NMSU’s Department of Biology presents

The 30th Annual Biosymposium
PROGRAM

8:30am – Coffee and poster setup

9:10am - Opening remarks, poster schedule reminder announcements

9:20am - Gizelle Hurtado and Karen E. Mabry - Boldness and aggression in Merriam’s kangaroo rat: an urban tolerant species?

9:40am - Angela Medina-García, Jodie M. Jawor, and Timothy F. Wright - Bright or Bold? Personality but not Stress, Affects Responsiveness in Cognitive Tasks in Budgerigars.

10:00am - Matthew J. Gould, Dr. James W. Cain III, Dr. Gary W. Roemer, Dr. William R. Gould, and Stewart G. Liley - American Black Bear Density in Three New Mexico Mountain Ranges.

10:20am - Megan Lettenberger, Youn Ji Nam, and Jennifer Curtiss - Nep1 regulates metabolism through different neuropeptides in Drosophila melanogaster.

10:40am – 11:00am – coffee break

11:00am - M. Isabella Chavez, Jonathan C. Teske, and Emily Indriolo - Analysis of COPI Arabidopsis thaliana stigmas during compatible pollination.

11:20am - Lynsey Kovar, Andrea Eveland, and Rajiv Parvathaneni - Data Mining to Identify Genetic Loci Controlling Inflorescence Traits in Maize.

11:40am - Sealtiel Ortega and C. Donovan Bailey - A Computational Method for the Assembly of Small Complex Genomes from Complex Datasets.

12:00pm - Cody Champion and John Xu - Pentose phosphate pathway inhibition elevates oxidative stress and impedes fecundity in Anopheles gambiae.

12:20pm – lunch and poster session – please stand by your poster during the allotted time for judging. Poster presenters, please keep your discussions with judges limited to 10 minutes so that they can make it to all presenters.

12:20 – 1:20pm – odd numbered posters

1:20 – 2:20pm – even numbered posters
2:30pm – Biosymposium clean-up and tear down. Awards for the best talks and posters will be announced at Biology seminar on October 6th.

n.b.
Talks are 15 minutes with 3 minutes for questions.
G = grad student; UG = undergrad
**MORNING SESSION TALK ABSTRACTS**

**Boldness and aggression in Merriam’s kangaroo rat: an urban tolerant species?**
Gizelle Hurtado [G] and Karen E. Mabry
Department of Biology, New Mexico State University, Las Cruces, NM.

Urban development can fragment and degrade habitat, which can have profound impacts on wildlife behavior. In urban areas, individuals may occur in close proximity to each other and experience high levels of disturbance, which may favor increased boldness and aggression in urban-dwelling wildlife. We investigated the influence of urbanization on boldness and aggression and the correlation between these traits in Merriam’s kangaroo rat (*Dipodomys merriami*). We predicted that kangaroo rats living in urban areas would be more bold and more aggressive than kangaroo rats in wildlands, that the two traits would be positively correlated, and that the correlation would be stronger in urban areas. We live trapped kangaroo rats at 4 urban and 4 wildland sites in and around Las Cruces, NM and assessed aggression using a mirror image stimulation test and boldness using a predator scent exposure. We found no difference between urban and wildland kangaroo rats in either aggression or boldness. We found a positive correlation between aggression and boldness, but there was no difference in the strength of the correlation between urban and wildland areas. These results indicate that kangaroo rats may be tolerant of urbanization, if habitat patches within urban areas are similar to wildland habitats.

**Analysis of COPI Arabidopsis thaliana stigmas during compatible pollination.**
Maria I. Chavez1* [UG], Jonathan C. Teske1, and Emily Indriolo1
1Department of Biology, New Mexico State University, Las Cruces, NM.

A crucial step in the process of flowering plant reproduction is the recognition of a compatible pollen grain, leading to fertilization. Recent research has demonstrated that vesicle trafficking plays a critical role in pollen acceptance in the *Brassicaceae* including the exocyst complex. Exo70A1 is required vesicle delivery at sites of polarized secretion. However, many questions remain in the field as to the identification of the receptor(s) that recognize compatible pollen grains through the basal pollen response that activates the transportation of secretory vesicles to the plasma membrane. To identify likely candidates in the basal pollen response, we have performed quantitative proteomics of *B. rapa* stigmas in compatible and self-incompatible pollinations. One of these likely compatible factors that was identified is the Coat Protein I complex (COPI). We are interested in the role that the COPI complex plays in the stigma during a compatible pollination. This is being analyzed through T-DNA knock-out *A. thaliana* plants as well as stigma specific knock-downs of each individual subunits. To test the function of each COPI subunit in pollen-pistil interactions, we will characterize the phenotype using the following assays on RNAi plants; aniline blue imaging of pollen tube growth, seed set of stigmas...
pollinated with wild-type pollen, and pollen hydration of wild-type pollen. These experiments will provide new insight into plant sexual reproduction, specifically the intra-cellular and vesicle trafficking activities of COPI in the stigma during compatible pollination.

