

2nd ANNUAL

TTABSS

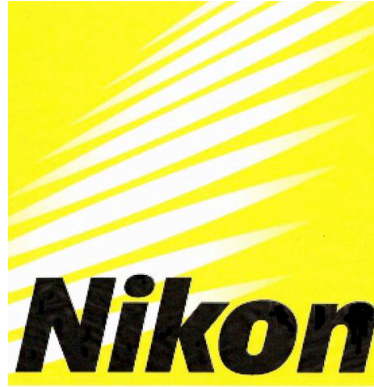
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Texas Tech Annual Biological Sciences Symposium

Texas Tech University
Department of Biological Sciences
Lubbock, Texas
1-2 April 2011

SPECIAL THANKS TO OUR EVENT SPONSORS



AND EVENT CONTRIBUTORS



ACKNOWLEDGEMENTS

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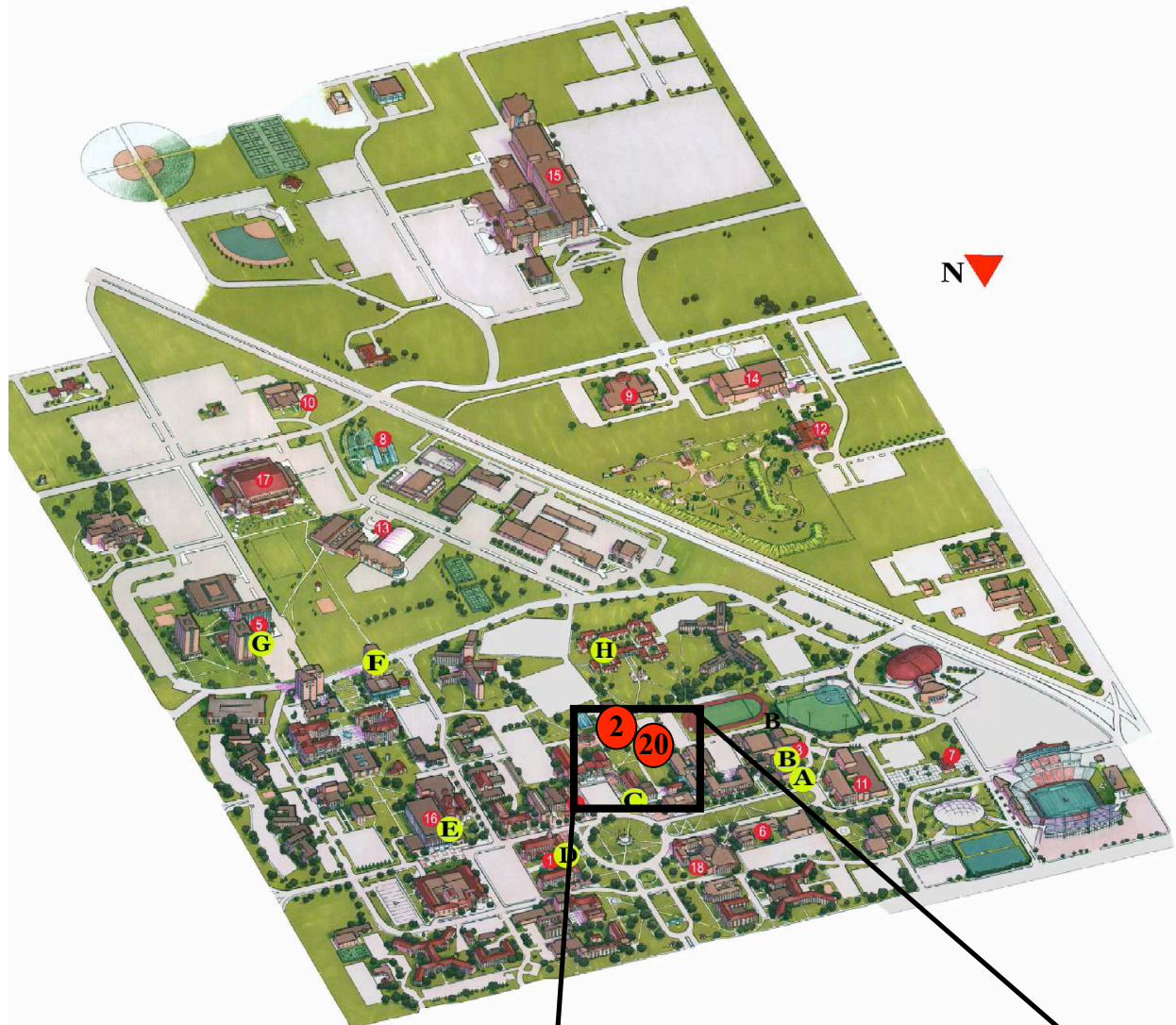
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TEXAS TECH UNIVERSITY CAMPUS MAP & PARKING



