Biosymposium 2019

Saturday, April 6th.

Hosted by the NMSU Department of Biology

The committee would like to take the time to thank everyone for their participation and support of NMSU Biology's Biosymposium.

This includes:

- presenters
- judges
- audience
- volunteers from the BGSO
- Biology staff for support
- Department of Biology for financial support
- the organizing committee

Biosymposium schedule

8:50-9:00	opening remarks
9:00-9:15	A. Kulkarni
9:15-9:30	S. Mitra
9:30-9:45	Y. Kandel
9:45-10:00	A. Moon
10:00-10:15	K. Young
10:15-10:30	coffee break
10:30-10:45	D. Pal
10:45-11:00	N. Ashraf
11:00-11:15	I. Terrazas
11:15-11:30	Y. Zheng
11:30-11:45	M. Najaf-Panah
11:45-12:00	C. Campos
12:00-2:00	posters and lunch
12:00-1:00	odd posters
1:00-2:00	even posters
2:00-2:15	P. Houde
2:15-2:30	R. Coryell
2:30-2:45	A. Dominguez
2:45-3:00	S. Lee
3:00-3:15	B. Pipes

P1. Resolving relationships in *Leucaena* through reference guided and *de novo* transcriptomics

Alexander L. Abair[1], Madhugiri Nageswara-Rao[1], Diana V. Dugas[1], Colin E. Hughes[2], C. Donovan Bailey[1]

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The genus *Leucaena* (Leguminosae, Caesalpinioideae, Mimosoid clade) contains 24 species, some of which have a long history of use in Mesoamerica as food, shade, and even spiritual medicine. Their native range is restricted to the Americas, but *Leucaena leucocephala* (and a few other species) have spread around the tropics where they are currently used in tropical agroforestry systems as fodder for cattle, soil stabilizers and fertilizers, shade, and biofuels. This genus, which contains diploid and allotetraploid species, serves as a model system for investigating the role of spontaneous backyard garden hybridization in early domestication, but the precise relationships of species remain unclear. Previous work recognized three well-supported clades of diploid *Leucaena*. However, the relationships among species within the largest clade (Clade 1) remain poorly resolved, confounding attempts to infer origins of the five allotetraploid species. In this study, we use a sequenced diploid genome (*Leucaena trichandra*) and whole seedling-derived transcriptome data from all diploid *Leucaena* species to infer both reference-guided and *de novo* phylogenetic hypotheses for *Leucaena*. Once a robust phylogeny is inferred from conserved orthologous genes, future work will attempt to elucidate the evolutionary history of *Leucaena* ssp. in a geographical context.

P2. Investigating the mechanisms driving polarity reversal during epithelial-mesenchymal transitions in the sea urchin embryo

Zebib Sielu Abraha, Silvia Sepulveda-Ramirez, Leslie Toledo and Charles B. Shuster

Department of Biology, New Mexico State University, Las Cruces, New Mexico, USA

Epithelial to Mesenchymal Transitions (EMT) are an evolutionary-conserved process where epithelial cells lose cell-cell contacts, reverse apico-basal polarity, and assume a mesenchymal phenotype that allows them to be invasive and migrate. Hence, understanding both transcriptional regulation and the morphological changes driving EMT during development could provide insights into the regulation of EMT in pathologies such as cancer metastasis. The sea urchin embryo provides an excellent model for studying EMTs in that in each embryo, 16-24 primary mesenchyme cells (PMCs) undergo EMT 20 hours post-fertilization by ingressing from the vegetal pole into the blastocoel. The transcriptional repressor Snail, which is upregulated in metastatic carcinomas, is thought to drive EMT through the downregulation of E-cadherin. Indeed morpholino or CRISPR downregulation of Snail in sea urchin embryos disrupts PMC ingression. However, how Snail controls other aspects of EMT i.e. the reversal of apico-basal polarity is unknown. Preliminary data suggests that prior to ingression, vegetal cells internalize the apical polarity protein Par-6 into intracellular vesicles in a manner similar to E-cadherin. We hypothesize that Snail directs Par-6 clearance from the apical cortex, and to test this hypothesis, we will overexpress/downregulate Snail and examine the effects of these perturbations on Par-6 localization in live and fixed embryos. Additionally, we will examine candidate Snail targets that may affect Par complex localization, such as the polarity protein Crumbs. Current efforts are focused on developing Whole Mount In-situ Hybridization (WMISH) and live cell probes for these proteins, as well as overexpression and CRISPR-Cas9 constructs for manipulating Snail expression.

T7. Understanding the underlying mechanisms of cell death in mitotically arrested cancer cells

Naghmana Ashraf, Roaa Kassim, and Charles B. Shuster

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Drugs targeting mitotic spindle have been employed to treat cancer for over three decades. However, the actual mechanisms by which mitotic arrest drives cell death remain poorly understood. Data from our lab indicate that simultaneous inhibition of spindle assembly and the phosphaotidylinositide-3-kinase (PI3K) pathway increases the kinetics of mitotic cell death and potentiates apoptosis in HeLa cells. Nevertheless, it is unclear whether cells die during mitosis or first they undergo accelerated mitotic slippage. To better understand this combinatorial effect and the underlying mechanisms of cell death, we have developed a series of constructs that will allow us to simultaneously monitor caspase activation and mitotic arrest. To monitor caspase activation, a caspase cleavage site was inserted between a myristoylation sequence and mApple, creating a red membrane tag that is mobilized into the cytoplasm upon initiation of apoptosis. This biosensor also contains a C-terminal viral peptide 2A sequence that allows for expression of a second open reading frame (such as fluorescent tubulin or cyclin B), enabling us to determine cell cycle status during mitotic cell death in living cells. HeLa cells expressing these biosensors displayed a range of cellular responses to mitotic arrest, ranging from apoptosis during mitotic arrest to mitotic slippage and cell survival. Using these biosensors, we aim to monitor morphological changes in mitotically arrested cancer cells in the absence of PI3K activity to investigate how PI3K inhibition shifts the kinetics of the cell death. Such studies can help in increasing the efficacy of cell killing through anti-mitotic drugs.