**Nep1 regulates metabolism through different neuropeptides in *Drosophila melanogaster***

Megan Lettenberger [UG], Youn Ji Nam, and Jennifer Curtiss

*Department of Biology, New Mexico State University, Las Cruces, NM*

Obesity is a crisis in this nation with 60% of adults being either overweight or obese. Mammalian nepriyls (NEP) is a zinc-metallo-endopeptidase whose function is associated with metabolism and obesity. The mechanism of how NEP regulates metabolism and obesity is not yet known, but previous studies have shown that NEP neuropeptide substrates also regulate metabolism. We are studying the function of *D. melanogaster* Nep1, which is homologous to mammalian NEP, to better understand similar metabolic pathways in humans. We are using epistasis to identify potential Nep1 substrates in the context of metabolism. Hemizygous Nep1 loss-of-function mutants (Nep1<sup>5</sup>) are more resistant to starvation than controls. Homozygotes for mutations in the AstA gene (AstA<sup(SK1)</sup>/AstA<sup(SK1)</sup>), which encodes the Allatostatin A neuropeptide, are also more resistant to starvation than controls, but heterozygotes (AstA<sup(SK1)</sup>/+) don’t show the phenotype, suggesting that AstA<sup(SK1)</sup> is a recessive allele. We found that Nep1<sup>5</sup>/Y; AstA<sup(SK1)</sup>/+ mutants are more resistant than either Nep1<sup>5</sup> hemizygotes or AstA<sup(SK1)</sup>/+ heterozygotes. Thus the AstA<sup(SK1)</sup> mutation dominantly enhances the Nep1<sup>5</sup> phenotype. These results suggest that Nep1 cleaves and activates AstA in the context of metabolism. Similar experiments suggest that Nep1 cleaves and inactivates small Neuropeptide F, which is the *D. melanogaster* version of mammalian Neuropeptide Y.

**Pentose phosphate pathway inhibition elevates oxidative stress and impedes fecundity in *Anopheles gambiae***

Cody Champion [G] and John Xu

*Department of Biology, New Mexico State University, Las Cruces, NM*

Unabated oxidative stress in mosquitos can result in reduced fecundity and even death. Reducing power from internal sources is essential for oxidative stress defense. The primary system used to create this reducing potential is the pentose phosphate pathway (PPP). We examine oxidative stress induction via paraquat (PQ), 6-aminonicotinamide (6AN), which is a PPP inhibitor, and alleviation of oxidative stress by lycopene. We fed these compounds to female A. gambiae then performed egg counts and biochemical assessments. Both PQ and 6AN feeding increased oxidative stress levels and decreased fecundity. Cod-feeding with lycopene attenuated these effects. 6AN, when fed with PQ, resulted in a normal egg number due to inactivation of NADPH production which is required for PQ toxicity. 6AN resulted in a high NADP+:NADPH ratio indicating that the PPP is inhibited and is a major producer of NADPH. Oxidized:reduced glutathione ratio was increased by both
6AN and PQ indicating that both of these compounds result in increased global oxidative stress. These antioxidants and pro-oxidants can provide a manipulatable link between mosquitoes and egg production capacity which can be used to design novel and effective vector control strategies, which may influence insecticide sensitivity, infection susceptibility, fecundity, and longevity.

A Computational Method for the Assembly of Small Complex Genomes from Complex Datasets.
Sealtiel Ortega [UG], C. Donovan Bailey
Department of Biology, New Mexico State University, Las Cruces, NM.

Complex prokaryotic and eukaryotic genomes have proved difficult to assemble through conventional assembly methods using short read next generation sequencing data. Long read datasets (e.g., PacBio and Nanopore) have helped resolve the complexities caused by large repeats, structural recombination, and genome duplication. Though helpful, there are still many challenges in assembling these long read datasets, especially since not all the reads in a dataset may belong in a particular assembly and therefore can have drastically different levels of sequence coverage. Due to these difficulties, the assembly and publication of some groups’ smaller complex genomes, such as plant mitochondrial genomes, have lagged behind the publication of nuclear genomes from the same organism. Here we present “Reference-Seeded Iterative Long-reads Assembler” as an assembly method that allows for quick and simple assemblies of complex genomes and/or simple genomes from complex data sets (e.g., metagenomics samples). RILA employs novel methods that allow users to target specific aspects of a dataset, allowing for a rapid and efficient assembly. Here we establish RILA’s ability to assemble chloroplast and mitochondrial genomes from Oryza sativa, Arabidopsis thaliana, and Leucaena trichandra PacBio SMRT datasets.

