23rd Annual Undergraduate Research Poster Symposium
April 15, 2016

AGENDA

2 - 3 p.m. Keynote Address – Memorial Union Alumni Room (MU 202)

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

Keynote Address
"Undergraduates in Butterfly Research at ASU:
Contributions, Fates, and Lessons”
Ron Rutowski, PhD
Professor Emeritus
School of Life Sciences, Arizona State University

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 B/C (MU 241 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

Please visit the virtual symposium site at the following address:
https://sols.asu.edu/symposium
ACKNOWLEDGMENTS

Undergraduate research programs in the School of Life Sciences, and this poster symposium in particular, are supported through the generosity and contributions of many. Monetary support for our programs come from the School of Life Sciences at Arizona State University, National Institute of General Medical Science of National Institutes of Health, and individual faculty research grants from a variety of institutions and agencies. Off-campus research organizations, including Translational Genomics Research Institute, Barrow Neurological Institute, Scottsdale Healthcare, Mayo Clinic Arizona, USDA Arid Lands Research Laboratory, The Phoenix Zoo, Desert Botanical Gardens and the University of Arizona College of Medicine, and their resident scientists have generously opened their doors and supported excellent research experiences for a number of our students. Within the School of Life Sciences, the Life Sciences Visualization Laboratory, the Facilities Office, the Business Office, the Graduate Programs Office, the Undergraduate Programs Office, the Academic Advising Office, and the SOLS Administration Office have provided essential logistic, administrative, and other support services. 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 program would not exist. For all of 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

Carol Bear
Coordinator Senior, SOLUR

Madhavi Chakravadhanula, PhD
Project Coordinator, IMSD
Evaluation of Various Designs of Nicotine Vaccines

Adaralegbe, Jimi¹; Liu, Xiaowei²; Sokalingam, Sriram²; Arutla, Viswanath²; Hecht, Sidney²,³; and Chang, Yung¹,²

¹School of Life Sciences, Arizona State University, Tempe AZ; ²Center for Infectious Diseases and Vaccinology, The Biodesign Institute at Arizona State University, Tempe AZ; ³School of Molecular Sciences, Arizona State University, Tempe AZ

Nicotine plays a major role in tobacco smoking dependence. Nicotine (Nic) vaccines have been used to treat nicotine addiction. In this study, we describe the use of DNA nanostructure as a vaccine platform for rational design of nicotine-specific vaccines. To induce the antibody responses focused on free nicotine, we synthesized a series of hapten linkers, which were designed to increase nicotine-specific responses, but lower the responses made toward linkers or carrier proteins. Some candidates were identified to fulfill these criteria. In addition to conjugating nicotine to the carrier protein, we have recently managed to incorporate the nicotine hapten into DNA nanostructure. The assembled nicotine vaccine containing nicotine on both protein and DNA was tested for its immunogenicity. In our preliminary study, we found a much higher level of anti-nicotine antibody responses elicited by this combined vaccine than DNA-Nic vaccine that does not have nicotine incorporated into the DNA nanostructures. This study will be further validated with additional tests.

Identifying the Function of Tyramine in the Mouse Uterus

Agre, M., Obayomi, B., and Baluch, D.P.

School of Life Sciences, Arizona State University, Tempe AZ

Pregnancy and the birthing process are natural events but still little is known about the signaling mechanism(s) that induce contractions. Globally, premature labor occurs in 12% of all pregnancies resulting in 15 million babies born preterm. Even though the cause of preterm labor can vary, understanding the signaling pathway that regulates muscle contraction could provide additional treatment options to stop premature labor. The uterus is composed of smooth muscle and in conjunction with the associated nerve fibers, forms a plexus which covers the muscle fibers. The plexus has swollen areas called varicosities that contain neurotransmitters. Within the uterine tissue, the smooth muscle receives opposing inputs from the sympathetic and parasympathetic parts of the ANS. Smooth muscle can be stimulated or modulated by many sources such as neurotransmitters (i.e. norepinephrine), hormones (i.e. epinephrine) and chemicals (i.e. nitrous oxide). In this study we are focusing on an alternative modulator of smooth muscle activity, a monoamine produced in the catecholamine biosynthesis pathway called tyramine. During catecholamine biosynthesis dopamine, tyramine, octopamine, and norepinephrine are all derived from the tyrosine precursor. Tyramine has been associated with peripheral vasoconstriction, increased cardiac output, increased respiration, elevated blood glucose and release of norepinephrine (McCabe-Sellers et al., 2006). Our data has found tryramine and its specific receptor TAAR1 to be localized at the uterine neuromuscular junction in relation to muscular contraction. Ongoing research is focused on distinguishing if there is synchronous or alternating signaling, between the epinephrine and octopamine pathways, which regulate muscle contraction.
High Glucose-mediated Oxidative Stress Impairs Vasodilation of Small Resistance Skeletal Muscle Arteries from Mourning Doves (Zenaida macroura)

Ahmed, Zoha S.1; Jarrett, Catherine L.; Faust, James J.1; and Sweazea, Karen L.1
1School of Life Sciences, Arizona State University, Tempe AZ; 2School of Nutrition and Health Promotion, Arizona State University, Phoenix AZ

Plasma glucose concentrations are naturally 1.5-2 times higher in birds than mammals of similar body mass. In mammals, hyperglycemia is associated with superoxide-mediated endothelial dysfunction resulting in hypertension. In contrast to mammals with hyperglycemia, oxidative stress is typically low in birds. This apparent avian resistance to oxidative stress may be attributed to higher antioxidant status. Therefore, we hypothesized that endothelium-dependent vasodilation of isolated arteries from mourning doves (Zenaida macroura) would not change after acute exposure to high glucose. Mourning doves were captured in Tempe, Arizona using walk-in style funnel traps. Following euthanasia with sodium pentobarbital (200 mg/kg body mass), small resistance cranial tibial arteries were isolated, cannulated and pressurized in a vessel chamber. Isolated arteries were then exposed to either physiological (20 mM/L) or high (30 mM/L) glucose concentrations for 1 hour at 41°C. Endothelium-dependent vasodilation was assessed by pre-constricting the arteries to 50% of resting inner diameter with increasing doses of phenylephrine (PE) followed by increasing doses of the endothelium-dependent vasodilator acetylcholine (ACh; $10^{-9}$ to $10^{-5}$ M, 5 min per step) in the superfusate. Inner diameter was continuously measured using edge-detection software from which percent reversal of PE-induced tone was calculated. Moreover, superoxide concentrations were assessed by dihydroethidium (DHE) microfluorography in separate arteries pre-exposed to 20mM or 30mM glucose. Contrary to our hypothesis, exposure to high glucose increased vascular superoxide concentrations by 168.9±42% (p=0.0072) and impaired endothelium-mediated vasodilation.

Developing Breath-Based Diagnostics to Detect P. aeruginosa Exoproducts in CF Lung Infections

Anderson, Darrin; Dacasin, Nathan; Bhebhe, Charity; and Bean, Heather D.
School of Life Sciences, Arizona State University, Tempe AZ

Cystic fibrosis (CF) is a genetic disease affecting approximately 30,000 persons in the U.S. (70,000 worldwide). The genetic defect causes the body to produce thick, sticky mucus that clogs the airways of the lungs and also impairs the lungs' ability to clear out inhaled microorganisms, which leads to life-threatening lung infections. The leading cause of CF lung infections is Pseudomonas aeruginosa. Although P. aeruginosa is a ubiquitous bacterium, its opportunistic nature makes it a particularly dangerous pathogen to those with compromised immune systems, including those afflicted with CF. In addition, due to its ability to adapt to the lung environment through phenotypic and genotypic changes, P. aeruginosa can cause infections that last for years to decades. Early P. aeruginosa treatment is essential for long-term patient outcomes; once the infection is established, strains of the bacteria that are mucoid (slimy), quorum-sensing deficient, non-motile and antibiotic resistant are established, and these traits are correlated to lung function declines. The goal of this project is to phenotype and genotype P. aeruginosa CF lung isolates for exoproduct production. In particular, we are focused on P. aeruginosa proteases, surfactants, exopolysaccharides, quorum sensing molecules, and siderophores. The quantities of these exoproducts will be correlated to the isolates' metabolomes to discover unique volatile biomarkers of P. aeruginosa phenotypes, leading to new, improved medical devices for early diagnosis and characterization of chronic lung infections.
Moving from Resistance to Value: Applying Expectancy Value Theory (EVT) to Student Experience with Active Learning in College

Cooper, Katelyn M.; Ashley, Michael; and Brownell, Sara E.

School of Life Sciences, Arizona State University, Tempe AZ

The BIO Bridge summer program was designed to prepare incoming first-year students to be successful life sciences majors at Arizona State University. The two-week program exposed students to a highly structured active-learning biology curriculum that was developed to maximize student success in BIO 51: Biological Thinking, the first course in a three semester active-learning introductory biology sequence. Interviews with BIO Bridge students supported previous evidence which suggests that engaging in active learning activities improves in-class performance and that this type of engagement may be especially helpful for under prepared students. BIO Bridge students reported utilizing strategies to engage in active learning in ways that maximized their learning experiences. Consistent with expectancy value theory, students perceived that their early exposure to active learning during the BIO Bridge program improved their confidence in their ability to actively engage with biology content, increased the value they placed on active learning activities, and decreased their resistance to active learning. As the biology community continues to transition biology courses to be more student-centered, introducing at-risk students to active-learning early and providing them with strategies to maximize their experience may be an important step in improving student retention.

Suppression of Breast Cancer Cell Proliferation by Bexarotene and Novel RXR Agonists

Bains, Supreet1,2; Shahani, Pritika2; Wagner, Carl2; Marshall, Pamela A.2; Kaneko, Ichiro2; Heck, Michael2; and Jurutka, Peter W.2,3

1School of Life Sciences, Arizona State University, Tempe Campus, Tempe AZ; 2School of Mathematical and Natural Sciences, Arizona State University, West Campus, Glendale AZ; 3University of Arizona, College of Medicine, Department of Basic Medical Sciences, Phoenix AZ

The ligand-bound estrogen receptor (ERα) stimulates expression of target genes to drive ERα-positive breast cancer growth, and one such E2 target gene includes A-Myb, a potent driver of hematopoietic/epithelial cell proliferation. One strategy to combat breast cancer in a clinical setting is to attenuate estrogenic activity in breast tissue. Previous experiments show that the FDA-approved drug bexarotene (Bex), which is used to treat cutaneous T-cell lymphoma (CTCL), may also be effective against other cancers. Bex binds to the retinoid-X-receptor (RXR), a nuclear receptor implicated in many biological pathways, and Bex may also serve as an estrogen signaling antagonist. The purpose of this study was to examine if bexarotene is able to suppress the proliferation of ERα-positive breast cancers cells, and if Bex can inhibit the expression of proliferation genes such as A-Myb. In addition, novel drug analogs of bexarotene were also tested. All experiments were performed using a human breast cancer cell model (MCF-7). Results revealed that neither bexarotene nor its analogs significantly inhibit cell proliferation in the MCF-7 breast cancer model, alone or in combination with Tamoxifen. Yet, when observing the effect of Bex on the expression of the estrogenic target gene A-Myb using qR T-PCR, there was evidence of down-regulation. Although the impact of Bex/analogs on MCF-7 cell proliferation did not reach statistical significance in proliferation assays, bexarotene may still hold promise as an anti-estrogenic compound with therapeutic potential, and we are exploring other breast cancer models as well as cytotoxicity assays to further test bexarotene in this context.
Developing Breath-Based Diagnostics to Detect \textit{P. aeruginosa} Exoproducts in CF Lung Infections

Anderson, Darrin; Bhebhe, Charity; Dacasin, Nathan; and Bean, Heather D.

