

ASU SCHOOL OF LIFE SCIENCES

**24<sup>th</sup>** annual

UNDERGRADUATE

**RESEARCH**

POSTER SYMPOSIUM



Keynote address  
Nancy Gonzales, PhD



FRIDAY, **MARCH 17, 2017** | 2-5 P.M.

POSTER PRESENTATIONS | 3-5 P.M.

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*School of Life Sciences is an academic unit of  
the College of Liberal Arts and Sciences*

**ASU** School of  
**Life Sciences**  
Arizona State University

School of Life Sciences  
**24th Annual Undergraduate  
Research Poster Symposium  
March 17, 2017**

## **AGENDA**

2 – 3 p.m. Keynote Address – Memorial Union Pima Room (MU 230)

Welcome

Kevin McGraw, PhD  
Professor, School of Life Sciences  
Director, SOLUR Program

Cheryl Conrad, PhD  
Professor, Department of Psychology

Keynote Address

“A Recipe to Reduce Health Disparities:  
Grit, Family Engagement, and Educational Equity”

Nancy Gonzales, PhD  
Department of Psychology

An Invitation from Sigma Xi, The Scientific Research Society  
Karen Sweazea, PhD, ASU Chapter President

3 – 5 p.m. Student Poster Presentations & Refreshments  
Memorial Union Ventana A/B/C (MU 241 A, B, and C)

3 – 3:30 p.m. Even Number Posters

3:30 – 4 p.m. Odd Number Posters

4 – 4:30 p.m. Even Number Posters

4:30 – 5 p.m. Odd Number Posters



# ACKNOWLEDGEMENTS

Undergraduate research programs and this poster symposium in particular, are supported through the generosity and contributions of many. Monetary support for our programs comes from the School of Life Sciences, the College of Liberal Arts and Sciences, the Institute for Social Science Research, and Knowledge Enterprise Development at Arizona State University, the National Institute of General Medical Science of the National Institutes of Health, and research grants awarded to individual faculty members from a variety of institutions and agencies. External research partners, including the Translational Genomics Research Institute, Barrow Neurological Institute, HonorHealth, Mayo Clinic Arizona, USDA Arid Lands Research Laboratory, Phoenix Zoo, Desert Botanical Gardens, and the University of Arizona College of Medicine-Phoenix, and their resident scientists have generously opened their doors and provided stimulating research experiences for a number of our students. Within the School of Life Sciences, the VisLab, the Facilities Office, the Business Office, the Undergraduate Programs Office, the Undergraduate Advising Office, and the Administrative Office have provided essential logistic, administrative, and other support services. Within the College of Liberal Arts and Sciences, the Research and Graduate Initiatives team and the Events team have been instrumental in the strategic planning and collaborative effort that is required to manage such an event across disciplines. We are grateful for the support and effort of Dean of the College of Liberal Arts and Sciences, Patrick Kenney, Assistant Vice President of Research Development in OKED, Cheryl Conrad, and Professor and Associate Dean of Faculty, Nancy Gonzales. Finally, we especially acknowledge the faculty mentors, both on- and off-campus. Without their outstanding contributions to the research experiences and intellectual growth of our students, the programs would not exist. For all this support, we are very, very grateful.

Kevin McGraw, PhD  
Professor, School of Life Sciences  
Director, School of Life Sciences Undergraduate Research (SOLUR) Program

Stuart Newfeld, PhD  
Professor, School of Life Sciences  
Director, Initiative for Maximizing Student Development (IMSD) Program

Michael Angilletta, Jr., PhD  
Professor, School of Life Sciences  
Associate Director, Undergraduate Programs, School of Life Sciences

Bertram Jacobs, PhD  
Director and Professor, School of Life Sciences

Madhavi Chakravadhanula, PhD  
Project Coordinator, IMSD

Kenro Kusumi, PhD  
Associate Dean of Research & Graduate Initiatives  
Professor, School of Life Sciences

## ABSTRACTS

(Alphabetical by Presenter's Name)

### 56 Inhibition of PKR activation by vaccinia virus' E3 protein

Alattar, Hamed; Foster, Clayton; Cotsmire, Samantha; Pearcy, Matthew J.; and Jacobs, Bertram L.  
*School of Life Sciences, Arizona State University, Tempe AZ*

Vaccinia virus (VACV) is a cytoplasmic, double-stranded DNA orthopoxvirus. Unlike mammalian cells, vaccinia virus produces double-stranded RNA (dsRNA) during its viral life cycle. The protein kinase R (PKR) is one of the principal host defense mechanisms against orthopoxvirus infection. PKR can bind double-stranded RNA and phosphorylate eukaryotic translation initiation factor, eIF2 $\alpha$ , shutting down protein synthesis and halting the viral life cycle. To combat host defenses, vaccinia virus encodes E3, a potent inhibitor of the cellular anti-viral eIF2 $\alpha$  kinase, PKR. The E3 protein contains a C-terminal dsRNA-binding motif that sequesters dsRNA and inhibits PKR activation. We demonstrate that E3 also interacts with PKR by co-immunoprecipitation. This interaction is independent of the presence of dsRNA and dsRNA-binding by E3 indicating that the interaction is not due to dsRNA-bridging. PKR interaction mapped to a region within the dsRNA-binding domain of E3 and overlapped with sequences in the C-terminus of this domain that are necessary for binding to dsRNA. Point mutants of E3 were generated and screened for PKR inhibition and direct interaction. Analysis of these mutants demonstrates that dsRNA-binding but not PKR interaction plays a critical role in the broad host range and of VACV. Nonetheless, full inhibition of PKR in cells in culture requires both dsRNA-binding and PKR interaction. Because E3 is highly conserved among orthopoxviruses, understanding the mechanisms that E3 uses to inhibit PKR can give insight into host range pathogenesis of dsRNA producing viruses.

### 32 Effects of biogeomorphic and geomorphic variation on transient storage in Sycamore Creek

Armijo, Nicholas; Handler, Amalia; and Grimm, Nancy  
*School of Life Sciences, Arizona State University, Tempe, AZ*

Stream transient storage occurs where flow paths have a significantly lower velocity relative to the main channel. Transient storage plays an important role in stream nutrient cycling and retention because it allows for more reactions to occur along any given reach. Previous studies have shown that biogeomorphic and geomorphic variation along stream channels can alter transient storage exchange, but the combined effect of the relationship varies. We examined how vegetation and geomorphic factors affect transient storage in Sycamore Creek, Maricopa County, Arizona. We conducted reach surveys of vegetation cover, flow type, substrate type, sinuosity, and cross-sectional area. We performed a total of four hydrologic tracer (sodium chloride) injections in three reaches of Sycamore Creek. We monitored the tracer movement with conductivity sensors at two locations downstream of the injection point. Based on the patterns of conductivity over time, we used the one-dimensional transport model with inflow and storage (OTIS) to derive transient storage zone size and exchange rate. We found large substrate particle size and high sinuosity were associated with a large transient zone area and exchange coefficient. Presence of islands in the stream channel was associated with higher transient storage exchange. Transient storage zone size and exchange rate were not associated with stream discharge, main channel cross sectional area, or vegetation presence. Our data indicates that geomorphic variables are an important control on stream transient storage zone size and exchange rate. Future studies will include more detailed vegetation surveys and target stream reaches with variable sinuosity and substrate types.

## 52 Socio-political Effects of Military Sexual Trauma on Veteran Female PTSD Victims

Bartee, Dante A.

*Department of Justice Studies, Arizona State University, Tempe AZ*

Post-traumatic stress disorder (PTSD) in the military has been thoroughly researched for male combatants. However, there is very little research on the effects of PTSD on female veterans, particularly when dealing with military sexual trauma (MST). This project researches the socio-political factors involved in MST in female victims and the resulting PTSD. The research that has been done has primarily focused on psychological risk factors such as childhood abuse and psychiatric family history. However, this research focuses on factors such as socio-economic status, education and military rank and their effects on the rates of MST and resulting PTSD. And as there is an ever-increasing number of women entering the military force, MST and the PTSD that often accompanies it are an ever-growing problem. With this research, we hope to use a different lens in combating MST and find more comprehensive solutions to PTSD because of MST.

## 50 Cell extrinsic regulation of OLIG2-mediated glioma invasion

Belmont, Laura<sup>1</sup>; Singh, Shiv K.<sup>1</sup>; Cascio, Costanza Lo<sup>1</sup>; Szeto, Emily<sup>1</sup>; Eschbacher, Jennifer<sup>2</sup>;  
Sanai, Nader<sup>2,3</sup>; and Mehta, Shwetal<sup>1</sup>

*<sup>1</sup>Barrow Brain Tumor Research Center, Barrow Neurological Institute, Phoenix, AZ; <sup>2</sup>Department of Pathology, St. Joseph's Hospital and Medical Center; <sup>3</sup>Department of Neurosurgical Oncology, Barrow Neurological Institute Phoenix, AZ*

Glioblastoma multiforme (GBM) is the most aggressive, infiltrative, and lethal brain tumor in adults with high mortality rates. Despite major research efforts in the diagnosis and treatment of GBM, the overall survival is 14 months. The poor survival is attributed to the presence of highly invasive cells which are resistant to conventional therapies. Hence, the tumors almost always recur, and there is no standard-of-care for recurrent GBM. In glioblastoma, it has been proposed that migrating tumor cells undergo a switch from proliferation to invasion. However, the molecular mechanism involved in the regulation of this switch from proliferation to invasion/migration in GBM is poorly understood. We have recently shown a novel role for lineage-specific transcription factor, OLIG2 in promoting glioma invasion. We found that glioma cells expressing low levels of phosphorylated OLIG2 (pOLIG2<sup>low</sup>) are highly invasive while those expressing high levels of phosphorylated OLIG2 (pOLIG2<sup>high</sup>) are less invasive but proliferate at higher rate. In addition, modulating the phosphorylation status of OLIG2 was sufficient to switch the cellular phenotype from invasive to proliferative. Here, we demonstrate how cell intrinsic factors determine OLIG2 phosphorylation levels and cell extrinsic factors can trigger dephosphorylation of OLIG2 and thus invasion. We have employed patient-derived xenograft models and short-term glioma stem-like cultures to address how signals from the surrounding tumor cells and the microenvironment can induce a switch in glioma cells from proliferation to invasion.

## 68 An Evaluation of the Cognitive Effects of Clinically Used Combination Hormone Therapy

Berns-Leone, Claire; Prakapenka, Alesia; Hiroi, Ryoko; Pena, Veronica; Northup-Smith, Steven; Melikian, Ryan; Patel, Shruti; Ladwig, Ducileia; Croft, Corissa; and Bimonte-Nelson, Heather  
*Department of Psychology, Arizona State University, Tempe, AZ*

Estradiol (E2) and Levonorgestrel (Levo) are two hormones commonly used in hormone therapy (HT) to decrease symptoms associated with menopause. Both of these hormones have been shown to have beneficial effects on cognition when given alone in a rodent model of menopause. However, it is unknown whether these hormones, when taken in combination, are beneficial, null, or harmful to cognition. This is a critically important question given that these hormones are often given in combination. This thesis is composed of two studies examining the cognitive effects of E2 and Levo using a rat model of surgical menopause. Study 1 assessed how the dose of E2 treatment in rats impacted cognitive performance, and found that low dose E2 enhanced working memory performance. Next, based on the results from Study 1, Study 2 used low dose E2 in combination with different doses of Levo to examine the cognitive effects of several E2 to Levo ratio combinations. The results from Study 2 demonstrated that the combination of low dose E2 with high dose Levo at a 1:2 ratio impaired cognition, and that the ratio currently used in HT, 3:1, may also negatively impact cognition. Indeed, there was a dose response effect indicating that working and reference memory performance was incrementally impaired as Levo dose increased. The findings in this thesis suggest that the E2 plus Levo combination is likely not neutral for cognitive function, and prompts further research in preclinical models as well as in menopausal women, in order to optimize HT.

## 61 Phenotypic Analysis of *P. aeruginosa* Isolates from Cystic Fibrosis Lung Infections

Bhebhe, Charity; Ellison, Darrin; Misra, Leanne; Montes, Seth; and Bean, Heather D.  
*School of Life Sciences, Arizona State University, Tempe AZ*

Cystic fibrosis (CF) is a genetic disease that affects 70,000 people worldwide, with 30,000 of them living in the US. The defect creates thick, sticky mucus that clogs airways and inhibits the ability of the lungs to clear out microorganisms that are trapped from the environment. This makes persons with CF highly susceptible to lung infections, which causes inflammation and results in damage to the lungs, eventually leading to death. *Pseudomonas aeruginosa* is a major cause of infection in the CF lung, with 80% of adults becoming chronically infected with the pathogen. Once the bacteria establish themselves in the lungs, they develop mechanisms that enhance their survival in the host and are correlated with lung function declines, including conversion to mucoidy, antibiotic resistance, and quorum sensing deficiencies.