Data Mining to Identify Genetic Loci Controlling Inflorescence Traits in Maize
Lynsey Kovar¹ [UG], Andrea Eveland², and Rajiv Parvathaneni²
¹Department of Biology, New Mexico State University, Las Cruces, NM, ²Donald Danforth Plant Science Center, St. Louis, Missouri.

Cereal crops such as maize, wheat, and rice bear their grains on elaborate flowering structures called inflorescences. Therefore, traits controlling inflorescence architecture, e.g. the length, number and position of branches and flowers, contribute directly to grain yield. In order to produce more high-yielding crop varieties, we need to understand the molecular mechanisms underlying inflorescence architecture traits in cereal crops like maize. The rise of next generation sequencing and a growing number of published genomes enable identification of loci that can be used to improve traits like yield in model crops. Here, RNA-seq datasets describing early ear and tassel development in maize were integrated and mined for candidate loci pertaining to inflorescence development. Co-expression networks were constructed from these data and used to identify
genes of interest that are co-expressed with known regulators of inflorescence architecture. MNase data was then used in conjunction with Genome-Wide Association Study data to further refine our genes of interest based on proximity to putative enhancer regions. By using a tissue-specific genomics approach and a variety of datasets, we were able to identify candidate loci that are hypothesized to be acting in pathways of interest, such as enhancers of gene expression, which may give rise to subtle effects on inflorescence architecture.

Bright or Bold? Personality but not Stress, Affects Responsiveness in Cognitive Tasks in Budgerigars. Angela Medina-García [G], Jodie M. Jawor, and Timothy F. Wright

A current aim of the field of animal cognition is to understand the fitness consequences of individual variation in cognition. In order to study maintenance and fitness effects of this variation, it is paramount to understand how other traits may influence variation, such as personality and physiological factors. We investigated the effects of personality and stress on responsiveness and performance in cognitive tests. We measured exploration, neophobia, sociability and the corticosterone stress response in 42 captive budgerigars. Birds were tested on four cognitive tasks: problem solving, spatial memory, detour reaching, and seed discrimination. Neophobia/exploration scores determined responsiveness only in the detour reaching and discrimination tasks. The overall level of neophobia in responsive individuals was associated with their ability to habituate to the cognitive devices, but not with performance. Stress response did not co-vary with responsiveness or cognitive performance in any task. Our results suggest that personality traits can affect individual responses in select cognitively demanding situations, and should be considered when measuring cognition with novel tasks.


Modeling population dynamics and setting harvest levels for wildlife populations requires estimates of both state variables (e.g., abundance) and transition rates (survival and recruitment). To assist in these endeavors, we estimated American black bear density for 5 study areas in 3 New Mexico mountain ranges. We collected hair samples from black bears using non-invasive genetic sampling methods, and used a suite of microsatellite loci to individually genotype hair samples. We estimated density in a spatially explicit capture-recapture framework. We identified 725 individuals; the sex ratio for each study area was approximately equal. Our density estimates varied within and among mountain ranges from a low of 16.55 bears/100 km² (95% CI: 11.64–23.53) to a high of 25.75 bears/100 km².
(95% CI: 13.22–50.14). Overall detection probability was low primarily a result of some hair samples failing to produce a complete genotype, which we speculate was due to exceedingly high levels of UV radiation coupled with heightened exposure that collectively degraded the DNA. Despite sampling difficulties, we were able to produce density estimates for New Mexico black bear populations with levels of precision comparable to estimated black bear densities made elsewhere in the U.S.

POSTER SESSION ABSTRACTS

1. Analysis of microtubule pulling forces during pronuclear migration and centration in the sea urchin egg.

Leslie Toledo [G] and Charles B. Shuster. Department of Biology, New Mexico State University, Las Cruces, NM.

Following fertilization, a microtubule aster is nucleated from the sperm centrosome, which mediates pronuclear migration as well as the centration of the fused zygotic nucleus. We applied a quantitative imaging approach to understand the forces that mediate nuclear migration following fertilization. Pronuclear movements occurred in two phases: 1) a rapid first phase where the female pronucleus was pulled towards the male pronucleus and the sperm aster; and 2) a slower second phase where the zygotic nucleus migrated towards the cell center. The sperm aster was dispensable, since parthenogenetically-activated eggs underwent nuclear centration using a microtubule array organized around the female pronucleus. Dynein inhibition blocked both phases of migration, by disrupting pronuclear-associated and cortical dynein activities, respectively. Among the factors known to recruit dynein to the cortex is the PAR complex (Cdc42, Par6, Par3 and atypical PKC), which is found in the egg cortex following fertilization. aPKC inhibition had no significant effect on migration or centration following fertilization, but did affect pronuclear centration in parthenogenetically activated eggs, suggesting that the PAR complex exerts a minor influence on dynein recruitment. Current efforts are focused on identifying additional factors that recruit dynein, which in turn applies pulling forces to effect nuclear migration.