P3. Characterization and Localization of COPI subunits and their isoforms during early compatible pollination events in *Arabidopsis thaliana*

Michael Anthony Balogh[1], Daniel Cabada Gomez[2], Emily Indriolo[1]

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Coat Protein Complex 1 is a vesicular coat protein that is mainly involved in retrograde transport from the *cis*-Golgi to the Endoplasmic Reticulum and may serve roles in endosomal functions. COPI is comprised of 7 subunits, and, in higher plants like *Arabidopsis thaliana*, each of these subunits has at least one additional isoform present. It has been shown previously that RNAi of COPI subunits causes mislocalization of transmembrane proteins and fragmentation of Golgi structures. From the perspective of cell interactions during a compatible pollination event in plants, vesicle trafficking is crucial for the germination and growth of a pollen tube eventually resulting in seed formation. Preliminary data has revealed that the α1-COPI subunit contributes significantly to processes involved in pollen pistil interactions as the *α1-copi* mutants exhibit reduced pollen grain adherence, germination, tube growth, and decreased seed set. Other subunit mutants, such as *β-copi* and *β′-copi*, appeared close to the wild type, while *γ-copi* and *ε-copi* has slightly reduced phenotypes but not as severe as the *α1-copi*. Confocal fluorescent microscopy will be utilized to observed where the subunits are localizing during transient expression in *Nicotiana benthamiana*, using a constitutive 35S promoter, and 10 minutes after a compatible pollination event in *A. thaliana* using a stigma specific SLR1 promoter. The α1-COPI subunit may be localizing to a different area of the cell during a compatible pollination event when compared to the transient expression in *N. benthamiana.* I predict α1-COPI will localize to the early endosomal vesicles as recycling of cell surface transmembrane proteins that are needed for compatible pollinations and subsequent seed formation.

P4. The regulation of nutrient storage, developmental duration and lifespan by the *Neprilysin-like 15* gene in *Drosophila melanogaster*

Surya Jyoti Banerjee, Michael Burnett, Jennifer Curtiss

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The *Drosophila melanogaster* has been used to investigate the human metabolic diseases such as obesity, diabetes, cardiac dysfunction and lifespan as the underlying mechanisms are remarkably conserved. The *D. melanogaster Neprilysin-like 15* (*Nepl15*) gene encodes a secreted neprilysin devoid of conserved catalytic residues. Our study showed that *Nepl15* mRNA levels were significantly higher in the wild type larval fat body and in adult fly abdomen (which contains fat body) compared to other tissues. The fat body of *D. melanogaster* is analogous to the human liver and is responsible for nutrient sensing and storage. We hypothesized that *Nepl15* plays a critical role in nutrient homeostasis. We have demonstrated that adult age-matched flies in which the *Nepl15* gene has been knocked out ($Nepl15^{ko}$) feed normally but have less stored triglycerides and glycogen compared to wild-type flies, suggesting that *Nepl15* is essential for proper nutrient storage. Consistent with these results, $Nepl15^{ko}$ flies show delays in development and are more susceptible to starvation but live longer when food is in adequate supply. Our data also indicates that flies overexpressing *Nepl15* in all tissues have increases in glycerides and glycogen. Interestingly, overexpression of *Nepl15* specifically in the gut results in increased glycerides but not glycogen, whereas overexpression specifically in the fat body results in increased glycogen but not glycerides, suggesting *Nepl15* has different roles in different tissues. Future studies of *Nepl15* can elucidate the underlying mechanism of nutrient storage and identify novel ways to control human obesity and related diseases.

T 11. Genetic structure and diversity in wild and captive populations of the critically endangered blue-throated macaw (*Ara glaucogularis)*

C.I. Campos[1], A. Martinez[1], I. Berkunsky[3], J.A. Diaz-Luque[4] M.A. Russello[2], T.F. Wright[1]

Department of Biology, New Mexico State University, Las Cruces, NM, USA; [2]Department of Biology, University of British Colombia, Okanagan, Canada; [3]Universidad Nacional del Centro de la Provincia de Buenos Aires, Tandil, Buenos Aires, Argentina; [4]Proyecto de Conservación de la Paraba Barba Azul, The World Parrot Trust, Sachojere, Beni, Bolivia

A key aspect in the conservation of endangered populations is understanding their underlying genetic structure. The blue-throated macaw is endemic to Bolivia and is one of the most endangered species of macaw, with an estimated 250 birds remaining in the wild. Like many parrots, the blue-throated macaw has sizeable populations in zoos and private ownership. This raises interesting questions about the genetic diversity within, and the genetic relatedness between wild and captive populations. Our goal is to assess genetic variation in wild and captive populations to inform conservation efforts for this highly endangered species. We genotyped 56 wild individuals from Bolivia and 58 captive individuals from the US, Canada and Bolivia at 12 polymorphic microsatellite loci to determine genetic diversity and relatedness. We examined population structure using a Bayesian clustering approach and calculated population F statistics to determine the extent of population structure. Our results using STRUCTURE show that wild Bolivian populations are genetically distinct from captive populations; this result was echoed by a significant pairwise Fst value of 0.059 between the two populations. Ongoing analyses will test for the presence of population bottlenecks and inbreeding in both captive and wild populations. These results will help inform ongoing efforts to manage wild populations and augment them with the release of captive-bred individuals.

P5. Noshing on vibrio - how grazing "outside the host" determines "fitness inside the host"

D. Cheam, P. Gonzalez, B. Hueffmeier, and M. Nishiguchi

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Vibrio fischeri can aggregate under stable conditions as a nonmobile community called a biofilm. Certain protozoans have a preference to feed on biofilms depending on the age and type of bacteria within the biofilm community. Protist grazing pressure can have multiple effects on bacterial biofilms including decreasing growth rates to triggering defense mechanisms that confer an increase in fitness. *V. fischeri* is a bacterial symbiont that resides in the light organs of sepiolid squids, forming a beneficial association by producing luminescence for a behavior termed counter-illumination. During the symbiosis, *Vibrio* bacteria produce biofilms within the squid light organ, allowing them to grow in high cell density, which regulates luminescence production. Given that *Vibrio* bacteria form biofilms both outside and inside the squid host, various factors may select for specific attributes for optimal biofilm production. Therefore, we examined whether biotic factors (e.g. grazing) outside the squid host were important for increasing biofilm fitness during symbiosis. We measured growth rates of eight different strains of *V. fischeri* to determine their ability to adapt to protozoan grazing pressure by using an experimental evolution approach. Late (24 hour) biofilms were exposed to the protozoans *Acanthamoeba castellanii* and *Tetrahymena pyriformis* after 30 generations. One strain of *V. fischeri* had a significant increase over time in biofilm formation over 30 generations of grazing pressure by *T. pyriformis*. Results of this study will provide a window to specific trade-offs that occur outside the squid that provide a fitness advantage in this beneficial association.

P6. Differences in energy production between skeletal muscle and electric organ of *Sternopygus macrurus*

Kevin A. Cisneros, Matthew Pinch, and Graciela A. Unguez

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

The electric organ (EO) in the weakly electric fish *Sternopygus macrurus* is derived from skeletal muscle fibers. Recently, Pinch et al demonstrated that the adult EO has basically the same transcript composition as that of skeletal muscle. However, skeletal muscle is composed largely of two main phenotypes: slow-twitch and fast-twitch fiber types. Which muscle phenotype is most expressed by adult electrocytes (i.e. EO cells)? Interestingly, electrocytes in *S. macrurus* are driven by motoneurons at a constant frequency of 50-200Hz – an activation pattern not experienced by any muscle cell. This study aims to determine the glycolytic and oxidative phosphorylation profile of electrocytes to ask whether energetically, electrocytes are similar to slow- or fast-twitch muscle fibers. To do this, we will examine the morphology and spatial distribution of mitochondria in electrocytes and muscle fiber types by analyzing images already obtained from longitudinal and transverse frozen tail cryosections (20 μm-thick) stained for qualitative enzyme histochemistry and tissue prepared for transmission electron microscopy to study mitochondria shape, arrangement and distribution. These data represent the first quantitative comparison of mitochondrial properties in electrocytes and skeletal muscle fibers.