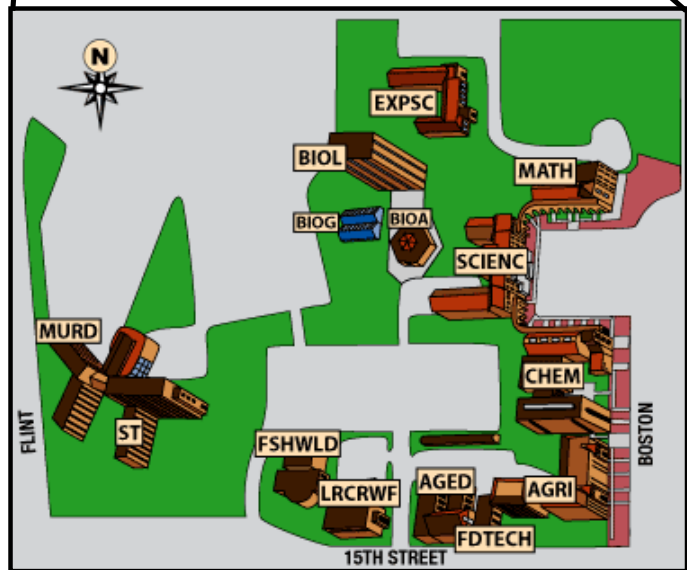
- 2** Biological Sciences Building
- 20** Experimental Sciences Building

BIOL – Biological Sciences Building

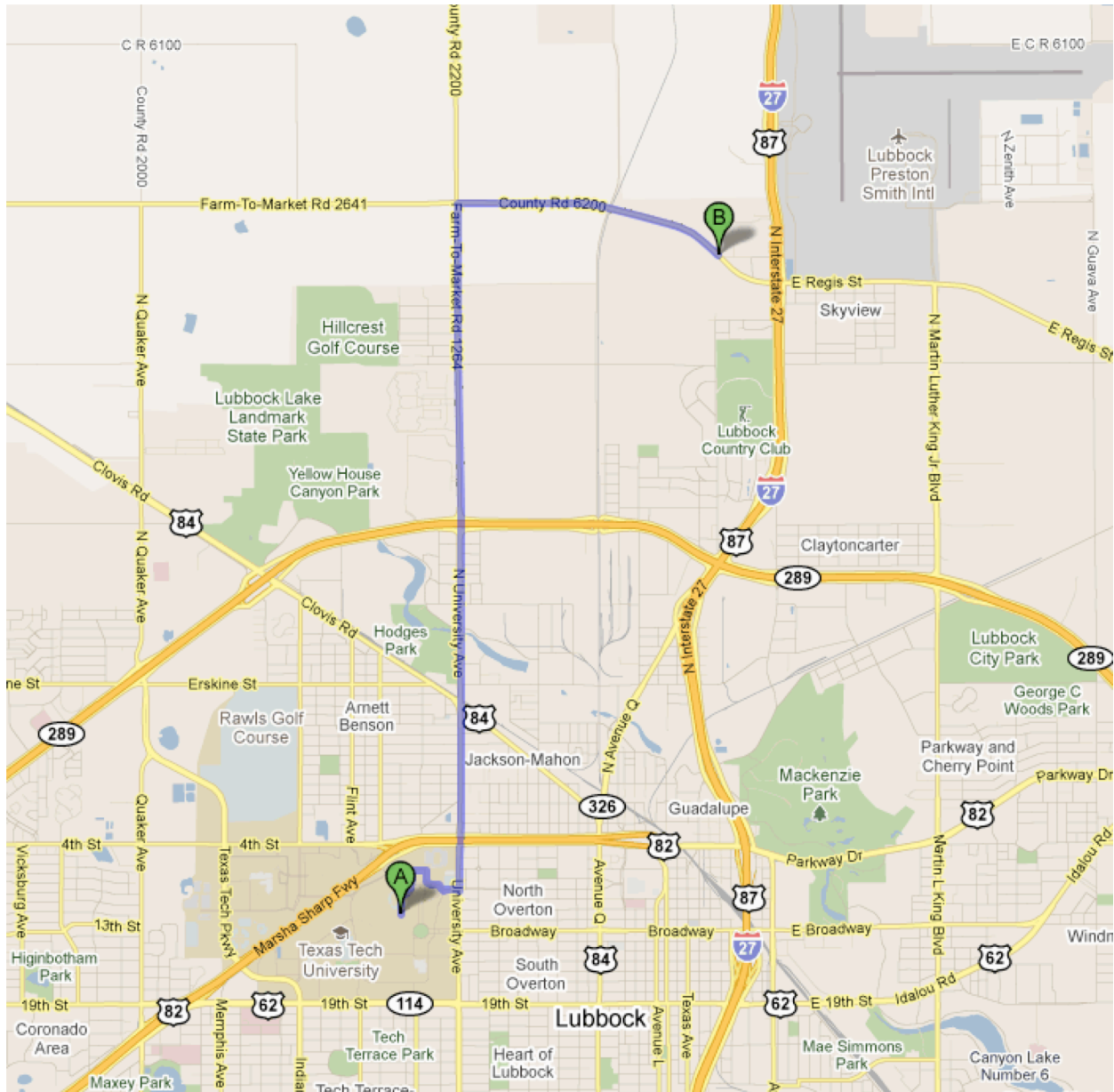
Enter 15th St. via Flint Ave. Visitor parking will be available for off-campus registrants through the kiosk on April 1st. Lot will be open April 2nd.

EXPSC – Experimental Sciences Building

Enter Canton Ave. via Drive of Champions. Visitor parking will be available for off-campus registrants through the kiosk on April 1st. Lot will be open April 2nd.



