that leads to hypersensitivity of nociceptors (Im and Galko 2011), the mechanisms of chemical hypersensitivity remain unknown. *Drosophila* larvae express nociceptive behaviors when exposed to high concentrations of hydrochloric acid (Lopez-Bellido et al., 2019). Acid sensitive ion channels (ASIC) are proton-gated and belong to the degenerin/epithelial sodium channel (DEG/ENaC) family. Acid sensing in mammals is mediated by TrpA1 and ASICs channels. In Drosophila, a mutation of the DEG/ENaCs (ppk19 and ppk30) has been shown to disrupt acid nociception (Jang et al. 2022). We find that ppk1 is required for chemical –allodynia (sensitivity to innoxious stimuli). In comparison to thermal-allodynia, dTrpA1 and painless are dispensable. This finding suggests that there may be a wound-initiated mechanism that sensitizes nociceptive sensory sensors. TMEM 16 channels are primarily Calcium-active Chloride Channels (CaCCs) in mammalian cells. It has been shown that a mutation in CaCCs (subdued) has a key role in nociceptor development in *Drosophila* (Jaszczak et al. 2022). We find that subdued is required for chemical-allodynia. Correspondingly, subdued is a mediator for thermal nociception (Jang et al., 2025). We find that acid damage induces a unique loss of nociceptive sensitivity, and that wound induced allodynia is sensitized to chemical stimulus in a ppk1 and subdued dependent but TrpA1 independent mechanism. Mapping allodynia pathways may reveal conserved mechanisms for developing targeted chronic pain therapies.

Talk 14:

Effects of Stormflow Events on Water Quality in the New Mexico Rio Grande River Basin

Caleb Fyock, Dr. Geoffrey Smith, Dr. Connie Maxwell, Kaustuv Neupane

Department of Biology, New Mexico State University; New Mexico Water Resources Research Institute

Stormflow events strongly influence water quality by increasing erosion and microbial contamination in surface waters. In the Rio Grande, Rincon Arroyo, and Butler-Cothern subbasins, elevated levels of Escherichia coli concentrations and turbidity pose risks to public health and intensify downstream flooding. This study evaluates stormflow effects on water quality using two watershed-scale experiments and monitoring of the Rio Grande and Las Cruces wastewater treatment plant. In the Rincon Arroyo, a paired watershed design compared two control watersheds with two restored watersheds containing one-rock structures intended to reduce sediment and *E. coli* loads. A second study in the Butler-Cothern subbasins on the West Mesa employed four automatic ISCO samplers to assess the effectiveness of a single, one-rock structure, by comparing stormwater influent and effluent. Additionally, weekly sampling of the Rio Grande and wastewater effluent provided regional context during agricultural and non-agricultural flow periods. Results from the Rincon Arroyo were highly variable and did not establish a clear link between watershed restoration and reduced *E. coli* and turbidity. Data from the Butler-Cothern subbasins were limited but suggest one-rock structures may reduce sediment loads and *E. coli* concentrations downstream. River monitoring results indicate stormflow events significantly increase both turbidity and *E. coli* concentrations, with multiple sampling sites exceeding the EPA recreational standard of 400CFU/100mL. Microbial source tracking analyses were used to differentiate contamination from human, cattle, and general ruminant sources across study sites.

Talk 15:

Corticosterone Receptor Expression Varies Across Tissues in Chronically Stressed Budgerigars

Negin A. Jazi, Alondra Villalba, Alyssa Hernandez, Amelia Clayshulte Abraham, Jodie M. Jawor, Timothy F. Wright

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Early life stress can trigger the release of glucocorticoid (GC) hormones and have profound effects on multiple physiological systems. Chronic stress may alter expression of glucocorticoid (GR) and mineralocorticoid (MR) receptors, which bind corticosterone and regulate stress responses. However, whether these changes occur uniformly across peripheral tissues remains unclear. In this study, we compared GR and MR expression across non-reproductive organs in budgerigars (Melopsittacus undulatus) exposed to a 3-week chronic stress protocol during the juvenile period and/or adulthood in a fully crossed design. Using qPCR, we quantified GR and MR expression in kidney, liver, pectoralis muscle, and pancreas. We observed tissue-specific patterns rather than a uniform receptor response to stress. In liver, GR expression decreased under both juvenile and adult stress, contrary to prediction, while MR remained relatively stable. In kidney, both GR and MR showed inconsistent treatment effects. In muscle, MR expression exceeded GR across treatments and appeared downregulated under stress. In pancreas, GR expression increased with stress exposure, consistent with glucocorticoid involvement in glucose homeostasis, whereas MR changed little. Overall, MR expression was higher in liver and muscle, while kidney exhibited comparatively lower GR and MR expression. These findings highlight distinct, tissue-specific roles of GR and MR in maintaining homeostasis and mediating chronic stress responses across life stages.

Poster Presentations

Ordered Alphabetically by First Author's Surname

Poster 1:

Effects of Electrical Treatments on Total Phenolic Biosynthesis and Associated Gene Expression in *Brassicaceae*

Shakil Ahmed[1], Jaspreet Thind[2], Erik Lehnhoff[3] and C. Donovan Bailey[1*]

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Plant secondary metabolites are crucial for plant adaptation and survival. Phenolics are essential for plant defense, stress responses, and human health. Phenolics are one class of secondary metabolites induced by a wide variety of abiotic and biotic stress factors. However, in experimental systems, some of these phenolic-inducing factors can be difficult to control precisely. Here, we investigate whether easily controlled, but previously underexplored, electrical treatments can be applied to manipulate phenolic production. This study uses members of the *Brassicaceae* family to investigate 1) the effects of low-current electrical treatments on total phenolic accumulation in kale and 2) patterns of differential gene expression in the phenolic biosynthetic pathway in the closely related species *Arabidopsis thaliana*. For the total phenolics experiment, 64 kale plants were exposed to a range of electrical treatments for one week, and total phenolic content quantified at each time point. Similarly, we investigated gene expression along the phenolic pathway following a 0.025 mAh application for 2 hours in A. thaliana. The results of the total phenolic experiment show that phenolic content varied with electrical treatment, and the 0.1 mAh treatment showed a significant increase. The RNA-seq study identified significant upregulation of one or more genes at each early step in the phenolic pathway, as well as along the subsequent branch of the pathway for the production of p-coumaroyl shikimate and downstream products. This study provides new insights into how direct electrical treatments can serve as a controlled stressor to enhance plant secondary metabolite production.