2. Inhibition of PI-3 kinase signaling potentiates the apoptotic response to mitotic arrest.

Roaa Kassim [G] and Charles B. Shuster. Department of Biology, New Mexico State University, Las Cruces, NM.

Anti-mitotic drugs represent a common strategy for cancer chemotherapy by blocking mitotic spindle assembly. Kinesin Spindle Protein (KSP) inhibitors arrest cells in mitosis with limited side effects in clinical trials. However, they are not as effective as Taxol, which has deleterious effects on non-dividing cells. Recent studies suggest that the ability of cells to maintain energy levels during mitosis could account for the differential responses of cancer cells to mitotic arrest. To determine if manipulating cellular metabolism could potentiate the efficacy of KSP inhibitors, we arrested cells in mitosis in the absence or presence of the PI3-kinase/AKT/mTOR inhibitors, and probed for the induction of apoptosis.
Treatments were performed using cell line that undergoes apoptosis immediately following mitotic failure (HeLa), as well as a second line that survives mitotic arrest (MCF-7). In both cases, simultaneous inhibition of KSP and PI3-kinase/AKT/mTOR induced apoptosis more effectively than mitotic arrest alone. Lastly, we found that increased glucose had a protective effect, further supporting the notion that the ability to survive mitotic arrest depended on the ability to maintain energy levels. If confirmed, this may represent a novel approach for potentiating the anti-tumor activity of KSP inhibitors in the clinic.

3. Factors influencing spindle orientation during early development.
Aaron Rodriguez [UG], Leslie Toledo, and Charles B. Shuster.
Department of Biology, New Mexico State University, Las Cruces, NM.

Following fertilization, the embryo undergoes precisely patterned cleavages that differentially partitions factors that influence cell fate. In Echinoderms such as sea urchins and sand dollars, the spatial patterning of the early divisions is critical to establishing the embryonic axis, but little is known about how this process is regulated. We hypothesize that the PAR complex recruits dynein to the cell cortex, which then influences the orientation of the mitotic spindle. Using time-lapse microscopy, we observed that PAR inhibition results in abnormal cleavage patterns. Current efforts are focused developing new reagents to validate these results.

4. Cuticular conductance in Juniper and Oak.
Mikayla Pulliam [UG], Sanna Sevanto, and Natalie McBranch.
Los Alamos National Laboratory, NM.

In the southwest, temperatures are rising and drought conditions are increasing due to climate change. We investigated how climate change will affect the trees living in these conditions by studying the stomata of juniper and oak trees. Stomata are pores found on the epidermis of leaves, and control the gaseous exchange of carbon dioxide and water throughout the plant. Stomatal conductance is the rate at which this exchange between water and carbon dioxide occurs. In ample conditions, the stomata remain open when exposed to sunlight. However when leaves dry out in drought conditions, they close their stomata to prevent water loss as a survival mechanism. Even if the stomata are closed to prevent water from escaping, there is typically still some water loss through the cuticular tissue of the plant. This is known as the cuticular conductance rate. This unintended water loss can be the reason for tree mortality in drought. We recorded the rate of water loss due to cuticular conductance in leaves of juniper and oak at two different temperatures: 20°C, and 40°C to observe water loss rates at a moderate temperature compared to an extreme temperature to understand tree mortality due to heat and drought.
5. Call similarity and strength of social behavior in Budgerigars (*Melopsittacus undulatus*).

*Clara Hansen [UG], Angela Medina-García, and Timothy Wright.*

Department of Biology, New Mexico State University, Las Cruces, NM.

Budgerigars are small parrots that, along with humans, are among a few species of animals capable of vocal learning and sound imitation as adults. Adult budgerigars within a social group will develop shared contact calls through vocal learning. One hypothesis for the evolution of this ability is that shared vocalizations facilitate social interactions between group members. Here we test the possible correlation between the number of contact call types and strength of social associations within a group of five captive female budgerigars. Contact call recordings and behavioral observations were conducted for a period of four weeks. We predicted that pairs of birds with strong affiliative associations would have more shared contact calls than pairs with weak associations. Results indicated no correlation between contact call strength and social association strength. We are currently replicating this experiment with the same group of female budgerigars and with male groups to test the consistency and generality of this initial result.


*Mahsa Shirani [G], Tyson McCabe, Rajan Koirala, Melissa Jarmel, Sanford Simon, and Barbara Lyons.*

Department of Chemistry and Biochemistry, New Mexico State University, Las Cruces, NM.