MAP/DIRECTIONS TO SPIRIT RANCH



FROM EXPERIMENTAL SCIENCES BUILDING PARKING LOT

1. Head north on Canton Ave toward 7th St – go 0.3 mi
2. Turn right at Drive of Champions – go 0.1 mi
3. Drive of Champions turns right and becomes Akron Ave/Boston Ave/Red Raider Ave (Continue to follow Akron Ave) – go 0.2 mi
4. Turn left at Glenna Goodacre Blvd – go 0.1 mi
5. Turn left at University Ave – go 4.3 mi
6. Turn right at County Rd 6200/Farm-To-Market Rd 2641 E – go 1.7 mi

LOCAL RESTAURANTS

ON CAMPUS

Name	Address	Phone
The Market	Stangel-Murdough Hall	N/A
Student Union Food Court	Student Union Building	N/A
Sam's Place	Murray Hall	N/A

WALKING DISTANCE (EAST OF CAMPUS)

Name	Address	Phone
Bar PM	1211 University Avenue	(806) 747-2720
Chili's Grill & Bar	607 University Avenue	(806) 744-2025
Chimy's Cervceria	2417 Broadway	(806) 763-7369
Cricket's Grill & Draft House	2412 Broadway	(806) 744-4677
Dion's	905 University Avenue	(806) 747-4800
Firehouse Subs	411 University Avenue	(806) 747-9600
Freebirds World Burrito	1201 University Avenue	(806) 741-0900
Jimmy John's	2413 Broadway Avenue	(806) 740-0002
Littlepanda	1221 University Avenue	(806) 722-0888
Mesquites Sports Grill & Bar	2419 Broadway	(806) 744-9277
One Guy from Italy's Pizza	1101 University Avenue	(806) 747-1226
Raising Canes Chicken Fingers	907 University Avenue	(806) 744-8552
Rocky LaRues	2420 Broadway #B	(806) 747-6366
Ruby Tequila's Mexican Kitchen	413 University Avenue	(806) 747-7829
Sazon Restaurant	1205 University Avenue	(806) 687-2572
Spanky's	811 University Avenue	(806) 744-5677
Starbucks	801 University Avenue	(806) 744-8234
Subway	1109 University Avenue	(806) 744-1535
Which Wich Superior Sandwich	1021 University Avenue	(806) 472-9424

SHORT DRIVING DISTANCE (INSIDE LOOP 289)

Name	Address	Phone
Arby's	2422 19th Street, Suite 6037	(806) 744-2535
Burger King	2405 19th Street	(806) 762-2282
Café J	2605 19th Street	(806) 741-5400
Fuzzy's Taco Shop	2102 Broadway	(806) 740-8226
Gardski's Loft	2009 Broadway	(806) 744-2391
Great Wall Restaurant	1625 University Avenue	(806) 747-1264
IHOP Restaurant	1627 University Avenue	(806) 744-5153
Josie's Authentic Mexican Food	2332 19th Street	(806) 796-0192
Long John Silver's	2344 19th Steet	(806) 765-7339
McCallister's Deli	2415 19th Street	(806) 740-0022
McDonald's	2339 19th Street	(806) 747-5536
Quizno's	2312 19th Street #100	(806) 771-7827
Schlotsky's Deli	3719 19th Street	(806) 793-5542
Skooner's Grill & Bar	1617 University Avenue	(806) 749-7625
Wendy's	2401 19th Street	(806) 741-0955

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Awards Banquet

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Opening Social/Vendor Show

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Faisal Ali Bin Anwarali Khan

Plenary Speaker/Program

Adam W. Ferguson

Poster Competition

Tyla Holsomback

Registration

Roxy J. Larsen

Vendor Show

Michael Panasci

**TEXAS TECH ANNUAL BIOLOGICAL SCIENCES SYMPOSIUM
2ND ANNUAL MEETING
1-2 APRIL 2011
TEXAS TECH UNIVERSITY–LUBBOCK**

PROGRAM-AT-A-GLANCE

FRIDAY, 1 APRIL

- 5:00 pm – 8:00 pm** **Registration, EXPSC 1st Floor Lobby**
- 5:00 pm – 8:00 pm** **Opening Social & Vendor Show, EXPSC 2nd & 3rd Floors**
- 6:00 pm – 7:30 pm** **Poster Session, EXPSC 3rd Floor (Poster Hanging 5:30 – 6:00 pm)**

SATURDAY, 2 APRIL

- 8:00 am – 11:30 am** **Registration – BIOL Lobby**
- 8:00 am – 8:15 am** **Continental Breakfast – BIOL Lobby**
- 8:15 am – 8:30 am** **Welcome – LH 100**
- 8:30 am – 9:45 am** **Oral Presentations – BIOL 101, BIOL 106**
- 9:45 am – 10:15 am** **Break – BIOL Lobby**
- 10:15 am – 11:30 am** **Oral Presentations – BIOL 101, BIOL 106**
- 11:30 am – 1:00 pm** **Lunch – On Your Own**
- 1:00 pm – 2:15 pm** **Oral Presentations – BIOL 101, BIOL 106, EXSPC 120**
- 2:15 pm – 2:45 pm** **Break – BIOL Lobby**
- 2:45 pm – 3:45 pm** **Oral Presentations – BIOL 101, BIOL 106, EXSPC 120**
- 3:45 pm – 4:00 pm** **Break – BIOL Lobby**
- 4:00 pm – 5:00 pm** **Plenary Presentation (Dr. Darin Carroll) – LH 100**
- 5:00 pm – 6:00 pm** **Open**
- 6:00pm – 9:00pm** **Awards Banquet – Spirit Ranch (see previous map/directions)**