School of Life Sciences, Arizona State University, Tempe AZ

Cystic fibrosis (CF) is a genetic disease affecting approximately 30,000 persons in the U.S. (70,000 worldwide). The genetic defect causes the body to produce thick, sticky mucus that clogs the airways of the lungs and also impairs the lungs' ability to clear out inhaled microorganisms, which leads to life-threatening lung infections. The leading cause of CF lung infections is \textit{Pseudomonas aeruginosa}. Although \textit{P. aeruginosa} is a ubiquitous bacterium, its opportunistic nature makes it a particularly dangerous pathogen to those with compromised immune systems, including those afflicted with CF. In addition, due to its ability to adapt to the lung environment through phenotypic and genotypic changes, \textit{P. aeruginosa} can cause infections that last for years to decades. Early \textit{P. aeruginosa} treatment is essential for long-term patient outcomes; once the infection is established, strains of the bacteria that are mucoid (slimy), quorum-sensing deficient, non-motile and antibiotic resistant are established, and these traits are correlated to lung function declines. The goal of this project is to phenotype and genotype \textit{P. aeruginosa} CF lung isolates for exoproduct production. In particular, we are focused on \textit{P. aeruginosa} proteases, surfactants, exopolysaccharides, quorum sensing molecules, and siderophores. The quantities of these exoproducts will be correlated to the isolates' metabolomes to discover unique volatile biomarkers of \textit{P. aeruginosa} phenotypes, leading to new, improved medical devices for early diagnosis and characterization of chronic lung infections.

Chronic Variable Stress Leads to Down-Regulation of Organic Cation Transporter 3

Boyll, Piper\textsuperscript{1}; Paode, Pooja R.\textsuperscript{1}; Fonseca, Emmanuel\textsuperscript{2}; Ortiz, J. Bryce\textsuperscript{2}; Talboom, Joshua S.\textsuperscript{1}; Molinaro, Jeremiah\textsuperscript{1}; Conrad, Cheryl D.\textsuperscript{2}; and Orchinik, Miles\textsuperscript{1}

\textsuperscript{1}School of Life Sciences, Arizona State University, Tempe AZ; \textsuperscript{2}Department of Psychology, Arizona State University, Tempe AZ

Monoamine neurotransmitters (e.g., serotonin, norepinephrine, and dopamine) are powerful modulators of mood and cognitive function in health and disease. We have been investigating the modulation of monoamine clearance in select brain regions via organic cation transporters (OCTs), a family of nonselective transporters. OCTs are thought to complement the actions of selective monoamine transporters in the brain by helping to clear monoamines from the extracellular space; thus, assisting to terminate the monoamine signal. Of particular interest, stress hormone (corticosterone; CORT) inhibits OCT3-mediated transport of monoamines, putatively prolonging signaling. Our lab supports this outcome and demonstrated that stress levels of CORT block OCT3 transport in the rat hypothalamus, an effect that likely underlies the rapid, stress-induced increase in local monoamines. These data led to the hypothesis that the stress-sensitive OCT3 is a mechanistic link between stress and depression, or anxiety. We examined the effect of chronic variable stress (CVS) on OCT3 expression in "limbic" and hypothalamic regions in the rat brain. Animals subjected to CVS (14-days with random stressor exposure two times/day) showed reduced body weight gain, indicating that CVS was perceived as stressful. In situ hybridization data confirmed that OCT3 mRNA is expressed in the hippocampus, amygdala, and hypothalamus. Analysis of Western blot data by two-way ANOVA revealed a significant treatment effect on OCT3 protein levels, with a significant decrease in OCT3 protein in the amygdala and hippocampus in CVS rats, compared to controls. These data suggest that OCT3 may be a target for development of novel treatments for mood disorders.
Genetic Diversity on the Human X Chromosome Does Not Support a Strict Pseudoautosomal Boundary

Brotman, Sarah M.; Cotter, Daniel J.; and Wilson Sayres, Melissa A.

School of Life Sciences, Arizona State University, Tempe AZ; The Biodesign Institute at Arizona State University, Tempe AZ

Unlike the autosomes, recombination between the X and Y chromosome is often thought to be constrained to two small pseudoautosomal regions (PARs) at the tips of each sex chromosome. The PAR1 spans the first 2.7 Mb of the proximal arm of the human sex chromosomes, while the much smaller PAR2 encompasses the distal 320 kb of the long arm of each sex chromosome. In addition to the PAR1 and PAR2, there is a human-specific X-transposed region (XTR) that was duplicated from the X to the Y. The XTR is often not excluded from X-specific analyses, unlike the PARs, because it is not thought to routinely recombine. Genetic diversity is expected to be higher in recombining regions than in non-recombining regions (nonPARs). In this study, we investigate patterns of genetic diversity in noncoding regions across the entire X chromosome of a global sample of 26 unrelated females. We observe that genetic diversity in the PAR1 is significantly greater than the nonPAR. However, rather than an abrupt drop in diversity at the pseudoautosomal boundary (PAB), there is a gradual reduction in diversity from the recombining through the non-recombining region, suggesting that recombination between the human sex chromosomes spans across the currently defined PAB. In contrast, diversity in the PAR2 is not significantly elevated compared to the nonPAR, suggesting that recombination is not obligatory in the PAR2. Finally, diversity in the XTR is higher than the surrounding nonPAR regions, providing evidence that recombination may occur with some frequency between the X and Y in the XTR.

Direct Nose-to-brain Delivery of Targeted Polymeric Nanoparticles

Chung, Eugene P.; Prakapenka, Alesia V.; DiPerna, Danielle M.; McCall, Rebecca L.; and Sirianni, Rachael W.

School of Life Sciences, Arizona State University, Tempe AZ; Brain Tumor Research Center, Barrow Neurological Institute, Phoenix AZ; Interdisciplinary Graduate Program in Neuroscience, Arizona State University, Tempe AZ; Biological Design Graduate Program, Arizona State University, Tempe AZ; School of Biological and Health Systems Engineering, Arizona State University, Tempe AZ

The goals of this study were 1) to examine the regional differences in CNS delivery of nanoparticles surface modified with the rabies virus glycoprotein (RVG) targeting ligand after intranasal administration and 2) to elucidate the mechanism by which this occurs. Healthy Balb/C mice were intranasally administered either RVG targeted or non-targeted poly(lactic-co-glycolic acid) (PLGA) nanoparticles loaded with a DiR fluorescent dye and were sacrificed at 0.5, 2, or 6 hours post administration. At 0.5 hours post-administration, DiR were readily detected in the CNS with greatest delivery to the olfactory bulb, significantly greater than all other CNS regions with exception of the cervical spinal cord (p<0.05). This was followed by rapid clearance across all CNS regions by 2 hours with no significant regional differences (p>0.05). However, specific delivery to the trigeminal nerve at this time point showed over 3x greater delivery of payload with the RVG nanoparticle compared to the control. This confirms the trigeminal nerve as a major transport pathway for direct nose-to-brain delivery of nanoparticles and highlights the targeting potential for this formulation. To determine the mechanism of delivery, a separate nanoparticle formulation was created in which Rhodamine-B dye was either covalently conjugated or freely encapsulated within the nanoparticle in order to assess whether an intact nanoparticle or just the payload is being transported to the CNS. While no significant differences in total delivery to the brain,
spinal cord, or trigeminal nerve were seen at 30 minutes, suggesting that whole nanoparticles can be transported, further experiments are required.

54 Understanding the Role of Repair Response During Localized Tissue Damage in *D. melanogaster*

Contreras Rodriguez, Jesus¹; Lupone, Teresa²; Beckett, Chaz¹; Almajan, Ashley³; Leek, Ty⁴; Marsh, Tyler⁴; Hussain, Sabahat⁵; Broatch, Jennifer⁴; and Hackney-Price, Jennifer F.⁴

¹School of Molecular Sciences, Arizona State University, Tempe AZ; ²College of Science of Health Care Delivery Health Solutions, Arizona State University, Phoenix AZ; ³College of Nursing & Health Innovation, Arizona State University, Phoenix AZ; ⁴School of Mathematical and Natural Sciences, Arizona State University, Glendale AZ

Proper developmental fidelity ensures uninterrupted progression towards sexual maturity and species longevity. However, early development, the timeframe spanning infancy through adolescence, is a fragile state since organisms have limited mobility and responsiveness towards their environment. Previous studies have shown that damage during development leads to an onset of developmental delay which is proportional to the extent of damage accrued by the organism. In contrast, damage sustained in older organisms does not delay development in response to tissue damage. In the fruit fly, *Drosophila melanogaster*, damage to wing precursor tissues is associated with developmental retardation if damage is sustained in young larvae. No developmental delay is observed when damage is inflicted closer to pupariation time. Here we use microarray analysis to characterize the genomic response to injury in *Drosophila melanogaster* in young and old larvae. We also begin to develop tools to examine in more detail, the role that the neurotransmitter dopamine might play in mediating injury-induced developmental delays.

5 Selective Serotonin₁B Receptor Agonist Attenuates Methamphetamine Self-administration

Cotter, Austin¹; Garcia, Raul¹; Leslie, Kenneth¹; Bonadonna, John Paul¹; Ennis, Katie¹; Benson, Thomas²; Olive, M. Foster²; and Neisewander, Janet¹

¹School of Life Sciences, Arizona State University, Tempe AZ; ²Department of Psychology, Arizona State University, Tempe AZ

Prior research in our lab has found that the serotonin₁B receptor (5-HT₁B R) agonist CP 94,253 (CP) attenuates the reinforcing properties of cocaine following abstinence. Methamphetamine is a psychostimulant that has similar pharmacological effects on the serotonin neurotransmitter system as cocaine; therefore, we hypothesized that CP would attenuate the reinforcing properties of methamphetamine. Male Sprague-Dawley rats were trained to lever press for methamphetamine self-administration pre- and post-abstinence. In the first study, we tested the effects of CP on a range of methamphetamine doses (0.003-0.3 mg/kg, i.v.) under a fixed ratio 5 (FR5) schedule. In the second study, we tested the effects of CP on the incentive motivation for methamphetamine (0.05 mg/kg, i.v.) on a progressive ratio (PR) schedule. In the third study, we examined if the effects of CP on methamphetamine (0.1 mg/kg, i.v.) were 5-HT₁R-mediated by testing whether a 5-HT₁R antagonist (SB 224,289) would reverse the agonist's effects on a variable ratio 5 (VR5) schedule. Additionally, we examined the effects of 5-HT₁R ligands on spontaneous locomotion. Pre-abstinence on a FR5 schedule, CP attenuated methamphetamine intake only at high doses while post-abstinence CP attenuated intake at all doses. Pre- and post-abstinence on PR and VR5 schedules, CP attenuated methamphetamine intake. Furthermore, during pre-abstinence on a VR5 schedule, SB 224,289 reversed the attenuating effects of CP. Neither CP
nor SB 224,289 had an effect on spontaneous locomotion. CP attenuates methamphetamine self-administration both pre- and post-abstinence. These findings suggest that 5-HT_{1B}R agonists may be useful for treating stimulant drug abuse. Financial Support: R01DA011064, R01DA025606

21 Hippocampal BDNF Downregulation Prevents Recovery from CA3 Dendritic Retraction Induced by Chronic Stress

Daas, Eshaan J.\(^1\); Ortiz, J. Bryce\(^2\); Paode, Pooja R.\(^1\); and Conrad, Cheryl D.\(^2\)

\(^1\)School of Life Sciences, Arizona State University, Tempe AZ; \(^2\)Department of Psychology, Arizona State University, Tempe AZ

Chronic restraint stress impairs hippocampal-dependent spatial ability and induces dendritic retraction in hippocampal neurons, while a post-stress recovery period reverses these effects. Brain-derived neurotrophic factor (BDNF) is important for hippocampal function and neuronal structure. We previously demonstrated that hippocampal BDNF is necessary for recovery from spatial memory deficits resulting from chronic stress (Ortiz et al., 2014). This study aimed to determine whether hippocampal BDNF downregulation prevents recovery from dendritic retraction in chronically stressed rats. Male Sprague Dawley rats were either infused with viral vectors against BDNF (shRNA) or a scrambled sequence (Scr) in the CA3 region of the dorsal hippocampus. Rats were then assigned to chronic stress or unstressed controls (Con). Brains were extracted immediately following the end of chronic stress (Str-Imm) or following a 21-day post-stress recovery period (Str-Rec). One hemisphere of the brain was flash frozen for ELISA, while the other was processed for Golgi Stain. Short and long shaft hippocampal CA3 neurons were traced using a light microscope and a camera lucida drawing tube. Dendritic complexity was determined by quantifying number of bifurcations and dendritic length. The data corroborate past findings that chronic stress reduces dendritic complexity, which reverses with a post-stress recovery period. New findings reveal that BDNF knockdown appeared to hinder the recovery of neuronal architecture: Str-Rec-shRNA rats had decreased CA3 dendritic complexity compared to the Str-Rec-Scr rats. Together with our previous report, these data suggest that BDNF mediates the enhancement of CA3 dendritic arborization and improvement in hippocampal-dependent spatial cognition following chronic stress.