Fibrolamellar hepatocellular carcinoma (FL-HCC) is a rare cancer of the liver, and affects adolescents and young adults. In almost all cases there is no history of underlying primary liver disease such as cirrhosis or viral hepatitis. FL-HCC represents less than 0.1% of all liver cancer, with little known about development. FL-HCC tumors do not respond well to chemotherapy and surgical resection remains the only effective therapy. Protein kinases regulate a wide range of cellular processes during growth and development, making them an integral part of signaling in diseases such as cancer. Activity of the PKA catalytic domain is regulated by four different regulatory subunit isoforms, Rία, Rία, Rίβ and Riiβ. The isoforms are believed to confer differing signal specificity. A gene fusion event in FL-HCC patients has recently been discovered. A deletion in chromosome 19 results in the fusion of PKA to the N-terminal J domain of DNAJB1, and therefore the expression of a chimeric protein, DNAJB1-PKA. Although not fully substantiated, it is believed this mutation is directly implicated in the development of FL-HCC. We believe the binding of this chimeric protein to its regulatory domains may be different than the binding of wild type PKA.

7. Neophobic tendencies and their effect on social position within networks of male budgerigars.

*Elise Boyd [UG], Zoe Sullenger, Angela Medina-García, and Timothy F. Wright.*

Department of Biology, New Mexico State University, Las Cruces, NM.

An individual's personality may have important effects on the structure
of a social network, that individual’s position in that social network, and therefore individual fitness. The aim of this study was to investigate whether neophobia, or an individual’s response towards new objects, is correlated with position within a social network of adult male budgerigars, *Melopsittacus undulatus*. Neophobic tendencies were tested with multiple novel objects, and a novel food item across several time points. Latency to feed in each condition was used to measure neophobia for each individual. Five groups, each composed of six males and three females each, were observed for several weeks. Both agonistic and affiliative interactions in each group were used to generate social networks and calculating association strength between pairs of individuals within each group. While strong social preferences were observed, no correlation was found between neophobia and position within social networks. Considering the highly social nature of budgerigars, it is possible that individual neophobic tendencies may not reflect individual ability or willingness to interact with conspecifics.

8. Reacting sulfite oxidase model complexes with acids

*Katarina Schwalenstocker [G], Feifei Li.*

Department of Chemistry and Biochemistry, New Mexico State University, Las Cruces, NM.

One area of bioinorganic chemistry involves modeling enzymes using small molecules. An example of this is the complexes $[\text{Bu}_4\text{N}]_2[\text{Mo}^{\text{VI}}\text{O}_2(\text{mnt})_2]$ and $[\text{Bu}_4\text{N}]_2[\text{Mo}^{\text{VI}}\text{O}(\text{mnt})_2]$ (mnt=maleonitriledithiolate) which model the active site of the sulfite oxidase enzyme. Sulfite oxidase is a molybdenum-centered enzyme that catalyzes the conversion of sulfite (SO$_3$) to sulfate (SO$_4$). Sulfite oxidase is present in many different species, including humans. Sulfite oxidase deficiency, though rare, can be fatal. The role of protons/acid in enzyme activity, including sulfite oxidase, is poorly understood, but can be illuminate by reacting these small model complexes with acids. It appears that reacting these complexes with tosyllic acid creates many different species in equilibrium. Reacting these complexes with trifluoroacetic acid results in the formation of the $[\text{Bu}_4\text{N}]_2[\text{Mo}(\text{mnt})_3]$ molecule for the $[\text{Bu}_4\text{N}]_2[\text{Mo}^{\text{VI}}\text{O}_2(\text{mnt})_2]$ di-oxo complex and a new complex for the $[\text{Bu}_4\text{N}]_2[\text{Mo}^{\text{VI}}\text{O}(\text{mnt})_2]$ mono-oxo complex.

9. Lower intraspecific aggression associated with lower genetic diversity in invasive urban colonies of the rough harvester ant *Pogonomyrmex rugosus.*

*Aldo F. Ramirez [UG], Grace Smith Vidaurre, and Timothy Wright.*

Department of Biology, New Mexico State University, Las Cruces, NM.

Ants include some of the most successful and widespread urban invaders. Rough harvester ants (*Pogonomyrmex rugosus*) are found throughout urban habitats in the Southwest, likely as a result of invasion from neighboring rural areas. Founder effects following urban invasion are expected to decrease genetic diversity within colonies and increase genetic similarity between colonies, and thus lower intraspecific aggression. We conducted 350 trials comparing inter-colony aggression within and between
urban and rural settings. In trials conducted between neighboring colonies, urban colonies displayed lower aggression than rural colonies. In contrast, urban and rural colonies showed similar levels of aggression towards non-neighbors from the same setting and across the two settings. We assessed genetic diversity within colonies using three microsatellite loci. Preliminary results for three markers and six colonies per setting indicate that urban colonies exhibit lower genetic diversity than rural colonies. These results suggest lower genetic diversity within neighboring urban colonies has led to lower intraspecific aggression among neighboring colonies.