Poster 2:

Using Differential Gene Expression Analysis to Investigate *Heteropsylla cubana* Herbivory Responses in the Genus *Leucaena*.

Mst Tasrin Aktar[1], Vinavi A. Gamage[2] and C. Donovan Bailey[1]

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Leucaena, a genus of fast-growing leguminous plants, includes important for fuel, timber, food, forage, soil development, medicine, and livestock feeding. However, plantations of *Leucaena* are often affected by the psyllid *Heteropsylla cubana*, which limits agricultural and agroforestry use by damaging 80% or more of the foliage and resulting in heavy defoliation and reduced growth. There have been several studies on psyllid infection in *Leucaena*, but the genetic and molecular basis of *Leucaena's* defense response remains largely unexplored. This limits knowledge of which metabolic and hormonal signaling pathways may confer resistance traits. In this study we use *L. cruziana* as a model to investigate differentially expressed genes associated with herbivory-exposed leaves in two populations: highly resistant (HR) vs. mildly susceptible (MS). Twelve treatment and twelve control plants from each population were selected, and plant materials were collected from three biological replicates for both treatment and control plants. RNA-Seq studies were carried out to identify differentially expressed genes in treatment vs. control. Preliminary results with the HR population identify several candidate genes with strong upregulation in the treatment group compared with controls. Further functional identification of these genes indicates activation of herbivore-response pathways. The identification of these gene systems could be useful in the *Leucaena* plant breeding program to develop psyllid-resistant *Leucaena* varieties.

Poster 3:

Involvement of anillin and septins in atypical cleavages

Alan Araiza[1], John Henson[2], Charles B. Shuster[1]

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Asymmetric cell divisions are a key feature of early development and are achieved either through spindle repositioning or structures called polar lobes (PLs). These PLs are observed only during the first two cleavages in some mollusc and annelid embryos and are hypothesized to sequester developmental determinants, as removal of the PLs in Ilyanassa embryos leads to developmental failures. Although the implications of PL removal have been described for some species, little is known about how the Polar Lobe Constriction (PLC) forms or how it relates to the contractile ring (CR). The PLC initiates early in cytokinesis, but the orientation of PLC appears to violate the canonical rules for establishing the cleavage plane. Thus, PLs remain an enigma from both a developmental and cell biological standpoint. In sea urchins, the core CR components (myosin II, anillin and septins) appear as foci or nodes, which aggregate to form a functional CR, and the placement of these ring components are ultimately under the control of the Chromosomal Passenger Complex (CPC). However, in PLs, the CPC kinase Aurora B is required only late in PL formation, suggesting that canonical cytokinetic signaling is dispensable for PLC initiation. Preliminary data in scallop embryos suggests that anillin localizes to the CR, but not PLC. However, it remains unknown whether septins are a component of the PLC, or if anillin contributes to PLC formation. Using a variety of cell and molecular biology techniques, we hope to better understand the role of these proteins during PLC in scallop embryos.

Poster 4:

Role of Notch-Delta signaling during muscle development in the sea star

Chinyere Awaogu, Angela Korte, Francina Montenegro and Charles B. Shuster

Department of Biology, New Mexico State University.

Embryonic development occurs in an orchestrated and precise manner from fertilization through the larval or juvenile stages. Central to the proper specification and organization of the germ layers is a conserved toolkit of signaling pathways that act in concert or antagonistically to control specification and morphogenesis. Sea star larvae have two populations of muscle (aboral and esophageal) that appear shortly after gastrulation. Previous work in the lab identified high molecular weight splice forms of the actin-binding protein tropomyosin (Tpm-L) that were muscle-specific, and Tpm-L transcripts could be detected in muscle precursors while they were still associated with the archenteron. Notch-Delta acts as a critical signaling pathway throughout animal development, and to determine whether Notch-Delta influences muscle development, Patiria miniata embryos were placed in either DMSO or DADT during late gastrulation, when muscle precursors have already been specified. Examination of live or immunolabeled five-day larvae revealed that both control and DADT-treated embryos had Tpm-L positive esophageal- and aboral muscle cells. Subtle differences in esophageal muscle organization could be detected. However, there was a dramatic increase in the number of aboral muscle cells, which control the opening and closing of the mouth. Moreover, preliminary results suggest that DADT-treated embryos had an impaired ability to ingest algae compared to their counterpart. Together, these results suggest that Notch plays an intrinsic role in muscular development, and current efforts are focused on defining the spatial and temporal dynamics of Notch signaling during this process.

Poster 5:

Characterizing immune genes in *Triatoma rubida*, a possible vector of Chagas Disease in the Southwestern United States.

Gabrielle N. Baca and Maria G. Castillo

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Triatomines are hematophagous insects and known vectors of the parasitic protozoan *Trypanosoma cruzi*. *T. cruzi* is the causative agent of Chagas disease, a potentially fatal disease and for which there is no vaccine. Chagas disease, once thought to be exclusively endemic in South and Central America, is now endemic in the United States and consequently, there is a pressing need to study triatomine species present in the U.S. Like humans, insects have a complex immune system that protects them from pathogens and provides tolerance towards symbiotic microorganisms. Immune characterization of triatomine insects has been extensively studied in species indigenous to South and Central America, but little is known regarding species present in the U.S. In New Mexico, one of the most abundant triatomine species is *Triatoma rubida*, and yet it is severely understudied. In this study, we aim to identify and characterize crucial immune genes in our local species of triatomine, *T. rubida*, using the available genomes of other triatomine species as reference. Genes known for their role in response to parasite infections were selected and include alpha macroglobulin, complement component C1q, and the mannose binding lectin receptor. Through RNA extraction and subsequent cDNA synthesis, we will use specific primers that amplify these target immune genes to validate their presence in *T. rubida*. Investigating the immune system present in local insect vectors is vital to understanding how resident triatomine species respond to *T. cruzi* and how we may develop novel vector control measures to prevent/limit the transmission of *T. cruzi*. Impact of RNA interference, the front-line antiviral defense of mosquito vectors, on the outcomes of within-cell competition between sylvatic and human-endemic strains of dengue virus