43 Developing Breath-Based Diagnostics to Detect \textit{P. aeruginosa} Exoproducts in CF Lung Infections

Anderson, Darrin; Bhebhe, Charity; Dacasin, Nathan; and Bean, Heather D.

School of Life Sciences, Arizona State University, Tempe AZ

Cystic fibrosis (CF) is a genetic disease affecting approximately 30,000 persons in the U.S. (70,000 worldwide). The genetic defect causes the body to produce thick, sticky mucus that clogs the airways of the lungs and also impairs the lungs’ ability to clear out inhaled microorganisms, which leads to life-threatening lung infections. The leading cause of CF lung infections is \textit{Pseudomonas aeruginosa}. Although \textit{P. aeruginosa} is a ubiquitous bacterium, its opportunistic nature makes it a particularly dangerous pathogen to those with compromised immune systems, including those afflicted with CF. In addition, due to its ability to adapt to the lung environment through phenotypic and genotypic changes, \textit{P. aeruginosa} can cause infections that last for years to decades. Early \textit{P. aeruginosa} treatment is essential for long-term patient outcomes; once the infection is established, strains of the bacteria that are mucoid (slimy), quorum-sensing deficient, non-motile and antibiotic resistant are established, and these traits are correlated to lung function declines. The goal of this project is to phenotype and genotype \textit{P. aeruginosa} CF lung isolates for exoproduct production. In particular, we are focused on \textit{P. aeruginosa} proteases,
surfactants, exopolysaccharides, quorum sensing molecules, and siderophores. The quantities of these exoproducts will be correlated to the isolates’ metabolomes to discover unique volatile biomarkers of *P. aeruginosa* phenotypes, leading to new, improved medical devices for early diagnosis and characterization of chronic lung infections.

8  **Male Mutation Bias in Drosophila**

Daly, Samantha; Amidan, Ashley; and Wilson Sayres, Melissa A.

School of Life Sciences, Arizona State University, Tempe AZ; Center for Evolution and Medicine, The Biodesign Institute at Arizona State University, Tempe AZ

Male mutation bias is founded on the idea that most mutations are due to errors during replication. Male gametes, which undergo more cell divisions than female gametes, should similarly accumulate and pass on more mutations than female gametes. This "male mutation bias" has been observed across mammals and in birds. This project focuses on identifying if the male mutation bias also exists in insects and if it does, whether it varies in magnitude across species. Due to the two papers previously written on male mutation bias in insects (both in flies) yielded conflicting results, we looked at the genomes for 12 Drosophila species and three outgroups across eight data subsets looking for evidence of male mutation bias. Because some species have larger X-chromosomes, due to chromosomal fusions, we conducted analysis both including these species and additions, and excluding them. We also analyzed several regions of the genome, some known to be directly affected by natural selection, and others that we expect to experience lower levels of selection, and so be more representative of the neutral mutation rate. For each dataset we compute X/A substitution rate ratios and estimated male mutation bias (alpha). The results section includes a table showing one subgroup of data – the coding exon region for 13 Drosophila species. Preliminary results show that some species exhibit male mutation bias while other do not. We are currently working on the complete analysis of eight subgroups of data with statistical analysis.

33  **A Novel Approach to Monitor and Understand the Rate of Mutational Adaptation to Targeted Cancer Therapy**

De Luca, Valerie⁴; Trent, Jeffrey³; Hendricks, William³; Zismann, Victoria²; Taila, Matthew²; Yin, Holly³; Sereduk, Chris³; Poorman, Kelsey²; Wilson Sayres, Melissa¹⁴; Maley, Carlo¹⁵; and Sekulic, Alex⁶

¹School of Life Sciences, Arizona State University, Tempe AZ; ²Integrated Cancer Genomics Division, TGen, Phoenix AZ; ³Cancer and Cell Biology Division, Cellular Genomics Collaborative Center, Scottsdale AZ; ⁴Center for Evolution and Medicine at The Biodesign Institute at Arizona State University, Tempe AZ; ⁵Virginia G. Piper Center for Personalized Diagnostics at The Biodesign Institute at Arizona State University, Tempe AZ; ⁶Department of Dermatology, Mayo Clinic, Scottsdale AZ

Resistance to BRAF inhibitors (BRAFi) in cutaneous malignant melanoma (CMM) patients exemplifies the current challenge to genomics-guided drug treatments. While over half of BRAF-mutant CMM patients experience tumor reduction with BRAFi such as Vemurafenib, their response is often short-lived due to the emergence of resistance. Many studies have identified genomic mechanisms driving BRAFi resistance. Yet, surprisingly little is known about the impact of targeted therapies, drug combinations, and dosing strategies on the rate of tumor adaptation; and no assay has been established to measure such a variable. We hypothesize that drug concentration and adaptation rate are positively correlated. As proof of principle, the BRAF**V600E** CMM suspension cell line SKMEL-1 will be grown from 100 million cells to 1 billion cells
in the presence of vehicle, Vemurafenib IC\textsuperscript{10}, IC\textsuperscript{30}, and IC\textsuperscript{50}. Serial passaging and growth rate analysis will continue until the change in growth rate plateaus. Adaptation rate will be calculated as the change in growth rate for each condition from Passage 1 until recovery. We predict that at higher doses, growth rate will recover more quickly across serial passages than at lower doses. Drug-resistant cells will then undergo genomic characterization to identify resistance drivers, which will also be assessed longitudinally to chart evolutionary dynamics. In summary, the goal of the project is to develop a novel in vitro assay to quantify and compare the adaptation rate of tumor cells under the influence of various therapeutic regimes in a large-scale system that captures the standing variation of a detectable lesion.

22 **Role of Accumbens Nicotinic Acetylcholine Receptors in Cue-induced Nicotine Seeking and Synaptic Plasticity**

Del Franco, Armani\textsuperscript{1,2}; Powell, Gregory\textsuperscript{1,2}; Pagni, Broc\textsuperscript{1}; Goenaga, Julianna\textsuperscript{1}; Scofield, Michael D.\textsuperscript{3}; and Gipson-Reichardt, Cassandra D.\textsuperscript{1}

\textsuperscript{1}Department of Psychology, Arizona State University, Tempe AZ; \textsuperscript{2}School of Life Sciences, Arizona State University, Tempe AZ; \textsuperscript{3}Neurosciences, Medical University of South Carolina, Charleston SC

**Aims:** Addiction to nicotine (NIC) produces long-term neuroadaptations that could contribute to relapse vulnerability. In the nucleus accumbens core (NAcore), glutamatergic signaling and synaptic plasticity has been shown to be involved in cue-induced nicotine seeking and may be modulated by nicotinic acetylcholine receptors (nAChRs). We investigated the effects of two intra-NAcore nAChR antagonists, methyllylcacoantin (MLA) or dihydro-β-erythroidine (DHβE), on cue-induced NIC seeking and relapse-associated synaptic plasticity as measured by changes in dendritic spines on NAcore medium spiny neurons.

**Methods:** Male Sprague Dawley rats were trained to self-administer NIC (0.02 mg/kg/infusion, paired with a light + tone cue). Rats then went into extinction for 14 days. Following intra-NAcore infusion of either MLA (11 nmol), DHβE (84 nmol), or aCSF, rats were placed into cue-induced reinstatement for 15 min, then transcardially perfused, and tissue was prepared for morphological analysis. Systemic injections (MLA; 0, 2.5, 10 mg/kg, i.p. or DHβE; 0, 3, 9 mg/kg, s.c.) were administered 30 min prior to 2 hour reinstatement sessions.

**Results and Conclusion:** Our results indicate that systemic nAChR antagonist injections do not significantly affect reinstatement of lever pressing as intra-NAcore infusions do. Furthermore, intra-NAcore infusion of MLA significantly alters the distribution of spine head diameters relative to aCSF and DHβE infusion. The location of the blocked receptors as well as their ability to modulate glutamate transmission and synaptic activity within the NAcore remains unclear, thus future research will explore the impact of acetylcholine signaling on neurotransmission and synaptic plasticity.

2 **Neural Correlates Underlying the Effect of Value on Recognition Memory**

Elliott, Blake L.; Blais, Chris; and Brewer, Gene A.

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In the present research we examined behavioral and neurophysiological correlates of value-directed recognition memory. Participants encoded words in multiple study phases that were assigned either high or low point values and were instructed that it was more important to remember the higher value words than the lower value words in order to increase their score on a subsequent word recognition test. Subjective states of recollection (i.e., “Remember”) and familiarity (i.e., “Know”) were assessed at retrieval. High
value words were discriminated more effectively than low value words and this difference was primarily driven by increases in Remember responses with no difference in Know responses. A corresponding parietal old-new effect (500-800 ms post-stimulus) over posterior electrodes differentiated neurophysiological correlates of high and low value words. Overall, the behavioral and neurophysiological data add to previous evidence that two distinct processes support recognition memory decisions, and that value-directed encoding results in a greater effect on subjective states of recollection.

39 How Does Water Availability Affect Macronutrient Balance?

Farington, Ruth H.1,2; Rogers, Stephen1; Learned, Jennifer1; and Cease, Arianne J.3
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Limited water in arid environments can create periods of prolonged stress for organisms. Inhabitants, specifically insects, must adapt behavioral strategies alongside physiological mechanisms to reduce and regulate water loss to survive. To fulfill water requirements animals may face a dietary trade-off. We used the Australian plague locust (Chortoicetes terminifera) to test how water availability influences macronutrient balance. In initial experiments, we gave locusts a choice of low and high protein:carbohydrate diets under ample water conditions and showed the lab colony preferred a ratio of 1 protein : 1.2 carbohydrate. We are currently conducting experiments where locusts are exposed to different levels of water availability: ad lib, no water, or water on one day over a three-day time period. We are measuring their self-selected protein to carbohydrate intake target. We hypothesize that consuming carbohydrate-biased diets may enable locusts to better adapt to arid environments based on two potential mechanisms. There is some evidence to suggest that high protein diets require more water to process. In addition, high carbohydrate diets increase lipid stores which can later be metabolized into water during drought conditions. In the future, I hope to add field-based studies to determine if this relationship is ecologically relevant for locusts and additional species to have a multi-genus comparison that could reveal an evolutionary relationship.