T13. **"It's getting hot in here"- Temperature adaptation increases symbiotic competence in the sepiolid squid-*Vibrio* mutualism**

R.L. Coryell, M.K. Nishiguchi

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Beneficial microbes such as *Vibrio fischeri* are uniquely adapted to a dual lifestyle that allows for survival and persistence in the environment and inside their animal host. Symbiotic vibrios form mutualistic associations with squids in the genus *Euprymna* (Cephalopoda: Sepiolidae) throughout the Pacific, from temperate waters off the southern coast of Australia to tropical waters of the Indo-west Pacific. Given that *V. fischeri* has such wide physiological breadth, we examined the extent to which *V. fischeri* can accommodate temperature stress in order to identify trade-offs that affect host colonization and symbiotic fitness. Using an experimental evolution approach, we adapted five strains of symbiotic *V. fischeri* from different geographic locations to five treatment temperatures for 2000 generations *in vitro* to determine whether temperature adaptation influences symbiotic fitness. Generation time, luminescence, biofilm formation, and motility were used to determine the physiological response of these evolved vibrios compared to their ancestors. Lines evolved at high temperatures were able to colonize juvenile host squids better than their ancestor despite decreased levels of luminescence. Interestingly, lower temperature evolved strains had decreased levels of light, longer generation times, reduced biofilm formation, and lower colonization efficiency. Our results indicate that our evolved *V. fischeri* demonstrate adaptation to a range of temperatures but differ in their ability to colonize their squid hosts. These findings will provide insight as to whether beneficial bacteria such as *V. fischeri* can acclimatize to environmental variability, and still maintain a sustainable association in the face of climate change.

P.7 A putative transporter gene *swnT* is involved in efflux of the mycotoxins swainsonine and slaframine of the fungus *Slafractonia leguminicola*

S. Das[1] and R. Creamer[2]

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The fungus *Slafractonia leguminicola*,is a plant pathogen that causes black patch disease in red clover plants (*Trifolium pretense L.)* and also infects other legumes such as soybean, kudzu, cowpea etc. It produces two indolizidine alkaloids: slaframine and swainsonine that are harmful to livestock grazing on clover hay or pasture infested with the fungus causing slobbers syndrome and locoism respectively. The mechanism by which the fungus secretes these toxins is poorly understood. This project addresses the role of the toxin transporter in this fungus. All swainsonine-producing fungi, including *S. leguminicola,* share orthologous gene clusters, "SWN," among which *swn*T is putative a transmembrane transporter. Not all swainsonine producing fungi have this *swn*T transporter. To study the role of *swnT* in transportation of these two mycotoxins in *S. leguminicola, swnT* was silenced using RNA interference (RNAi). A silencing construct pSilent-swnT was made by engineering pSilent-1, which includes inverted repeat transgenes (IRT) of the transmembrane transporter gene *swn*T and a hygromycin resistance casssette. *Slafractonia leguminicola* was transformed with this fungal construct was done using PEG-mediated transformation. Transformation of *S. leguminicola* with pSilent-swnT construct should reduce *swnT* transcript levels in a knockdown mutant compared to wild type and be accompanied by a reduction in both swainsonine transport into media. Since nothing is known about the slaframine biosynthetic pathway, we anticipate determining if it uses the same or a different transport mechanism. This research will help elucidate the plant-pathogen interaction and how these toxic alkaloids are transported by the fungus.

T14. Contrasting the root zone microbial communities of the invasive Lehmann lovegrass and native black grama grass, and investigating their responses to climate manipulation

Andrew Dominguez[1], Dr. Erik Lehnhoff[2], Dr. Nicole Pietrasiak[1]

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The invasive perennial grass, *Eragrostis lehmanniana* (Lehmann lovegrass), was introduced to the Southwestern United States in the 1930s to mitigate degraded soil. *Lehmann lovegrass*, drought tolerant with an extended growing period, was well-suited for its introduced climate. It has since outcompeted native grasses in many rangelands. Yet, belowground impacts are poorly understood, and the role the microbial community associated with *Lehmann lovegrass* may play in its competitiveness is unclear. We investigated the microbial community of root zone soils under Lehmann lovegrass and the native perennial grass, *Bouteloua eriopoda* (black grama). Soil samples of each grass were taken from 18 plots, premonsoon (June 2017) and postmonsoon (November 2017). Plots were divided into three treatments including rainout (-80% precipitation), rain-on (+80% precipitation), and control (ambient). MiSeq Illumina Sequencing was used to sequence the archaeal, bacterial, and fungal communities of each soil sample. Statistical analysis indicated treatment effects on the diversity of black grama microbial communities sampled in November while lovegrass communities did not change. Also, we detected differences between the fungal communities of the two grasses. These interesting patterns reveal first insights into the temporal dynamics of soil microbial root zone communities when exposed to changes in precipitation amounts.

P8. Assessment of Population Size and Dialect Presence in the Endangered Yellow-Naped Amazon, *Amazona auropalliata*

M. Dupin[1], C.R. Dahlin[2], T.F. Wright[1]

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Successful planning for species conservation requires a thorough understanding of behavior and communication in wild populations that have the potential to host reintroduced individuals. A lack of knowledge about cultural dynamics such as shared vocalizations could result in the failure of reintroduced individuals to assimilate into a population. Yellow-naped amazons, *Amazona auropalliata*, have undergone a recent and rapid decline in Costa Rica, an area that once harbored a healthy population. Population data are scarce or missing throughout other parts of their range in Mexico and Central America. This study aims to evaluate population numbers and geographic variation in contact calls across the yellow-naped range and determine whether geographically distinct dialects have emerged or have been maintained as population numbers have dwindled. Contact calls and roost count data were collected during 2018 from 8 different sites in Chiapas, Mexico. We find northern subpopulations have experienced drastic decline and exhibit strong call divergence. These calls are structurally different to those from the southern-most region of the parrot's range, suggesting the presence of dialects at both ends of the range. These results suggest that as the number of individuals in the wild declines, contact call structure may be subject to rapid change which could impact the success of reintroductions.