DETAILED SCHEDULE OF EVENTS

FRIDAY PM 5:00 – 8:00	REGISTRATION Experimental Sciences 1st Floor Lobby
5:00 – 8:00	OPENING SOCIAL & VENDOR SHOW Experimental Sciences 2nd & 3rd Floors
6:00 – 7:30	POSTER SESSION Experimental Sciences Building 3rd Floor
	1 – UNDERSTANDING THE INFLUENCE OF AMPHIPHILIC MOLECULAR INTERACTIONS OF THE LIPID BILAYER ON THE FUNCTION OF TRANSMEMBRANE ION CHANNELS AND TRANSPORTERS. <u>Andrew Armstrong</u> and Pablo Artigas
	2 – SPATIAL EXPLORATION AS AN ASSESSMENT OF LEARNING IN TWO ANURAN SPECIES. <u>Amanda J. Arner</u> and Ximena E. Bernal
	3 – ASSESSMENT OF INFORMATION SOURCES IN LEARNED PREDATOR RECOGNITION OF TADPOLES. <u>Lynne E. Beaty</u> and Ximena E. Bernal
	4 – EFFECTS OF DEER HERBIVORY ON PLANT COMMUNITIES IN CENTRAL TEXAS. <u>Will Brewer</u> , Kent M. Rylander, and Dylan W. Schwilk
	5 – DEVELOPING NEW STRATEGIES FOR COMBATING CHRONIC WOUND INFECTIONS. <u>Allie Clinton</u> , Chase Watters, and Kendra Rumbaugh
	6 – SELECTION OF BITING SITES ON ANURAN HOSTS BY FROG-BITING MIDGES (<i>CORETHRELLA</i> SPP). <u>Priyanka de Silva</u> , Cesar Jaramillo, and Ximena E. Bernal
	7 – INFLUENCE OF THE MENSTRUAL CYCLE PHASES ON EXERCISE-INDUCED BRONCHOSPASM AND ITS EFFECT ON ENDURANCE PERFORMANCE. <u>Melissa R. Iñigo</u> and Joaquin U. Gonzales
	8 – SPECTROSCOPIC STUDIES OF THE DIMERIZATION OF ATP-BINDING CASSETTE (ABC) NUCLEOTIDE-BINDING DOMAINS (NBDs). <u>Srinivasan Krishnan</u> , Maria E. Zoghbi, and Guillermo A. Altenberg
	9 – WATER-USE STRATEGIES OF OAKS (<i>QUERCUS</i> , <i>FAGACEAE</i>) FOUND IN THE SKY ISLAND SYSTEM OF THE DAVIS MOUNTAINS, TEXAS, USA. <u>Russell Lackey</u>
	10 (Not Competing) – REEVALUATION OF AFRICAN <i>MUS</i> IN BOTSWANA USING DNA, CYTOGENETICS, AND MORPHOLOGY. <u>Molly M. McDonough</u> , Cibele G. Sotero-Caio, Patrick J. Lewis, Monte L. Thies, Matlhgonolo Tswiio, and Robert J. Baker
	11 (Not Competing) – PHYLOGENETICS AND PHYLOGEOGRAPHY OF THE <i>HIPPOSIDEROS BICOLOR</i> (CHIROPTERA: HIPPOSIDERIDAE) COMPLEX BASED ON MITOCHONDRIAL DNA, MORPHOLOGY AND ECHOLOCATIONS. <u>Faisal Ali Anwarali Khan</u> , M. T. Abdullah, Ibnu Maryanto, Fahma Wijaya, and Robert J. Baker

SATURDAY AM 8:00 – 11:30	REGISTRATION Biology Lobby		
8:00	CONTINENTAL BREAKFAST Biology Lobby		
8:15	WELCOME Lecture Hall 100		
	I. PROPOSAL Biology 106	II. CELL/MOLECULAR BIOLOGY & MICROBIOLOGY Biology 101	
8:30	12 – POPULATION GENETICS OF THE AMERICAN CROCODILE IN COIBA MARINE NATIONAL PARK, PANAMA <u>Ashish Bashyal</u> , Miryam V. Anaya, Gad Perry and Llewellyn D. Densmore	17 – THE INVOLVEMENT OF PROTEIN PHOSPHATASE 2A IN AUXIN TRANSPORT PATHWAY <u>Jian Chen</u> , Yinfeng Zhu, Rongbin Hu, and Hong Zhang	
8:45	13 – MORPHOMETRIC AND GENETIC VARIATION AMONG SIX MONOTYPIC GENERA OF THE SUBFAMILY PHYLLOSTOMINAE (CHIROPTERA: PHYLLOSTOMIDAE) <u>Juan P. Carrera-E.</u> , Carleton J. Phillips, and Robert J. Baker	18 – abh1 sgs3 DOUBLE MUTANT MANIFESTS NOVEL PHENOTYPES SUGGESTING AN INTERACTION BETWEEN mRNA PROCESSING AND POST TRANSCRIPTIONAL GENE SILENCING <u>Fan Jia</u> and Christopher D. Rock	
9:00	14 – FIRE SURVIVAL STRATEGIES OF OAKS IN THE TRANS PECOS MOUNTAINS <u>Maria S. Gaetani</u>	19 – ANTISENSE TRANSCRIPTION AND SMALL RNA REGULATION OF ARABIDOPSIS AUXIN RESPONSE FACTOR ARF12/22 GENES IN OVULES <u>Yingwen Jiang</u> , Manoj P. Samanta, and Christopher D. Rock	
9:15	15 – EAVESDROPPING BY BLACK-TAILED PRAIRIE DOGS (<i>CYNOMYS LUDOVICIANUS</i>) ON ACOUSTIC SIGNALS OF KILLDEER (<i>CHARADRIUS VOCIFERUS</i>) <u>Elizabeth F. Watson</u> and Kenneth A. Schmidt	20 – EXAMINATION OF 35S::ATMYB90 TRANSGENE SILENCING USING DICER LIKE KNOCKDOWN LINES IN NICOTIANA TOBACCUM. <u>Nancy L. Layland</u> and Jeff Velten	
9:30	16 – PHOTOSYNTHETIC RESPONSE OF THE INVASIVE GRASS <i>PHALARIS ARUNDINACEA</i> AND THE NATIVE SEDGE <i>CAREX STRICTA</i> THAT IT REPLACES TO CLIMATE CHANGE AND NITROGEN AVAILABILITY <u>Elizabeth Waring</u> , Zhiyu He, and A. Scott Holaday	21 – COLIFORMS DETERMINATION IN MUNICIPAL DRINKING WATER, MAHENDRANAGAR, NEPAL <u>Narayan P. Kandel</u> , Govinda P. Dhungana, Puran Chalise, Naresh Chaudhari, Madan S. Bohara, and Yam K. Kandel	