10. Factors related to telomere length in Puerto Rican parrot chick (*Amazona vittata*)

Brian Ramos-Güivas1, Bridgett von Holdt2, Taras K. Oleksyk3, and Timothy F. Wright1.

1Department of Biology, New Mexico State University, Las Cruces, NM, Princeton University, Princeton, NJ, 2University of British Columbia-Okanagan, British Columbia.

Shortened telomeres have been related to decreased lifespan and long term detrimental effects in a variety of organisms. Early life stressors play an important role in shortening telomeres. In birds, both a lack of food provided by the parents and a larger clutch size may increase stress in young chicks and can be reflected on the weight of the chicks and age of fledging from nest. We investigated how these factors may relate to telomere length in wild-hatched chicks of the Puerto Rican parrot. To measure telomere length, we use a fraction of the blood samples taken for sexing of chicks between 40 to 55 days after chick hatching. A total of 22 wild born chicks were sampled from 9 wild nest. We use relative quantification to measure telomere length via q-PCR of telomere and B364 as reference gene. Preliminary results show no strong relation of telomere length with any of the variables measured. We found high variance in telomere length within each nest. This high variance may be due to the difference of age among siblings, or parental food allocation between chicks. I will follow up by analyzing food allocation by parents and hatching sequence effect on telomere length.

11. Detecting genomic signatures of selection in an invasive parakeet (*Myiopsitta monachus*)

Grace Smith Vidaurre1 [G], Andrew J. Veale2, Michael A. Russello2, and Timothy F. Wright1

1New Mexico State University, Las Cruces, NM, 2University of British Columbia-Okanagan, British Columbia.

Human movement and trade have greatly accelerated the rate of biological invasions across the globe. We do not understand how diverse species become successful invaders in light of anthropogenic change. Do species that invade new habitats adapt to anthropogenic selection pressures following invasion, or does anthropogenic change in the native range promote pre-adaptation to subsequent invasion elsewhere? Naturalized monk parakeet (*Myiopsitta monachus*) populations have established in cities across the Northern hemisphere as a consequence of the pet trade. These populations are an ideal natural experiment for investigating evolutionary processes following invasion. Previous research shows low
neutral genetic diversity among naturalized populations compared to native South American populations. Such patterns suggest that either naturalized populations are adapting to new selective regimes, or populations are experiencing population bottlenecks and founder effects. I am using a genotyping-by-sequencing approach to identify genes under selection and identify demographic relationships between native and naturalized populations. This study is the basis for upcoming fieldwork in South America to determine whether parakeet populations demonstrate signatures of adaptation to human disturbance in the native range.

12. The effects of increased perceived predation risk on lay-date in black-throated blue warblers (*Setophaga Caerulescens*).

*Dominique L. Hellmic*¹ [G], Mike S. Webster², and Sara A. Kaiser³.

¹Department of Biology, New Mexico State University, Las Cruces, NM. ²Cornell University, Ithaca, NY, Smithsonian Conservation Biology Institute, Washington, DC.

Recent studies have found that perceived predation risk alone is capable of substantial declines in adult fitness, parental investment, and net fecundity due to the adoption of costly, anti-predator behavioral responses. In this study we investigated the effects of increased perceived predation risk on lay-date in black-throated blue warblers. Previous study by Townsend et al. (2013) found that these warblers are able to adaptively advance their lay-date in warmer springs. We predicted that increased perceived predator abundance in warmer springs would potentially constrain this advancement in lay-date if the costs of avoiding peaks in predation risk outweighed the benefits of an increased chance of double brooding. We also predicted that females experiencing higher perceived risk would adopt additional, costly, anti-predator behaviors (i.e. increased vigilance). Using predator playback during the 2013 and 2014 breeding seasons we manipulated early perceived predation risk but found no relationship between this and lay-date. Neither did we see a significant increase in anti-predator responses by females. These results suggest that interactions between multiple demographic parameters (e.g. prey abundance, weather), methodological flaws in our experimental design, or the absence of a functional relationship between lay-date and predation risk may be responsible for our lack of evidence.

13. Rap1 affects recruitment of R7 photoreceptors and of cone cells in *Drosophila ommatidia*

*Crystal Hernandez* [UG], Philip Yost, and Jennifer Curtiss.

Department of Biology, New Mexico State University and NM-AMP.