The aim of our project is to phenotype and genotype *P. aeruginosa* lung isolates to identify new biomarkers for chronic lung infections. The phenotypes we are investigating are motility (swimming, swarming, and twitching), exoproduct production (proteases, alginate, and quorum sensing molecules), and antibiotic resistance. The data presented below represents the phenotypes of 32 strains of *P. aeruginosa* that were isolated from the sputum of CF patients. These data will be correlated to isolates' metabolomes to identify biomarkers of *P. aeruginosa* phenotypes that will lead to the development of improved medical devices for tracking chronic lung infections in CF patients.

## 60 Strong and Weak Indicators of Foreign Support

Briggs, Noah

*Department of Political Science, Arizona State University, Tempe, AZ*

When states support foreign insurgent groups, they change everything about the existing conflict. From Salehyan, et. al., 2011:

“Civil wars with outside involvement typically last longer, cause more fatalities, and are more difficult to resolve through negotiations. They introduce new actors into the conflict with agendas of their own, changing the bargaining dynamic to include both state and nonstate actors. Understanding why some groups receive foreign support is therefore critical for understanding how such conflicts unfold, and ultimately, how they are resolved.”

In order to better understand civil conflict, we need to understand what insurgent groups receive support from foreign states, why that support is given and accepted, and under what circumstances foreign states support insurgent groups. The research presented and its conclusions further refines our knowledge on the subject. I assume there are three sorts of ties that are used as indicators by foreign states and insurgent groups: political, ethnic or religious. My hypothesis is that religious or political ties more consistently lead to foreign support than do ethnic ties. While ethnic ties often denote common language and customs which may make communicating easier, both potential supporter states and insurgent groups place a premium on autonomy. Autonomy is maximized when both agents share the same goal. Ideology is amore definitive indicator of shared goals, so religious or political ties should more consistently lead to foreign support than ethnic ties. I explore this hypothesis using a seven step probability distribution.

## 34 Standard mapping protocols misestimate sex-linked gene expression

Brotman, Sarah M.<sup>1</sup>; Olney, Kimberly C.<sup>1</sup>; and Wilson Sayres, Melissa<sup>1,2,3</sup>

<sup>1</sup>*School of Life Sciences, Arizona State University, Tempe, AZ*; <sup>2</sup>*Center of Evolution and Medicine, Arizona State University, Tempe, AZ*; <sup>3</sup>*The Biodesign Institute, Arizona State University, Tempe, AZ*

There are several challenges to accurately inferring levels of transcription using RNA-sequencing (RNAseq) data, including detecting and correcting for reference genome alignment bias. However, one potential confounder of RNAseq analysis can result when applying a standardized pipeline to samples of different sexes in species with chromosomal sex determination. Because of the homology between the human X and Y chromosome, we expect that mis-mapping will routinely occur between these two chromosomes, artificially affecting estimates of sex-linked gene transcription. For this reason we tested alternative alignment scenarios on RNAseq samples from the brains of 5 genetic female and 5 genetic males to assess how inferences of differential gene expression patterns change depending on the reference genome. We first applied a standard alignment protocol where we aligned all individuals to the entire human reference genome, and computed differential expression between the set of male and female samples. Then, we realigned the female samples (46,XX) to the human reference genome with the Y chromosome removed, and the male samples (46,XY) to the human reference genome (including the Y chromosome), but with the pseudoautosomal regions of the Y chromosome masked out. The new strategy called 33 additional genes as being differentially expressed between the two sexes when the genetic female samples were mapped to the reference without the Y chromosome and the genetic males were mapped to the reference without the Y PARs. This research is providing essential insight into correcting genome alignment bias that can be used in future studies.

## 49 Fabrication of incubation chambers for long-term observations of cell development and behaviors under local electrical stimuli

Brown, Sierra-Rose<sup>1</sup>; Wang, Yuan<sup>2</sup>; Jiao, Xiangbing<sup>2</sup>; Li, Houpu<sup>2</sup>; and Qing, Quan<sup>2,3</sup>

<sup>1</sup>*School of Molecular Sciences, Arizona State University, Tempe, AZ;* <sup>2</sup>*Department of Physics, Arizona State University, Tempe, AZ;* <sup>3</sup>*The Biodesign Institute, Arizona State University, Tempe, AZ*

The growth, migration, and interaction between cells guided by electrical fields and surface topology gives important insight of the coupling between biochemical, electrical, and mechanical signaling pathways that reveal potential biomedical methods for accelerating wound-healing, nerve injury rehabilitation, and inhibition of metastasis of cancer cells. In order to precisely deliver electric stimuli to the cells and observe their real-time responses, here we use microelectrodes, surface topology control, and precise environmental control, allowing long-term modulation and imaging observations. To accomplish this, we went through several iterations of 3D modeling, 3D printing, and computer controlled milling machine to produce a prototype chamber composed of four major components: a well, a lid, equidistant chamber extensions, and gradual dorsal gradient. Microelectrode arrays, and micro-scale and nano-scale topological features were fabricated on a transparent cover slip and used as the substrate to grow the cells internally within the chamber. A customized external function generator is used to deliver programmed electric stimuli to the electrodes, as the cells are tracked via epi-fluorescent or total internal reflection fluorescent (TIRF) imaging. The device was successfully tested in two separate experiments, including the polarized movement of human epithelial cells (HaCat) under electric field stimulation, and the oriented actin fiber polymerization in dictyostelium cells on oriented microscale arrays and stripes. This new platform allows us to initiate systematic studies of the development and behaviors of variety of cells with precise delivery of local stimuli and modulations.

## 41 Plastid Genome Evolution in Cactaceae

Cassetta, Eric A.<sup>1</sup>; Sanderson, Michel J.<sup>2</sup>; and Wojciechowski, Martin F.<sup>1</sup>

<sup>1</sup>*School of Life Sciences, Arizona State University, Tempe, AZ;* <sup>2</sup>*Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ*

The Cactaceae, a diverse family of angiosperms that evolved about ~30 million years ago, is the most evolutionarily successful adaptive radiation of succulent plants distributed in arid and semi-arid regions of the New World. Cacti are remarkable for the evolution of extreme succulence in most members, diversity of growth forms, as model systems for ecological studies, and possession of a crassulacean acid metabolism (CAM) mode of photosynthesis. We found the plastid genome of the saguaro, *Carnegieia gigantea*, has been reduced in size by the loss of several genes necessary for photosynthesis (ndh genes) and one copy of the large inverted repeat (IR) region, making it the smallest plastid genome of any known obligate photosynthetic angiosperm. Plastid genomes from three species of columnar cacti closely related to saguaro and found in the Sonoran Desert (“senita”, “cardón”, “organ pipe”) together with genomes from species of earlier-diverging lineages (*Opuntia*, *Pereskia*) were assembled and compared to that of saguaro. Annotation of the plastid genomes of *Lophocereus schottii*, *Pachycereus pringlei*, and *Stenocereus thurberi* are similar in size and gene content/structure to that of saguaro, and like saguaro, their plastid genomes lack one copy of the IR and all plastid-encoded ndh genes, while the genomes of the *Opuntia* and *Pereskia* species also exhibit the IR loss, but contains most/all of the plastid ndh genes. Work is in progress to characterize these architectural differences – gene losses and other minor rearrangements – more fully to determine the pattern(s) of plastid genome evolution more broadly among cacti.

## 42 Effects of Land Use on Denitrification Potential in Oak Creek

Caulkins, Corey; Palta, Monica M.; and Grimm, Nancy B.  
*School of Life Sciences, Arizona State University, Tempe, AZ*

Denitrification is a microbial process in which nitrate ( $\text{NO}_3^-$ ) is reduced into dinitrogen gas ( $\text{N}_2$ ). Previous work suggests that areas with high concentrations of ambient  $\text{NO}_3^-$  are likely to have higher denitrification rates than areas that are nitrogen limited. Our experiment seeks to address how potential denitrification rates in Oak Creek (near Sedona, AZ) are influenced by a land use gradient. We hypothesize that  $\text{NO}_3^-$  is an important limiting factor to denitrifiers in Oak Creek, and differences in  $\text{NO}_3^-$  inputs between land-use types result in differing rates of denitrification, with higher  $\text{NO}_3^-$  concentrations facilitating higher denitrification rates. Land use within the study area transitions from relatively undeveloped land north of Sedona, to urbanized land in downtown Sedona, to agriculture (primarily vineyards) in Cornville. Of the three land use categories, we expect that agricultural land generates the highest  $\text{NO}_3^-$  inputs into Oak Creek, and that these sections of the creek therefore have the highest potential denitrification rates. We expect that undeveloped land will show the opposite trend. In order to test our proposed relationship, we established two study sites in each land-use zone, collected sediment and water samples, and measured additional properties. We then used the sediments to perform a denitrification enzyme assay (DEA) in the lab, creating low-oxygen microcosms for each sediment type. Gas samples were taken from each microcosm at four different time points, capturing the change in headspace gas composition over time. Following sample analysis, we plan to assess significant drivers of potential denitrification in Oak Creek.

## 15 Simulating conformational transitions of the transmembrane symporter Mhp1

Colburn, T.; Seyler, S.; and Beckstein, O.  
*Department of Physics, Arizona State University*

The function of many proteins depends on large-scale conformational changes. Because these conformational transitions are rare events, it is very difficult to investigate them with equilibrium molecular dynamics (MD) simulations, which have otherwise become an important tool to study the molecular mechanisms of macromolecular systems. A variety of techniques — such as the Dynamic IMportance Sampling (DIMS) method and various elastic network-based approaches — have been developed to overcome timescale limitations and produce physically plausible trajectories between putative metastable states. We sought to characterize a number of different path generating and sampling methods, including DIMS with and without an implicit membrane model, by producing multidirectional trajectories of the transmembrane nucleobase symporter Mhp1. All trajectories were compared to one another using Root-Mean-Square Distances (RMSDs), structural order-parameters and Path Similarity Analysis (PSA). In particular, PSA showed that while trajectory generating methods were broadly similar, paths from each method were also clearly distinguishable.

## 48 The Lepidoptera of North America Network (LepNet)

Cooper, Dylan; Hays, Brennan; Takimoto, Brian; Nguyen, Justin; Nguyen, John; Martinez, Jose; Lee, Sangmi; and Franz, Nico  
*Hasbrouck Insect Collection, School of Life Sciences, Arizona State University*

The Hasbrouck Insect Collection (ASUHIC) is one of 27 collections currently contributing to the NSF funded "Lepidoptera of North America Network" (LepNet) project (<http://www.lep-net.org/>). LepNet is a collaborative on-line data portal which hosts digitized Lepidoptera specimen records. The insect order Lepidoptera, which includes the butterflies and moths, is one of the largest and most ecologically significant clades of plant-feeding and pollinating insect. ASUHIC and other LepNet collaborators are working to digitize nearly 1.7 million specimen records representing the 14,300+ species known from North America in order to facilitate remote identifications as well as systematic and ecological research. As part of this initiative, we are currently digitizing and georeferencing the nearly 10,863 specimens, and providing high-quality images of each species through the LepNet portal. The dynamically published data are available on-line at <http://symbiota4.acis.ufl.edu/scan/lepnet/portal/index.php>.

## 51 The role of specific serotonergic circuitry on psychostimulant self-administration

Cotter, Austin; Garcia, Raul; Ennis, Katie; and Neisewander, Janet L.  
*School of Life Sciences, Arizona State University, Tempe, AZ,*

Rodent drug self-administration provides a model to study addictive properties of psychostimulants. Our lab has found that a serotonin<sub>1B</sub> receptor (5HT<sub>1B</sub>R) agonist CP 94,253 (CP) attenuates these properties. While studies utilizing selective ligands for 5HT<sub>1B</sub>R have shown the 5HT<sub>1B</sub>R as responsible for these changes, the circuitry which CP works on to attenuate reinforcement remains unknown. We hypothesize that selectively targeting dorsal raphe nucleus (DRN) projections to the ventral tegmental area (VTA) will produce effects like CP. Designer Receptors Exclusively Activated by Designer Drugs (DREADDs) will be used to test behavioral effects of silencing 5-HT<sub>1B</sub>R-expressing serotonin neuronal projections (selected with a SERT promoter) from the DRN to the VTA. A viral-mediated inhibitory DREADD injected into the DRN (where serotonin is synthesized) should be expressed at axon terminals in the VTA (where 5HT<sub>1B</sub>R are found). Clozapine-N-oxide (CNO), the DREADDs agonist with no endogenous effects, will be injected into the VTA before self-administration tests so behavioral changes from localized inhibition of 5HT<sub>1B</sub>R can be observed. Preliminary research has resulted in an optimized stereotaxic surgery allowing for the concurrent implementation of cannulae into the DRN and VTA of rats. Injection of retrobeads through the VTA cannulae has allowed us to verify that projections from the DRN reach the VTA, and immunohistochemistry on these brains has allowed us to verify that the retrobeads travel back up the serotonergic projections. We will need to test that a CNO injection into the VTA inhibits neurons expressing the DREADD and run rodent cohorts through drug self-administration.