SATURDAY AM 9:45 – 10:15	BREAK Biology Lobby		
	III. PROPOSAL Biology 106	IV. UNDERGRADUATE/ECOLOGY Biology 101	
10:15	22 – THE EFFECTS OF TRICLOSAN AND METHYLTRICLOSAN ON GENE EXPRESSION DURING EARLY EMBRYONIC DEVELOPMENT IN SOUTH AFRICAN CLAWED FROGS (<i>XENOPUS LAEVIS</i>) <u>Meghan M. Cromie</u> , James A. Carr, Ernest E. Smith, and Mike R. Wages	27 – A SURVEY OF THE ACTIVITY PATTERNS OF MEDIUM TO LARGE MAMMALS IN THE SOUTHERN ROLLING PLAINS OF TEXAS <u>Erika Mitchell</u> and Joel Brant	
10:30	23 – CREATION AND ANALYSIS OF TRANSGENIC COTTON PLANTS EXPRESSING A SUMO (SMALL UBIQUITIN RELATED MODIFIER) E3 LIGASE SIZ1 <u>Neelam Mishra</u> and Hong Zhang	28 – ASSOCIATIONS BETWEEN ADULT FEMALE BODY SIZE AND FITNESS IN ODONATES <u>Kelly S. Baker</u> and Nancy E. McIntyre	
10:45	24 – THE ROLE OF SMALL RNAS IN ABIOTIC-STRESS RESPONSES IN PEANUT (<i>ARACHIS HYPOGAEA</i>) <u>Meenakshi Mittal</u> and Paxton Payton	29 – EFFECT OF REDUCED DAILY SOIL TEMPERATURE VARIABILITY ON A SOIL MICROBIAL COMMUNITY IN THE CHIHUAHUAN DESERT <u>Nirmala Dhungana</u> , Natasja C. van Gestel, Veronica Acosta-Martinez, and John C. Zak	
11:00	25 – ENHANCING COTTON FIBER ELONGATION AND CELLULOSE SYNTHESIS BY MANIPULATING FRUCTOKINASE ACTIVITY <u>Thiya Mukherjee</u> , Mariana Ivanova, Marisela Dagda, David Granot, and A. Scott Holaday	30 – REPRODUCTIVE PHENOLOGY OF INSECTIVOROUS BATS IN MALAYSIA: IMPLICATIONS FOR CLIMATE CHANGE <u>Nurul Ain Elias</u> , Rosli Hashim and Tigga Kingston	
11:15	26 – CULTURE AND ISOLATION OF “NTAD GENE CLUSTER” PRODUCTS FOR FUNCTIONAL ANALYSIS IN ADDICTION AND RELAPSE <u>Kenneth D.W. Griffith</u> and Brenda E. Rodgers	31 – CHARACTERIZATION OF THE ABIOTIC NICHE OF THE AMERICAN HOG-NOSED SKUNK (<i>CONOPATUS LEUCONOTUS</i>) USING ECOLOGICAL NICHE MODELING: PAST AND PRESENT VIEWPOINTS <u>Adam W. Ferguson</u> , Richard E. Strauss, and A. Townsend Peterson	
11:30 – 1:00	LUNCH On Your Own		