Cell fate specification is controlled in part by signaling among cells, but the mechanisms remain unclear. Each of the 800 facets (ommatidia) of the *Drosophila melanogaster* eye contains 8 photoreceptors (R1-6 detect motion and R7, 8 detect color), as well as 4 cone cells that produce a lens. The identity of each cell is specified entirely by the order in which it is recruited via signaling among ommatidial precursors. Here, we show that expression of a dominant negative version of Rap1 small GTPase (*Rap1N17*) in the R4
precursor results in premature expression of the R7 marker Prospero during larval development, together with an increase in R7 photoreceptors and a decrease in cone cells at the pupal stage. Expression of constitutively active Rap1 (RapV12) in the R4 precursor has no effect on timing of Prospero expression in larvae, but results in a decrease in R7 photoreceptors and an increase in cone cells in pupae. The R7 fate is interchangeable with cone and other photoreceptor cell fates depending on the relative levels of EGFR and Notch signaling they receive. Thus, our results suggest that Rap1 affects EGFR and/or Notch Signaling during cell fate specification in the Drosophila eye.

14. Lost in untranslation: Effects of evolution in different avian host species on structural variation in the 5’ untranslated region of the West Nile virus genome.

Stacey L. Scroggs [G], Johnny A. Sena, Gregory D. Ebel, and Kathryn A. Hanley. Department of Biology, New Mexico State University, Las Cruces, NM.

West Nile virus (WNV) has a positive-sense, single stranded RNA genome flanked by 5′ and 3′ untranslated regions (UTRs), which form secondary structures. Structural elements are required for viral replication, and there appears to be strong selective pressure to conserve these structures. To date, structural analysis has relied on consensus sequences, which may miss or misrepresent dynamics within the viral quasispecies. We hypothesized that mutations are more likely to occur in single stranded (SS) regions of the UTRs compared to double stranded (DS) regions, as the former mutations have less effect on structure. To test this, we conducted next-generation sequencing of WNV populations that had undergone 5 passages, in triplicate, in 3 bird species (N = 45 populations) as well as the input virus (WNV99). Ten randomly-chosen reads of the 5’ UTR with at least 1 mutation were selected per bird, passage, and replicate for analysis. Crow-passaged WNV had more 5’ UTR mutations in SS locations compared to the expected distribution (p=0.002) at passage 2, whereas, sparrow- and robin-passaged WNV had more 5’ UTR mutations in SS locations at passage 3 (p<0.005 for both).

15. Spatial distribution of mosquitoes that vector Zika, dengue, and West Nile virus in New Mexico.

Stephanie Mundis† [G], Nathan Lopez-Brody‡, Michaela Buenemann‡, and Kathryn A. Hanley‡.

†Department of Biology and ‡Department of Geography, New Mexico State University, Las Cruces, NM.

A current, accurate understanding of vector distribution is vital for countering the threat of mosquito-borne disease. In New Mexico, the distributions of Aedes aegypti and Aedes albopictus, the vectors of Zika, chikungunya, and dengue, are essentially unknown. Thus, in this study, a clustered, stratified random sampling design was employed to collect mosquitoes across 24 counties in New Mexico. Sampling represented six land cover classes: Agricultural, Barren, Forest, Rangeland, Urban, and Wetland, resulting in 178 site visits from June 13th to September 10th 2016. Using morphological keys, all mosquitoes were identified to the genus level and
all *Aedes* species were identified to the species level. Overall, 940 mosquitoes have been collected and identified. The results from our analyses indicate that *Aedes aegypti* is present in urban areas in five counties while *Aedes albopictus* was collected in an urban site in Roosevelt County. Culex species, which are vectors of West Nile, were found in all land cover classes, with the majority collected in urban areas. In future work we will create species distribution models of key vector species to better predict where they are likely to occur, as well as project distributions of these species under climate change conditions.

16. An exploration of the temporal stability of social networks in the budgerigar (*Melopsittacus undulatus*)
Zoe Sullenger [UG], Elise Boyd, Angela Medina-García, and Timothy F. Wright.
Department of Biology, New Mexico State University, Las Cruces, NM.

Social network structure and temporal dynamics in avian species, particularly in Psittaciformes, are poorly understood. Previously, social networks in captive monk parakeets, *Myiopsitta monachus*, were shown to stabilize quickly and remain stable for over a month. In this study we examined social networks in another parrot, the budgerigar, *Melopsittacus undulatus*. Five groups, each composed of six males and three females, were observed using focal animal sampling. We used social interaction data from these observations to generate social networks every 3-4 days, and then calculated correlations between social interaction matrices at ten time points. Results suggest budgerigar social networks do not stabilize, and instead remain variable for weeks to months after initial group formation. This lack of stability in social networks may reflect the nomadic lifestyle and opportunistic breeding shown by budgerigars in their native habitat.