## 46 Development of novel model organisms for cancer research

Culbertson, Michelle<sup>1,2</sup>; Fortunato, Angelo<sup>2</sup>; Martinez, Ruby<sup>1,3</sup>; Bolbolan, Saba<sup>1,3</sup>; Colorafi, Abbey<sup>3,4</sup>; and Maley, Carlo<sup>3,4</sup>

<sup>1</sup>*School of Molecular Sciences, Arizona State University, Tempe, AZ*; <sup>2</sup>*Biodesign Institute, Arizona State University, Tempe, AZ*; <sup>3</sup>*Biodesign Institute, Arizona State University, Tempe, AZ*; <sup>4</sup>*School of Life Sciences, Arizona State University, Tempe, AZ*

The evolution of multicellular organisms required cellular cooperation in order to facilitate tissue specialization and differentiation. However, cancer disrupts this cooperation and changes how normally clonal cells interact. This project seeks to understand this process by investigating potential cancer growth and progression in simple model organisms. The organisms chosen are those in which no cancer-like phenomena have previously been reported, to determine if they have molecular mechanisms preventing cancer development. The organisms include *Trichoplax adhaerans*, the only known species of the Placozoa phylum, *Macrostomum lignano*, a species of non-parasitic flatworms, and *Tethya wilhelma*, a demosponge. These organisms contain only a few cell types and a relatively simple morphology which make them ideal models for investigating mutagenesis and contain numerous well-conserved genes often involved in human cancers. We have developed protocols for culture and have optimized mutagenesis methods, using chemical and physical agents. Following mutagenesis, the animals are examined for cellular and morphological changes, visualized by phase contrast, differential interference contrast microscopy, and differential staining. New phenotypes have been observed and will be further studied with histological and molecular techniques, including genome sequencing. These findings will either show that cancer can develop in the earliest branches of animals, or that there are cancer resistance mechanisms in those animals. They may also illuminate how cancer develops from mutated cells and disrupts multicellular collaboration, and potentially identify molecular pathways involved in DNA repair and cancer prevention.

## 64 Investigating the relationship between CA3 dendritic restructuring and CA1 dendritic complexity

Daas, Eshaan J.; Ortiz, J. Bryce; Flegenheimer, Aaron; Le, Brittany; and Conrad, Cheryl D.  
*Behavioral Neuroscience and Department of Psychology Arizona State University, Tempe, AZ*

Chronic restraint stress leads to apical dendritic retraction in CA3 pyramidal neurons. When chronic stress ends, a post-stress recovery period results in an enhancement in dendritic complexity. We investigated the relationship between CA3 and CA1 pyramidal neurons to determine whether dendritic restructuring in CA3 neurons leads to changes in the dendritic complexity of CA1 neurons. Adult male Sprague-Dawley rats were restrained (wire mesh, 6h/d/21d) and brains were removed soon after restraint ended (Str-Imm) or after a 21d post-stress recovery period (Str-Rec). In addition, BDNF downregulation targeting the CA3 region prevents enhancement in dendritic complexity following recovery in chronically stressed rats, providing robust conditions to investigate the CA3-CA1 relationship. Consequently, rats were infused into the CA3 with either an AAV vector with a coding sequence against BDNF (shRNA) or a sequence with no known mRNA complements (Scr). Apical and basal dendritic complexity of CA3 and CA1 was quantified by counting total dendritic bifurcations and dendritic intersections using the Sholl analysis (20  $\mu$ m distances from soma). Apical CA3 dendritic retraction was found in Str-Imm-Scr and Str-Rec-shRNA. For the CA1, gross dendritic bifurcation differences were not detected, but Sholl analysis revealed regionally-enhanced dendritic complexity that varied by distance from the soma at distal (Str-Imm-Scr) and medial (Str-Rec-Scr) apical dendrites and proximal basal dendrites (Str-Rec-shRNA). Moreover, a correlation of all groups revealed a significant relationship between CA3 apical dendritic complexity and CA1 basal dendritic complexity. The results demonstrate that chronic stress-induced CA3 apical dendritic retraction may relate to region-specific changes in CA1 dendritic complexity.

## 2 Measuring Male Mutation Bias in *Drosophila*

Daly, Samantha M.<sup>1</sup>; Narang, Pooja<sup>1</sup>; Amidan, Ashley<sup>1</sup>; and Wilson Sayres, Melissa A.<sup>2</sup>

<sup>1</sup>*School of Life Sciences, Arizona State University;* <sup>2</sup>*Center for Evolution and Medicine, The Biodesign Institute, Arizona State University*

Male gametes, which undergo more cell divisions than female gametes, should similarly accumulate and pass on more mutations than female gametes, creating a male-bias in the observed mutation rate. This “male mutation bias” has been observed across mammals and in birds. Our project focuses on identifying whether male mutation bias also exists in insects and if it does, whether it varies in magnitude between species. We analyzed the genomes from 12 *Drosophila* species and three outgroup species across eight genomic subsets. Because some species have larger X-chromosomes, due to chromosomal fusions, we conducted analysis both including these species and fused regions, and excluding them. We also analyzed several regions of the genome; some known to be directly affected by natural selection and others expected to experience lower levels of selection, more representative of the neutral mutation rate. For each dataset we computed X/A substitution rate ratios and estimated male mutation bias (alpha). Results show that some *Drosophila* species exhibit patterns of substitution on the X and autosomes consistent with male mutation bias while others do not, giving no evidence for strong male mutation bias across *Drosophila*.

## 37 N-Acetylcysteine inhibits cue-induced nicotine seeking and relapse-associated rapid, synaptic plasticity

Del Franco, Armani<sup>1,2</sup>; Powell, Gregory<sup>1,2</sup>; Kupchik, Yonatan<sup>3</sup>; Spencer, Sade<sup>4</sup>; Garcia-Keller, Constanza<sup>4</sup>; Stankeviciute, Neringa<sup>4</sup>; Schwartz, Danielle<sup>4</sup>; Goenaga, Julianna<sup>1</sup>; and Gipson, Cassandra D.<sup>1</sup>

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Cigarette smoking is a leading cause of preventable death, and addiction to nicotine produces long-lasting, stable changes in brain synaptic physiology that possibly contribute to the vulnerability to relapse. Compounds targeting the dysregulation of glutamatergic signaling in promoting smoking cessation are not as well studied as those of cocaine, and relapse rates remain high. Cues associated with nicotine can precipitate nicotine-seeking behavior, and recently we showed that cue-induced nicotine seeking is associated with rapid, transient synaptic plasticity in the nucleus accumbens core (NAcore). It was unknown, however, if N-Acetylcysteine (NAC), an antioxidant and cystine prodrug that has shown promise as a pharmacotherapy in the treatment of various mental health disorders, could restore nicotine-induced alterations in glutamatergic signaling and synaptic plasticity thought to underlie relapse vulnerability. When NAC was administered (100 mg/kg, i.p., across five sessions) during extinction from nicotine self-administration, there was a significant reduction in cue-induced nicotine seeking using a preclinical model of relapse (reinstatement) after 15 min. Additionally, NAC inhibited the rapid increase in NAcore AMPA/NMDA ratio and increase in NMDA current decay. As withdrawal from nicotine self-administration has been associated with a decrease in NAcore expression of glial glutamate transporter (GLT-1), we examined the ability of a lower dose of NAC (30 mg/kg) to restore sodium-dependent glutamate uptake as well as expression of GLT-1 protein. Decreased levels of GLT-1 expression were not restored at a 30 mg/kg NAC dose, nor were differences in spine head diameter observed. Dose dependent impacts on reinstatement were also observed.

## 24 Evading resistance: measuring melanoma's adaptation rate in different drug environments to identify the best course of treatment

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The development of BRAF and MEK inhibitors has revolutionized treatment for patients with BRAF-mutant melanoma. Yet, despite improvements in survival conferred by these therapeutics, the majority of patients relapse with drug-resistant disease. Studies have identified mutations that drive resistance to these targeted agents, but surprisingly little is known about the rate at which resistance develops. There is evidence that resistance arises from pre-existing clones rather than from *de novo* mutations, but a need remains for understanding how different drugs affect the fitness of clones within a tumor population and promote or delay the emergence of resistance. To this end, we have developed a novel assay that quantifies the *in vitro* rate of adaptation by analyzing the progressive change in sensitivity of a melanoma cell line to different treatments. Cells derived from a shared parental population are split into subpopulations and treated continuously with drug or vehicle. Divergence from the parental drug sensitivity is analyzed through serial drug-dose-response curves. Our assay considers cell heterogeneity, impact of starting population size, and clinically-relevant treatment methods. To test feasibility, we performed a proof-of-theory for the MEK inhibitor E6201 in the BRAF V600E-mutant melanoma cell line A375. The data shows divergence from parental sensitivity as early as 27 days. We were able to quantify this rate of divergence, and we equate this value to rate of adaptation. We conclude that our system design was successful and anticipate that with future developments, our assay will prove helpful in identifying treatment options that circumvent or delay resistance.

## 7 Expression of recombinant Zika virus-like particles in *Nicotiana benthamiana*

Di Palma, Michelle; Naji-Talakar, Siavosh; Mor, Tsafir; Mason, Hugh; Damos, Andrew; and Meador, Lydia

Zika virus is a member of Flaviviridae family of RNA viruses composed of a single stranded positive sense RNA genome. Zika virus particles contain a lipid bilayer, one genome RNA and three distinct viral proteins: capsid (C), envelope (E), pre-membrane (prM) cleaved by furin resulting to membrane (M). Development of virus-like particles (VLPs) in plant expression hosts such as *Nicotiana benthamiana* will allow production of vaccine candidates at substantially less cost and time due to the ease of manipulating plant vectors. The Bean Yellow Dwarf virus plant vector constructs allow expression of single proteins or co-expression of multiple proteins within *Nicotiana benthamiana* utilizing *Agrobacterium tumefaciens* infiltration. Initial confirmation of single expression of E, M and prM will verify the ability for *Nicotiana benthamiana* to correctly produce and post-translationally modify each protein. The prM protein is cleaved by furin to express M; this step may have a role in proper protein formation of VLPs and excluding prM may hinder the expression or function of VLPs. The M protein is very small and detection methods other than western blot may need to be implemented to elucidate the protein. Acid precipitation may be used to remove Rubisco background noise which will partially denature and precipitate the proteins of interest requiring further investigation on the stability of all proteins under acidic conditions. Successful co-expression of the Zika E, M and prM may lead to viable expression of VLPs allowing for the production of transgenic plants to further progress vaccine candidates.

## 20 **The survey matters: instructors using different surveys to measure acceptance of evolution may be reaching different conclusions**

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Instructors who teach evolution often find it useful to gain formative feedback on whether their students accept evolution. However, a review of the literature shows more than 40 unique surveys used to poll students on their attitudes towards evolution and past essays from leaders in the field have implied that these different survey tools are not equivalent, but thus far these claims have not been tested. We surveyed 1200 college students on their acceptance of evolution using three different surveys from the research literature to determine whether they will lead to relatively equivalent results in a regression. Additionally, we surveyed students on their prior biology background, socioeconomic status, race, and religiosity. We ran three different regression analyses using the three surveys of acceptance of evolution as our dependent variable but kept all independent variables constant in each regression. We found that these different survey measures produced very different results. In one model, the relationship between race and acceptance of evolution was mediated by religiosity, while in the others it was not. Also, the strength of the relationships of all variables to acceptance of evolution was different across all regressions. If researchers and teachers are using different surveys, they may get inconsistent results. These data indicate a need for a consensus tool in evolution education to measure acceptance of evolution both for research conclusions and formative feedback for teachers who would like to gain information about their students' attitudes towards evolution.