Poster 6:

Impact of RNA interference, the front-line antiviral defense of mosquito vectors, on the outcomes of within-cell competition between sylvatic and human-endemic strains of dengue virus

Lindsey G. Biehler[1], Kathryn A. Hanley[1]

[1]Department of Biology, New Mexico State University

Dengue virus (DENV) has previously emerged from the sylvatic (wildlife) cycle at least four times, resulting in the four serotypes that circulate today in the human-endemic cycle. The ancestral sylvatic transmission cycle involves non-human primates and forest-dwelling *Aedes mosquito* species, while the human-endemic cycle involves humans and the peridomestic mosquito species *Aedes aegypti* and *Aedes albopictus*. The sylvatic cycle of DENV remains extant in both Asia and Africa, and spillover into humans occurs with some regularity, but these events have not led to emergence of new human-endemic lineages of DENV in recent times. A major focus in our lab is understanding the factors that limit DENV emergence, one of which may be within-mosquito competition. We have previously demonstrated that sylvatic DENV are competitively inferior than human-endemic DENV in Ae. albopictus C6/36 cells. However, subsequent studies revealed that this cell line lacks a functional RNA interference (RNAi) pathway, the main defense of mosquitoes against arboviruses. In the current study, we quantified the outcome of concurrent and lagged co-infection of sylvatic and human-endemic DENV strains in Ae. albopictus U4.4 cells, which are capable of mounting an RNAi response to infection.

Poster 7:

Determining the role of the small GTPase Rap1 in morphogenesis during *Drosophila melanogaster* eye development

Samantha Brazil[1], Jennifer Curtiss[1]

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Morphogenesis is the process by which cells, tissues, and organisms develop their shape and structure, which are essential for proper physiological function. A classic example of morphogenesis is the development of a frog, which transitions from a spherical egg to an elongated tadpole with an oval-shaped head and long tail. Defects in morphogenesis can lead to congenital birth defects, affecting roughly 3%-5% of births and, consequently, leading to infant mortality. In epithelial tissues, morphogenesis is driven by cell adhesion and actomyosin contractile forces, with E-cadherin playing a key role in cell-to-cell adhesion and allowing cells to move and change shape. *Drosophila melanogaster*, commonly known as the fruit fly, is a traditional model system to study morphogenesis. Their compound eyes exhibit a precise pattern of cell shapes that enable proper function, providing insight into how morphogenetic processes are regulated. The small GTPase Rap1 is a molecular switch and is involved in signaling pathways related to cell adhesion and actomyosin contractility, which both play a critical role in morphogenesis. We aim to determine if Rap1 is interacting with a gene involved in morphogenesis. We have knocked down the expression of Rap1 in specific cell types in the Drosophila eye, which leads to a rough eye phenotype. We are performing dissections to determine which cell types are being affected. We plan to perform a genetic screen to identify which genes involved in morphogenesis are interacting with Rap1.

Poster 8:

Breeding Behavior and Mate Selection in Artibeus jamaicensis

Aimee Coletti[1], Alexis Ortiz[1], Jessica Pulgarin[1], Alana Pedersen-Kamaka[1], Daniella Sanchez[1], Karen E. Mabry[1], Teri J. Orr[1]

[1]Department of Biology, New Mexico State University

Numerous mating systems have evolved over time, especially in the ecologically diverse order *Chiroptera* (bats). One species of bats is of particular interest, exhibiting specialized reproductive strategies during pregnancy. This species, *Artibeus jamaicensis* (the Jamaican Fruit-Eating Bat) is known to have a harem-style breeding system; a mating system involving one or two males associated with a large group of females. However, individual interactions and behaviors that establish these groups are unknown. We predict that individual breeding behaviors will influence mate selection and establishment of harem groups. To examine these behaviors, video footage was coupled with a Passive Integrated Transponder (PIT) tag identification system. Captive bats were monitored in two simultaneous, week-long trials with five females and two males in each trial for a total of twelve individuals. Recording on four cameras occurred daily from 12am to 11:59pm each of the seven days. Video footage was cross referenced to data from the PIT tag reader to identify interacting individuals. Interactions between individuals were categorized as: approach, bonding, sparring, copulation, or "other" by three observers blind to bat identities. Footage was accessed through Windows Media Player or Mac QuickTime Player. Here we present our preliminary findings, and their importance for expanding our understanding of the factors that drive mate choice and their effects on fitness in mammal breeding systems.

Poster 9:

Diversification of Modern Birds Driven by Early Paleogene Climate Patterns

Meig Dickson[1]

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Most major modern bird groups first appeared in the fossil record during the early Paleogene, the period following the extinction of non-avian dinosaurs 66 million years ago. Much of the resulting diversity occurs not in the immediate wake of the extinction event, but ten million years later. This corresponds with the Paleocene-Eocene Thermal Maximum, a major global warming event that occurred between the Paleocene and Eocene epochs. The thermal maximum is theorized to have caused dramatic changes in global biodiversity, including spurring the diversification of major placental mammal clades. The perceived paucity of Paleocene avian fossils has prevented similar studies as to the true drivers of the diversification the non-passerine families. Here I conduct a broad scale analysis of avian fossil diversity across the Paleocene-Eocene transition in the wake of shifts in global temperature, taphonomic patterns, and diversity of other tetrapods. While ordinal radiations potentially occurred due to the available ecospace following the end-Cretaceous extinction, the spread of pan-tropical habitats during the thermal maximum seems to have further increased family-level diversity in the earliest Eocene. Furthermore, avian fossilization rates in the Paleocene are not as poor as once thought, but average compared to non-placental tetrapods. This indicates that occurrence rates of avian fossils are most likely reflective of actual diversity patterns and not taphonomic bias. These patterns point to the expansion of novel tropical habitats possibly spurring avian cladogenesis like seen in placental diversification at the start of the Cenozoic Era.