P9. Genome wide association analyses for salinity tolerance at seed germination in elite alfalfa germplasm

Arshdeep Singh Gill, Harpreet kaur, Ian Ray

Soil salinity is a major limitation to crop production throughout the world particularly in arid irrigated environments. Selection for resistance to salt tolerance would be greatly facilitated by the identification of genes involved in salt tolerance. Genome Wide Association Studies (GWAS) have shown great potential for uncovering genes/loci of interest in plants. The objective of this study was to identify molecular markers associated with salt tolerance for seed germination in alfalfa. An elite population of 265 half-sib families was evaluated by germinating twenty-five seed of each family in 1% sodium chloride (NaCl) solution in a randomized complete block design. Genotyping by sequencing (GBS) approach was used for genotypic characterization of half-sib families, and GWAS was performed with 7280 single nucleotide polymorphisms (SNPs) markers. GWAS identified three and nine SNPs significantly associated with salt tolerance in the year 2017 and 2018, respectively. Eight markers were repeatedly found significant in both years. Most significant markers associated with salt tolerance were found on chromosome 1,3, 5 and 7. The significant markers identified for salt tolerance by GWAS explained 10.9% to 32.9% of phenotypic variation. Gene Expression Omnibus (GEO) database search identified a total of 97 genes in the vicinity of significant markers whose expression significantly changed under salt stress. Blast search in UniProt database found that 17 out of above genes have been implicated in the stress tolerance pathways making them potential candidate genes for salt tolerance at seed germination.

T12. Phylogeny and biogeography of New Zealand's extinct Adzebill (Aves: Gruiformes)

Peter Houde[1], Alexander Boast[2], Kieren Mitchell[2]

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Biogeography may reflect the influence of plate tectonics on organismal evolution. For example, New Zealand is home to several of the most ancient lineages among various groups of living birds, including kiwis, moas, Kea, and Rifleman. These relicts might have been stranded in New Zealand due its breakup from the Mesozoic supercontinent Gondwana, some 85 MYA – but they weren't. Phylogenomic timetree analyses conclude that they diverged too recently from their respective nearest relatives to have originated in Gondwana. The Adzebill, too, was endemic to New Zealand. It was a large flightless bird that was extirpated by Polynesian immigrants in prehistoric times. Some contend, based on comparative anatomy, that the Adzebill was most closely related to flightless Kagu of New Caledonia, another Gondwanan fragment. Proponents of the Gondwana paradigm of early avian origins speculate that continental vicariance caused the divergence of the Adzebill and Kagu from a flightless ancestor. Using ancient DNA from fossil bone and eggshell, we sequenced the complete mitochondrial genome of the Adzebill as well as all of its potential relatives, including 98 of the 148 species of living rails. We find that the Adzebill diverged recently from small rail-relatives of Madagascar. It is not related to the Kagu. Rails are notorious for losing their powers of flight after colonizing remote Pacific islands devoid of predators. The Adzebill probably did, too. Coincidentally, New Zealand's kiwi also recently diverged from Madagascan endemics, the elephant birds. Although now discredited, these are popularly cited as textbook examples of Gondwana vicariance biogeography.

T3. Widespread Insecticide Resistance in yellow fever mosquitoes (*Aedes aegypti* L.) from New Mexico, USA

Yashoda Kandel, Julia Vulcan, Stacy D. Rodriguez, Emily Moore, Hae-Na Chung, Soumi Mitra, Joel J. Cordova, Kalli J. L. Martinez, Alex S. Moon, Aditi Kulkarni, Paul Ettestad, Sandra Melman, Jiannong Xu, Michaela Buenemann, Kathryn A. Hanley, Immo A. Hansen.

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Using insecticides with the same mode of action over multiple years is likely to promote rapid evolution of insecticide resistance. The resistance status of yellow fever mosquito populations from New Mexico has not been assessed. We collected Ae. aegypti from different cities in southern New Mexico and tested them for resistance against pyrethroids and an organophosphate. We sequenced parts of the para gene of these mosquitoes to look for knockdown-resistance mutations. We found pyrethroid resistance is common in Ae. aegypti from southern New Mexico. We identified a single point mutations in the para gene of the majority of mosquitoes from New Mexico that is associated with pyrethroid resistance.

***T1. Wolbachia pipientis* occurs in field-caught *Aedes aegypti* mosquitoes in New Mexico and Florida, USA.**

Aditi Kulkarni[1], Wanqin Yu[1], Jinjin Jiang[1], Concepcion Sanchez[1], Ajit K. Karna[1], Kalli J.L. Martinez[1], Kathryn A. Hanley[1], Michaela Buenemann[2], Immo A. Hansen[1], Rui-de Xue[3], Paul Ettestad[4], Sandra Melman[4], Dagne Duguma[5], Mustapha Debboun[5], Jiannong Xu[1].

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Wolbachia species are natural endosymbionts of approximately 60% of all insect species; including some disease vectors. The bacteria are transmitted vertically and manipulate host reproduction through a mechanism known as cytoplasmic incompatibility. Furthermore, certain *Wolbachia* strains can interfere with viral replications in infected mosquitoes, therefore are being used in novel mosquito and arbovirus control strategies. The mosquito *Aedes albopictus* is commonly infected with *Wolbachia*. However, it is controversial if a natural *Wolbachia* infection exists in *Aedes aegypti*, a primary vector for arboviruses including dengue and Zika virus. During a microbial survey in field caught *Ae. aegypti* from New Mexico, *Wolbachia* infection was identified by a two-step PCR assay. The PCR products were sequenced to confirm *Wolbachia* infection and identify the *Wolbachia* strains. *Wolbachia* infected *Ae. aegypti* were detected in samples collected in all eight surveyed locations during May-November 2017. *Wolbachia* prevalence at these locations ranged from 15-100%, with an average prevalence of 57.4% among the 148 individuals screened. Further, we have also identified *Wolbachia* from the wild-caught *Ae. aegypti* from St. Augustine, Florida, with a low prevalence of 4.3%. These bacteria were however not detected in *Ae. aegypti* populations from Deer Park, Harris County, Texas. A *Wolbachia* infected *Ae. aegypti* colony has been established from pupae collected in Las Cruces, NM in 2018. The maternal transmission of *Wolbachia* by the infected LC strain to the progeny when crossed with uninfected Rockefeller strains has provided the ultimate evidence for the presence of *Wolbachia* sequences in New Mexico *Ae. aegypti* populations.

T15. Environmental heterogeneity and post-fire seed bank diversity in the Mojave Desert of North America

Steven Lee[1], Robert Klinger[2] and Scott Ferrenberg[1]

[1]Department of Biology New Mexico State University, Las Cruces, NM, USA; [2.] U.S. Geological Survey, Western Ecological Research Center, Fresno, CA, USA

Plant communities in arid ecosystems are prone to major changes in structure after burning, but how these changes impact the below ground soil seed banks are largely unknown. Soil seed banks allow plants to disperse across time, playing an important role in post fire trajectories of a system. We utilized a chronosequence design to assess seed bank diversity across 111 unburned reference plots and 432 plots that burned one or more times between 1972 and 2010 in the Mojave Desert. We calculated several common metrics of species diversity and asked: (1) what the relative influence of fire (frequency and severity) and environment (climate and topography) are on seed bank diversity; (2) are patterns of seedbank diversity consistent with the intermediate disturbance hypothesis (IDH); and, (3) do patterns of seed bank diversity differ from a community with a random (neutral) structure. Here we discuss the preliminary results and what they may mean for desert plant communities recovering from fire.