44 Nutritional and Dietary Treatment Study For Children & Adults With Autism

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Autism has been linked to nutritional, metabolic, and digestive problems. This study aims to determine the effect of a combination of six nutritional and dietary supplements (vitamins, minerals, essential fatty acids, carnitine, digestive enzymes, and gluten-free, casein-free diets) on the symptoms of people with autism. Previous studies have successfully used this approach to treat these problems individually and over short periods. During 12 months, this study used a behavioral metric on two autism groups: one that received treatment (TG) (n=19) and one that received no treatment (NTG) (n=16). The behavioral metric, Vineland Adaptive Behavior Scales, Second Edition, was used to assign a neurotypical age to the participants by quantifying sets of behavior. A T-Test was used to determine the significance of the difference between the initial and final subscale data for the treatment and non-treatment groups. Three of the Vineland subscales showed a significant difference: written (TG: 1.6 +/- 3 years; NTG: -0.2 +/- 1.9 years; p < 0.05), domestic (TG: 2.2 +/- 2.3 years; NTG: -0.2 +/- 1.9 years; p < 0.05), and coping skills (T: 3.2 +/- 4 years; NTG: -0.2 +/- 4.7 years; p < 0.05). The total average of the Vineland was 20 +/- 18 months for the treatment group
and 5 +/- 19 months for the non-treatment group with a p ≤ 0.05. A combination of nutritional and dietary treatments over 12 months led to significant overall improvements in Vineland developmental age, including significant improvements on the written, domestic, and coping subscales.

37 Influence of City Food on the Gut Microbiome of House Sparrows (*Passer domesticus*)

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Birds living in cities have increased access to human-derived refuse. In fact, house sparrows (*Passer domesticus*) are commonly seen in heavily-populated areas in which these potential food sources are readily available (parks, restaurant patios, etc). In contrast to the urban populations that regularly consume human-derived foods, rural house sparrows consume mainly seeds. Therefore, we are interested in understanding how the gut microbiome differs in birds living in rural versus urban populations. We hypothesize that urban birds will have a different gut microbiome profile associated with measures of increased risk for cardiovascular disease than rural conspecifics. To test this, ten adult house sparrows of both sexes will be captured from both urban and rural locations and both blood and fecal samples obtained. The gut microbiome will be analyzed by 16S rRNA analysis. Variations in body mass, plasma glucose, fatty acids and proteins in each bird along with changes in the antioxidants carotenoids and uric acid will be measured for each bird. Gizzard samples will also be collected to measure sugar and fat intake. It will then be determined whether changes in the gut microbiome are associated with changes in these other variables. The results of this study will lead to a better understanding of the effects of urban diets on the nutritional physiology of house sparrows.

58 Characterization of the Protist Hindgut Community in *Heterotermes aureus*

Garcia, Mikaela D.; Jasso-Selles, Daniel; Merrell, Trevor L.; Peterson, Katalina D.; and Gile, Gillian H.  
*School of Life Sciences, Arizona State University, Tempe AZ*

*Heterotermes aureus* (Rhinotermitidae) is the most common subterranean termite in the dry and hot Sonoran Desert and the most destructive urban termite pest in Arizona. As generalist feeders, they are often found in and burrowed around deadwood. Wood eating termites like *H. aureus* have gut dwelling symbiotic protists to help them break down their lignocellulose diet. This obligate symbiotic relationship is ancient, dating back to the common ancestor of termite and the wood roach, *Cryptocercus*. Each termite and *Cryptocercus* species (except for termites in the family Termitidae) has a characteristic assemblage of protist symbionts. We collected *H. aureus* from an empty lot in Gilbert, Arizona and characterized the hindgut protist community with morphological and molecular methods. The hindgut eukaryotic microbiome of *H. aureus* was previously reported to consist of unnamed species of *Holomastigotooides*, *Spirotrichonympha*, and *Pseudotrichonympha* and our light microscopical observations agree with these classifications. We isolated single cells of each protist with micropipettes, amplified and sequenced the small subunit ribosomal RNA gene (SSU rDNA) and performed phylogenetic analyses. Each protist branched as expected: *Pseudotrichonympha* within the Trichonymphidae, and *Holomastigotooides* and *Spirotrichonympha* in the Spirotrichonymphidae. Based on their distinct host species and differences in their SSU rDNA sequences, we suspect the *H. aureus* protists should be considered new species.
Relationships Between Courtship Behavior, Morphology, and Structurally Based Plumage Coloration in Anna's hummingbirds (*Calypte anna*)

Givens, Jessica L.; Simpson, Richard K.; and McGraw, Kevin J.  
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Sexually selected traits often reveal attributes of individual quality to potential partners or rivals. Hummingbirds display some of the most exaggerated traits in animals, including rapid flight, elaborate courtship displays (e.g. dives, shuttles), and brilliant plumage, yet we know very little about the expression of and relationship among these hummingbird traits. The traits may covary if they reveal common indices of quality, or may independently vary if they serve different functions. I am exploring the relationships between body morphology, courtship behavior, and iridescent plumage coloration in male Anna’s hummingbirds (*Calypte anna*), a common breeding species in the Phoenix metropolitan area. We use spectrometry to measure reflectance characteristics of plucked feathers from the crown, gorget, back, and belly. We elicit and record courtship behaviors in the field and measure spatial locations and display angles of males (relative to the female) from video recordings. We measure morphology with bill, tarsus, and mass measurements. After analyzing the relationships between these traits, we can begin to place them in an urban context and assess what environmental factors may be affecting them, such as human impact or differences in learning.

Targeted Delivery DNA-Tetrahedron Assembled Therapeutics

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We are optimizing the conditions to increase the internalization of a DNA tetrahedron nanostructure into a B cell lymphoma line. The structure exhibits delivery potential for targeted vaccines that could be applicable to cancer therapeutics. The initially low immunogenicity of the structure is increased via addition of CpG. Other molecules may be added to further increase the immune response. Upon efficient internalization we will optimize the specificity of targeting by decorating the TH assembly with specific antibodies or peptides. This specificity will be utilized to deliver drug-loaded tetrahedron structures to B cells targeted for destruction.

Monoamine Oxidase A Co-localized with Organic Cation Transporter 3 in Rat Brain Neurons

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Serotonin (5-HT) is a neurotransmitter involved in the regulation of sleep, mood, appetite, and emotion. Monoamine oxidase A (MAO-A) is an enzyme that metabolizes monoamines, preferentially 5-HT. This study investigated a novel metabolic pathway for 5-HT that depends upon the presence of MAO-A and organic cation transporter 3 (OCT3) in neurons. OCT3 is a little-studied, polyspecific transporter for monoamines, including 5-HT. Our hypothesis is that 5-HT can be cleared after transport via OCT3 into neurons containing MAO-A, in addition to the well-known reuptake via specific 5-HT transporters. We looked for co-localization using immunofluorescent double-labeling against NeuN (a marker of adult neurons) and MAO-A, and against OCT3 and MAO-A. Immunopositive cells in hippocampus, amygdala, hypothalamus, cortex, and prefrontal cortex were visualized using epifluorescent microscopy; co-localization was determined through semi-quantitative measures using superimposed images of MAO-A
and NeuN labeling or MAO-A and OCT3 labeling. We found MAO-A in neuronal cell bodies in all the study regions. Most, but not all, MAO-A cells were neurons and most, but not all, MAO-A cells contained OCT3. These data provide evidence for a previously undescribed metabolic pathway for 5-HT that depends upon OCT3. Further, since the activity of OCT3 is inhibited by stress hormones, the presence of OCT3 in MAO-A-containing neurons supports the hypothesis that this is a stress-sensitive 5-HT clearance, and therefore signaling, pathway. This pathway is likely applicable for understanding dopamine and norepinephrine metabolism as well as 5-HT.

14 A Review of the Weevil Genus Pachnaeus: Morphology, Geographic Distribution, and Phylogenetic Analyses

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The weevil genus Pachnaeus Schönherr, 1826 (Curculionidae: Entiminae) is known to contain species that are citrus pests. The adults feed on leaves and young shoots while the larvae consume the roots, resulting in the damage or death of the plant. This has been a known issue since 1908 and has had wide spread economical and agricultural impacts. Despite their economic importance, species of Pachnaeus have not been the subject of a systematic revision. At present there are seven described species within Pachnaeus from Cuba, Jamaica, Puerto Rico, Mexico, and the United States. The last publication detailing Pachnaeus is Marshall (1916), giving reasons for a genus wide revision. Herein a review of the genus Pachnaeus is conducted utilizing taxonomic descriptions, comparative morphological documentations, geographic distribution, and phylogenetic analyses. This review has resulted in the documentation and description of several new species from Cuba, Panama, Bahamas, and the Cayman Islands. Based on newly reconstructed morphological and molecular phylogenies, we test the monophyly of Pachnaeus and investigate its phylogenetic placement. Our phylogenetic insights also necessitate generic membership transfer to Pachnaeus of several species currently placed in Exophthalmus.

58 Characterization of the Protist Hindgut Community in Heterotermes aureus

Garcia, Mikaela D.; Jasso-Selles, Daniel; Merrell, Trevor L.; Peterson, Katalina D.; and Gile, Gillian H.
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Heterotermes aureus (Rhinotermitidae) is the most common subterranean termite in the dry and hot Sonoran Desert and the most destructive urban termite pest in Arizona. As generalist feeders, they are often found in and burrowed around deadwood. Wood eating termites like H. aureus have gut dwelling symbiotic protists to help them break down their lignocellulose diet. This obligate symbiotic relationship is ancient, dating back to the common ancestor of termite and the wood roach, Cryptocercus. Each termite and Cryptocercus species (except for termites in the family Termitidae) has a characteristic assemblage of protist symbionts. We collected H. aureus from an empty lot in Gilbert, Arizona and characterized the hindgut protist community with morphological and molecular methods. The hindgut eukaryotic microbiome of H. aureus was previously reported to consist of unnamed species of Holomastigotoides, Spirotrichonympha, and Pseudotrichonympha and our light microscopical observations agree with these classifications. We isolated single cells of each protist with micropipettes, amplified and sequenced the small subunit ribosomal RNA gene (SSU rDNA) and performed phylogenetic analyses. Each protist branched as expected: Pseudotrichonympha within the Trichonymphidae, and Holomastigotoides and Spirotrichonympha in the Spirotrichonymphidae. Based on their distinct host species and differences in their SSU rDNA sequences, we suspect the H. aureus protists should be considered new species.
51  The Proteomic Profile of Chronic Stress and Recovery in the Hippocampus

Kachemov, Marketta1,2; Garcia, Krystine2; Paode, Pooja1,3; Rosenow, Matthew2; David, Victoria2; Saltzman, Marissa2; Conrad, Cheryl D.3; Pirrotte, Patrick2; and Orchinik, Miles1
1School of Life Sciences, Arizona State University, Tempe AZ; 2Center for Proteomics, Translational Genomics Research Institute, Phoenix AZ; 3Department of Psychology, Arizona State University, Tempe AZ

The stress response facilitates our ability to deal effectively with threatening situations, but exposure to severe or chronic stressors can lead to undesirable neural, physiological, and behavioral outcomes. Chronic stress is associated with structural changes in the rat hippocampus, with corresponding deficits in learning and memory. Recent studies have uncovered an inherent neuroplasticity that allows the hippocampus to recover from these stress-induced neural changes. Underlying mechanisms likely involve several different cellular and molecular pathways. In order to gain a more comprehensive understanding of these pathways, we investigated differences in protein expression throughout the timeline of chronic stress and recovery. Male Sprague-Dawley rats were randomly assigned to chronic restraint stress for 6hr/d/10d or 6hr/d/21d, stress for 6hr/d/21d followed by a recovery period of no stress for 10 or 21 days, or a control group. The proteome from the hippocampus of these rats was sequenced using liquid chromatography tandem mass spectrometry (LC-MS/MS) and analyzed.

We hypothesized that the neural recovery process involves a suite of proteins associated with neuronal plasticity, including synaptic and cytoskeletal proteins and neurotrophins. So far we have found that structural proteins, such as collagen alpha chain, neurofilament light, tubulin, and vimentin were significantly altered by chronic stress. In contrast, proteins necessary for neuron growth and development, such as myelin-associated glycoprotein, F-box/LRR-repeat protein 16, and homer protein homolog 3, were significantly altered in the recovery period. Collectively, these results will provide a resource for further investigations into the mechanisms of the brain’s recovery from chronic stress.