## 58 **Monitoring the Environmental Conditions Present during Incidences of Narrow-headed Gartersnake Activity during Brumation**

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Narrow-headed gartersnakes (*Thamnophis rufipunctatus*) are a threatened piscivorous species endemic to the southwestern United States and northern Mexico. Their coloring ranges from olive to charcoal, with a yellow underside and red or brown spots covering the back. Narrow-headed gartersnakes typically go through brumation, a period of winter dormancy exhibited by ectothermic vertebrates. However, field biologists have observed narrow-headed gartersnake activity in the field during their typical brumation period. We used an array of motion sensing cameras to track the activity of four adult female narrow-headed gartersnakes housed in an outdoor, climate-controlled enclosure. We observed activity during the months leading up to, during and following brumation while recording temperature and barometric pressure to determine if environmental conditions could help predict activity. If incidences of activity during brumation are positively correlated to barometric pressure rather than temperature, then there may be some survival strategy used by narrow-headed gartersnakes to track barometric pressure. If barometric pressure can be used to predict narrow-headed gartersnake activity, this information would be beneficial for field biologists trying to understand why these snakes are active at a time when energy expenditures are costly.

## 55 Does extending the washout period following chronic stress leave intact the beneficial effects of shorter post-stress washout pe

Flegenheimer, Aaron; Ortiz, J. Bryce; Nishimura, Kenji; Martin, Logan; Shah, Vrishti; Daas, Eshaan; Judd, Jessica; Le, Brittany; Padilla-Garcia, Diego; Vracar, Iva; and Conrad, Cheryl D.  
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Chronic stress often leads to cognitive deficits, especially within the spatial memory domain mediated by the hippocampus. When chronic stress ends and a no-stress period ensues (i.e., washout, WO), spatial ability improves, which can be better than non-stressed controls (CON). The WO period is often the same duration as the chronic stress paradigm. Given the potential benefit of a post-stress WO period on cognition, it is important to investigate whether this potential benefit of a post-stress WO period has long-lasting effects. In this project, chronic restraint (6hr/d/21d) in Sprague-Dawley rats was used, as it is the minimum duration necessary to observe spatial memory deficits. Two durations of post-stress WO were used following the end of chronic restraint, 3 weeks (STR-WO3) and 6 weeks (STR-WO6). Immediately after chronic stress (STR-IMM) or the WO periods, rats were tested on various cognitive tests. We corroborated past studies that chronic stress impaired spatial memory (STR-IMM vs CON). Interestingly, STR-WO3 and STR-WO6 failed to demonstrate improved spatial memory on a radial arm water maze task, performing similarly as STR-IMM. Performance outcomes were unlikely from differences in anxiety or motivation because rats from all conditions performed similarly on an open field task and on a simple object recognition paradigm, respectively. However, performance on object placement was unusual in that very few rats explored, suggesting some degree of anxiety or fear. Given the unusual findings, the findings will be discussed in terms of potential procedural differences from past work and in terms of WO outcomes.

## 57 Comparative gene expression analysis of reptilian vs. mammalian musculoskeletal development

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Mammals and reptiles display differences in their musculoskeletal anatomy, particularly in their axial and limb structures. These differences arise in embryonic stages, and this study focuses on comparing the expression of genes for musculoskeletal development in reptilian (green anole lizard, *Anolis carolinensis*) and mammalian (mouse, *Mus musculus*) models at comparable developmental stages. We are carrying out *in situ* hybridization analysis using specific antisense RNA probes for transcription factors that direct muscle development (*myog*) and skeletal development (*sox5*, *sox6*, and *sox9*), and also a marker of muscle differentiation (*myh3*). Based on previous studies in the mouse, we expect to observe similar gene expression in lizard developing tissues but different patterning of muscle groups and skeletal structure. In addition, green anoles are distinct in that they are capable of regenerating their musculoskeletal tissue after tail breakage, and these gene markers will be useful in future studies of the tail regrowth process in lizards.

## 10 **Comparison of the nutritional physiology of urban and rural house sparrows (*Passer domesticus*)**

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House sparrows (*Passer domesticus*) are often considered urban exploiters as they heavily utilize human-related resources such as bird feeders, discarded foods, and nest boxes. According to the 2015 U.S. Census Bureau, Maricopa County currently has the second highest population growth in the nation. With increasing urban expansion, it is important to assess potential impacts of urbanization on birds. To date, there is conflicting evidence as to whether urbanization affects body mass and nutritional physiology of house sparrows. Reports indicate that the health and nutrition of wild birds can be estimated from measures of nutrients in the blood. The purpose of the current project therefore, was to measure these variables in wild urban and rural house sparrows. Plasma and liver samples were collected from n=13 rural and n=7 urban birds. There were no significant differences in body mass between populations. In addition, while there were no significant differences in circulating triglycerides or free glycerol concentrations between urban and rural house sparrows, urban birds had significantly greater blood glucose compared to rural birds. In contrast, rural birds had significantly more plasma uric acid and liver free glycerol. Higher blood glucose suggests greater accessibility of this nutrient in an urban setting whereas the elevated uric acid suggests greater protein availability in the rural habitat. Finally, elevated liver free glycerol in rural birds suggests they may metabolize more fat but could also indicate that urban birds have greater glycerol gluconeogenesis. While the results from this study demonstrate that the nutritional physiology of birds living in the city is different, additional research is needed to determine whether these variations impact the health of urban birds.

## 67 **Male Anna's hummingbirds (*Calypte anna*) orient their shuttle display towards the sun**

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Animals often have unique behaviors and traits that they use as signals during courtship. Hummingbirds have some of the most exaggerated signaling traits, including their rapid flight, elaborate courtship displays (e.g. dives, shuttles), and brilliant iridescent plumage. These rapid displays contain complex behaviors that have previously been difficult to discern with the naked eye. Using Anna's hummingbirds (*Calypte anna*) as a model species, we video-recorded male courtship displays to better understand the temporal characteristics of these rapid displays and specifically how color and behavior interact with each other during courtship. We have characterized and examined the traits of a male's shuttle display, including his angle of orientation, vertical position, and horizontal position relative to the female and sun during his display. Thus far, we have found that males tend to selectively face the sun when doing their shuttle displays to females, most likely to optimize the intensity of plumage coloration while displaying.

## **54 The use of a G-quadruplex aptamer on a DNA tetrahedron nanostructure to target cancer**

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An ideal cancer therapy would be biocompatible, affordable, easy to make, and most importantly, specific. DNA nanostructures which fulfill those requirements have been shown to exhibit targeting abilities through the use of conjugated molecules. G-quadruplex aptamers contain guanine nucleotides that can bind to each other in planar conformations giving the aptamer a unique structure. Nucleolin is a protein that can be overexpressed on cancer cells, making it an ideal target for specific cancer therapeutics. It is the structural conformation and the affinity for nucleolin protein that we seek to utilize. Linking a G-quadruplex aptamer to a DNA tetrahedron nanostructure increases the binding ability of the aptamer compared to free aptamer as well as a random nonspecific aptamer. This increased binding could be utilized to specifically deliver a drug-loaded DNA assembly to cancer cells.

## **13 Analysis of Rapid Expansion Experienced by ASUHIC**

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The Arizona State University Hasbrouck Insect Collection (ASUHIC) is one of the eminent research collections of arthropods in the southwest United States. In 2011, when collection activities were resumed, approximately 700,000 specimens were found present in the collection. However, our legacy specimen holdings were in great need of physical re-curation and re-organization into a modern, phylogenetic classification that reflects valid taxonomic names. In the past 3-5 years, the number of active students and also more senior (volunteer) collection members has risen to about 20 per semester. Through a combination of our own insect collecting activities, and also bulk donations of regional collections made by affiliates, we are growing at a rapid pace of 50,000-100,000 specimens annually. The process of reorganizing, identifying, and placing old and newly acquired specimens into their proper taxonomic locations in the collection is critical. We present an overview of current efforts involved in the curatorial process, provide data on taxonomic strengths and growth trends, and also analyze the changing geographic foci of our collection holdings. Nearly 80,000 ASUHIC specimen records are accessible on-line at [symbiota4.acis.ufl.edu/scan/portal/collections/misc/collprofiles.php?collid=1](http://symbiota4.acis.ufl.edu/scan/portal/collections/misc/collprofiles.php?collid=1).

## 23 Do Christian Biology Students Experience Stereotype Threat?

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While religious individuals are the majority group among the general public, they are the minority in science disciplines and they may be negatively stereotyped. Past research shows that religious students experience stereotype threat effects in the context of science communities because they perceive they are negatively stereotyped. However, it is currently unknown whether religious students in college biology classes experience stereotype threat effects on biology tests. Using a 2X3 experimental design, we tested whether religious students taking biology classes illustrate stereotype threat performance effects on questions taken from the GRE biology practice exam. Students self-reported their religiosity and were placed in one of three experimental conditions that were meant to illicit different levels of stereotype threat before answering questions from the GRE biology practice exam. We found that regardless of experimental condition religious students underperformed relative to their non-religious peers and that regardless of religiosity, those in higher level threat conditions performed worse than those in lower level threat conditions. However, we did not detect a religiosity/condition interaction effect that would be present if stereotype threat was activated in religious students. We hypothesize that if we control for prior academic ability that we would detect the interaction of religiosity and condition.

## 26 Evaluating the role of a multi-heme cytochrome c in electron transfer from an electrode surface to *Heliobacterium modesticaldum*

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*Heliobacterium modesticaldum* (*H. modesticaldum*) is an anaerobic photoheterotroph that can produce H<sub>2</sub> when other electron transfer pathways are restricted. In addition, electrons can be injected into this organism via an electrode and redox mediator in a light-dependent fashion, as shown recently by the Redding and Jones research groups. These factors make *H. modesticaldum* an ideal organism for use in a microbial photoelectrosynthesis cell, in which electricity can be used to power specific metabolic processes that produce a desired compound (e.g. H<sub>2</sub>). However, the injection of electrons into this organism has not yet been optimized. There is a gene (HM1\_0653) in the genome encoding a multi-heme cytochrome c that is similar to the proteins known to be used for exit of electrons in the well-known electrode-respiring bacteria (e.g. *Geobacteria*). RNA-sequencing in the Redding lab has shown that the HM1\_0653 gene is very poorly expressed in *H. modesticaldum*. Boosting expression of this cytochrome could lead to faster electron transfer into the cells and thereby more H<sub>2</sub> production. This hypothesis is being tested by cloning the HM1\_0653 gene into a plasmid behind a strong promoter and introducing it into *H. modesticaldum* using a transformation system recently developed in the Redding lab. To test that the protein is being highly expressed, SDS-PAGE/heme-staining will be conducted. The effect of HM1\_0653 on electron transfer will then be assessed by comparing the light-dependent current into cells containing the overproducing plasmid with control cells, as well as H<sub>2</sub> production.

## 25 **Generating a Georeferenced Tissue Collection of Arid-Adapted Darkling Beetles (Coleoptera: Tenebrionidae)**

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The family Tenebrionidae, the darkling beetles, contains over 4,000 described North American species, most of which are adapted to arid habitats. Tenebrionids express multiple adaptations for surviving in arid environments. Their diversity and adaptivity to arid environments make them ideal candidates for evolutionary and ecological studies. Despite their ubiquity in deserts of the southwest, darkling beetle distributions, evolutionary relationships, and biology are poorly known. We are currently working on sampling darkling beetle diversity from across western North America. A darkling beetle tissue collection comprised of molecular-quality voucher specimens is being generated from these ongoing field-sampling efforts. Specimens are databased, georeferenced, and made available on-line through the Symbiota Collections of Arthropods Network (SCAN, <http://symbiota4.acis.ufl.edu/scan/portal/index.php>). The distributional data which these specimens add to SCAN is being incorporated into an ongoing revision of the genus *Eleodes* Eschscholtz and the genetic resources being made available through this project make evolutionary analysis possible for these arid-distributed taxa. We have 170 specimens for 49 species catalogued in the tissue collection so far, only 5 of which have any sequences available on GenBank2, the National Institutes of Health genetic sequence database (<https://www.ncbi.nlm.nih.gov/genbank/>).

## 65 **Early Life Stress: An Increased Risk of Schizophrenia through Activation of the Complement Component Pathway**

Hoegh, Emily M.; Talboom, Joshua S.; and Orchinik, Miles  
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Schizophrenia is a debilitating disorder with poorly understood genetic and environmental risk factors. An allelic variant of complement component 4 (C4), a protein first identified in innate immune response, is strongly associated with schizophrenia. In the brain, activity of C4 leads to dendritic pruning, a process that may be causal in disease progression. Environmental factors, such as early life exposure to significant stressors also associate with increased risk of schizophrenia in later life. My hypothesis is that these factors do not act independently, but rather in tandem to influence disease etiology.

This hypothesis is supported by previous studies demonstrating that stress-induced elevation of glucocorticoids increases the transcription of C4. Direct and indirect mechanisms represent likely molecular mechanisms through which glucocorticoids act. Direct activation relies on the glucocorticoid receptor binding sites of the C4 promoter to increase C4 protein production through binding. Indirect activation proceeds through activated glucocorticoid receptors inhibiting the expression of the transcription factor nuclear factor-light-chain-enhancer of activated B cells (NF- $\kappa$ B), thereby leading to decreased expression of the C4 inhibitor CUB and Sushi multiple domains 1 (CSMD1).