P10. "You talkin to me?" Interspecies communication fosters collaboration between closely related symbionts in the sepiolid squid-*Vibrio* mutualism

K.E. Lopez[1], A.A. Chavez-Dozal[1], I.V. Ike-Newton[1], W. Yu[1], R. Lami[2], and M.K. Nishiguchi[1]

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The beneficial association between squids in the family Sepiolidae (Mollusca: Cephalopoda) and bioluminescent bacteria in the family Vibrionaceae form a unique relationship that provides a model to study the interactions between animals and bacteria. Sepiolid squids from the Mediterranean Sea (genus *Sepiola*) are unique in that these squids serve as hosts for two bioluminescent bacterial species: *Vibrio logei* and *Vibrio fischeri*. *Vibrio* bacteria produce unique communication molecules known as acyl-homoserine lactones (AHLs) that are used to modulate light via quorum sensing (QS). Since *V. logei* and *V. fischeri* differ in many of their physiological properties, we examined whether these species produce AHLs that could be "understood" by the other species, and whether the regulatory genes controlling AHL production and subsequently luminescence are genetically distinct. We have identified a number of *V. fischeri* and *V. logei* strains isolated from the same host light organ in order to determine whether both species can "identify" each other's AHLs. Using a biosensor assay, we evaluated the type of AHL that is being produced by each species of *Vibrio*. To determine whether specific luminescence regulators are activated by these AHLs, we created a null mutation on the response regulator gene *luxO* in *V. fischeri* to determine whether mutations at this locus affect the ability of bacteria to communicate within and between both species during symbiosis. Understanding how different species of bacteria communicate inside an animal host will provide insight as to how symbiotic bacteria evolve cooperative mechanisms in complex beneficial associations.

P11. Tracking the growth of mat-forming cyanobacteria using auto-fluorescence signal of photosynthetic pigments

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Cyanobacteria are photosynthetic prokaryotic organisms known to be sources of valuable bio-compounds. However, investigations on their potentials are limited to only a few unicellular or heterocytous species which grow in liquid cultures as homogeneous suspensions. Most other species that are filamentous often form structured mats or colonies, which makes it difficult to measure their growth rate in experimental conditions. To break through this challenge, we examined the potential of a microassay which used a 96-well plate to measure growth by auto-fluorescence signal of the phycobilisomes and chlorophyll *a*. We applied this method to study the effect of two media type on 6 cyanobacteria species with varying morphology – from unicellular and filamentous heterocytous form, to filamentous form that build compact mats. We also validated the method by comparing auto-fluorescence in *vivo* with auto-fluorescence of extracted pigments, and compared growth rate measured by auto-fluorescence signal with the traditional dry weight method. Additionally, we recorded changes in the surface area of the colonies on a daily basis. Our investigation revealed the first insights to the potentials of this microassay for further application, and for the first time, the process of mat-formation in the studied mat-forming species.

P12. The characterization and completion of thioester-containing proteins in the freshwater snail, *Biomphalaria glabrata*

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Schistosoma mansoni is a trematode parasite and cause of the human disease schistosomiasis, affecting over 200 million people in tropical and subtropical countries. *S. mansoni* parasites require the infection of an intermediate host, the freshwater snail *Biomphalaria glabrata*. Interestingly, there are resistant and susceptible snail strains that have genetically based susceptibility to schistosome infections. Although, the molecular mechanisms that lead to protection in *B. glabrata* are not fully understood, the host's humoral immune components are known to play an important role. One such group of molecules are the thioester-containing proteins (TEPs), which have been reported in both vertebrates and invertebrates. TEPs are traditionally classified into three subfamilies: 1) alpha-2-macroglobulins (A2Ms); 2) components of the complement system; and 3) thioester proteins (TEP/CD109). TEPs have shown to be involved in immunological functions against pathogens including blocking proteolytic attacks, opsonization, and cell lysis. Using the recently published snail genome, 12 members of the TEP superfamily have been identified in strains of *B. glabrata*, these include three members from the A2M group, three complement C3-like molecules, and six classical TEP-related proteins. The present study reports the characterization of *B. glabrata* TEP transcripts and their phylogeny. Results show high sequence identity between snail strains and the presence of conserved protein domains, such as the characteristic GCGEQ thioester motif. Phylogenetic analysis clustered these TEPs into the three main groups alongside homologues from other species. This study offers new information regarding variations in TEP DNA and protein sequences between snail strains and the evolution of TEP molecules.

P.13 Transformation vs Conjugation: Developing a superior genetic tool for the for *Vibrio fischeri* genetic engineering tool-box

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The bioluminescent marine bacterium *Vibrio fischeri* has been used as a model to study mechanisms of environmental specificity in mutualistic associations with animal hosts. *V. fischeri* colonizes the interior of the light organ of sepiolid squids (Cephalopoda: Sepiolidae) and produces luciferase-based light which provides ventral counter-illumination camouflage for the squid while hunting at night. Previously developed techniques based on genetic engineering of *V. fischeri* have relied on a cumbersome tri-parental mating to introduce trans-genetic material into *V. fischeri* via conjugation. Since *V. fischeri* can also be induced to uptake foreign DNA through transformation, we have optimized an alternative technique which utilizes induced transformation to introduce trans-genetic material into *V. fischeri*. This alternative technique has the advantage of reduced time, cost, and simplicity, as well as being able to introduce linear DNA (such as PCR constructs) in addition to the standard plasmid constructs. We have studied the effect of several parameters on transformation efficiency, including *V. fischeri* culture conditions and trans-gene composition. We find that lower culturing temperatures, higher culture cell densities, and longer post-transformation recovery times all lead to increased transformation efficiencies. Additionally, plasmids display an order of magnitude higher transformation efficiency compared to linear DNA fragments. This ability to introduce foreign DNA into *V. fischeri* with direct transformation rather than conjugation will enable more efficient molecular genetic analysis and flexibility in vector construction for *V. fischeri*, increasing our knowledge of how this bacterium interacts with its host squid during symbiosis.

P14. Increasing node support in deep neoavian branches by non-coding data filtering.