38  How do MiRNAs Increase Risk for Type 2 Diabetes

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The prevalence of obesity in the United States has more than tripled in the past 3 decades and represents a major medical, social and financial burden. The Latino population is at increased risk for obesity and related diseases such as type 2 diabetes. While rates of type 2 diabetes are increasing in younger populations, little research has been conducted within the pediatric age group. Lifestyle interventions are the first line of prevention against the development of type 2 diabetes. However, data suggest that there is considerable variability in how individuals at risk for type 2 diabetes respond to lifestyle intervention. Genetic factors may help explain individual variability in diabetes risk reduction following lifestyle intervention. MicroRNAs (MiRNAs) are small, non coding RNA’s that regulate gene expression and have emerged as potential biomarkers for identifying risk and for type 2 diabetes in adults. Whether MiRNA can be used as biomarkers of risk reduction following lifestyle intervention among Latino youth at risk for type 2 diabetes in unknown. Therefore, the purpose of this study is to identify alterations in MiRNA expression between Latino youth with prediabetes who respond and those who do not respond to lifestyle intervention. This study will explain if genetic factors explicate how prediabetic, obese Latino youth respond and do not respond to lifestyle intervention. These actions may help explain how MiRNAs may predict diabetes risk reduction following lifestyle intervention. These observations may explain the mechanisms that lead to the risk in type 2 diabetes.
Developing Breath-Based Diagnostics to Detect P. aeruginosa Motility and Antibiotic Resistance in CF Lung Infections

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The primary cause of lung function decline and eventual death for persons with cystic fibrosis (CF) is pulmonary damage from chronic bacterial lung infections, with *Pseudomonas aeruginosa* responsible for half of all CF infections, and establishing chronic lung infections in 75% of adults with CF. During chronic infection, *P. aeruginosa* acquire phenotypes, such as antibiotic resistance, loss of motility, and mucoidy, that are significantly correlated to lung function decline. However, accurately diagnosing these phenotypes in the clinical microbiology laboratory is incredibly challenging due to rapid phenotypic switching by the bacteria once they are cultured outside of the lung environment. The long-term vision of the Bean Lab is to identify volatile biomarkers to detect these clinically-important bacterial phenotypes directly from the patients' breath, making it possible to detect the pathogens and their phenotypes in situ.

The goal of this project is to phenotype and genotype *P. aeruginosa* CF lung isolates for motility and antibiotic resistance. In particular, we are focused on *P. aeruginosa* swimming, swarming, and twitching motilities, and resistance to cephalosporin, fluoroquinolone, carbapenem, aminoglycoside, monobactam, and polymyxin antibiotics. These traits will be correlated to the isolates' volatile metabolomes to identify biomarkers of these *P. aeruginosa* phenotypes, which will be developed into breath-based diagnostics for early, non-invasive detection and characterization of chronic lung infections.

Exposure to Sunlight Facilitates Subsequent Leaching Losses from Plant Litter in the Sonoran Desert

Leesley, Dionne R.; Robertson, Sarah K.; Deegan, Taylor A.; Bliss, Michael S.; Tomes, Alexander R.; and Day, Thomas A.
School of Life Sciences, Arizona State University, Tempe AZ

Recent studies have shown that exposure to sunlight can be an important driver of plant litter decomposition via photodegradation. Leaching from plant litter during precipitation events is another potential driver of decomposition. We explored how the combination of exposure to sunlight and leaching influence plant litter decomposition. In a previous study, leaf litter of 12 species that was exposed to sunlight for 22 months in the Sonoran Desert lost more mass than litter that did not receive UV or UV/blue sunlight. We used litter from that study to assess whether exposure to sunlight influenced subsequent leaching losses, via a lab assay that quantified leaching losses associated with immersion of litter in warm water for 1 hr. Leaching losses were substantial (mean mass loss 24%) and were greater from litter that had been exposed to more sunlight in the field study, illustrating that exposure to sunlight facilitated subsequent leaching losses. Litter mass loss during the previous experiment was positively correlated with subsequent leaching losses in the lab assays. Therefore, the more mass lost in the field, the more subsequently lost via leaching. Our findings illustrate that photodegradation accelerates subsequent leaching losses from relatively old litter. In the context of climate change predictions of more extreme precipitation events (larger but less frequent), we suggest that photodegradation and leaching may become stronger drivers of decomposition in the Sonoran Desert. Plant litter exposed to extended periods of sunlight punctuated by large precipitation events could experience faster decomposition rates via greater photodegradation and leaching losses.
28 Linking Livestock Grazing Practices with the Nutritional Ecology of Grasses and Locusts in West Africa

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1School of Life Sciences, Arizona State University, Tempe AZ; 2School of Sustainability, Arizona State University, Tempe AZ

A locust outbreak can cause a significant amount of damage to crops and vegetation when it occurs. In Senegal, West Africa, the Senegalese locust *Oedaleus senegalensis* is shown to be abundant in pasture and fallow fields compared to crop fields (Toure et. al 2013). We have selected three field sites across Senegal to test our hypothesis that the nutritional status of plants is linked to this observed pattern in the behavior of the locust. Studies have shown that in Inner Mongolia overgrazed fields have high populations of *Oedaleus asiaticus* compared to more moderately grazed pastures because overgrazed fields contain plants with low nitrogen contents (Cease et. al 2012, 2015). We will test to see if a similar mechanism is happening in Senegal by investigating the relationship between agricultural practices, plant nitrogen content, and Senegalese locusts. Understanding the relationship between the Senegalese locust and the nutritional status of plants in grazing fields and crop fields will provide valuable information that could be used to develop policies that promote landscape sustainability, farmer livelihood, and decrease the probability and severity of locust plagues.

53 HIV-1 Virus Like Particles as Stimulators of Innate Immunity

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Development of a safe but effective vaccine against HIV-1 is an attractive strategy for the prevention of new infections needed for pandemic control. Clinical trials have indicated that viral vector and subunit based prime-boost vaccines have protective capacities against HIV-1 infection though low efficacy1. HIV virus-like particles (VLPs) produced in *Nicotiana benthamiana* plants have potential natural adjuvancy due to their method of production involving a gram-negative bacteria making them a good candidate as a vaccine component2. To assess this immunogenic potential, we seek to characterize the VLPs’ interaction with and activation of the innate immune system. Data shows activation of many toll-like receptors (TLRs) due to the presence of a variety of possible pathogen associated molecular patterns (PAMPs) along with the VLPs. Fully enveloped VLPs harbor and protect nucleic acid from nuclease treatment which can be abrogated if digested in the presence of a membrane disturbing detergent. Presence of these PAMPs and their activation of TLRs confer intrinsic adjuvant properties to these plant-derived VLPs; a beneficial property if used as a booster to a vaccine.
MKX Regulation of Macrophage Recruitment during Chronic Muscle Damage Associated with Muscular Dystrophy

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Duchenne Muscular Dystrophy (DMD) is a muscular degenerative disease characterized by striated membrane instability that stimulates continuous cycles of muscle repair. The productive sterile inflammatory response necessary for healthy muscle repair transitions to a pathological chronic inflammation associated with fibrosis and an increase in immature fibers. The balance between pro-inflammatory macrophage (M1) and anti-inflammatory macrophage (M2) needed to promote myolysis followed by tissue repair is regulated by an intricate feedback loop between muscle, neutrophils and macrophages mediated by Th1 and Th2 cytokines and chemokines. Pathology is created by the failure of the muscle to resolve inflammation and the presence of a pro-fibrotic species of the M2. Finding treatments that ameliorate fibrosis are essential for extending ambulation of dystrophy patients. Mohawk (Mkx), a homeobox transcription factor, has been shown to be essential for the initiation of a robust inflammation response to acute injury. This study aims to examine the potential of Mohawk (Mkx) as a regulator of the inflammation response to chronic damage associated with muscular dystrophy. The mdx mouse is a well-studied mouse model that recapitulates muscle necrosis, chronic inflammatory response and fibrosis associated with muscular dystrophy. Utilizing Flow cytometry, quantitative RT-PCR and histological analysis, the diaphragms and quadriceps muscles of adult Mkx−/−mdx and Mkx+/+mdx mice were analyzed at three critical time points (4 weeks, 3 months and 7 months). The results of these studies will be discussed.

Characterization of TolC-AcrB Interactions in Efflux Pumps in Escherichia coli

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The spread of antibiotic resistant bacteria is currently a pressing global health concern, especially considering the prevalence of multi-drug resistance. Efflux pumps, bacterial machinery involved in various active transport functions, are capable of non-specific removal of antibiotics from the periplasmic space, frequently conferring multi-drug resistance. Many aspects of efflux machinery's structure, functions, and inter-protein interactions are still not fully understood; further characterization of these components of efflux will provide a strong foundation for combating this resistance mechanism. In this project, we further characterize the channel protein TolC as a part of the AcrAB-TolC efflux pump complex in Escherichia coli by first determining the specificity of compensatory mutations in TolC as a response to defects in AcrA and AcrB, and then identifying TolC residues that might influence TolC aperture dynamics or stability when altered. Specificity of compensatory mutations was determined using an array of TolC mutants, previously generated from defective AcrA or AcrB, against a different mutant AcrB protein; these new mutant combinations were then analyzed with efflux and antibiotic susceptibility assays. A vancomycin sensitive mutant – a phenotype that has been associated with constitutively open yet unengaged TolC channels – was then used to generate vancomycin-resistant revertants which were evaluated with DNA sequencing, protein quantification, and efflux assays to identify residues important for TolC aperture dynamics and protein stability and complex activity.
Characterization of the Protist Hindgut Community in *Heterotermes aureus*

Garcia, Mikaela D.; Jasso-Selles, Daniel; Merrell, Trevor L.; Peterson, Katalina D.; and Gile, Gillian H.
*School of Life Sciences, Arizona State University, Tempe AZ*

*Heterotermes aureus* (Rhinotermitidae) is the most common subterranean termite in the dry and hot Sonoran Desert and the most destructive urban termite pest in Arizona. As generalist feeders, they are often found in and burrowed around deadwood. Wood eating termites like *H. aureus* have gut dwelling symbiotic protists to help them break down their lignocellulose diet. This obligate symbiotic relationship is ancient, dating back to the common ancestor of termite and the wood roach, *Cryptocercus*. Each termite and *Cryptocercus* species (except for termites in the family Termitidae) has a characteristic assemblage of protist symbionts. We collected *H. aureus* from an empty lot in Gilbert, Arizona and characterized the hindgut protist community with morphological and molecular methods. The hindgut eukaryotic microbiome of *H. aureus* was previously reported to consist of unnamed species of *Holomastigotoides*, *Spirotrichonympha*, and *Pseudotrichonympha* and our light microscopical observations agree with these classifications. We isolated single cells of each protist with micropipettes, amplified and sequenced the small subunit ribosomal RNA gene (SSU rDNA) and performed phylogenetic analyses. Each protist branched as expected: *Pseudotrichonympha* within the Trichonymphidae, and *Holomastigotoides* and *Spirotrichonympha* in the *Spirotrichonymphidae*. Based on their distinct host species and differences in their SSU rDNA sequences, we suspect the *H. aureus* protists should be considered new species.