Poster 10:

Alternative splicing in electric fishes: detection of transcript variants of ube2d3 within the context of the electric organ and skeletal muscle tissues

Emily D. Earnest, Franchesca Ortega, Eliha M. Hernandez, Sandra Rios Alba, and Graciela A. Unguez

Department of Biology, New Mexico State University

Electric organ (EO) cells, or electrocytes, are evolutionarily derived from skeletal muscle (SM) cells and have evolved independently at least six times in electric fish species. These non-contractile organs retain some structures of their SM precursors but gain the ability to produce continuous high-frequency electric fields. Knowledge of how electrocytes acquire and continue to maintain distinct function from SM is limited. Recent studies of the electric fish *Sternopygus macrurus* revealed similar transcriptomes of adult EO and SM, despite the EO being non-contractile. We hypothesize that post-transcriptional modifications contribute to specialization and maintenance of these cell types. In this study, we focus on disproportional mRNA alternative splicing between the EO and SM of *S. macrurus* and two other electric fishes, *Eigenmannia virescens* and *Brienomyrus brachyistius*. Splicing detection software predicted disproportional usage of splice variants from multiple genes, including an exon skipping event in ube2d3. Our qualitative PCR data shows ube2d3 to be differentially spliced in *E. virescens* and *B. brachyistius*, but not in *S. macrurus*. The EO of both *E. virescens* and *B. brachyistius* favors the skipping isoform whereas SM favors the inclusion isoform, a pattern not detected in *S. macrurus*. Interestingly, these ube2d3 splice variants are highly conserved in both vertebrates and invertebrates, and they likely act as key components of the ubiquitin-proteasome system (UPS), a process important for protein degradation. Whether these variants play distinct roles in protein degradation that could contribute to the phenotypes of SM and EO is currently unknown.

Poster 11:

Ecophysiological adaptation in woodlandsnails (genus *Ashmunella*)

Thomas A. Everest[1], T. Mason Linscott[1]

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Understanding how organisms adapt to desert environments is critical to our understanding of evolution, ecology, and conservation. Woodlandsnails (genus *Ashmunella*) in the Southwestern US provide an ideal model for studying desert adaptation as they are one of the most diverse genera of land snails in North America, exhibit narrow-range endemism and island biogeography patterns, and exist across a wide range of habitats. In multiple mountain systems in Arizona, New Mexico, and Texas, we have identified two species morphotypes: smaller, flatter species with increased aperture dentition live in drier desert habitats at lower elevation, and larger, taller species with reduced aperture dentition live in wetter forest habitats at higher elevation. Previous workers have suggested that these two morphotypes independently colonized each mountain system. Alternatively, we hypothesize that an ancestral desert morphotype colonized each mountain system before independently diverging into an additional forest morphotype in each mountain system.

Poster 12:

Evaluating Thermal Stress Response of *Chlorella–Azospirillum* Model Using Continuous Cultures

Gabitzsch, Maya[1]; Corcoran, Alina[1]

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Algal-bacteria interactions underpin structure and function of aquatic interactions, yet we are only beginning to understand how these interactions might change under future climate scenarios. The *Chlorella*-*Azospirillum* model is a well-studied system in which the bacteria promote algal growth through the secretion of indole-3-acetic acid. However, studies have found that this compound alone is not enough to increase biomass and mitigate stress. Additionally, the co-culturing of *Azosprillum brasilense* with different *Chlorella* species yields inconsistent results, indicating that symbiosis is dependent on environmental and physiological conditions. My research aims to understand the interactions of co-cultures of *Azosprillum brasilense* and *Chlorella vulgaris* when subjected to temperature stress in continuous cultures. I implement continuous culture systems (chemostats) to co-culture these organisms at two temperatures: 27°C reflects optimal growth, while 35°C imposes stress relevant to future warming scenarios. Continuous culture is achieved through continuous medium inflow and culture outflow at a fixed dilution rate, allowing the culture to remain in the same growth phase throughout the experiment. By using continuous cultures, variables dependent on population size such as nutrients, pH, light, and metabolite accumulation are held constant. I establish triplicate co-culture and monoculture chemostats (w/v 100 mL) at dilution rate of 0.1 day^{-1}. Co-cultures will be inoculated on a 1:1 cell ratio with optical density (550), chlorophyll fluorescence, photosynthetic yield and cell counts measured daily. This study is the first to grow the *Chlorella*-*Azospirillum* model in continuous culture and highlight the utility in running chemostat experiments to understand algal bacteria interactions.

Poster 13:

Evaluation of Genetic Soil Disinfestation for Managing *Phytophthora capsici* in Chile Pepper

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Phytophthora capsici, a soil-borne fungal-like pathogen, can cause significant yield losses in chile pepper. Management of this virulent pathogen is challenging due to the presence of asexual motile zoospores and long-lived sexual oospores. Various management techniques, such as chemical, biological, and cultural approaches, have been employed; however, they have not provided complete control of the pathogen. The present study focused on an innovative strategy, genetic soil disinfestation, which exploits host resistance to reduce pathogen populations and their aggressiveness in the soil. Jalapeño (NuMex Vaquero, Early Jalapeño, and TAM-Jalapeño) and non-jalapeño cultivars (CM334 -resistant control, Numex Sandia select - susceptible control) were grown in pathogen-infested soil and rotated with a susceptible pumpkin cultivar under greenhouse conditions. Germination percentages were evaluated in both prior resistant and susceptible cultivars grown in pathogen-infested soil and treated soil, respectively. Disease incidence was reduced in the susceptible host, pumpkin, following jalapeño cultivation, supporting the genetic soil disinfestation strategy.