17. Understating how tumor cell clusters metastasize: Invasive leader cells express hemidesmosome proteins.
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Metastatic cancer cells detach from a primary tumor, migrate, and proliferate in a distant organ. Metastasis was thought to occur through dissemination of single tumor cells, but recent studies revealed an alternative mechanism in which tumor cell clusters migrate and colonize distant organs. When breast tumor organoids are cultured in a 3D matrix, tumor cell clusters invade using specialized leader cells that express cytokeratin 14 (K14). K14+ cells are enriched hemidesmosome mRNAs, suggesting hemidesmosome proteins could be involved in cell cluster metastasis. In this project we characterized expression of three hemidesmosome proteins (collagen XVII, collagen VII, and integrin β4) in mammary tumor organoids. Tumor organoids were isolated from MMTV-PyMT mice and embedded in each of two 3D matrices that model the tissue microenvironment of noninvasive or invasive breast cancer: matrigel and collagen I. Tumor organoids expressed hemidesmosome proteins in matrigel and collagen I; however expression of...
hemidesmosome proteins varied. In collagen I, β4, C17, and C7 proteins were expressed on invasive leader cells within a tumor cell cluster. In matrigel, β4 was expressed uniformly throughout the organoid border, C17 was expressed heterogeneously, and C7 was not expressed. Determining features of cell clusters involved in metastasis could enable novel treatments of metastatic breast cancer.

18. A Deadly intrusion: Competitive displacement among dengue virus strain in Sri Lanka
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Dengue virus, the agent of dengue hemorrhagic fever (DHF) infects approximately 400 million people worldwide. Dengue virus is primarily transmitted by the mosquito *Aedes aegypti*. This virus is exceptionally genetically diverse, and dengue strains regularly invade new geographic regions and displace existing strains. Particularly successful invasive strains often cause high rates of DHF. My project investigates the mechanisms underlying a series of dengue virus strain displacements in Sri Lanka. Specifically, we are testing the hypothesis that differences among strains in susceptibility to RNA interference, the fundamental mosquito immune defense against viruses, determines their invasion success. To test this hypothesis, we will knock down RNAi in live mosquitoes and then feed them on successful, invasive dengue strains or unsuccessful, displaced dengue strains. To date we have generated double stranded RNA (dsRNA) against Argonaut 2 (Ago2), a key enzyme in the RNAi pathway, as well as GFP control dsRNA, injected *Ae. aegypti* with these dsRNA, and used semi-quantitative PCR to measure Ago-2 and Actin mRNA at days 3, 6 and 12 post-injection. We have observed a ~25% knockdown Ago2 mRNA via rt-PCR. We will now feed these knockdown mosquitoes on our target strains of invasive and displaced dengue virus.

19. Paraquat feeding for study of bacterial participation in mosquito defense against oxidative stress.
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For anautogenous female mosquitoes, blood digestion results in heme associated oxidative stress, which is detrimental to various life traits, like fecundity and longevity. As an adaptation, mosquitoes have evolved certain antioxidant mechanisms to cope with the stress. However, little is known about the extent of defense capacity that mosquitoes have. Paraquat (PQ) is an herbicide that causes extensive damage to mitochondria through the production of free radicals and oxidative stress. In this study we examined the effect of PQ feeding on mosquito fecundity and mortality. Interestingly, blood feeding increased the mortality and decreased the fecundity of PQ fed mosquitoes, suggesting that the stress induced by blood meal and PQ both reached a level that exceeds the defense capacity of mosquitoes. In order to examine the contribution of the gut bacteria to the mosquito
antioxidant ability, bacterium (Elizabethking, Enterobacter or Pseudomonas) plus PQ feeding was applied to adult mosquitoes. The results showed that the single bacterium plus PQ feeding caused higher mortality. The 3 bacteria mixed sugar could relatively alleviate the mortality caused by the simple bacterial community structure, but still significantly higher than regular sugar, which demonstrated that the mosquito needs a complicated gut bacteria community for survival.

20. Characterization of type I-F of CRISPR-Cas system in strains of Serratia spp. from the mosquito gut.

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The mosquito Anopheles gambiae midgut ecosystem accommodates a diverse and dynamic microbiome. Within this microbiome, Serratia is an abundant genus. CRISPR-Cas system is an adaptive immune system in bacteria and archaea. In this study, two strains of Serratia spp., Ag1 and Ag2, were isolated from the mosquito midgut. There are two subtypes of type I CRISPR-Cas system, I-E and I-F, present in the genome. The I-F subtype consists of six cas genes. I-E subtype consists of seven cas genes. Possible origins of the spacer sequences of the CRISPR systems were examined by comparing spacers against the databases of phages and conjugative plasmids. Interestingly, there is an insertion in the I-F cas3 gene in Ag2 strain. The inserted DNA fragment was 1.5 kb with three coding regions. The type I-F system of both Serratia strains was functional. It was able to degrade the plasmids that carried engineered protospacers. Apparently, in the strain Ag2, the insertion in cas3 did not affect its function. Since Serratia is predominant in the microbial community in the mosquito gut, it will be interesting to know if the CRISPR system plays a role in shaping and stabilizing of the mosquito microbiome.

The Biosymposium committee thanks

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