Glucocorticoid receptors and C4 are richly expressed in the hippocampus, a region critical in memory consolidation, spatial, and declarative memory. I propose that stress-induced upregulation of C4 activity in the hippocampus promotes excessive synaptic pruning, contributing to specific deficits and hippocampal shrinkage seen in schizophrenia. This mechanism may reveal novel interactions between environmental and genetic risk factors in the etiology of schizophrenia through complement activation.

## 4 The Mathematical Physics and the Technical Mechanics of Time Travel

Hoogstra, Brandon

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The project analyzes both the mathematical physics and the technical mechanics associated with the theory of relativity as it applies to temporal distortion. More specifically, the research addresses the influence of relativistic time dilation and gravitational time dilation upon a point mass within a theoretical model of interplanetary travel throughout the universe. The model provides an account of the influence of a black hole upon the passage of time, including such factors as mass, angular momentum, and electrical charge. Equations are provided for calculating the discrepancy in time between that experienced by a terrestrial observer and that experienced by the traveling point mass. Examples of the empirical observations of the effects of gravitational factors and time delay are discussed. The project proposes future research into such topics of relevance as the influence of gravitational waves upon time dilation, the utilization of wormholes for purposes of time travel, and the existence of tachyons within the universe.

## 29 An Analysis of the Benchmark Test Izbench for Open-Source Compressors

Howell, Abigail A.<sup>1</sup>; Mertens-McConnell, Zach<sup>2</sup>; Cartwright, Reed A.<sup>1</sup>

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With the rising data output and falling costs of Next Generation Sequencing technologies, research into data compression is crucial to maintaining storage efficiency and costs. High throughput sequencers can produce up to 1.8 terabytes of data per run, and such large storage demands are even more important to consider for institutions that rely on their own servers rather than large data centers. Compression aims to reduce the amount of memory used by encoding the most frequently occurring symbols with the shortest bit codewords and by changing the order of the data to make it easier to encode. Depending on the probability distribution of the symbols in the dataset or the structure of the data, choosing the wrong algorithm could result in a compressed file larger than the original. In this study, 37 open-source compression algorithms were used to compress six types of genomic datasets (FASTA, VCF, BCF, GFF, GTF, and SAM) and evaluated on compression speed, decompression speed, compression ratio, and file size using the benchmark test Izbench. Compressors that outperformed the standard bioinformatics compressor Gzip were evaluated against one another by ratio and speed as well as transmission time through variable speed internet pipes. Our preliminary data found that the optimal algorithms for compression speed and ratio were dependent on the type of file format, and that the most efficient algorithms for transmitting compressed datasets through internet pipes were also dependent on file format as well as if the data was compressed on client or on the server.

## 11 Determination of new regulator for phoP.

Hua, Tangsiyuan; and Shi, Yixin

*SOLUR program, School of Life Sciences, Arizona State University, Tempe, AZ*

*E. coli* based gene expression screening for several PhoP-dependent genes. This is a blind screening so I do not know the regulators behind this part of the project, yet. I am using *E. coli* KEIO collection to search for these factors that either upregulate or downregulate PhoP/PhoQ two component system. I have been transducing lysates made from a library of *E. coli* strains to a WT strain with PhoP/PhoQ regulatory gene PYS1000-pagC-UP which contains pagC promoter and lacZ gene, that allows me to use Beta-galactosidase test to screen for possible candidate by comparing their expression under Low/High Mg<sup>2+</sup> environment. I have worked out a workable protocol for this project, and will expect more data soon.

## 44 Will this be on the test? Depends on the instructor! Exploring differences in instructor exam decisions in introductory biology

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From the literature, we know that there is variation in course exam structure from different instructors teaching the same course, including characteristics such as open or closed-ended questions and/or the cognitive difficulty of individual questions. We also know from a large set of literature that differences in exam structure can impact student learning as well as student performance on the exam. Given that we know that instructors administer different types of exams than other instructors, any variation in exam structure may be impacting students differently, whether it be their course grade or their understanding of the course content, it begs that question, why are these exams different? To start to answer this, a key step would be to characterize what decisions instructors make when constructing their exams as it is usually the case that instructors are principally responsible for constructing their own exams. Currently, there is no prior research on this area to our knowledge. Thus, we set out on an exploratory interview study in order to characterize what decisions instructors of the same course make when constructing their exams. A total of seven introductory biology instructors teaching the same course participated in a semi-structured interview. We found that despite teaching the same course, the decisions that instructors made when constructing their exams highly varied. In this poster presentation, we will highlight the differences in the decisions instructors make as well as any common or interesting factors that influence these decisions.

## 33 Recombinant Immune Complex Vaccine Methods Applied to Zika Virus

Hunter, Joseph G.; Damos, Andy; and Mason, Hugh

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Zika virus has recently become a focus of the scientific community across multiple disciplines due to outbreaks across Central and South America. These outbreaks not only revealed Zika virus' role in causing Microcephaly and Guillain-Barré syndrome but also drove vaccination research in a way not seen in recent memory. Herein is discussed the application of a tried vaccination method using recombinant immune complexes (RICs) applied to the Zika virus envelope proteins. RICs aggregate to produce an imitation of the natural immune response, increasing immunogenicity of the vaccine. The envelope protein of Zika virus was focused on as it is readily accessible to the immune system and is thought to induce neutralizing antibodies.

## 27 The Role of Protist Parasites in the Particle Flux of the Ocean

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It is well known that marine plankton play a significant role in the cycling of carbon and nutrients in the oceans. Single celled eukaryotes known as protists contribute their fair share to this ecological phenomenon, yet the nuances of their impact on carbon particle aggregation and sinking requires further research. Analysis of DNA 18s DNA amplicons retrieved from the water column and particle traps has shown that parasitoids known as Marine Alveolates (MALVs) are overrepresented in the aggregates found in these traps. This suggests that organisms that are infected by MALVs are more likely to aggregate and sink. The aim of this research is to see if there is a correlation between those MALVs found in the traps and MALVs previously characterized from anoxic environments. Using phylogenetic trees constructed from the gene sequences obtained as well as existing sequences from GenBank, we could show that anoxic MALVs are more frequently associated with aggregates collected from particle traps at 150m depths, although a fair amount of oxic and suboxic representatives can be found in these traps as well. On the other hand, anoxic MALV sequences were rarely retrieved from higher up in the water column.

## 43 The Role Division of Labor Plays in Generating Hypometric Relationships between Colony Size and Metabolic Rate in California Seed

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In colonies of seeds harvester ants (*Pogonomyrmex californicus*), relationships among colony size and collective physiological traits, specifically metabolic rate, have been found to be consistent with the  $\frac{3}{4}$  power law that we observe across individual organisms. We've found that the division of labor index positively correlates with colony size. We aim to further explore the relations between these qualities and address the question of how the behavioral mechanisms ensure the validity of the  $\frac{3}{4}$  power law at the colony level. We founded 24 pleometric queens' colonies of California seed harvester ants in the lab in July of 2016. We conducted behavior scanning and metabolic rate measurement on colonies from October 2016 to February 2017. Here we present that division of labor emerges spontaneously during the colony ontogeny. The data suggest that division of labor is an energy-saving mechanism based on the preliminary analyses. Applying the hierarchy cluster analysis, we found that resting behavior is key when looking at task allocation and collective metabolic process. In the future, we plan to study the relationships within groups of ants performing particular tasks such as brood care, foraging, and even trash maintenance.

### 35 Changes in miRNA species following lifestyle intervention among obese Latino youth with prediabetes.

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Obesity and related health disparities including type 2 diabetes disproportionately impact Latino youth. These health disparities may be the result of gene-environment interactions, but limited research has examined these interactions in the pediatric age group. Lifestyle intervention is the cornerstone for preventing diabetes among high-risk populations and epigenetic and genetic factors may help explain the biological mechanisms underlying diabetes risk reduction following lifestyle changes. MicroRNAs (miRNAs) are small, non-coding RNAs that regulate gene expression and have emerged as potential biomarkers for predicting type 2 diabetes risk in adults but have yet to be applied to youth. Therefore, the purpose of this study was to identify changes in miRNA expression among Latino youth with prediabetes (6 participants, 4 females, 2 males, age 14-16) who participated in a 12-week lifestyle intervention focused on increasing physical activity and improving nutrition-related behaviors. Whole blood collected at baseline and post intervention was processed using the PAXgene blood miRNA extraction kit. Next generation sequencing results of miRNA expression levels was quantified using programs CAP-mirSEQ and EdgeR. From the analysis, 2,823 miRNAs were identified. Of those, 22 miRNAs were found to be significantly ( $P < 0.05$ ) altered in response to the intervention. Seven of the miRNAs identified have previously been characterized in relation to diabetes related outcomes, while 5 of the miRNAs are novel (miR-5701, miR-6747-3p, miR-3127-3p, miR-6783-3p, miR-4661-5p). The preliminary results of this study suggest that alterations in miRNAs in response to lifestyle intervention are related to type 2 diabetes and could shed light into the biological mechanisms underlying lifestyle-induced diabetes risk reduction in youth.

### 39 Influencing the Rhamnolipid Production of *P. aeruginosa* with Environmental Changes to Resemble the CF Lung

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Cystic fibrosis (CF) is a genetic disease that affects the production of mucous in the lungs, leaving the lungs susceptible to infection. *P. aeruginosa* is a gram-negative bacterium that opportunistically infects the CF lung, which often lead to chronic infections. During this progression, *P. aeruginosa* adopts phenotypes that are linked with negative patient outcome. Rhamnolipid production is an exoproduct phenotype of *P. aeruginosa* regulated by quorum-sensing genes, which are often mutated in chronic CF lung infections. The ultimate goal of our work is to develop new diagnostics for detecting *P. aeruginosa* from a patient's breath. For this project, we are interested in manipulating the environmental conditions of *P. aeruginosa* to represent the CF lung, and measure the change in rhamnolipid production that results. We selected 35 *P. aeruginosa* strains that were isolated from CF lung infections, and grew them in different temperatures (30°C, 37°C, 40°C) and in the presence of *Staphylococcus aureus* metabolites, simulating a co-infection, and measured rhamnolipids production in each condition. These results will be combined with information on the metabolic changes that occur in the difference environments to identify putative biomarkers of rhamnolipids. These biomarkers can be used to identify biomarkers of reduced rhamnolipid production to detect this *P. aeruginosa* phenotype in chronic CF lung infections.

## 40 SBI-183 Inhibits Enzymatic Function of Quiescin Sulfhydryl Oxidase 1

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Quiescin Sulfhydryl Oxidase 1 (QSOX1) is an enzyme that catalyzes the formation of disulfide bonds in protein folding. Numerous cancer cell types, including breast, prostate, pancreatic, colon, and lung, overexpress QSOX1 while non-malignant cells do not. Additionally, QSOX1 facilitates invasion and metastasis of cancer cells. SBI-183 is a compound that was identified as a potential QSOX1 inhibitor in high throughput screening of 50,000 compounds. The goal of this research was to confirm that SBI-183 inhibits QSOX1. The inhibition of QSOX1 by SBI-183 was quantified in a fluorescence assay, in which greater fluorescence suggested more enzymatic activity. QSOX1 alone in the fluorescence assay had a relative fluorescence of ~2200, and QSOX1 without DTT substrate had a relative fluorescence of ~0. Increasing concentrations of SBI-183 inhibitor cause the relative fluorescence to continually decrease and plateau at ~1000 with 100  $\mu$ M SBI-183. Additionally, SBI-183 is being tested for the ability to suppress tumor cell growth and invasion. These results suggest that SBI-183 does inhibit QSOX1, although not completely. Future studies using medicinal chemistry techniques to modify SBI-183 to increase the solubility and inhibitory activity will require monitoring with each iteration of the inhibitor.

## 36 What's in a name? The importance of students perceiving an instructor knows their names in a high enrollment biology classroom

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Learning student names has been promoted as an inclusive classroom practice, but it is unknown whether students value having their name known by an instructor. We explored this question in the context of a high-enrollment active learning undergraduate biology course. Using surveys and semi-structured interviews, we investigated whether students perceived that instructors know their name, the importance of instructors knowing their name, and how instructors learned their name. We found that while only 20% of students perceived their names were known in previous high-enrollment biology classes, 78% of students perceived that an instructor of this course knew their name. However, instructors only knew 53% of names, indicating that instructors do not have to know student names in order for students to perceive that their names are known. Using grounded theory, we identified nine reasons why students feel that having their names known is important. When we asked students how they perceived instructors learned their names, the most common response was instructor use of name tents during in-class discussion. These findings suggest that students can benefit from perceiving that instructors know their names and name tents could be a relatively easy way for students to think that instructors know their name.