Poster 14:

Detection of transcript variants of tp63 in the skeletal muscle and electric organ of electric fishes

Eliha M. Hernandez, Emily Earnest, Sandra Rios Alba, Franchesca Ortega, and Graciela A. Unguez

Biology Department New Mexico State University

The electric fish *Sternopygus macrurus* contains a muscle-derived electric organ (EO) that is non-contractile and creates an electric field, allowing it to navigate and interact with its environment. Transcriptome studies comparing adult muscle and EO of *S. macrurus* showed that relatively few genes were highly differentially expressed between these two tissues, despite having dramatically different cellular structures and functions. To date, how the EO acquires and retains such different functions from its muscle precursors is unknown. It could be that post-transcriptional processes are especially important in regulating these two cell types. Here, we study the disproportional usage of splicing variants between the SM and EO of *S. macrurus* and two additional electric fishes, *Eigenmannia virescens* and *Brienomyrus brachyistius*. We focused on the gene tp63, because, according to published research, it generates transcript variants with important roles in muscle development. We detected two transcript variants, TAp63 and ΔNp63, in the EO and SM of these three species. Our qualitative PCR data show a tissue-specific expression pattern of these isoforms only in *S. macrurus*. The post-transcriptional regulation of tp63 is unique to *S. macrurus* and may play a role in cell identity and distinct functions between its adult EO and SM.

This work was supported by the NIH Undergraduate Research Training Initiative for Student Enhancement (U-RISE) and the New Mexico State University’s Ronald E. McNair Postbaccalaureate Achievement Program, PR/Award Number P217A220314.

Poster 15:

Impacts of Sorghum-Barley Crop Rotation on Chile Pepper Growing Season

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Crop rotation may offer an effective strategy to reduce weed pressure and weed management costs in chile pepper. A field study was conducted to evaluate the effects of prior-season crops on weed density, hand hoeing time, nitrogen requirement, yield, and economic returns in spring-sown chile pepper. Treatments included summer fallow followed by (fb) winter barley, summer fallow fb winter fallow, sorghum fb winter fallow, and sorghum fb winter barley. Results indicated that the sorghum–barley rotation reduced broadleaf weed density in chile pepper by 21% compared with summer fallow fb winter fallow. Hand-hoeing time during the fourth through sixth week of the chile pepper growing season was reduced by 17 to 27% following sorghum fb barley. However, the sorghum–barley rotation increased nitrogen requirements by 24%, compared to summer fallow fb winter fallow. Chile pepper fruit yield did not differ among treatments. Economic analysis revealed that barley following either fallow or sorghum increased crop production costs, which reduced net economic benefits relative to other rotations, despite comparable yields. Overall, replacing both summer and winter fallows with sorghum and barley, respectively, provided measurable weed suppression and labor savings in subsequent chile pepper production. However, sorghum-barley rotations may cause an increase in costs, relative to fallow, that are not offset by labor savings.

Poster 16:

The Role of Rap1 in Primary Pigment Cell Development in the *Drosophila* melanogaster eye

Delaram Jafari[1], Jennifer Curtiss[1]

Department of Biology[1], New Mexico State University[1]

Morphogenesis requires dramatic cell shape changes, which are powered by contractile force generated by actin and myosin, as well as through cell adhesion. It remains unclear how factors that promote cell fate ultimately lead to changes in cell shape. The *Drosophila* eye contains ~750 ommatidia in an exquisitely precise hexagonal arrangement that enables tight packing and acute vision. One morphogenetic event that occurs during pupal development involves a group of four cone cells that signal via the Notch pathway to adjacent cells on either side, forming primary pigment cells. The primary pigment cells then enwrap the cone cells, separating them from interommatidial cells. It is likely that actomyosin contractility and/or heterophilic cell adhesion are involved in the enwrapment process; however, the mechanisms underlying this process remain unclear. Rap1, a Ras-family small GTPase, regulates diverse functions. To determine whether Rap1 has a role in primary pigment cell enwrapment, we employed the UAS-GAL4 system to drive the expression of dominant-negative Rap1 ($Rap1N^{17}$) in primary pigment cells. We found extra primary pigment cells in some ommatidia. Additionally, our time-lapse observations revealed that these extra cells originated from interommatidial cells. Time-lapse imaging shows that the primary pigment cells initially begin to enwrap the cone cells. However, later during morphogenesis, interommatidial cells will often invade the primary pigment cells to replace them. This resembles defects observed in Notch mutants, suggesting that Rap1 and Notch are both involved in this process.

Poster 17:

Many sites, many stories: Context-dependent fungal responses to global change drivers

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Soil fungal communities play central roles in carbon cycling, nutrient dynamics, and soil structure, yet their responses to global change drivers remain difficult to generalize across ecosystems. Much of the existing literature is based on single-site or single-driver studies, limiting broader inference. To address this gap, this study examined how soil fungal communities respond to three major global change drivers, drought, warming, and nitrogen enrichment, across multiple ecosystems using a consistent analytical framework. Soil samples were collected from nine Long-Term Ecological Research (LTER) sites in the United States and Puerto Rico, and three non-LTER sites representing the Mojave, Chihuahuan, and Great Basin deserts. Fungal communities were characterized using high-throughput sequencing of the ITS2 region. Site-level environmental context emerged as the dominant factor structuring fungal community composition and diversity. Alpha and beta diversity metrics showed that fungal communities were largely resilient to experimental drought, warming, and nitrogen enrichment at the cross-ecosystem scale, with variation driven primarily by ecosystem identity rather than treatment. However, indicator species analysis revealed clear, stressor-specific taxonomic responses, demonstrating that global change effects were concentrated within subsets of responsive fungal taxa rather than expressed as community-wide restructuring. These findings indicate that fungal responses to global change are strongly context dependent and primarily expressed through trait-mediated taxonomic filtering rather than shifts in overall diversity or functional guild composition. This work highlights the importance of integrating environmental context and indicator-based approaches to interpret fungal community responses to global change and predict their implications for ecosystem functioning under future climate scenarios.

Poster 18:

SkitoSnack 2.0 - a Bloodmeal Alternative for *Anopheles* and *Aedes* Mosquitoes.