Linking Immunologic and Epidemiologic Models of Virus Transmission and Susceptibility

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Memory CD8+ T-cells can persist in the absence of antigen, primed for immediate activation and proliferation if later exposed to the same antigen. These cytotoxic lymphocytes provide long-term immunity following an acute infection. Previous results suggest that naive CD8+ T-cell injection has a minimal immunological effect as a vaccination method when challenged through cohousing with an infectious carrier. Therefore, our current study focuses on a memory CD8+ T-cell therapy using lymphocytic choriomeningitis virus (LCMV) specific splenocytes, which should activate and proliferate at an accelerated pace compared to that of naive T-cells. LCMV is a natural murine pathogen which also poses a zoonotic infection threat to humans, and the effect of immune cell vaccination therapies for LCMV is not fully understood. We will be observing the effect of multiple splenocyte doses on overall disease, infection, and memory CD8+ T-cell response to the virus. It is hypothesized that treatment will result in an accelerated immune response after mice are challenged by exposure to congenital carrier "spreader" mice. Symptoms of disease, weight, clinical score, and mortality rate will be measured to quantify the accelerated immune response. Infection will be verified initially through plaque assays and at a later time using ELISA testing. CD8+ T-cell response will be monitored using PBMC measurement specific for Thy1.1+ memory T-cells. Our findings will elucidate the possible outcomes of anti-viral treatments and vaccines focused primarily on memory CD8+ T-cells.
Establishing a Mouse Model for Congenital LCMV Infection

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¹School of Life Sciences, Arizona State University, Tempe AZ; ²Center for Infectious Diseases and Vaccinology, The Biodesign Institute at Arizona State University, Tempe AZ

Pathogens such as lymphocytic choriomeningitis virus (LCMV) cause spontaneous abortions in mice when exposure occurs during early pregnancy; however, exposure at later stages of pregnancy and after birth causes a chronic, lifelong infection associated with T cell tolerance. Although tolerated, the virus is responsible for major neurological effects that impair the behavior of these mice. To study the evolution and neuropathogenesis of the virus, we needed mice chronically infected with LCMV. To establish congenital infection, newborn C57BL/6J mice were intra-cerebrally (i.c.) injected with the Armstrong strain of LCMV. Infanticide between days three and ten after inoculation resulted in almost 100% mortality, and surviving mice were seronegative for the virus. A smaller dose of the virus was used when infecting two additional litters, but mortality was not changed. After reviewing literature on other LCMV strains, we noticed that intraperitoneal (i.p.) injection has reduced mortality compared to i.c. injections. Therefore, LCMV Armstrong was i.p. injected into four litters of mice, resulting in a much higher rate of survival after ten days. Although it is unknown what percentage of mice are chronically infected, the reduction in mortality makes it more likely that chronically infected mice have survived.

Meal Consumption Is Ineffective at Maintaining or Correcting Water Balance in Western Diamondback Rattlesnakes, Crotalus atrox

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While water is a critical resource, free-standing water is rare in desert environments. Thus many desert-adapted species utilize either metabolic (that produced during metabolism) or dietary (that found in food) water to meet their hydric needs. While it is widely suspected that snakes can fulfill their water needs solely through dietary water intake, this has never been empirically tested. Therefore, we hypothesize that meal consumption will be equally effective at rehydrating rattlesnakes compared to drinking. We predicted that both moderately and severely dehydrated Crotalus atrox will improve their hydration state after consuming a meal. Our results indicated that C. atrox hydric state does not benefit from meal consumption. In fact, meal consumption resulted in an acceleration of dehydration rates as compared to no meal consumption. These results demonstrate that C. atrox and likely other rodent-eating desert reptiles, rely on free-standing water and that changes in precipitation frequency could have drastic effects on these species.
Interactions Between the HIV-1 Protein gp41 and Calmodulin and its Effect on Cytotoxicity When Expressed in *Nicotiana benthamiana*

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HIV-1 virions display two surface proteins, gp120 and gp41, with key antibody targets. Gp120 protein is very immunogenic but highly mutable and used by HIV as a decoy. The gp41 protein is also immunogenic but is more highly conserved in specific regions. Using a modified version of gp41, deconstructed gp41 (dgp41), we may expose the membrane proximal external region (MPER). The MPER is a target for broad neutralizing antibodies (bNAbs) such as 2F5, 4E10, 10E8. These antibodies are very valuable in the immune system, however, they may take years to develop in an infected patient. Gp41 is highly toxic in plant and mammalian expression systems. Recent data suggests this could be due to ER stress through a calmodulin (CaM) dependent Ca\(^2+\) signaling pathway. Gp41 binds CaM at its C-terminus. In this project, we will clone a point mutation, A835W, into the dgp41 gene. This mutation has been shown to disrupt CaM interactions with gp41 and reduces cytotoxicity in mammalian cell culture. If this mutation succeeds in preventing CaM to bind to dgp41, then we may produce the dgp41 protein with reduced toxicity in the plant system. We can then proceed to make transgenic plants which can successfully express the protein and further the progress of achieving a HIV vaccine.

Organizing the Weevil Collection in the Arizona State University Hasbrouck Insect Collection (ASUHIC)

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The Arizona State University Hasbrouck Insect Collection (ASUHIC) is experiencing rapid growth, containing about 850,000 arthropod specimens to date. One of the main organisms of study by ASU entomological taxonomists are the weevils (Coleoptera: Curculionoidea). There are over 60,000 known species of weevil in the world. Species of weevil are continuously being added the Symbiota Collection of Arthropods Network database (SCAN, [http://symbiota4.acis.ufl.edu/scan/portal/](http://symbiota4.acis.ufl.edu/scan/portal/)), and the focus on this group by specialists working with ASU has led to many discoveries and new species. The goals of this current project are to (1) reorganize the weevil collection in phylogenetic order, (2) create an inventory of all weevils in the ASUHIC, and (3) update the nomenclature of each genus and species. Since beginning on this project, 260 insect drawers have been inspected with confirmation of the higher classification, genera and species contained in each. The first part of this goal has been accomplished, in that all weevil genera within the ASUHIC have been digitized and reorganized. The second and third goals of this project continue to advance, as a convenient and digitally accessible inventory has been created and the nomenclature of each species is consistently being updated and digitized. All information derived from this project will be digitally available for the purpose of aiding in the curation of the ASUHIC.
The Southwest Collection of Arthropods Network (SCAN, http://symbiota4.acis.ufl.edu/scan/portal/) is a data portal built on the Symbiota software collections database system. The portal facilitates rapid taxonomy- and/or geography-driven searches and dynamic specimen mapping and species identification tools. The Arizona State University Hasbrouck Insect Collection (ASUHIC) has been involved in the SCAN project in cooperation with over 80 institutional collections throughout North America. Our predecessors made a significant contribution to SCAN data entry. Recently, we have been tasked with organizing the orders Mantodea, Blattodea, and Hemiptera collections by family. To account for the increasing collections received through donations and collecting, we have created additional space within the collection. Furthermore, we have updated the validity of nomenclature and their organizations to the most recent classifications. From when the project launched in early 2012 up to March 1, 2016, over 5,300,000 arthropod specimen data have been digitized, and information entry continues steadily. Utilizing these data, we wish to fulfill two main goals. The first (1) is to acquire data on the total number of insect specimens collected throughout Arizona and accurately describe the taxonomic classification of each individual. The second goal (2) is to analyze patterns in species distribution, phenology, location, abundance, plant and animal association, etc. across the Southwestern region.

Chronic stress significantly alters brain morphology and cognitive function. In the hippocampus, these changes can recover following chronic stress when a no-stress recovery period ensues. Mounting evidence implicates BDNF in the hippocampus' stress recovery process; however, it is unclear when in the stress and recovery processes BDNF plays a significant role. Some studies indicate that hippocampal BDNF levels are reduced following chronic stress, whereas others show no change. Differences between studies may be due to varying durations of stress, the type of stressor used, and/or the method of quantification (e.g., protein versus mRNA). With regards to differential durations of stress, BDNF levels may change midway through longer chronic stress paradigms, but return to normal before the end of the stress period. A similar process may be involved for the post-stress recovery phase. The purpose of this study was to investigate BDNF proteins levels in the hippocampus and other key limbic structures sensitive to stress at midway and end points of the chronic stress and post-stress recovery periods. Male rats were stressed using wire mesh restrainers for 6 hours per day. Time groups included 10 days (10d) stress, 21d stress, 10d stress followed by 10d recovery, and 21d stress followed by 21d recovery. Brain tissue was immediately collected after stress or recovery; tissue from the CA3 region of the hippocampus was punched and will be analyzed for BDNF protein levels using an ELISA, a method effective at detecting even low endogenous levels of protein. Optimization of the ELISA is ongoing.
**Toward Robotic Assessment of Proprioception in 3D Space**

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Proprioception is defined as a person's sense of body position and movement in space. Many different central nervous system disorders can impair an individual's proprioception, making even the simplest of tasks very difficult to perform. Currently, the method of measuring proprioception in the clinic is useful for assessing loss of function, but is not remarkably accurate in people with typical proprioception ability. Furthermore, all of the previous research done on developing a reliable and accurate paradigm to measure proprioception has been done in two-dimensional space. The purpose of this project is to develop an accurate and reliable paradigm to measure proprioception, so that further research can be performed and rehabilitation programs can be developed. This project is novel in that participants' proprioception is analyzed in three-dimensional space; as people do not just move in two-dimensional space, it is very important to be able to look at their proprioception in all three dimensions. A 7 degree of freedom robotic arm is coupled to the participant and is used for the assessing proprioception. Preliminary data has been collected on multiple subjects and has been using d', a measure of sensitivity derived from signal detection theory. The results show that individuals are better able to detect differences in position as the distance between the reference and target position increases. Furthermore, the data shows a consistent pattern in participant responses, which provides evidence that the paradigm that is being tested is reliable across subjects, and matches the previous 2 dimensional data.

**Evaluating the Effectiveness of Synthetic FBS**

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Cell culture based research is one of the foundational forms of experimentation— which transitions to future studies involving tissue, and eventually animal and human trials. In 2014, the R&D market cost for cell culture was valued at 16.35 billion, and costs related specifically to media, sera, and reagents comprised 23% of that total. One of the largest costs involved in cell culture work is sera [i.e. fetal bovine serum, newborn calf and adult bovine serum] which provides nutrients, growth factors, and hormones to cells to simulate their natural environment. Since 2003, the cost of fetal bovine serum has tripled, which has affected the research efforts of many labs. Recently a pharma company in Montana developed a "synthetic" serum where they have identified key factors that are required by cell cultures in an attempt to reduce cost, overuse of cattle for serum production, and create a consistent product that should not vary in content between seasons or herds. This study compared the effects that standard FBS and the synthetic Fetalgro supplemented media had on cell growth, differentiation, and behavior. Neuroblastoma cells were imaged using brightfield, epi-fluorescent, and confocal microscopy to observe any morphological changes which included the cytoskeleton [tubulin and actin] and were probed for the neuroblastoma cell lineage marker, nestin, which is no longer expressed in transformed cells. To evaluate any change in behavior, cells were also observed through live cell, time lapse microscopy. From these results it appears that Fetalgro is an acceptable substitute for FBS in culture media.
Characterization of the Protist Hindgut Community in *Heterotermes aureus*

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*Heterotermes aureus* (Rhinotermitidae) is the most common subterranean termite in the dry and hot Sonoran Desert and the most destructive urban termite pest in Arizona. As generalist feeders, they are often found in and burrowed around deadwood. Wood eating termites like *H. aureus* have gut dwelling symbiotic protists to help them break down their lignocellulose diet. This obligate symbiotic relationship is ancient, dating back to the common ancestor of termite and the wood roach, *Cryptocercus*. Each termite and *Cryptocercus* species (except for termites in the family Termitidae) has a characteristic assemblage of protist symbionts. We collected *H. aureus* from an empty lot in Gilbert, Arizona and characterized the hindgut protist community with morphological and molecular methods. The hindgut eukaryotic microbiome of *H. aureus* was previously reported to consist of unnamed species of *Holomastigotoides*, *Spirotrichonympha*, and *Pseudotrichonympha* and our light microscopical observations agree with these classifications. We isolated single cells of each protist with micropipettes, amplified and sequenced the small subunit ribosomal RNA gene (SSU rDNA) and performed phylogenetic analyses. Each protist branched as expected: *Pseudotrichonympha* within the Trichonymphidae, and *Holomastigotoides* and *Spirotrichonympha* in the Spirotrichonymphidae. Based on their distinct host species and differences in their SSU rDNA sequences, we suspect the *H. aureus* protists should be considered new species.