## 18 Characterization of a Synergistic Network of Malate Exporters in *Escherichia coli*

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Besides being a key metabolite in the citric acid cycle, L-malate is an important specialty chemical used in the food, pharmaceutical, and polymer industries. It is also a desirable renewable chemical with the potential for mass production from biomass. The export of organic acids represents a potential bottleneck for bioproduction, but malate export has not been characterized in bacterial hosts. In this work, we use a reverse genetics approach to characterize a malate export system and explore whether this export system can enhance production in an L-malate biocatalyst. Ten candidate genes were evaluated for a role in malate export in an L-malate producing *Escherichia coli*. One transporter of the dicarboxylate uptake family (Dcu) and two transporters of the dicarboxylate anion: sodium symporter (DASS) family together appear to play a primary role in malate export. Combinatorial evaluation of the transporters demonstrates that TtdT and DcuA play a crucial role in this synergy, and removal of these genes results in elevated intracellular L-malate concentrations.

## 45 Functional Characterization of *Escherichia coli* Multi-Drug Efflux Pump Protein AcrB

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Antibiotic resistance is one of the biggest concern to global health today. Due to naturally occurred processes and/or misuse of antibiotics by human, multi-drug resistant bacteria are emerging every day. In *Escherichia coli*, multi-drug resistance can be achieved by the AcrAB-TolC efflux system. AcrB, a trimer protein which function as the multi-drug efflux pump contribute to the efflux of a broad spectrum of antibiotics. Previous study has shown that Y49S, a second-site substitution in AcrB overcome the drug hypersensitivity phenotype of F610A. *In silico* study of Y49 in the binding monomer revealed that it can interact with R239 in the extrusion monomer. However, little has been known for the role of R239. In this study, we aimed to further expand our knowledge on the efflux pump protein AcrB by trying to elucidate (1). How a second-site substitution R239A in the periplasmic domain affect rate of efflux? (2). What is the effect of efflux pump inhibitor MBX2319 on the efflux rate of *E. coli*? Mutants were constructed by site direct mutagenesis and Live Cell N-phenyl-1-naphthylamine Efflux Assay, Minimum Inhibitory Concentration Assay as well as selective antibiotic plates were used to fulfill these two aims. Recent results states that the second-site substitution R239A can overcome the functional defect of F610A hypersensitive mutation and optimization of integrating efflux pump inhibitor into efflux assay is currently in progress. Understanding the function of suppressor mutations and inhibitor can help us further understand efflux pump function in bacteria and may give insight on the development of novel efflux pump inhibitors to fight against the emerging multi-drug resistance.

## 1 An Improved Microtiter Bioreactor System for Organisms with Combustible Substrates

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Microorganisms that consume combustible gas mixtures, such as methanotrophs, are of great scientific interest due to their ability to generate value-added products from unused natural gas feedstocks. Microtiter reactor systems, which allow 96-well plates to be used as microbioreactors, can accelerate engineering efforts of these organisms by enabling screening of large numbers of cultures. However, the reactor systems currently being used for this purpose are still those designed for heterotrophs. These systems have small chambers (3L) and require a constant flow of a methane/air mixture to function. This constant flow significantly increases the costs and safety risks associated with operating the system. A mass-balance analysis suggested that a larger chamber (20L) would allow for the elimination of the gas flow while maintaining consistent performance.

An improved reactor system was machined from acrylic using a CNC router. The system was tested using 192 microreactors inoculated with exponential-phase *Methylobacterium buryatense* 5GBS1 at an OD<sub>405</sub> of 0.05. The chamber was filled with an air/methane mixture and shaken at 200rpm. There were no measurable changes in chamber methane concentration over single day periods. Over three days, reactors on the two plates grew to average OD<sub>405</sub> values of 0.321 and 0.251. The difference between the two is statistically significant, but can be explained by non-uniformities in diffusion cover compression that will be remedied in future iterations. There were no statistically significant correlations in growth across the individual plates. Overall, these results are proof-of-concept for cost-effective and safer microtiter reactors that operate without constant gas flow.

## 73 The Development of Reproductive Health Access

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Although women in the US used contraception for many centuries, social norms dictated the extent to which physicians and individuals could disseminate family planning knowledge. During the 1800s, the moral standards of Victorian Era society contributed to the belief that distributing contraceptives and teaching women about birth control would lead to sexual promiscuity and the collapse of family values. That belief influenced the support for the passage of the US federal Comstock Act of 1873. This act hindered access to and distribution of material related to contraception and abortion by labeling those items as obscene. Subsequent state laws reinforced regulation of contraception and abortion at the state level. That led to a large number of unplanned and often unwanted pregnancies, harmful attempts at self-abortions, and more women left with unanswered questions about family planning and reproductive health. Social and political attitudes towards contraception and abortion in the 1900s were examined through primary source documents to answer two questions: In what ways did reproductive health advocates dismantle legal barriers to contraception and abortion in Arizona during the 20th century? and How did this improve access to reproductive health? After analysis of this controversial time period, it was determined that the work of four influential reproductive health advocates contributed to the rise of maternal and child health clinics, education of farming and rural communities, and support for the distribution of federal funding for family planning services.

## 22 The Evolutionary Origin of *Spirotrichonympha* in the Termite Genus *Reticulitermes*

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*Reticulitermes tibialis* is in the family Rhinotermitidae and is native to the western United States. In Arizona it is considered the most widely distributed subterranean termite. Like other members of the Rhinotermitidae family, *R.tibialis* is dependent on gut protist symbionts to digest its wood food. The termite genus *Reticulitermes* belongs to a monophyletic group with the termites from the *Coptotermes* and *Heterotermes* genera. Termites from these two genera always contain three genera of protists which are *Pseudotriconympha*, *Holomastigotoides* and *Spirotrichonympha*. However, termites in the genus *Reticulitermes* have a protist community more similar to the distantly related termite *Hodotermopsis*. *Reticulitermes* only has one protist genus in common with its relatives in *Coptotermes* and *Heterotermes*, the parabasalian, *Spirotrichonympha*. One hypothesis for this is that *Reticulitermes* somehow lost all of its hindgut community and replaced it with the hindgut community of *Hodotermopsis*. In order to shed light on this mystery, we sequenced the 18S ribosomal RNA gene (18S rDNA) from *Spirotrichonympha* in *R.tibialis* and performed phylogenetic analyses to determine whether *Spirotrichonympha* sequences from *R.tibialis* are more closely related to those from *Hodotermopsis* or to those from *Coptotermes* and *Heterotermes*. Observing our phylogenetic analysis we found that our *Spirotrichonympha* sequence from *R.tibialis* did form a monophyletic group with *Spirotrichonympha* sequences from *Hodotermopsis* and therefore is more closely related to sequences from *Hodotermopsis* instead of *Heterotermes* and *Coptotermes*. This is consistent with the earliest ancestor of *Reticulitermes* having replaced its hindgut community with that of *Hodotermopsis*.

## 7 Expression of recombinant Zika virus-like particles in *Nicotiana benthamiana*

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Zika virus is a member of Flaviviridae family of RNA viruses composed of a single stranded positive RNA genome. Zika virus particles contain a lipid bilayer, one genome RNA and three distinct viral proteins: envelope (E), pre-membrane (prM) cleaved by furin resulting to membrane (M) and capsid (C). Development of virus-like particles (VLPs) in plant expression hosts such as *Nicotiana benthamiana* will allow production of vaccine candidates at substantially less cost and time due to the ease of manipulating plant vectors. The Yellow Bean Dwarf virus plant vector construct allow expression of single proteins or co-expression of multiple proteins within *Nicotiana benthamiana* utilizing *Agrobacterium tumefaciens* infiltration. Initial confirmation of single expression of E, M and prM will verify the ability for *Nicotiana benthamiana* to correctly produce and post-translationally modify each protein. The prM protein is cleaved by furin to express M; this step may have a role in proper protein formation of VLPs and excluding prM may hinder the expression or function of VLPs. The M protein is very small and detection methods other than western blot may need to be implemented to elucidate the protein. Acid precipitation may be used to remove Rubisco background noise which will partially denature and precipitate the proteins of interest requiring further investigation on the stability of all proteins under acidic conditions. Successful co-expression of the Zika E, M and prM may lead to viable expression of VLPs allowing for the production of transgenic plants to further progress vaccine candidates.

### **3 Optimizing Expression and Purification of the Human TRPM8 Ion Channel**

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Transient Receptor Potential Melastatin 8 (TRPM8) is a primary cold sensor in human body. It is also involved in a variety of human diseases such as prostate cancer, pancreatic cancer, diabetes, and obesity. Since its discovery in 2001, studies have been done to better understand TRPM8 function which gives it its physiological roles and potential for therapeutic intervention. Post-translational modifications of proteins are widespread phenomena in cellular physiology. To answer the question of how post-translational modifications affect TRPM8 function, the proteins are expressed and purified from mammalian cells (HEK293) and bacterial cells (*E. coli*). The purified proteins with and without posttranslational modifications are subjected to planar lipid bilayer electrophysiology experiments to compare its function in a lipid bilayer context. Here, we discuss the process of optimizing the transfection, expression and purification of TRPM8 from mammalian cells in addition to the preliminary data on planar lipid bilayer experiment.

### **19 Evaluating the Effectiveness of Alternative FBS on Neuroblastoma Cells**

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Cell culture based research is one of the foundational forms of experimentation that transitions into future studies involving tissue and eventually animal and human trials. It is estimated that the R&D market cost for cell culture was valued at 16.35 billion in 2014—with one of the largest monetary investments being sera [i.e. fetal bovine serum (FBS), newborn calf and adult bovine serum] which provides nutrients, growth factors and hormones to cells to simulate their natural environment. It was reported that since 2003, the cost of FBS has tripled—which has affected the research efforts of many labs. To address this surge in price, numerous pharma companies have begun to develop their own alternatives to traditional sera, using well-known key factors required by cell cultures in an attempt to reduce cost and create a consistent product that should not vary in content between seasons or herds of cattle. This study compared alternative sera to standard FBS and evaluated the affects it had on growth, behavior, and differentiation of neuroblastoma cells. Cells were imaged using confocal microscopy to observe cytoskeletal changes, as well as live cell microscopy to observe any changes in behavior. Additional lab analysis was preformed to quantify common serum elements and identify composition differences between serum types. From these results, it appears that alternative serum is an acceptable substitute for FBS in culture media for a short time—but for prolonged growth, cells may require additional hormones and growth factors typically provided through FBS for sustained healthy growth.

## 21 Utilization of Dielectrophoretic Microfluidic Channels in Protist Separation to Enable Symbiosis Research

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Rapid separation of species in a community is desired in microbiology. Dielectrophoresis is the movement of uncharged particles in non-uniform electric fields, and it can separate whole cells based on their physical differences. Research in termite hindgut communities brought about the need for simplified, low cost, and quick protist isolation. For example, *Heterotermes aureus* has a characteristic hindgut community comprising three protists ranging from 10-250  $\mu\text{m}$ . In order to study *H. aureus* protists, they currently must be separated by the laborious process of manual micropipette cell picking. Dielectrophoretic channels have previously been used to separate  $<10 \mu\text{m}$  biomolecules, but cannot currently separate larger protist cells. A novel dielectrophoretic separation device is being fabricated that can handle the separation of larger scale cells. Our process is inexpensive, quick, and allows for the separation of larger, more complex samples. The successful development of a microfluidic channel on this scale can have innumerable uses in microbial community ecology, microbial genomics, and symbiosis research.