Anjali Karki[1], Hailey A. Luker[1], Naga Narendra Reddy Potlapalli[2], F. Omar Holguin[2], Meenakshi Berwal[3], Patricia V. Pietrantonio[3], and Immo A. Hansen[1]

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SkitoSnack, an artificial blood-meal alternative, was developed in 2018 for rearing *Aedes aegypti* mosquitoes in laboratory culture. This artificial blood-meal diet has a long shelf life and can effectively support the long-term rearing of *Ae*. *aegypti*. However, *Anopheles* mosquitoes often do not engorge on it. Therefore, in this study we optimized the SkitoSnack recipe for rearing *Anopheles stephensi* mosquitoes. We added, removed or changed individual components from the original recipe and measured engorgement rates, egg numbers, and hatching rates. We identified a new recipe that can effectively support the continuous rearing of *An*. *stephensi*. We then tested this new diet with *Ae*. *aegypti* and found engorgement rates, egg numbers, and hatching rates were not statistically different from those of blood-fed females. Using a modified FlyPAD feeding system, we showed that *Ae*. *aegypti* ingested significantly larger meal volumes of the new diet compared to bovine blood, showing a strong preference for it. Our findings support that our new diet is an effective blood-meal alternative for the rearing of both *Anopheles* and *Aedes* mosquitoes. We named the new recipe SkitoSnack 2.0.

Poster 19:

Identifying determinants of cancer cell fates in response to mitotic arrest

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Anti-mitotic drugs that induce mitotic delay have been employed in the clinical treatment of multiple cancer types for several decades. However, different cancer cell types exhibit variable cell fate responses to mitotic arrest, including mitotic cell death or slippage back into interphase, at which point cells may undergo cell cycle arrest, die, or continue to cycle. Previous work from the lab and others have shown a high degree of heterogeneity in tumor cell responses to mitotic arrest, both between cell lines and amongst individual cells. These differences in cellular responses may be a contributing factor to the variable efficacy of anti-mitotic drugs. In an effort to identify factors whose differential expression may determine whether a cell can survive mitotic delay, we conducted RNA-SEQ on three cervical cell lines: a cancer cell line that dies in response to mitotic delay, a cancer cell line that survives mitotic delay, and a noncancerous cell line that survives mitotic delay and arrests in G1. Additionally, RNA-SEQ was performed on the same lines cultured in the presence of a PI3K inhibitor, which has been shown to sensitize some lines to mitotic cell death. Preliminary analysis of differentially expressed genes have identified the proto-oncogene c-Myc as a gene whose expression correlates with mitotic cell death, as well as anti-apoptotic factors (Bcl-2 and Bcl-xL) whose expression correlates with cell survival. Current efforts are focused on confirming differential expression by Western blotting, and applying RNA interference and over-expression approaches to shift cell fates in these cell lines.

Poster 20:

The Salvador-Warts-Hippo Signaling Pathway Regulates Primary Follicle development in *Aedes aegypti* mosquitoes

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Aedes aegypti mosquitoes are the principal vector of major emerging and re-emerging infectious diseases that are of both medical and veterinary significance. Despite advances in mosquito control measures, *Aedes aegypti* continues to expand its global distribution, this its burden. An emerging target for mosquito control is by interfering with key regulators of reproduction. *Aedes aegypti* are anautogenous, meaning they require a blood meal for successful production of eggs. After a blood meal, a series of signals induce the process of vitellogenesis, which is the massive synthesis of yolk proteins in the fat body organ and deposit into the ovaries to support the developing oocyte. We have used a phosphoproteomics analysis of the mosquito fat body to uncover signaling pathways that may play a role in vitellogenesis. We have utilized RNAi to knockdown the gene expression of two key proteins in the hippo/warts signaling pathway. Our findings suggest that the core kinase 'hippo' and transcriptional co-activator 'yorkie' regulate egg development and can be a potential target for mosquito control.

Poster 21:

The effects of acid exposure on *Drosophila* development rate and outcomes

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Drosophila larvae exposed to hydrochloric acid have been observed to have smaller pupae sizes than larvae not exposed to the same acid. While pupation size does not significantly impact adult sizes it does represent a metric for efficiency of development. *Drosophila* larvae exposed to other harmful stimuli have been shown to exhibit a retinoid-regulated “developmental checkpoint” that delays their progression from larvae to pupae. This project will investigate whether larval acid exposure induces delayed development and size changes in pupae by recording pupation rates and characterizing the size differences of *Drosophila* larvae and pupae after acid exposure. The results are expected to provide evidence that Drosophila pupae either speed up or slow down their pupae development after exposure to hydrochloric acid, decreasing size as a morphological response to damage. The results may impact the fundamental understanding of epidermal and neurological responses to harmful stimuli throughout organismal development with applications to medicine, including treatments for chronic pain and autism.

Poster 22:

Effects of Peri-Conception Maternal Immune Activation on Wool Characteristics at Weaning

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Maternal immune activation around the time of conception influences reproductive success and offspring development. Immune challenges including infection can disrupt the maternal environment, potentially affecting fetal growth and long-term production traits. However, the effects of maternal immune activation during distinct stages of follicular development prior to conception on consequent lamb production traits, including wool quality, remain unclear. Therefore, this study evaluated maternal immune challenges during the peri-conception period on wool characteristics in lambs at weaning. Estrus-synchronized ewes received subcutaneous injections of saline (CON), 1.5 µg/kg body weight lipopolysaccharide (LOW), or 3.0 µg/kg body weight lipopolysaccharide (HIGH) on d 5, 10, and 15 of the estrous cycle. These treatments were designed to induce repeated immune challenges during distinct follicular development prior to breeding. Wool samples were collected 60 days of age and analyzed using an Optical Fiber Diameter Analyzer to assess wool quality. Average fiber diameter did not differ among maternal treatment groups at 60 d of age ($P = 0.14$). However, fiber uniformity tended to differ, as lambs from high-dose ewes showed lower standard deviation and coefficient variation of fiber diameter compared to control lambs ($P = 0.06$), with low-dose lambs intermediate. The coefficient of variation of fiber diameter was lower in high-dose lambs than controls ($P = 0.05$).