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Recent advances in genomic technologies have provided researchers with more data and new methods to manage it. Phylogenetics has benefited immensely as this new data has increased the resolution and accuracy of inferred lineages and clarified otherwise unclear relationships. The deep neoavian branches of avian phylogenetic history have proven especially difficult to resolve even with the increased scope of sources of phylogenetic information. Insertions and deletions mutations (indels) represent a form of character data that are measurably more phylogenetically informative than nucleotide data. Nonetheless, indel data have traditionally been omitted from phylogenetic analyses due to concern that unreliable sequence alignment could compromise their homology. Our goal is to determine whether an automated pipeline to filter more questionably-aligned indels from the data set can improve phylogenetic signal. We scored indels as present or absent from the introns of 2500 orthologous genes in 48 taxa representing at least every order in class Aves. We filtered indels using the NCBI toolkit DUSTmasker at different threshold levels to mask low-complexity sequences across all loci. Gene trees were generated using RAxML and a multi-species coalescent analysis was completed using ASTRAL. Results were assessed by bootstrap scores and tree topology. Filtering resulted in higher support for some deep branches, but, local shifts in topology caused previously supported relationships to fall apart. A balance between masking low-complexity sequences and maintaining sufficient phylogenetic signal is at play. Further refinements in parameters are necessary to accurately filter indels for phylogenetic inferences.

P15. Expression of the immune-related thioester-containing proteins (TEPs) in the *Biomphalaria glabrata* embryonic (Bge) cell line

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The *Biomphalaria glabrata* embryonic (Bge) cell line is the only molluscan cell line available and was established over 40 years ago from embryos of a susceptible strain of *B. glabrata* snails. Since then, Bge cells have been used in numerous studies aiming at a better understanding of host-parasite interactions, especially in the research of snail-schistosome recognition and defense mechanisms. In order to define the role of thioester-containing proteins (TEPs) in snail defense we have tested the expression of these proteins in Bge cells. TEPs are a diverse family of proteins most of them characterized by the presence of an active thioester-containing domain that is used to bind and target molecules. Traditionally TEPs are divided into three groups: alpha-2-magroglobulin, complement-like, and insect-TEPs. In preliminary results we confirmed the presence and expression of *B. glabrata* TEPs in Bge cells, including members of all three major groups and we are currently working to obtain full-length transcript sequences from this cell line to compare with those found in resistant and susceptible snail strains. Furthermore, we will study TEPs transcript expression in Bge cells in response to exposure to parasite products including *Schistosoma mansoni* larval transformation products (LTPs), lipopolysaccharide, peptidoglycan, and zymosan. These studies will aim to further understand the immune role that TEPs have in *B. glabrata* snails and determine if any of these genes could be important elements for snail-host susceptibility to *S. mansoni* infections.

T2. Efficacy of EPA 25B List chemicals in reducing attraction rate in mosquitoes towards human host

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In 1996 the Environmental Protection Agency of the U.S. published a list of ingredients for minimum risk pesticides. We performed Y-tube olfactometer bioassays to test the efficacy of 21 different ingredients in reducing attraction rates of female yellow fever mosquitoes (Aedes aegypti) to humans. We tested five commercial repellent products (Swamp gator, Babyganics, Repel Naturals, Honest Repellent and Burt's Bees) that only contained EPA 25(B) list ingredients. Cinnamon Oil effectively reduced the attraction rate in mosquitoes up to 1hour. Peppermint, Spearmint, Lemongrass, Cedar wood and Garlic Oil effectively reduced attraction after initial application but lost efficacy after 30 minutes. Only Burt's Bees Insect Repellent was effective up to 30 minutes. Pure ingredients from the EPA 25 B list as well as commercial sprays containing these only have short term repellency effects.

T4. GAPDH response to bacterial challenge in *Anopheles gambiae* mosquitoes

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Anopheles gambiae mosquitoes are the primary vector for malaria, and cause morbidity to hundreds of thousands of people per year. Most mosquito-borne diseases are transmitted from a host to a female mosquito via a blood meal. Mosquitoes must rely on their non-specific innate immunity to eliminate the pathogen from their body to prevent septicemia. The innate immune system is composed of hemocyte cells and membrane proteins, which target the pathogen for destruction either through phagocytosis or through four pathways (IMD, Toll, JAK/STAT, and RNAi). The mosquito immune system requires energy and intermediate molecules from glycolysis to eliminate the pathogen and prevent septicemia. We attempted to inhibit Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) using dimethyl fumarate (DMF), and found a significant difference in mortality between the DMF and sugar fed mosquitoes post bacterial challenge. We hypothesize that GAPDH is involved for protection against pathogens and in immunity. This led us to posit GAPDH has other roles besides glycolysis. We fed mosquitoes 10mM DMF mixed in 10% sugar for 3 days, then challenged the mosquitoes with bacterial injections and found an increased mortality phenotype. We performed a western blot and found a decrease in protein between unchallenged and challenged sugar-fed mosquitoes. We then analyzed transcriptome data from bacterial challenged, sugar fed mosquitoes, and found a decrease in GAPDH transcripts in the infected compared to the naïve. This result was unexpected, as a decrease in protein levels normally causes an increase in transcripts. We plan on investigating this startling development further.

T10. The evolution of Pentatricopeptide repeats in the legume plant family

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Cellular energy is produced in mitochondria and chloroplasts through oxidative phosphorylation and photosynthesis, processes that require fine-scale control of gene expression. Organellar genomes have fewer promoters and longer mRNA half-lives than their prokaryotic ancestors, requiring more gene expression regulators, such as RNA-binding proteins. PPRs are a large family of modular RNA-binding proteins involved in post-transcriptional mechanisms that are almost entirely specific to organellar mRNA. PPR genes have a high rate of evolution and play an imperative role in organellar function. In this study, sixteen legume genomes have been investigated. We identify PPR gene locations, classify each into their appropriate gene subfamily, infer organellar sub-localization and syntenic relationships, and investigate patterns of PPR diversification through phylogenetic studies. Each open reading frame (ORFs) within an input genome was aligned against the 11 Hidden Markov Model (HMM) profiles, which currently define PPR motifs. Based on the PPR domain architecture as well as start and ending positions of both hmmsearch matches and annotation genes, PPRs have been mapped on each chromosome/scaffold. Thus, the main purpose of this study is to identify all defined PPRs in each legume and understand their sub classification, organelle destination, related functions, and eventually patterns of diversification.

T6. Rho GTPases, branched actin networks and the control polar body extrusion during oocyte maturation

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The actomyosin cytoskeleton determines cell shape and drives cell shape change. Work in the lab has demonstrated that during cytokinesis, linear-unbranched actin filaments form the contractile ring whereas branched actin (nucleated by Arp2/3) is cleared from the cell equator. Unbranched and branched actin networks are under the control of the GTPases Rho and Rac, respectively, and these molecular switches are functionally and spatially segregated in both crawling and dividing cells. We are interested in understanding how this regulatory scheme functions in oocytes, where meiotic divisions are highly asymmetrical to ensure conservation of cytoplasm in the future gamete (egg) while still reducing chromosomal ploidy. During meiosis, there is a local depression of cortical tension at the site of polar body extrusion, suggesting that polar body extrusion occurs through a combination of myosin-based contractility and a local depression of cortical tension, possibly created by local activation of Arp2/3. We hypothesize that while Arp2/3 is dispensable for symmetric divisions, Arp2/3 (and Rac) is essential for meiosis. Sea star oocytes undergoing meiosis in the presence of an Arp2/3 inhibitor or dominant-negative mutant of Rac fail to form a polar body. Current efforts are focused on characterizing the localization dynamics of Arp2/3, Rac, Rho and myosin II to determine how these factors coordinately regulate polar body extrusion. Lastly, we have also developed an optogenetic tool to locally activate Arp2/3 in response to 405 nm light to stimulate branched actin networks to determine how Arp2/3 affects myosin II recruitment and polar body morphology.