Evolutionary Assessment of a Novel Type of Angle-Dependent Plumage Coloration in Parrots

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Animals use a diverse array of mechanisms (e.g. pigmentary, structural) to generate their brilliant colors. Parrots are well known for their marvelous rainbow of plumage colors, and we have observed a novel type of angle-dependent coloration in several parrot species that is produced through the differential coloration of barbs and barbules within a given feather that changes as a function of observation angle. This unique angle-dependent coloration may provide directional abilities to communicate with specific receivers or in specific lighting environments. To better understand the evolutionary significance of this type of coloration, we are using photography and spectrometry to analyze color and feather morphology and comparing color properties to the habitat of many parrot species in order to test the Light Environment hypothesis. Our results should provide valuable information about the pressures underlying the evolution of brilliant colors in an animal group that is beloved by fanciers and pet owners for their elaborate plumage hues.
Methane gas in the atmosphere, resulting from both natural and anthropogenic sources, has increased dramatically since the industrial revolution. Some microorganisms act as a sink for methane, using methane as a carbon and energy source. These microorganisms, methanotrophs, carry out aerobic and anaerobic methane oxidation and are ubiquitous in the environment. As these organisms may be integral to addressing shifts in methane concentrations in the atmosphere this study is focused on understanding the biological and geochemical parameters that underpin the distribution of methanotrophs in the environment. Based on bioenergetic calculations of methane oxidation coupled to oxygen, for hot springs in Yellowstone, methane oxidation is a strongly energy-yielding process (Shock et al., 2010), therefore we predict that aerobic methanotrophy will be widespread in hot springs. If it is not, then other chemical or physical parameters such as competitive inhibition by ammonia or degassing of oxygen may influence the distribution of methanotrophy. To test these predictions we have carried out field in situ microcosm activity assays for biological methane oxidation in hot spring sediments in Yellowstone National Park. Preliminary results show that methane oxidation is widespread across a range of geochemical parameters, but may be inhibited by high concentrations of ammonia in the environment. Enrichments for methanotrophs agree with these results with methane depletion being observed in cultures having N2 as a nitrogen source versus cultures with NH3 as the nitrogen source. Furthermore, we have detected methanotrophy in a hot spring with a temperature of 90°C, well above the currently known upper temperature limit of 72°C.

Age-Related Decline of Anoxia Tolerance in Adult Drosophila melanogaster

Cell death occurring from anoxia is considered to be the cause of many human diseases such as heart attack and stroke. Interestingly enough, we still have a poor understanding of the underlying mechanisms causing cell death and variation in survival of anoxia. Drosophila melanogaster are particularly interesting models for studying responses to anoxia as they can survive many hours of anoxia and most of their metabolic pathways are similar to humans. We hypothesized, based on studies with humans, that younger flies would have a higher anoxia tolerance than older adults. We exposed adult Drosophila, ages 1, 3, 5, 7, 9, and 12 days old, to six hours of anoxia. Survival was assessed 24 hours post-treatment. Seventy nine percent of adults one day past eclosion survived six hours of anoxia; while only 10% of twelve-day-old adults survived. Additionally, we measured ATP in 1 and 12 day old Drosophila in different durations of anoxia. In anoxia, ATP levels declined rapidly to near-zero levels in both one and 12 day old adults; thus the better capacities of young adults to survive anoxia are not due to a better capacity to keep ATP elevated. This age-related decline in anoxia tolerance may be due to loss of capacities to prevent or repair anoxia-related damage. Overall, these data show that patterns of age-associated variation in tolerance to anoxia are similar in Drosophila and mammals, suggesting that Drosophila may be underutilized models for studies of the genetic and biochemical mechanisms of pathology of stroke and heart disease.
Viral protein U (Vpu) is a type-III membrane protein of HIV-1. Vpu assists with the budding and release of newly synthesized virions from an infected cell by binding to and then deregulating various host proteins. For example, Vpu neutralizes the cellular host factor BST-2 by binding it with its transmembrane domain and subsequently targeting it for degradation. BST-2 tethers virions to the cellular membrane, preventing their release. Vpu also induces proteasomal degradation of the CD4 T-cell receptor. This experiment attempts to delineate a structural model of Vpu using Nuclear Magnetic Resonance (NMR) spectroscopy. Further understanding of the structure of Vpu may reveal new targets for future HIV-1 antiviral medications and therapies. We report the expression of Vpu in Escherichia coli using the pelB signal peptide. The protein was extracted using detergents, and then purified by immobilized metal affinity chromatography (IMAC). We show further purification and characterization using size exclusion chromatography. A second IMAC purification was performed to exchange the protein in NMR compatible detergents. We finally report our preliminary data from the NMR spectra obtained from Vpu in complex with various detergent micelles.

Hyperactivation of ERK/MAPK Signaling in GABAergic Neurons Leads to Altered Cortical Neuron Number and Morphology

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The extracellular regulated kinases (ERK1 and ERK2) are key components of the canonical Ras/ERK signaling cascade, which controls important aspects of development. Aberrations in this pathway are associated with a group of neurocognitive syndromes called RASopathies, which lead to phenotypic abnormalities such as facial dysmorphia, cardiac defects, and neurological delay and epilepsy. The incidence of RASopathies is approximately 1:2000. While previous studies have implicated GABAergic interneurons in the neurological deficits observed in RASopathies, the mechanisms remain poorly understood. In this study, we have investigated the effects of hyperactive ERK signaling on the number and morphology of cortical GABAergic inhibitory interneurons. Our results reveal that there is a significant decrease in the number of cortical GABAergic interneurons in mutant mice. Interestingly, this decrease in number is limited to a subset of fast-spiking GABAergic interneurons that express Parvalbumin. Morphological assessment of Parvalbumin-expressing interneuron somal sizes did not appear to differ between mutants and controls. However, mutants exhibited increased dendritic arbor complexity in comparison to littermate controls. This increase in dendritic complexity suggests that the remaining Parvalbumin-expressing GABAergic interneurons may innervate more target cells. Further understanding of the cellular responses to hyperactive ERK signaling will assist in additional characterization of these phenotypes as well as the development of preventative medicine to reverse the defects that result from aberrant signaling.
52 Effects of Hypoxia and Hyperoxia on Thermal Tolerance and Flight Performance of
_Drosophila melanogaster_

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Animals are thought to die at high temperatures because proteins and cell membranes lose their structural integrity. Alternatively, a newer hypothesis (the oxygen and capacity limitation of thermal tolerance, or OCLTT) states that death occurs because oxygen supply becomes limited at high temperatures. Consequently, animals exposed to hypoxia are more sensitive to heating than those exposed to normoxia or hyperoxia. We hypothesized that animals raised in hypoxia would acclimate to the low oxygen supply, thereby making them less sensitive to heating. Such acclimation would be expressed as greater heat tolerance and better flight performance in individuals raised at lower oxygen concentrations. We raised flies (Drosophila melanogaster) from eggs to adults under oxygen concentrations ranging from 10% to 31% and measured two aspects of thermal tolerance: 1) the time required for flies to lose motor function at 39.5°C at normoxia (21%), referred to as knock-down time, and 2) flight performance at 37°C, 39°C, or 41°C and 12%, 21%, or 31% oxygen. Contrary to our prediction, flies from all treatments had the same knock-down time. However, flight performance at hypoxia was greatest for flies raised in hypoxia, but flight performance at normoxia and hyperoxia was greatest for flies raised at hyperoxia. Therefore, flies acclimated flight performance but not thermal sensitivity according to oxygen supply during development. Our data does not support the OCLTT hypothesis, but instead supports the beneficial acclimation hypothesis, which proposes that acclimation improves the function of an organism during environmental change.

30 Evaluating Phage Effect on Heterotrophic Decomposition in Amazon Peatland Soils

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Little is known about the diversity and role of bacteriophages in carbon (C) rich ecosystems such as peatlands in tropical and temperate regions. To better understand how bacteriophages influence organic C cycling to final products like CO2 and CH4, phage communities and phage like particles were isolated or manipulated from freshwater sources from Amazon peatlands. Here we present initial findings on bacteriophages and their effects on heterotrophic bacteria, which in turn affects C cycling and decomposition to CH4 in peatlands. To assess diversity, phages were enriched from water samples from Amazon peatlands by filtering to remove organic matter and bacteria, and iron flocculation to bind the phages and allow for precipitation onto a filter. Phage community enrichments were screened using an OD absorbance and cross-streaking method, against 50 heterotrophic bacterial isolates obtained from the same Amazon peatlands to identify phage hosts. Once a host was found, the phage was isolated. Total phage community numbers were assessed using fluorescent microscopy. The efficiency of iron flocculation was determined using fluorescent microscopy counts of phage pre and post extraction method. The effect of iron flocculation on infectivity was determined by counting plaques pre and post extraction method. Selected phages will be sequenced for accurate identification. Our results provide the groundwork for further characterizing the role that bacteriophage play in C cycling and greenhouse gas production from Amazon peatland soils.
Genome Size and Chromosome Number Evolution in Early Diverging Species of Flowering Plant Genus *Medicago* (Fabaceae)

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There is a relative lack of basic information about chromosome number and genome size in the genus *Medicago*, especially for the early diverging species, in sections Buceras, Lunatae, and Platycarpae. Some of the few published chromosome numbers, e.g. 2n=28 and 44, differ from those of the rest of the genus, which are mostly 2n=16 or polyploids thereof, although some cases of aneuploid reduction (2n=14) do exist. As part of a larger study of the genome and chromosome number evolution in *Medicago*, we obtained genome size data using flow cytometry for 44 accessions of 14 currently recognized early diverging species, with a focus on *Medicago monantha*. Chromosome numbers were obtained using standard cytological methods. For each accession, sequence data for two molecular markers was obtained; phylogenetic analyses using those sequences were performed using maximum parsimony and Bayesian inference. Interestingly, our data support the hypothesis that there are at least two geographically isolated entities within the currently recognized species *M. monantha* that differ in chromosome number and genome size. Our data also indicate that both polyploidy (whole genome duplication) and aneuploidy (variation in number less than an entire set) events played a part in the genome evolution of these species. These data not only provide insight into the delimitation of the early diverging species, and clarify the relationships among these species of *Medicago* but also help build a foundation for more in-depth research concerning the evolution of chromosome number and genome size within the entire genus.

Regulation of *Mycobacterium tuberculosis* Cytochrome *bd* by the Essential PrrAB Two-component System

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In 2014, *Mycobacterium tuberculosis* (*Mtb*) caused 1.5 million deaths and latently infected another 2 billion people globally. The success of *Mtb* as a pathogen is dependent on its ability to adapt to the intracellular environment of macrophages and persist within the human host. To survive within the human host, *Mtb* utilizes two-component systems (TCSs) to sense environmental cues and respond by altering gene expression. The PrrAB TCS was initially identified during early stages of *Mtb* intracellular replication in human macrophages and was subsequently deemed essential for *Mtb* viability. This TCS consists of PrrB, a membrane-bound histidine kinase, and PrrA, a transcriptional regulator with a receptor domain and DNA-binding domain. Upon phosphotransfer, PrrA binds to target DNA sequences to modulate gene expression. We have generated phosphomimetic (D58E) and phosphoablative (D58A) forms of PrrA to mimic these phosphorylation states. In 2014, diarylthiazole (DAT) was identified as an anti-tuberculosis compound which targets PrrB, thus confirming our hypothesis that the PrrAB TCS serves as a bona fide drug target. *Mtb* PrrA D58E overexpression repressed *cydA*, one of the genes encoding the cytochrome *bd* terminal oxidase which is induced during hypoxia and chronic *Mtb* infection. Conversely, DAT-mediated PrrB inhibition induced *cydA* expression. Electrophoretic mobility shift assays.
demonstrated the PrrA specifically binds to the cydA promoter. These data reveal that the PrrAB TCS represses the non-proton-pumping cytochrome bd terminal oxidase, an enzyme that enables Mtb to transition from acute to chronic infection of mouse lungs and tolerate nitrosative and oxidative stresses.