SATURDAY PM	V. EVOLUTIONARY BIOLOGY Biology 106	VI. ECOLOGY Biology 101	VII. CELL/MOLECULAR BIOLOGY & MICROBIOLOGY Experimental Sciences 120
1:00	32 – PHYLOGENETIC RELATIONSHIPS AND TRIBAL DIVERGENCE TIMES IN THE SUBFAMILY NEOTOMINAE <u>Megan S. Corley</u> , Roy N. Platt, Brian R. Amman' and Robert D. Bradley	37 – THE IMPACTS OF NITROGEN UTILIZATION AND ALLOCATION STRATEGIES ON PHOTOSYNTHESIS FOR AN INVASIVE GRASS, PHALARIS ARUNDINACEA, IN COMPARISON TO THE NATIVE SEDGE, CAREX STRICTA <u>Hasitha Guvvala</u> and A. Scott Holaday	42 – CHARACTERIZATION OF PA2783: A MEMBER OF THE <i>PSEUDOMONAS AERUGINOSA</i> Vfr REGULON <u>Aysegul Balyimez</u> , Michael San Francisco, and Abdul Hamood
1:15	33 – MOLECULAR AND ECOLOGICAL EVALUATION OF HYBRIDIZATION IN TWO SPECIES OF WOODRATS (<i>NEOTOMA FLORIDANA</i> AND <i>N. MICROPUS</i>) <u>Matthew R. Mauldin</u> , Ethan B. Rowell, Michelle L. Haynie, and Robert D. Bradley	38 – THE DIVERSITY AND ECOLOGICAL AND ECONOMIC SERVICES OF BATS IN A COFFEE-FOREST LANDSCAPE IN SOUTHWESTERN SUMATRA, INDONESIA <u>Joe Chun-Chia Huang</u> , Elly Rustiati Jazdyk, Meyner Nusalawo, Ibnu Maryanto and Tigga Kingston	43 – FUNCTION AND ANTI-MICROBIAL ACTIVITY OF POISON SAC PROTEINS FROM QUEEN RED IMPORTED FIRE ANTS (FORMICIDAE: SOLENOPSIS INVICTA) <u>Stephanie A. Lockwood</u> and Richard J. Deslippe
1:30	34 – MORPHOLOGICAL COMPARISON BETWEEN INSULAR AND CONTINENTAL POPULATIONS OF <i>VIPERA AMMODYTES</i> (SQUAMATA: VIPERIDAE) IN GREECE <u>Stephen A. Roussos</u> , Maria Dimaki, Ljiljana Tomovic, and Llewellyn D. Densmore III	39 – LEAF TRAITS AND LITTER FLAMMABILITY: UNDERSTANDING MULTI-SPECIES MIXTURES <u>Rita M. Quiñones-Magalhães</u> and Dylan W. Schwilk	44 – CHARACTERIZATION OF SODIUM/IODIDE TRANSPORT ACTIVITY IN THYROID AND EXTRATHYROIDAL TISSUES OF THE AFRICAN CLAWED FROG <i>XENOPUS LAEVIS</i> DURING METAMORPHOSIS <u>Sharanya Murali</u> , Mike Wages, Ernest Smith, and James. A. Carr
1:45	35 (Not Competing) – Y-CHROMOSOME AND MITOCHONDRIAL SEQUENCES INDICATE GENETIC INTROGRESSION IN MORPHOLOGICALLY-DISTINCT GROUND SQUIRRELS (GENUS <i>SPERMOPHILUS</i>) <u>Cody W. Thompson</u> , Frederick B. Stangl, Jr., and Robert D. Bradley	40 – AN ASSESSMENT OF GENETIC STRUCTURE AND DIVERSITY AMONG SWIFT FOX POPULATIONS IN THE UNITED STATES <u>Donelle L. Schwalm</u> , Warren B. Ballard, and Lisette P. Waits	45 – ANALYSIS OF <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> GENE EXPRESSION IN PLANKTONIC VERSUS BIOFILM LIFE CYCLE STAGES <u>W. Shalika D.K. Silva</u> , Nancy L. Carty, Uzma Qaisar, Abdul N. Hamood, and Michael J.D. San Francisco
2:00	36 – PHYLOGENETIC RECONSTRUCTION OF <i>DERMANURA</i> : TESTING FOR CONGRUENCE AMONG MULTIPLE MOLECULAR MARKERS <u>Julie A. Parlos</u> and Robert J. Baker	41 – STARTING OFF ON THE RIGHT FOOT: EXPLORING LIFE HISTORY STRATEGIES AND SALT TOLERANCE IN SYMPATRIC FRESHWATER SNAILS <u>Jamie Suski</u> , Christopher Salice, and Reynaldo Patiño	46 – DEGRADATION OF HOST LIPIDS BY <i>LEISHMANIA</i> <u>Mattie C. Pawlowic</u> and Kai Zhang
2:15 – 2:45	BREAK Biology Lobby		