T16. Developing a versatile inducible CRISPR/cas9 gene regulation tool to enhance genetic studies in the *Vibrio fischeri - Euprymna scolopes* symbiosis

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The bioluminescent marine bacterium *Vibrio fischeri* has been used to study mechanisms of environmental specificity and bacterial-animal cross talk in mutualistic associations with sepiolid squids. *V. fischeri* colonizes the light organ of squids in the genus *Euprymna* (Cephalopoda: Sepiolidae), where symbiotically competent vibrios produce luciferase-based light for ventral counter-illumination camouflage for the squid. Light production is an energetically costly aerobic reaction, and *V. fischeri* can only produce bioluminescence when in high cell density. Although some of the biochemical pathways utilized during light production have been identified in *V. fischeri*, none have been measured *in situ*. Techniques to investigate the genetics underlying the production of this light, and other determinants of successful *V. fischeri* colonization have relied on traditional gene "knock-out" methods, which cannot provide information on the time-dependent expression of important colonization factors in *V. fischeri*. Therefore, we are expanding the repertoire of *V. fischeri* genetic techniques by developing a strain of genetically transformed *V. fischeri* carrying an inducible version of the *S. pyogenes* CRISPR cas9, which has no nuclease activity. When used in conjunction with transformation with a programable guide RNA plasmid, we can induce and suppress expression of *V. fischeri* genes (e.g. luminescence- *lux*) during the course of host colonization. This unprecedented ability to incrementally and reversibly control the expression of any *V. fischeri* gene throughout the normal course of host colonization will allow us to probe the timing and intensity of gene expression at a finer resolution, providing a window of how this beneficial symbiosis is regulated.

P16. Duet synchronization and the effect on reproductive success

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Duetting behavior is widespread in birds and has been hypothesized to serve multiple functions. The reproductive synchrony hypothesis states that duets function to synchronize their reproductive effort, which may be important in species with extensive biparental care. Understanding the function of duetting behavior can benefit conservation efforts for endangered species that rely on captive breeding to sustain wild populations. The Puerto Rican parrot, *Amazona vittata,* is a critically endangered species for which recovery efforts have focused on improving reproduction success captive pairs. Like many parrot species, the Puerto Rican parrot engages in extended pair duets. Using pairs in the captive breeding program, we investigated whether duetting behavior influences the number of fertile eggs per clutch. We predicted that pairs that display more temporal synchronization of duets will produce more fertile eggs than less synchronized pairs. We recorded duets of pairs in two captive populations prior the breeding season. Once the breeding season ended, we collected the number of fertile eggs across pairs. To evaluate synchronization of duets, we measured the difference in timing of the response by each individual and compared values between pairs. We found considerable variation in reproductive success among different pairs; analysis of temporal synchrony is ongoing. These results can positively influence restoration efforts of duetting bird's species, managers can identify better coordinated pairs that will produce more fertile eggs and contribute to a quicker recovery.

P17. Immunofluorescence study of adult and regenerating muscle and electric organ tissues in *Eigenmania virescens*

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Eigenmania virecens is a weakly electric fish of the Gymnotiform family found in the rivers of South America, most electric fish species known to date, *E. virecens* has a muscle-derived electric organ (EO) that produces electric signals for communication and navigation purposes. Previous studies in the closely related gymnotiform *Sternopygus macrurus* showed that adult EO cells (i.e. electrocytes) continue to express muscle proteins, and that after amputation fast Myosin Heavy Chain (MHC) appear to fuse and give rise to electrocytes. Whether these observations are unique to *S. macrurus* remains unknown. The study will determine the myogenic phenotype of adult electrocytes and regeneration process of *E. virecens* using an immunofluorescence approach as done previously with *S. macrurus*. This data will begin to inform the extent to which the specific myogenic lineage is conserved among different electric fish species.

T8. Cortical granule motility in response to hormone stimulation during sea star meiosis

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Fertilization and proper development requires that a single sperm binds and enters the female oocytes. Upon sperm-binding, the oocyte or egg responds with the exocytosis of specialized vesicles called cortical granules (CGs), and the release of CG granule contents, prevents further sperm binding. Actin and the Rho GTPases that control the actomyosin cytoskeleton are known to have a fundamental part in oocyte maturation, but how these G proteins are regulated and how their actions control CG recruitment are less well understood. Work in the lab has established that in the sea star oocyte, there is a Rho-dependent burst of actin polymerization following hormone stimulation, and we hypothesize that this activation of Rho and actin plays a role in promoting translocation of CGs to the cell surface. To track CG movements following hormone stimulation, fluorescent protein tagged versions of sea star Rab 27 and Rab 3 were generated, and using these probes we tracked CG motility during oocyte maturation using 4D confocal microscopy. Image analysis has demonstrated a net movement of CG's toward the cell surface as well as two modes of motility; long distance, rapid movement deep in the cytoplasm and shorter movements closer to the membrane. The velocities and processivity of the deep cytoplasmic motility is suggestive of Myosin V-mediated transport, and current efforts are focused on quantifying vesicle motility in control oocytes prior to- and following hormone stimulation, as well as motility under conditions where Rho activity is blocked.

P18. Applying biophysical approaches to understand the mechanics and regulation of cells with isotropic cytoskeletons

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In motile cells, actin networks are organized such that branched actin networks (nucleated by Arp2/3) are found at the leading edge of the cell whereas linear (and contractile) actin networks are found in the rear. In large spherical cells, actin is enriched at the cell cortex to form an unpolarized, isotropic network. But in contrast to crawling cells, less is known about the regulation of isotropic actin networks. Previous work demonstrated that branched actin antagonizes contractile ring function during cytokinesis, and we hypothesize that branched actin may act as a break on global myosin II contractility. To quantitatively analyze the biophysical properties of the cell, we are applying MicroPipette Aspiration (MPA), which measures cortical tension. Prior to fertilization, cortical tension in the egg is approximately 1.27 nN/mm^2; but if eggs are artificially activated with Calyculin A (that activates myosin II), cortical tension rises 13-fold. Using this approach, we have characterized the changes in cortical tension in sea urchin eggs during the first cell cycle as well as when Rho and Arp2/3 are inhibited. We found a significant drop on tension in response to Rho kinase inhibition, but a small increase when Arp2/3 activity was blocked. MPA can also measure the mechanosensitivity of actin networks, and we predict that altering Arp2/3 and myosin II activity will affect how the actin cytoskeleton responds to physical stresses. We anticipate that these biophysical approaches will provide a more quantitative understanding of how the actin cortex is regulated to promote shape change in spherical cells.