## 63 Effects of major element compositions on mineral equilibria and melting in exoplanetary upper mantles

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With the launch of the Kepler Space Telescope in 2009, came the discovery of 348 earth-sized terrestrial planets. So far, we know little about what the interiors of these terrestrial planets are like or how melting of the interiors forms surficial crusts. Without the means to collect direct samples of exoplanet mantles and crusts, they must be created in the lab. The purpose of this project is to identify the likely mineral phases and melting behavior in a possible exoplanet upper mantle through experimentation. Spectral analyses give us an idea of the relative elemental abundances in a given solar system when compared to our own, which we use to extrapolate a mantle composition to study. In this study, a synthetic mix of elemental oxides is used to simulate exoplanet mantle compositions at temperatures of 1000-1500°C and pressures of 1-2 GPa to determine phase equilibria and the location of a likely mantle solidus. The composition being tested during our first set of experiments represents a planet with a higher Mg:Si ratio than terrestrial planets in our solar system, which is predicted to be the case for over 50% of observed exoplanet systems. The solidus at 2GPa is between 1200°C and 1300°C. The melt compositions provide insights into what the composition of the crust might be like on this exoplanet, which allows us to predict aspects such as plate tectonics and habitability

## 66 Peculiar Plumage Produces Angle-Dependence Across Parrot Phylogeny

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Studies of animal coloration provide key insights into the evolution of phenotype in many organisms and can have implications for species persistence, conservation, and domestication. Parrots are well-known amongst researchers and pet fanciers for their marvelous display of colors. The array of feather colors in parrots is produced by a variety of pigmentary and structural mechanisms. I have observed a novel type of angle-dependent coloration in many parrot species (Order Psittaciformes). This angle-dependence appears to be produced through the differential coloration of barbs and barbules within a given feather, such that the relative proportion of barb v. barbule coloration that is visible depends upon observation angle. Though we know some about the mechanisms and evolution of iridescence in animals ranging from beetles to birds, we know very little about this unique form of angle-dependent coloration in parrot plumage. With photographic and multiple-angle spectrophotometric data collected from a variety of sources (e.g. live birds, museum specimens), I am characterizing this novel form of angle-dependent coloration across different feather patches and species. I also am evaluating whether or not the lighting environment in which a species resides (e.g. open field, deep forest) predicts the presence of angle-dependent plumage coloration; I predict that angle-dependent coloration will be more prevalent in closed light environments. We believe that our fine-scaled investigation into the physical mechanisms at work and the phylogenetic analysis of angle-dependent coloration across parrot species will greatly contribute to the sparse body of research on parrots and the ecosystems that they inhabit.

## 59 A Specimen-Based Inventory of the Weevils of Sonora, Mexico

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Arizona and Sonora - Mexico's second-largest state - form an ecosystem gradient that remains poorly studied across the two bordering regions. Sonora's diversity of habitats range from coastal beaches and arid ecosystems to more humid, higher-elevated forests in the Sierra Madre Mountains. Based on (1) current assessments of vascular plant species diversity (ca. 4,000 species), and (2) expected diversity relationships between host plants and the specialized, plant-feeding beetles of the weevil superfamily (Coleoptera: Curculionoidea), we would expect as many as 1,000 weevil species to occur in Sonora. However, at present only 50-100 species have been confirmed as state records. Thus, the goal of this project is to create a comprehensive, specimen based inventory of the weevils of Sonora, to be published dynamically through the "Symbiota Collections of Arthropods Network" SCAN data portal (URL: [symbiota4.acis.ufl.edu/scan/portal/](http://symbiota4.acis.ufl.edu/scan/portal/)). The specimen material used for this project includes both legacy specimens from the ASU and other regional insect collections, and new material acquired through collecting trips by our collection members. The Sonora-based "Universidad de la Sierra" collaborates on the project. The processed specimen records, species distribution maps, weevil images, and taxonomic pages are accessible on-line at [symbiota4.acis.ufl.edu/scan/portal/checklist.php?cl=102](http://symbiota4.acis.ufl.edu/scan/portal/checklist.php?cl=102). Later project stages will include the production of taxonomic identification keys and systematic revisions.

## 71 Effects of Gut Bacteria on the Age-Related Decline of Anoxia Tolerance in Adult *Drosophila melanogaster*

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Cell death occurring from anoxia is the major pathology during heart attack or stroke. Humans vary substantially in their ability to survive anoxia, especially across ages, and the basis to this variation is not understood. *Drosophila melanogaster* have similar metabolic pathways to humans but have much better capacities to tolerate anoxia, suggesting that understanding mechanisms of anoxia tolerance in flies may provide insight for medicine. We exposed adult *Drosophila*, ages 1, 3, 5, 7, 9, and 12 days old, to six hours of anoxia and assessed survival 24-hours post-treatment. Seventy-nine percent of adults one day past eclosion survived; while only 10% of twelve-day-old adults survived; thus *Drosophila* show age-related decline in anoxia tolerance like humans. We measured ATP in 1 and 12-day old *Drosophila* in different durations of anoxia. In anoxia, ATP levels declined rapidly (< 30 min) to near-zero levels in both 1 and 12 day old adults; thus the better anoxia-tolerance of young adults is not due to a better capacity to keep ATP elevated. To test whether declining anoxia tolerance might be due to increasing bacterial load, we replaced their food daily, every third day, or every sixth day. At 12 days of age, each treatment group was exposed to six hours of anoxia and assayed for gut bacterial load. Anoxia tolerance was strongly and negatively affected by bacterial load. These data suggest that increasing bacterial load may play an important role in the age-related decline of anoxia tolerance in *Drosophila*.

## 8 Determining peak expression of a fusion protein in *N. benthamiana* for use as an immunotherapy for treating glioblastoma.

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The anti-CD3/Clx fusion protein (ACDClx) has promising potential as an immunotherapy for targeting glioblastoma cells and can be expressed in *N. benthamiana* plants via *Agrobacterium* infiltration. We have performed a time course study to determine the day in which expression of the fusion protein is highest post-infiltration in order to maximize protein yield for future experiments. Agroinfiltration of *N. benthamiana* leaves with a Geminiviral vector encoding ACDClx induces transient expression of the gene in order to produce the desired fusion protein within the plant. By expressing the protein in plant cells, we are able to produce suitable quantities of the protein in a timely and efficient manner as needed for further characterization and use in cell experiments. Current analysis of protein expression provides evidence that peak expression occurs 4-5 days post-infiltration. Further expression analysis is ongoing.

## 53 Inter-rater Reliability, Remote Evaluation, and Park Quality in the Phoenix Metro Area

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Location and quality of parks can make a significant difference in public health and quality of life in local communities. Parks serve as green spaces, places to exercise, socialize, and relax, among other functions, so it is important to evaluate their availability and quality to ensure that all have adequate access to the many services provided by parks. During our project we remotely evaluated the quality of parks in the Phoenix Metro Area, using Google Earth and a park assessment tool the research team created. In order to ensure the validity of our assessments we have to ensure that raters are coming to similar conclusions about the content and quality of the parks; this agreement is inter-rater reliability. Using Cohen's Kappa Coefficient, we analyzed the level of agreement between two independent raters, using a sample of 15 parks. Our results were mixed, and most ratings we found were in moderate agreement, indicating a necessity to refine the assessment tool. Overall, we came to meaningful conclusions about the clarity and effectiveness of the assessment tool, and made important insights into the strengths and limitations of remote assessment that we will use to continue this research.

## 16 Hydrolysis of Succinylcholine by Butyrylcholinesterase Mutant Expressed in *N. benthamiana* Plants

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Succinylcholine induced apnea is a common problem in pre-hospital medicine that affects 1/1800 patients who undergo rapid sequence intubation. This problem occurs when succinylcholine, a neuromuscular blocking agent, is not degraded and leads to long-lasting paralysis and apnea. A small percentage of the human population possess defective forms of the enzyme Butyrylcholinesterase, which is responsible for hydrolyzing succinylcholine. Previous studies have shown that wild type human butyrylcholinesterase (BChE) can be produced in transient-expression *N. benthamiana* plants, and can reverse the effects of succinylcholine induced apnea through enzyme replacement therapy. Mutants of the human form of BChE have also been developed to hydrolyze organophosphate nerve agents. The purpose of this study is to express these mutants in transient-expression *N. benthamiana* plants to see if they hydrolyze succinylcholine more efficiently.

In this study, we used MagnICON vectors to transform *N. benthamiana* plants with variants 3 and 4 of the BChE gene. We used GV3101 competent cells to transform *Agrobacterium tumefaciens* with the desired plasmid. The infiltration was performed with a needleless syringe. Bradford and Ellman protein assays were used to determine the highest protein expression day post-infiltration. Samples were tested for activity with butyryl cholinesterase's namesake substrate butyrylthiocholine. The Km and Vmax for Variant 3 were 0.1mM and 0.012 OD/min. The Km and Vmax for Variant 4 were 0.4mM and 0.01 OD/min. The tests for activity against succinylcholine have yet to be performed.

## 69 **Hyperactivation of ERK/MAPK Signaling Regulates Embryonic Cortical GABAergic Neuron Development**

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The extracellular regulated kinases (ERK1 and ERK2) are key components of the canonical ERK/MAPK intracellular signaling cascade. *De novo* mutations in regulators of this pathway occur in approximately 1:2000 births and are associated with a family of syndromes called RASopathies. The RASopathies are largely caused by mutations that hyperactive components of the ERK/MAPK pathway, and patients exhibit craniofacial dysmorphism, neurological delay, and epilepsy. While studies have implicated GABAergic interneuron dysfunction in learning deficits observed in models of RASopathies, the pathogenesis of the syndromes remains poorly understood.

In this study, we have investigated the effects of hyperactive ERK/MAPK signaling on the development of cortical GABAergic interneurons. Mice with hyperactive ERK/MAPK in GABAergic circuits display a decreased seizure threshold. At the cellular level, there is a significant neuronal migration issue that leads to a reduced number of GABAergic neurons in the sensory cortex of mutant mice by embryonic day 17. To examine whether this was a global effect on all GABAergic neurons, we immunolabeled subpopulations of GABAergic interneurons. Surprisingly, we only found significant decreases in Parvalbumin-expressing (PV) GABAergic interneurons in mutant mice. We then assessed the morphology of cortical PV neurons in mutants and controls. PV neuron somal sizes were not altered; however, mutants exhibited increased dendritic arbor complexity in comparison to littermate controls. This increase in dendritic complexity suggests that the remaining PV GABAergic interneurons may be receiving increased input. Further analysis of the cellular response to hyperactive ERK/MAPK signaling may assist in understanding the pathogenesis of neurological defects in RASopathies.

## 17 **The Development and Validation of Makeup and Sexualized Clothing Questionnaires**

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Today, there is an increasing amount of research documenting society's objectification of women. Additionally, various forms of media promote this objectification of women on a daily basis (Kilbourne, 2003). Body acceptance programs on college campuses have found that women often report feeling pressured to dress in a sexualized manner, cover up their so-called flaws with makeup, and be thin. Currently, no quantitative measures exist to assess the daily behaviors of women regarding the pressure women feel to wear makeup or dress in a provocative manner. Thus, the goal of the current studies was to develop brief self-report questionnaires aimed at assessing makeup and sexualized clothing use and attitudes in young women. In Study 1, items were developed from qualitative data collected by the Body Project Prevention Program (n = 403) to assess perceived pressure to wear make-up, discomfort when not wearing make-up, perceived pressure to wear sexualized clothing, and body image concerns regarding sexualized clothing. Exploratory factor analyses revealed Unconfident and Unease subscales for the Makeup Questionnaire (MUQ) and Body Dissatisfaction and Pressure subscales for the Sexualized Clothing Questionnaire (SCQ). Using a different sample of women in Study 2 (n = 153), confirmatory factor analyses supported the factor structure for the MUQ and SCQ. Study 2 showed that makeup use can predict self-objectification and pressure to wear sexualized clothing can predict shape and weight concern. These studies provide preliminary support for the factor structure of two novel measures aimed at assessing perceived pressure to wear makeup and sexualized clothing.

## 12 Enzymatic activity of *Mycobacterium tuberculosis* Fic toxin

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*Mycobacterium tuberculosis* (*Mtb*), the causative agent of tuberculosis, accounted for 1.8 million deaths worldwide in 2015. The *Mtb* Fic protein belongs to the novel family of Fic domain proteins that post-translationally modify target substrates by AMPylation. Fic domain proteins include toxins such as *Vibrio parahaemolyticus* VopS, which AMPylates threonine residues on small GTPases within mammalian host cells, ultimately resulting in cell death. Previous studies showed *Mtb* Fic hydrolyzes ATP. To assess *Mtb* Fic enzymatic activity, we expressed and purified recombinant *Mtb* Fic and the *Histophilus somni* IbpA Fic1 domain along with Rac1 small GTPase and *Mtb* GyrB. AMPylation activity of both Fic proteins were tested against purified Rac1 and GyrB proteins and *E. coli*, HeLa, and THP-1 protein lysates. While IbpA Fic1 AMPylated Rac1, recombinant *Mtb* Fic lacked in vitro AMPylation activity against all tested substrates. However, *Mtb* Fic hydrolyzed ATP, suggesting that the recombinant protein has enzymatic activity. Future studies include investigating additional target substrates, directed mutagenesis of the antitoxin protein, and the role of Fic in *Mtb* pathogenesis.

## 14 Effects of Grasshopper Management on Non-Target Arthropods

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Orthopteran insect pests, such as grasshoppers and Mormon crickets, pose a significant economic problem for rangeland managers across the United States, sometimes mounting over 1 billion dollars in annual losses. Chemical treatment is often used as an available, effective solution to this problem. The ramifications of such treatments, however, are not well understood.