SATURDAY PM	VIII. APPLIED BIOLOGY Biology 106	IX. ECOLOGY Biology 101	X. CELL/MOLECULAR BIOLOGY & MICROBIOLOGY Experimental Sciences 120
2:45	47 – UTILIZING A VIRAL GENE TOWARDS GENERATING INSECT-RESISTANT <i>ARABIDOPSIS</i> AND COTTON <u>Saranya Ganapathy</u> , Guoxin Shen, Hong Zhang, and Shan L. Bilimoria	51 – INTRODUCTION AND ESTABLISHMENT OF THE EASTERN GRAY SQUIRREL (<i>SCIURUS CAROLINENSIS</i>) IN NOVA SCOTIA, CANADA. <u>Howard M. Huynh</u> , Geoffrey R. Williams, Donald F. McAlpine, and Richard W. Thorington, Jr.	55 – AGO2 CLEAVAGES A PRE-MIRNA IN A RISC-LIKE MODE <u>Yonggan Wu</u> , Simon Rayner, and Lou Densmore
3:00	48 – PREDICTING SMALL-SCALE HOTSPOTS OF RED SNAPPER (<i>LUTJANUS CAMPECHANUS</i>) ABUNDANCE FROM LARGE-SCALE SPATIALLY REFERENCED DATA Sandra L. Diamond and <u>Tiffany L. Hopper</u>	52 – HETEROSPECIFIC ALARM CALL RECOGNITION AND UTILIZATION IN TIME AND SPACE <u>Amy M. Kuczynski</u> and Kenneth A. Schmidt	56 – SPHINGOLIPID DEGRADATION IN <i>LEISHMANIA</i> VIRULENCE <u>Wei Xu</u> , Ou Zhang, and Kai Zhang
3:15	49 – ROLE OF THYROID HORMONES IN GONADAL SEX DIFFERENTIATION OF ZEBRAFISH <u>Prakash Sharma</u> and Reynaldo Patino	53 – POPULATION-LEVEL EFFECTS OF CO-INFECTION BY <i>BARTONELLA</i> AND INTESTINAL NEMATODES IN <i>PEROMYSCUS LEUCOPUS</i> <u>Courtney A. Thomason</u> , Sarah Knowles, Andrea L. Graham, Amy B. Pedersen, and Rich Strauss	57 – AN INTRINSIC CRF SIGNALING PATHWAYS IN THE OPTIC TECTUM <u>Bo Zhang</u> , Mike Wages, Ernest Smith, and James. A. Carr
3:30	50 – CAUSE-SPECIFIC MORTALITY OF MULE DEER (<i>ODOCOILEUS HEMIONUS</i>) FAWNS IN CENTRAL ARIZONA <u>Nicole M. Tatman</u> , Warren B. Ballard, Mark C. Wallace, James deVos Jr., Paul R. Krausman, Ole Alcumbrac, C.A. Cariappa, and Chantel O'Brien	54 – PUBLIC INFORMATION USE IN A GROUND-NESTING SONGBIRD COMMUNITY <u>Janice K. Kelly</u> and Kenneth A. Schmidt	58 – MOLECULAR AND BIOCHEMICAL RESPONSES OF AN AMPHIBIAN PATHOGEN <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> UPON EXPOSURE TO THYROID HORMONE <u>Jose C. Thekkiniath</u> , Mithun R. Pasham, Mohammed Fokar, Susan San Francisco, and Michael J D. San Francisco
3:45 – 4:00	BREAK Biology Lobby		
4:00 – 5:00	PLENARY PRESENTATION Lecture Hall 100 CHASING JENNER'S VACCINE: ORTHOPOXVIRUSES AND THE ORIGINS OF VACCINATION. <u>Darin Carroll</u>		
5:00 – 6:00	OPEN		
6:00 – 9:00	AWARDS BANQUET Spirit Ranch		

ABSTRACTS

1 – UNDERSTANDING THE INFLUENCE OF AMPHIPHILIC MOLECULAR INTERACTIONS OF THE LIPID BILAYER ON THE FUNCTION OF TRANSMEMBRANE ION CHANNELS AND TRANSPORTERS

Andrew Armstrong¹ and Pablo Artigas¹

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The cell membrane is composed of a double layer of phospholipids called a lipid bilayer as well as many transmembrane proteins that facilitate the movement of molecules into and out of the cell. The lipid bilayer contains two distinct regions; a hydrophilic phosphate head region, and a hydrophobic hydrocarbon tail region. This property is referred to as amphiphilicity. The proteins embedded into the membrane are also amphiphilic and their hydrophobic regions need to match the length of the hydrophobic lipid tails in the bilayer. Many molecules including several with pharmacological applications are also amphiphiles. Although amphiphilic molecules have been used pharmaceutically for some time, their influence on the lipid bilayer properties and the subsequent change in function of transmembrane ion channels and transporters is not yet fully understood. To investigate the effects of amphiphilic molecular interaction with the lipid bilayer, ion channels were expressed in *Xenopus laevis* oocytes, and ion channel function was monitored using electrophysiological probes. We demonstrated that the amphiphilic molecule 2,3-butadione monoxime (BDM) enhances the activity of the cystic fibrosis transmembrane conductance regulator (CFTR) protein by effecting the lipid bilayer conformation. Further investigations were conducted using the application of an amphiphilic class of drugs known as dihydropyridines, which have common pharmacological use as calcium channel blockers to treat hypertension. Initial measurements indicate that nifedipine enhances the activity of the CFTR protein similar to the effects of BDM on CFTR activity.

2 – SPATIAL EXPLORATION AS AN ASSESSMENT OF LEARNING IN TWO ANURAN SPECIES

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Anuran amphibians exhibit a wide array of complex behaviors, most noticeably those associated with vocal communication and sexual selection. Learning has been studied to a great extent in higher order taxa such as mammals and birds, however little is known about learning ability in anurans. We predict that anurans exhibit higher cognitive function than once previously thought, despite their taxonomic location in relation to other groups that exhibit learning. Cane toads (*Rhinella marina*) and leaf litter toads (*Rhinella alata*) will be exposed to multiple trials in a novel arena containing hidden and exposed food resources. If learning occurs, individuals will show high exploration during initial trials (until available resources are located) and will locate resources more quickly during subsequent trials. Preliminary trials during July 2010 indicated that cane toads could learn to associate resources with a specific location (personal observation). Learning would be advantageous to this species, as they are known to colonize new areas, including urban interfaces. In contrast, leaf litter toads are highly specific in their habitat requirements and rarely seen in urban areas. Exploration and learning would not pose a great benefit to a species such as this, with a limited range of habitat preferences. Differences in learning ability between these species are expected, given their differing life history characteristics. However, if learning persists in both species, this result would suggest that

learning may be widespread among anurans providing evidence that this ability may be conserved across vertebrate taxa.