P19. The regulatory mechanism of chilling-induced dormancy transition from endo-dormancy to non-dormancy in *Polygonatum kingianum* Coll.et Hemsl rhizome bud

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Polygonatum kingianum Coll.et Hemsl (*P. kingianum*) is an important traditional Chinese medicine, but the mechanism of its rhizome bud dormancy has not yet been studied systematically. In this study, three dormancy phases were induced under controlled conditions, and changes occurring during the transition were examined, focusing on phytohormones and the cell wall. As revealed by HPLC-MS (High Performance Liquid Chromatography-Mass Spectrometry) analysis, the endo- to non-dormancy transition was association with a reduced abscisic acid (ABA)/gibberellin (GA_3) ratio, a decreased level of auxin (IAA) and an increased level of trans-zeatin (tZR). Transmission electron microscopy showed that plasmodesmata (PDs) and the cell wall of the bud underwent significant changes between endo- and eco-dormancy. A total of 95,462 differentially expressed genes (DEGs) were identified based on transcriptomics, and clustering and principal component analysis confirmed the different physiological statuses of the three types of bud samples. Changes in the abundance of transcripts associated with endogenous hormones, PDs and cell wall-loosening factors were analysed during the bud dormancy transition in *P. kingianum*. Furthermore, *nitrilase 4* (*NIT4*) and *tryptophan synthase alpha chain* (*TSA1*), which are related to IAA synthesis, were identified as hub genes of the co-expression network, and strong interactions between hormones and cell wall-related factors were observed. Biological experiments proved that 6-BA could promote the relief of rhizome bud endo-dormancy in P.kingianum by inhibiting ABA synthesis and improving auxin transport. This research will provide a good model for breaking rhizome bud dormancy in *P. kingianum*.

T5. Host identification of mosquito bloodmeals collected in diverse land cover types in Malaysian Borneo using COI barcoding

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Host preference of vectors, host density, and contact rates between vectors and hosts are important contributors to the rate of arthropod-borne virus (arbovirus) transmission. Land cover and land use change drive arbovirus transmission by influencing host and vector diversity, abundance, and distribution; as well as, interactions between hosts and vectors. Identification of bloodmeals from wild-caught mosquitoes can provide insight into host utilization and the potential role of mosquito species in disease transmission. This research sought to 1) collect and identify mosquito bloodmeals, using cytochrome oxidase subunit I (COI) barcoding, from a wide breadth of land covers, and 2) compare the complexity of host-vector networks across land covers in Sarawak, Malaysian Borneo. Land cover types sampled included: barren, high density buildings, low density buildings, mixed agriculture, oil palm plantation, swamp forests, secondary forests, and primary forests. A nested PCR protocol for amplification of the COI barcoding region, 658 base pairs, was performed with primers covering a broad range of vertebrate taxa on 134 abdomens from bloodfed

mosquitoes. A total of 116 bloodmeals were identified encompassing 10 genera of mosquitoes. A diverse range of hosts was identified representing reptiles, amphibians, birds, and mammals from 21 genera. Host and mosquito diversity decreased from forests to anthropogenically altered land cover types with secondary forests being the most and barren least diverse respectively. Humans were the most common host detected, 34% of the total bloodmeals identified, and acted as mosquito hosts in all land covers except, somewhat surprisingly, the most urban land cover type.

T9. Glucose-dependent GPER1 Expression Increases Tamoxifen-induced IGFBP-1 Production

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G protein-coupled estrogen receptor 1 (GPER1) is a seven-transmembrane receptor that mediates rapid cell signaling events stimulated by estrogens. While the role that GPER1 has in the modulation of E2-responsive tissues and cancers is well documented, the molecular mechanisms that regulate GPER1 expression are currently not well defined. The recently identified GPER1-dependent mechanism of tamoxifen action in breast cancer cells underscores the importance of identifying mechanisms that regulate GPER1 expression in this cell type. We hypothesized that GPER1 expression in breast cancer cells is sensitive to [D-glucose] and provide data showing increased GPER1 expression when cells were cultured in low [D-glucose]. To determine if the observed accumulation of GPER1 was AMPK-dependent, small molecule stimulation or inhibition of AMPK was performed. AMPK inhibition decreased GPER1 accumulation in cells grown in low [D-glucose] while the AMPK-activating compound AICAR increased GPER1 accumulation in cells grown in high [D-glucose] media. Additionally, transfection of cells with a plasmid expressing constitutively active AMPK resulted in increased GPER1 accumulation. To determine if [D-glucose]-dependent GPER1 accumulation altered breast cancer cell response to tamoxifen, cells grown in the presence of decreasing [D-glucose] were co-treated with tamoxifen and IGFBP-1 transcription was measured. The results from these experiments reveal that D-glucose deprivation increased GPER1-mediated and tamoxifen-induced IGFBP-1 transcription suggesting that [D-glucose] may increase breast cancer cell sensitivity to tamoxifen. Taken together, these results identify a previously unknown mechanism that regulates GPER1 expression that modifies one aspect tamoxifen action in breast cancer cells.

P20. Inferring Avian Phylogeny with mtDNA and Data Partitioning

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Recent advances in phylogenomics have allowed researchers to resolve most of the evolutionary relationships within birds. Despite this, the deepest relationships within the Neoavian rapid radiation event remain a mystery. Different phylogenies produced from large-scale genomic studies have generated a robust, consensus tree for the Neoavian Tree of Life, but with little consensus regarding the 8 deepest speciation events. In contrast, phylogenetic analyses using mitochondrial DNA (mtDNA) have produced conflicting phylogenies compared to the consensus phylogeny. But with an elevated substitution rate, lack of recombination, rapid coalescence time and reduced effective population size, mtDNA, in theory, should be an ideal molecular marker to track deep short internodes. Previous mtDNA analyses have also implemented little to no data partitioning and sampled less than 80 species per analysis. In this study, the utility of mtDNA is reevaluated by conducting phylogenetic analysis with 315 avian species with at least one species for each order. PartitionFinder 2, a more rigorous data partitioning method is also used. The

effects of data recoding (RY-coding) and removing compositionally heterogenous sites are also investigated. Our findings indicate that data partitioning and RY-coding increase bootstrap support and tree resolution. But despite this, we were not able to produce trees congruent with previous large-scale genetic analyses. We also find evidence that mtDNA may not provide enough phylogenetic signal to resolve the deep Neoavian divergences, possibly due to saturation and compositional heterogeneity.