To examine the effects of chemical management of grasshoppers on non-target arthropod populations in treated areas, samples were collected at Encino, New Mexico during summers of 2015 and 2016 by undergraduate and graduate student members of the Arizona State University Hasbrouck Insect Collection, in a funded partnership with Phoenix-based USDA-APHIS Center for Plant Health Science and Technology.

As part of the experimental approach, three 2000 acre plots were treated in June, 2015, using the novel control agents Diflubenzuron (Dimilin<sup>®</sup>) and Chlorantraniliprole (Prevathon<sup>®</sup>). Each plot contained three sampling sites, from which arthropods were collected using pitfall traps, malaise traps, and sweep net. Additionally, three sampling sites were established outside the treated areas as controls. Samples were collected at one week pre-treatment, then for four weeks immediately following the treatment, and finally for five weeks at one year following the initial treatment. Thousands of specimens are presently being sorted to order, dried, and weighed to obtain biomass data. In this poster, we provide data and analyses regarding the biomass of the 2015 malaise trap samples. Based on these preliminary outcomes, we explore how non-target arthropods are affected by the chosen insecticide treatments.

### **30 Ovarian Hormonal Status Influences 5-HT1B Receptor Agonist Effects on Cocaine Self-Administration**

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Nearly a decade after the NIH issued requirements for the inclusion of women in study populations, as many as one-fifth of NIH-funded, non-sex-specific studies failed to include women, leading to a large number of pharmaceutical drugs approved for consumer use that have not been tested for their effects across the female ovarian hormonal cycle and other sex-related differences. In addition, there are currently no effective pharmacological treatments for cocaine dependence, although previous evidence from our lab have shown that CP94253, a selective 5-HT1B receptor agonist, attenuates cocaine intake and cocaine seeking behavior in male rats. The aim of our study was to test the effects of CP94253 on cocaine intake during the estrus and diestrus phases of the rat estrous cycle, the phases during which levels of estradiol and progesterone are elevated respectively. Female Sprague-Dawley rats were trained on a fixed-ratio (FR5) schedule to self-administer 0.75mg/kg dose of cocaine intravenously and vaginal smears were taken daily to determine estrous cycle phase. After cocaine self-administration rates stabilized, rats were pretreated with either CP94253 (5.6 mg/mL) or saline (vehicle) 15 minutes before self-administering 0.75 mg/kg cocaine for one hour and 0.375 mg/kg for the second hour of testing during estrus and diestrus phases. This study is ongoing, however, our current data shows a significant difference in active lever response rates during estrus and diestrus phases, in addition to a significant increase in cocaine reinforcement rates during estrus.

### **31 Lizards fail to plastically adjust nesting behavior or thermal tolerance as needed to buffer populations from climate warming**

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In a rapidly warming climate, organisms must cope with the increasing temperature or alter its thermal niche. According to climate models, rising temperatures may pose a threat to ectotherms such as the plateau fence lizard (*Sceloporus tristichus*) if they lack the behavioral plasticity or thermal tolerance needed to survive and reproduce in a warmer environment. These lizards may mitigate the heat imposed on their nesting sites by digging deeper nests or preferentially nesting in shaded areas. To investigate this phenomenon, we exposed gravid female lizards to two different thermal environments and observed their effect on nesting behavior and thermal tolerance. Although the thermal treatment did not have a significant effect on nesting behavior, embryos that were exposed to the warmer treatment exhibited decreased thermal tolerance. Gravid females did not preferentially nest in regions with more shade and displayed decreased nesting depth on particularly warm days. These findings suggest that such behavioral plasticity and thermal tolerance in response to heat stress has not been under selection and further climate warming will be detrimental to this species.

## **70 How identity, biology content, and instructional practices impact religious students' sense of belonging in the biology classroom**

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In response to the growing need for science and technology-related solutions, there has been a call to increase the number of STEM graduates and the diversity of individuals within the sciences whom can bring unique perspectives in creating these solutions. In attempt to increase the number and diversity of STEM graduates, an abundance of research has been conducted that looks at underrepresented groups such as women, ethnic minorities, and first-generation college students. However, little research has examined the experiences of other groups that may struggle with persisting in a science-related major, such as religious students in biology. In this study, we focus on the experiences of students from Judeo-Christian religious backgrounds in their undergraduate biology classes that may have an effect on their sense of belonging in the biology community and their decisions to persist in biology. We interviewed 28 religious students enrolled in biology classes at a large research-intensive university in the Southwest United States. We analyzed the interview transcripts using grounded theory and content analysis. Our results indicate that religious students in biology must navigate two identities in the classroom: their religious identity and that as a biology student. These religious students also perceive disadvantages and advantages of being religious in biology classrooms. Furthermore, these students perceive that their religious identities are more relevant for certain topics of biology instruction, particularly evolution. These findings indicate that religious students face unique challenges in the biology classroom, which may influence their sense of belonging and retention in the discipline.

## **62 Effects of Water Availability During Gravidity on Performance and Growth of Neonate Children's Pythons (*Antaresia childreni*)**

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The embryonic developmental environment is crucial in an offspring's success after birth. For oviparous animals, specifically *Antaresia childreni*, there is a sensitive period post-ovulation leading us to the question of how depriving the female of water during gravidity would affect the "packaging" of the embryo in the oviduct and the later implications on the hatched neonates. Our results suggest that the offspring are buffered from the dehydrating conditions imposed on the female while gravid. Offspring from females in the water and no water treatment groups showed no significant differences in growth, snout to vent length, mass, and performance (swimming, strike tests).

## 47 Sex-bias gene expression in human placenta RNA-seq data

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Strong sex bias exists in several diseases such as breast and ovarian cancer, metabolic disorders, and autoimmune disease across the human populations. Analyzing patterns of sex-biased gene expression in early development tissue such as the placenta can help to better understand the molecular basis of disease. The placenta is a maternal-fetal tissue and sex-biased gene expression in the placenta may be contributing to the development of sex-biased disease later in life. Here we analyzed RNAseq from the placentas of 21 male and 19 female humans across four populations (African-American, European-American, East Asian American, and South Asian American). We tested the effects of a variety of filtering steps on our assessment of differential gene expression and found 67 differentially expressed genes between all male and all females samples. Furthermore, 45 genes are differentially expressed between the sexes in the African-American population, 58 in the European-American, 72 in the East Asian American, and 46 in the South Asian American population. This research contributes to a baseline understanding of differentially expressed genes in healthy human placentas between males and females, and across populations that can be used in future studies to better our understanding of the molecular basis of disease.

## 38 The Effects of Changes in Environmental Factors on the Protease Production of *P. aeruginosa*

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Cystic Fibrosis (CF) is a disease in which a genetic mutation causes the affected patients to build up thick mucus in their lungs, making them more susceptible to contracting life-limiting chronic lung infections. The microorganism that most commonly causes these lung infections in adults with CF is the opportunistic pathogen *Pseudomonas aeruginosa*. Once in the lungs of CF patients, *P. aeruginosa* can rapidly adapt to the environment with changes in its phenotype and genotype, some of which are correlated to worse patient outcomes. One of the exoproducts of *P. aeruginosa* that changes in the CF lung is protease, an enzyme that performs proteolysis or the catabolism of proteins by hydrolyzing peptide bonds. In chronic lung infections it has been noted that there is an overall decrease in the amount of protease produced. I hypothesize that changing environmental conditions will cause a change in the levels of protease production in *P. aeruginosa*. The goal of this project is to identify the effects of changes in temperature, oxygen availability and co-infection with *Staphylococcus aureus* on the protease production of *P. aeruginosa*. In the future, the genotypic and phenotypic data collected from these strains will be correlated with metabolomics data to identify potentially important biomarkers. These biomarkers will be used to create breath-based diagnostics, which will allow doctors to more easily diagnose lung infections and provide better clinical care.

## 72 **Breathe Big Beetle: Despite Hypermetry, Scarab Spiracle Scaling Requires Switch from Diffusive to Convective Gas Exchange**

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One hypothesis for why insects are smaller than vertebrates is that the blind-ended tracheal respiratory system challenges oxygen delivery for larger insects. Supporting this hypothesis, several studies have documented that larger insect species have larger gas transport structures than expected by isometric scaling. To further test this hypothesis, we performed the first inter-specific study of the scaling of spiracle size, using ten scarab beetle species, including some of the most massive insects. Using micro-CT, we measured the cross sectional area and depth of all eight spiracles. Areas of large spiracles in the anterior portion of the animal showed hypermetric scaling, varying approximately with mass<sup>0.8</sup>. However, because diffusive capacities scaled with lower slopes than metabolic rates, larger beetles had a 10-fold higher required PO<sub>2</sub> gradient across the spiracles to sustain oxygen consumption by diffusion. Despite this trend, calculations suggest that large beetles can exchange oxygen by diffusion across the spiracles at rest, but likely no beetles can do so during flight. Advective capacities through the spiracles scale with mass<sup>1.8</sup>, suggestive of a switch toward greater use of convection and/or reduced required pressures in larger beetles.

## 6 **Urban Water Insecurity: A Case Study of Homelessness in Phoenix, Arizona, USA**

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In this research project, we engage with the misconception that all people in the U.S. enjoy water security by examining the case of people experiencing homelessness in Phoenix, Arizona. Persons who experience homelessness are disproportionately at risk of dehydration and heat-related illness as they spend significantly more time outdoors and many have limited access to adequate water. Our data was collected using archival data, participant-observation, focal follows with water distributors that serve homeless populations, and expert interviews with diverse service providers. Our analysis follows this processual framework of water insecurity by focusing on sources of water, barriers to water acquisition, and impacts of insufficient access for persons experiencing homelessness. In this analysis, we focus on people living in three situations: shelters, encampments, and with no roof. We find that different economic sectors of the homeless population are affected in different ways. For those in shelter, the major problem is water replenishment during or after exposure to extreme heat. For those in encampments, the major problem is increasing physical and social isolation as a product of encampment raiding. For those with no roof, the major problem is inconsistent access to water fountains and water trucks. We also find many of the impacts of water scarcity lead back to the barriers to water acquisition, causing a cycle of water insecurity or homelessness. We conclude that persons who are experiencing homelessness have inconsistent and unreliable access to water for hydrating, maintaining hygiene, cooking, and cleaning for reasons that are largely social and structural.

## 5 **The Influence of Patriline on Task Division in Single Queen *Pogonomyrmex Californicus* Colonies**

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*Pogonomyrmex Californicus*, a species of harvester ants, colonies have polyandrous queens, meaning that each queen mates with multiple males before starting a colony. In some cases, *P. californicus* colonies can even be polygynous, meaning that multiple queens cooperate to produce workers in a colony. In previous studies, the colony size, worker age, and matriline of *Pogonomyrmex californicus* colonies were all found to influence task division to varying degrees, with matriline appearing to only have influence within their respective colonies. Since *P. californicus* colonies are also polyandrous, it would lead one to suspect influences of patriline in task division within colonies as well. To test this I observed task division within three colonies over four months, and collected the genotypic data of the workers I observed from each colony. The data collected is currently being analyzed to determine the extent to which task division is influenced by polyandry.

## 9 **Effects of Environmental Conditions on Pyocyanin Production in *Pseudomonas aeruginosa***

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Cystic Fibrosis (CF) is a genetic disease characterized by the inability to rid the respiratory tract of inhaled microorganisms because of production of thick mucus. As a result, microorganisms are able to colonize the lungs where they are exposed to varying environments during the course of years-long infections. Later in disease stage, the lungs of CF patients often consist of subpopulations of well-adapted bacteria, most commonly of *Pseudomonas aeruginosa* possessing a wide range of phenotypes, making these lung infections especially hard to target and eradicate.

One such phenotype represented in the lungs of cystic fibrosis patients is pyocyanin production. Pyocyanin is a pigment produced by *P. aeruginosa* with redox activity in respiratory tract epithelial cells that causes oxidative stress, deactivated cilia, and decreased capacity for ATP synthesis, leading to increased virulence of infection. Despite many studies quantifying the pyocyanin production of *P. aeruginosa* in infection isolates, much remains unknown about the effects that the unique CF lung environment has on *P. aeruginosa* phenotypes. I hypothesize that environmental conditions will affect pyocyanin production. In order to test this, I will examine how pyocyanin production changes as a result of temperature change, coinfection with *Staphylococcus aureus*, and oxygen depletion, all probable lung conditions in cystic fibrosis patients. Our goal as a lab is to identify volatile biomarkers associated with particular phenotypes of bacteria, including pyocyanin production, which can be used through breath-based diagnostics to more accurately detect lung infection phenotypes, leading to more effective treatments.