Poster 23:

Innate immunity in three overwintering sparrow species that differ in migratory status

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Migration is a strenuous activity requiring energetic tradeoffs among physiological traits, potentially including the innate immune system. The innate immune system acts as a nonspecific defense against infectious agents and likely plays a vital role in migratory success as migrating birds face novel pathogens at stopovers and overwintering grounds. We hypothesize that migratory distance impacts innate immune system strength, predicting reduced immune responses in long-distance migrants due to energetic tradeoffs, or alternatively, enhanced immunity for greater pathogen exposure during migration. White-crowned sparrows (*Zonotrichia leucophrys*; long-distance migrants), Brewer's sparrows (*Spizella breweri*; short-distance migrants), and black-throated sparrows (*Amphispiza bilineata*; residents) were captured in Las Cruces, New Mexico during two periods: overwintering (November-February) and pre-departure (March-April) and we collected blood and morphometric data during captures. Collected blood was used in bacterial killing assays (BKA) to measure the strength of the innate immune response. We did not detect statistically significant differences in bacterial killing ability (BKA%) between species (p-value=0.9797). However, we saw significant differences in BKA% between our two time periods (p-value=0.0158) and a decrease in BKA% from overwintering to pre-departure for Brewer's Sparrows (p-value=0.0127). This suggests the innate immune system is dynamically changing over time, perhaps in response to the impending demands of migration. Sampling is ongoing and will give better insight into the comparisons between species and shifts of immunity in our two time periods.

Poster 24:

Dissection of Anillin nuclear localization and function in sea stars

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The contractile ring is a transient assemblage of actin and myosin II filaments that constricts to partition the two daughter cells. A central organizer of contractile ring assembly is Anillin, a multidomain protein that links the contractile ring to the plasma membrane and integrates signals from the mitotic spindle to affect ring assembly and constriction. In many cells, including yeast and humans, Anillin is targeted to the nucleus during interphase and recruited to the cell equator during contractile ring assembly. However, more recent studies suggest that Anillin may have a cytoplasmic function during interphase at cytoskeletal domains under stress or tension. Sea Star Anillin contains a single bipartite Nuclear Localization Signal (NLS) in the N-terminal domain (that also mediates actin-binding) and is targeted to the germinal vesicle in G2-arrested oocytes. To explore the role of Anillin during both interphase and cell division, we designed site-directed mutagenesis primers to mutagenize the two basic clusters in the NLS, both individually and in combination, in fluorescent protein-tagged sea star Anillin. Single and double mutants will be expressed in both mammalian cells and sea star oocytes to determine the minimal alteration required to disrupt nuclear targeting. Control and NLS-mutant will then be followed through oocyte activation and meiotic progression to determine whether mutant Anillin localizes to the actin cytoskeleton during interphase and whether this precocious recruitment interferes with the normal cytoskeletal dynamics that accompany meiotic re-entry.

Poster 25:

Leptin receptors in *Artibeus jamaicensis*; a novel model to study energetic demands of pregnancies

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Pregnancy requires the navigation of precarious energy balances due to competing demands between maternal maintenance and offspring development. Females must be sensitive to energy stores, which is particularly problematic in bats, as they have high metabolism, demanding locomotion, and often low fat-stores. The nuances of the female response to changes in energy levels are poorly known and are less understood in *Artibeus jamaicensis* (Jamaican fruit-eating bat) pregnancies. These bats undergo two annual pregnancies that differ in length by two months: a phenomenon that raises questions about the energetic demands required for gestation and fetal development amongst the differing pregnancies. The placenta is an organ unique to pregnancy and can synthesize leptin, a hormone normally secreted by fat cells. Leptin serves key roles in reproduction, energy regulation, and immune responses by utilizing their receptor to trigger pleiotropic effects. We aim to test the hypothesis that *A. jamaicensis* delay their pregnancies when energy stores are too low to support reproduction. To examine this hypothesis, we addressed 3 questions: (1) Is immunohistochemistry effective for staining Ob-R in bats? (2) Do bats regulate Ob-R differently under the two types of pregnancy? and (3) Are there morphological differences in placentae between the two types of pregnancies? To address these questions, we quantified placental leptin receptors (Ob-R) and compared their expression between the two pregnancy types using immunohistochemistry and brightfield microscopy. Hematoxylin and Eosin-y (H&E) staining was used to distinguish any morphological differences of the placentae. Here we discuss our preliminary findings and outline future directions.

Poster 26:

Identifying Reservoir Hosts of Sin Nombre Virus Via Molecular Barcoding

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Deer mice within the *Peromyscus* genus are major reservoir host of Sin Nombre virus (SNV), the causative agent of Hantavirus Cardiopulmonary Syndrome (HPS) in humans. New Mexico experiences the highest per capita rates of HPS in the United States; a disease associated with a fatality rate of up to 40%. Despite its public health significance, much remains to be understood about the ecology and transmission dynamics of SNV within the context of climate change and wildfire disturbance. As wildfire frequency and intensity continue to increase across New Mexico and the western United States, it is critical to evaluate their effects on SNV transmission dynamics. One major barrier to understanding wildfire impacts on SNV is the difficulty of accurately identifying species within the Peromyscus genus from morphology alone. Additionally, recent taxonomic revisions have split Peromyscus maniculatus into two species, P. maniculatus and Peromyscus sonoriensis. This revision now identifies P. sonoriensis as the primary reservoir host for SNV, making accurate molecular identification essential for proper comprehension of SNV host-virus interactions. The primary objectives of this project were to utilize previously collected RNA from rodent tissue samples originating from sites with documented SNV transmission and varying degrees of wildfire impact for taxonomic identification. Complementary DNA (cDNA) was synthesized and amplified via polymerase chain reaction (PCR) using primers targeting the cytochrome b gene for molecular barcoding. Resulting sequences were compared to published Peromyscus sequences using NCBI BLAST, with ≥98% genetic similarity used to confirm species identity.

Poster 27:

Examining Nociception in *Drosophila* Larva After Acid Damage

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This poster presentation will focus on hyperalgesia (abnormal increase in sensitivity to pain) and hypoalgesia (abnormal decrease in sensitivity to pain) in larvae and how they relate to larvae nociception mechanics. Previous experiments suggest that larvae become hypoalgesic when initially exposed to an acid noxious stimulus, rested, and then exposed once again for a behavior dose. This created the question of if under the same process, but with a different behavior stimulus, would they show the same desensitization? The stimulus my project will be interested in for the behavior stimulus will be thermal stimuli. These experiments might help show how acid and thermal nociception differ. The hypothesis for my experiment is that *Drosophila* larvae will be hypoalgesic when stimulated with a thermal stimulus after an initial exposure to acid.