13 Spilling the Beans on Weevil Mouthparts

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Little research has been conducted specifically on the subject of weevil mouthparts. Existing research has mostly been conducted at high taxonomic levels, and sporadically describes characters without in-depth exploration. In this project, I perform a study of the comparative morphology of mouthparts in weevils representing two tribes. My study aims to document and observe the mouthparts of closely related weevils. The aim of the study is to elucidate patterns in their structures, understand and analyze these patterns, and through observing the shape, variations, differences and similarities, gain some understanding of the significance of structures in a phylogenetic/taxonomic context. Fifteen specimens are used to represent five genera. Mouthparts of specimens are dissected and viewed under a microscope. The mouthparts are imaged and compared visually in order to analyze these structures in a phylogenetic context.

9 Neuropathogensis of LCMV in Clone-13 Carriers

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Lymphocytic choriomeningitis virus (LCMV) is an arenavirus that infects about 10% of the rodent population in the wild. Rodents can be infected as adults or congenitally infected. In adult-infected immune response there is an anti-viral immune response while in congenitally infected carriers lack of response. When mice are infected with LCMV they will suffer from persistent infection without having an immune response. These persistently infected mice are typically called carriers or super-spreaders and are different from infected mice since they show no antibody response while having high titers of virus in their blood and body fluids. We have seen LCMV in the brain and nervous system which suggests neuropathogenesis is happening. Carrier infected mice are runted and neurological and physiological defects have been observed. We will be looking into the neurological effects of the virus at different gestational stages during vertical transmission from mother to fetus. This will happen by looking at both the histology of the brain as well as doing immunohistochemistry on the brain tissues. At different stages of gestation, the brain will be dissected from mice to see if there are any differences of the brain region sizes and immunological markers in the brain from persistently infected mice and mock-infected.
STEM education has been a priority in the United States to ensure there is a pipeline of future professionals who will continue research and education in these fields. It is estimated that by 2018 there will be 8.6 million STEM jobs available with 60% requiring skills possessed by only 20% of the workforce. Statistics such as this emphasis the importance of adequate training which will prepare students to enter the workforce. In the field of science, lab based courses are fundamental in career preparation, providing students with hands-on training and experience. One of the shortcomings of many lab-based courses is that they are of the "cookbook" type which limit the investigative process. As students become more advanced, it is important to introduce training in techniques that are used in basic research as well as the investigative reasoning for developing and interpreting research projects and the data collected from them. The Open Lab classroom not only provides a standard curriculum objectives but also adds a lab component that is similar to working in a research laboratory. The Cell Biotechnology [BIO451] course was developed in 2000 in an open lab format and not only covers the standard course content but also teaches students to how to culture and maintain cells for weekly experiments where they learn cutting edge techniques such as immunocytochemistry, DNA transfections, histology, FISH and microscopy. This poster will summarize some of the techniques and labs that are conducted within this course, detailing how they are developed, implemented and assessed.

Experiences of Religious Students in Biology Classes: Evolution, Ethics, and Perceived Advantages/Disadvantages of Being a Religious Biology Student

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 31 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.
Modeling Effects of Time Since Human Bottleneck on Genetic Diversity

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Much of our current knowledge on human evolutionary history has come from the study of patterns of diversity across our genome, which carry specific genetic signatures of demographic events. The focus of this research is on human population bottlenecks and the extent to which they affect autosomal diversity. This is relevant because anthropological evidence suggests there were population bottlenecks, but it is not known how many generations it takes before those bottlenecks leave a signature in genomic variation. In particular, we ask how many generations it takes before we are able to detect the effect of a population bottleneck on genetic diversity. We simulated varying times since abrupt contractions in the population to determine the moment at which genetic differences can begin to be detected between initial (pre-bottleneck) and final (post-bottleneck) population. Preliminary data suggests that the severity of the bottleneck is not present immediately after population contraction; instead it takes many generations before the existence of the bottleneck can be inferred from the genetic data. The results of these simulations will contribute to a deeper understanding of the effect of demography, specifically population bottlenecks, on patterns of observed genetic diversity and will aid in more accurate reconstructions of human history.

Creating an Artificial Antigen Presenting Cell System for HPV16 Proteins

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Background: High risk types of human papillomavirus (HPV) are known to cause cancer, including cervical (99%) and oropharyngeal cancer (70%). HPV type 16 is the most common subtype. Three antigens that are critical for integration or tumor progression are E2, E6 and E7. In this study, we developed a systematic approach to identify naturally-processed HPV16-derived HLA class I epitopes for immunotherapy development.

Methods: K562 cells, which lack HLA expression, were transduced with each HPV16 antigen using lentivirus and supertransfected with HLA-A2 by nucleofection. Stable cell lines expressing each antigen were selected for and maintained throughout the investigation. In order to establish a Gateway-compatible vector for robust transient gene expression, a Gateway recombination expression cloning cassette was inserted into the commercial Lonza pMAX GFP backbone, which has been experimentally shown to display high transfection expression efficiency. GFP was cloned into the vector and plain K562 cells were transfected with the plasmid by nucleofection.

Results: Expression of K562-A2 was tested at various time points by flow cytometry and A2 expression was confirmed. Protein expression was shown for the transduced K562 E7 by Western blot analysis. High transfection efficiency of the pMAX_GFP_Dest vector (up to 97% GFP+ cells) was obtained 48 hours post transfection, comparable to the commercial GFP-plasmid.

Conclusion: We have established a rapid system for target viral antigen co-expression with single HLA molecules for analysis of antigen presentation. Using HPV as a model system, our goal is to identify specific antigenic peptide sequences to develop immunotherapeutic treatments for HPV-associated cancers.
Developing Breath-Based Diagnostics to Detect *P. aeruginosa* Motility and Antibiotic Resistance in CF Lung Infections

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The primary cause of lung function decline and eventual death for persons with cystic fibrosis (CF) is pulmonary damage from chronic bacterial lung infections, with *Pseudomonas aeruginosa* responsible for half of all CF infections, and establishing chronic lung infections in 75% of adults with CF. During chronic infection, *P. aeruginosa* acquire phenotypes, such as antibiotic resistance, loss of motility, and mucoidy, that are significantly correlated to lung function decline. However, accurately diagnosing these phenotypes in the clinical microbiology laboratory is incredibly challenging due to rapid phenotypic switching by the bacteria once they are cultured outside of the lung environment. The long-term vision of the Bean Lab is to identify volatile biomarkers to detect these clinically-important bacterial phenotypes directly from the patients' breath, making it possible to detect the pathogens and their phenotypes *in situ*.

The goal of this project is to phenotype and genotype *P. aeruginosa* CF lung isolates for motility and antibiotic resistance. In particular, we are focused on *P. aeruginosa* swimming, swarming, and twitching motilities, and resistance to cephalosporin, fluoroquinolone, carbapenem, aminoglycoside, monobactam, and polymyxin antibiotics. These traits will be correlated to the isolates' volatile metabolomes to identify biomarkers of these *P. aeruginosa* phenotypes, which will be developed into breath-based diagnostics for early, non-invasive detection and characterization of chronic lung infections.

Size Matters? Hypermetric Spiracular Scaling and Gigantism in Scarab Beetles

Wagner, Julian; Duell, Meghan; and Harrison, Jon

School of Life Sciences, Arizona State University, Tempe AZ

One hypothesis for why insects are smaller than vertebrates is that possession of a blind-ended tracheal respiratory system possess physiological challenges for larger insects. If this is the case, we might expect to see that larger insects would have to have relatively larger gas transport structures. To test this possibility, we used the scarab beetles, the insect clade with the most massive species. We used full body micro-CT scans of 19 individuals of 11 species to measure the scaling pattern of the spiracles, which are the point of entrance of oxygen into the insect tracheal system. We measured cross sectional area of the spiracles' opening, as well as the depth from the opening to the valve structure behind the spiracles' atrium. Using the Fick's and Hagen–Poiseuille equations, we measured the scaling of spiracular area, resistance to diffusion (area/depth), and resistance to convection (area^2/depth). Data were log-transformed and we corrected slopes for phylogenetic relationships among the species. By all measures, the spiracles in the anterior portion of the animal showed hypermetric scaling, indicating that larger beetles have spiracles that have relatively low resistance to diffusion and convection compared to smaller ones. However, this pattern differed among subfamilies, with much more hypermetric scaling in the subfamily Cetoniinae as compared to Dynastinae. These findings suggest that in some but not all clades, larger beetles require relatively larger spiracles to enable gas exchange.
Male genitalia have significant morphological characteristics which historically are used to determine evolutionary divergence resulting from sexual selection. This principle is applied to the *Exophthalmus* genus complex to address its current polyphyletic nature by providing important morphological evidence to be used in genus reclassification. The focus of the study is on documenting the aedeagus character complex to explore morphological variations and evolutionary transformations under a phylogenetic context. The genitalia of over thirty species within the *Exophthalmus* genus complex were dissected and then analyzed under light microscopy in the ventral and lateral positions. The aedeagi display variation in shape and curvature for differentiation of the species.

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Manipulation Experiments on N₂O Reduction in Amazon Peatland Soils

Zamora, Zacary; Buessecker, Steffen; and Cadillo-Quiroz, Hinsby
School of Life Sciences, Arizona State University, Tempe AZ

A yet uncovered diversity of microbes are capable of using nitrous oxide (N₂O) to generate energy. The redox couple N₂O/N₂ is very powerful, with potential of 1.35V as compared to that of NO₃⁻/NO₂⁻ 0.43V. Novel peatlands of the Amazon show high potential to reduce N₂O under anoxic conditions thus increasing the importance of the understanding of these communities. In order to access its role in the peat ecosystem, microbial N₂O reduction was quantified and followed in incubations under induced and inhibiting conditions.

Nitrous oxide reductase (Nos) is the periplasmic enzyme that catalyzes the reduction of N₂O to N₂. Acetylene (C₂H₂) prevents the reduction of N₂O to N₂ by inhibiting Nos. Carbon Monoxide (CO) prevents the degradation of C₂H₂ by blocking all Nitrogenase based reactions (nitrogenase reduces acetylene). Acetylene Prepared slurries of tropical peat soil were manipulated with 200 μM nitrite (precursor of N₂O), CO and C₂H₂. All C₂H₂ treatments were effective for up to 6 days before being degraded by microbes. CO had no statistically significant effects. N₂O production observed in C₂H₂ treatments averaged 126.4(±2.67) ppm and 123.4(±5.68) ppm across days where C₂H₂ was viable and 14.5(±20.5) ppm in non-inhibited controls. Results indicated that there is high microbial reduction potential for nitrous oxide and that more studies observing N₂O reduction model in acidic soils (pH: 6.02).
# SOLUR Program, IMSD Program, and Symposium Participants 2015-16

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**Programs:**

- Hasbrouck
- IMSD: Initiative for Maximizing Student Development Program
- PZSOLS-CRTTP: The Phoenix Zoo & School of Life Sciences - Conservation Research Training Program
- SOLUR Fellow: School of Life Sciences Undergraduate Research Program - Fellow
- SOLUR Researcher: School of Life Sciences Undergraduate Research Program - Researcher
- SOLUR Apprentice: School of Life Sciences Undergraduate Research Program - Apprentice
- SOLUR - SRE: School of Life Sciences Undergraduate Research Program - 2015 Summer Research Experience