Poster 28:

Effects of salinity and temperature on predation by the bacterium, FD111, on *Nannochloropsis oceanica*

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Microalgae are one of the most powerful yet overlooked crops for a sustainable world because of their capability to recapture CO_2, provide alternative proteins, and produce renewable biofuels and eco-friendly products. *Nannochloropsis oceanica* is an economically important microalga due to its high nutritional content, rapid growth rate, and adaptability to extensive environmental stress. Like other crops, microalgae are vulnerable to losses from a variety of invaders, including predatory bacteria. Salinity and temperature are key abiotic factors that may shape the interactions between microalgae and bacteria. Therefore, understanding how these environmental factors regulate bacterial predation is crucial for large-scale microalgae farming in changing climates. The objective of this study is to examine how salinity and temperature influence the predation of the newly discovered predatory bacterium, FD111, on P7C12, a field-adapted strain of *N. oceanica*. To track algal growth health, we monitored the metrics of biomass (OD750, chlorophyll fluorescence) and photosynthetic efficiency of P7C12. We counted algal and bacterial cells using flow cytometry and quantified bacterial abundance using qPCR. At lower temperatures (23°C), no crash occurred, whereas crashes happened as the temperature increased (25, 27, 29°C). Although no salinity level completely prevented P7C12 crashes, fluctuations in crash time and severity across salinity gradients (16, 20, 25, and 30 PPT) imply a possible effect of salinity on crash dynamics. These findings could help improve commercial microalgae farming, as salinity and temperature impact bacterial predation, hence facilitating pest management of algal cultivation by figuring out optimal conditions to stabilize or mitigate algal crashes.

Poster 29:

Interplay between ORB2 and Isep (CG46385) in regulating spermatid individualization during *Drosophila melanogaster's* spermatogenesis

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Drosophila spermatogenesis depends on stored cytoplasmic mRNA, as transcription halts in early meiosis, and spermatid elongation and individualization depend largely on post-transcriptional gene regulation. In oocyte and zygote development, the cytoplasmic polyadenylation binding element protein (CPEB) regulates translation by acting as either a translational repressor or an activator, depending on whether it interacts with a deadenylase or a non-canonical Poly(A) polymerase, respectively. Recently, it was shown that the double zinc finger domain of the Drosophila CPEB ortholog ORB2, which is crucial for protein-protein interactions, is necessary for spermatid individualization. A CRISPR-Cas9 mutant in the isep gene, which is predicted to encode a non-canonical polymerase, also shows defects in individualization. We hypothesize that Isep and ORB2 interact to regulate translation and control the individualization stage of spermatogenesis. Using confocal microscopy, we found that ORB2 is co-expressed with Isep. Additionally, we observed that the ORB2 signal is dispersed throughout the axoneme (sperm tail) in isep mutants, whereas in the wild type, most of the signal is restricted to the axonemal tip. Using western blot analysis, we found that ORB2 protein levels were significantly higher in the mutant than in the wild type. From our findings, we conclude that Isep acts as a negative regulator of ORB2 at the translational level and promotes ORB2 protein localization in spermatid cysts.

Poster 30:

Is the formation of extracellular traps in *Biomphalaria glabrata* a defense strategy against Schistosoma mansoni larvae

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Extracellular traps (ETs) were first observed produced by human neutrophils as an innate defense mechanism. Shortly after their discovery, ET formation was documented in invertebrate immune cells (hemocytes) of several species including gastropods, implying this is a conserved ancient defense. ETs are large diffuse structures composed primarily of DNA and antimicrobial proteins that physically immobilize or neutralize invading pathogens for destruction by immune cells. The formation of ETs is a rapid and non-specific innate response, but specific stimuli can act as triggers. *Biomphalaria glabrata* is a snail of medical relevance due to its role as the intermediate host for the trematode parasite Schistosoma mansoni. Modeling previous experiments that induced the formation of ETs, hemocytes from two strains of *B. glabrata* (resistant BS-90 and susceptible BB-02) will be exposed to the larvae of *S. mansoni* and their secreted products to observe the possible formation of extracellular traps. Fluorescent microscopy will be used to visualize the formation of ETs produced by the snails' hemocytes. Our hypothesis is that hemocytes from *B. glabrata* produce ETs in response to *S. mansoni* and that these structures are more prominent in resistant hemocytes compared to susceptible. Quantification of ETs between hemocytes of both resistant and susceptible strains will determine if the formation of ETs is a defense strategy seen primarily in resistant phenotypes. If so, this will be the first time extracellular traps in *Biomphalaria glabrata* in response to *Schistosoma mansoni* will be reported.

Poster 31:

Impacts of early life and adult stress on neural circuits for vocal learning in adult budgerigars

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Early life stress can profoundly shape how individuals respond to stressors in adulthood by altering endocrine function and neural circuits critical for learning and stress regulation. When individuals experience stress, circulating glucocorticoids are released, and corticosterone can bind to both glucocorticoid (GR) and mineralocorticoid (MR) receptors, activating pathways that influence sensitivity to future stressors. GR and MR together can determine how strongly the hypothalamic–pituitary–adrenal (HPA) axis responds to and recovers from stress, making them informative targets for understanding how early experiences may shift both physiology and adult stress reactivity. To investigate how early experiences interact with later-life stress, we conducted a two-phase experiment in which individuals were randomly assigned to control or stress treatments as juveniles, matured to adulthood, and were then reassigned to either control or stress conditions for three weeks, generating four fully crossed treatment groups with mixed sexes. At the end of adult treatments, we collected blood and brains. Data include circulating corticosterone at the time of death and expression of GR and MR receptors within brain regions essential for vocal learning, as well as within the hippocampus, a central component of the HPA axis that modulates negative feedback and helps regulate the stress response. We predict that early life stress will alter GR and MR expression in both hippocampal and vocal learning regions, adult stress will elevate corticosterone and shift receptor profiles, and combined stress exposure will produce the strongest effects. Analyses are ongoing. This work ultimately aims to deepen our understanding of how stress across development influences neuroendocrine function, neural circuits for learning, and the brain's ability to regulate the stress response.