3 – ASSESSMENT OF INFORMATION SOURCES IN LEARNED PREDATOR RECOGNITION OF TADPOLES

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In predator-prey relationships, it is vital for prey to be able to recognize and respond appropriately to predation risk. Tadpoles are prey for many species and, as a defense, have evolved the ability to learn to recognize predators. Though tadpoles may learn predator recognition through first-hand experience (private information) or from other tadpoles (public information), it is uncertain how tadpoles value these different sources of information. Because there are costs and benefits to the use of private and public information, it is believed that animals differentially exhibit both strategies to obtain the greatest benefit. Previous studies conducted on birds and fish have examined the conditions in which animals will use either private or public information in a foraging context however, my proposed study is novel in that it will observe how tadpoles value private and public information when determining predator avoidance behavior. Cane toad (*Bufo marinus*) tadpoles will be exposed to three predator recognition learning treatments (private information, public information from other cane toad tadpoles, and public information from *Engystomops pustulosus* tadpoles) and their anti-predatory behavioral responses will be quantified. Differences in behavioral responses, which indicate how tadpoles perceive predation risk, will be used as a proxy for how tadpoles value different sources of information. If private information is more valued than public information, for example, then tadpoles will perceive the greatest predation risk in private information treatments and will exhibit the greatest behavioral change. Conclusions of this study will provide insights into learning theory and cane toad natural history.

4 – EFFECTS OF DEER HERBIVORY ON PLANT COMMUNITIES IN CENTRAL TEXAS

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Deer herbivory has significant effects on plant community structures. White tail (*Odocoileus virginianus*) and Axis deer (*Cervus axis*) populations have increased within central Texas in recent decades. Despite this, herbivory effects in Texas have been poorly studied. This population increase has led to increased browsing pressure and, consequently, may have caused a change in plant community composition. In 2005, deer exclosure plots and paired control plots were established to determine the effects of deer herbivory. Previous deer herbivory studies have found that results are often unique to particular plant communities, but in much past work, deer population densities and plant community have been confounded. Therefore, we tested herbivory effects in two adjacent different plant communities: riparian forest and mesquite savanna. Plant communities will vary between riparian woodland and mesquite savanna, accordingly deer herbivory patterns may change. Treatments and controls were established in an unreplicated, blocked design with five replicate plots in each treatment and plant community (N=20). After five years of browsing exposure, we measured species cover. Our results indicate fewer tree species inside controls for both savanna and riparian habitats. Vines occurred in forest exclosures only. Deer browsing decreased overall plant abundance and diversity. Increased browsing pressure, especially on vines and tree saplings and seedlings, has an effect on species richness and diversity on a community wide level. With increasing deer populations changing plant

community structures entire ecosystem structures may be altered. Continued community analysis is needed to further understand the effects of increasing deer herbivory in central Texas.

5 – DEVELOPING NEW STRATEGIES FOR COMBATING CHRONIC WOUND INFECTIONS

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Chronic wound infections have a profound effect on the morbidity and mortality of a large patient population and cost billions of dollars in direct medical costs annually in the United States. Chronic wound infections are typically polymicrobial and biofilm-associated. Biofilms are aggregates of bacteria enclosed in a tough polysaccharide shell, which protects the bacteria residing inside from antimicrobial agents and immune cells. In addition, the bacteria within a biofilm may exist in a dormant state, making antibacterial agents that target only actively dividing bacteria ineffective. This project was designed to investigate new therapeutic strategies for combating biofilm-related chronic wound infections. We hypothesized that we may be able to successfully target bacteria infecting chronic wounds and/or promote wound healing with biofilm disrupting agents and/or competition from a probiotic bacterial species. To test this hypothesis, we infected the wounds of mice with either *Pseudomonas aeruginosa* or *Staphylococcus aureus* and treated them with a glycoside hydrolase enzyme that catalyzes the hydrolysis of the poly-*N*-acetylglucosamine component of the biofilm matrix. This agent was used in combination with the commercially available wound care ointment Neosporin. For the probiotic approach, we used a ‘continual *in vivo* passage’ strategy as an attempt to identify an endogenous bacterial species that promoted healing. Thus far we have been unable to demonstrate efficacy using either experimental strategy. However, we are continuing to optimize our approach and it is possible that one or both treatments may be effective against other chronic wound pathogens.

6 – SELECTION OF BITING SITES ON ANURAN HOSTS BY FROG-BITING MIDGES (*CORETHRELLA* SPP)

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A critical challenge of obtaining a blood meal resides in locating an appropriate host. Once haematophagous insects reach their host, there is another step ahead, selecting a biting site. Optimal foraging theory predicts that biting insects should feed on their host on those areas that maximize blood intake while minimizing the costs. Here we investigate the biting sites of *Corethrella* species on túngara frogs, *Physalaemus pustulosus*, and treefrogs, *Dendropsophus ebraccatus* and *D. microcephalus*. The midges bite the tree frogs on a variety of body areas, but they exclusively bite túngara frogs on their nostril. We explore the reasons behind such differences in biting sites examining the properties of the skin of these species of frogs. For each frog species, we prepared histological samples of the dorsum and the area around the nostril. We collected frog-biting midges by playing advertisement calls of the frogs studied here. Microscopic slides of the mouth parts of midges were prepared to measure the length of their proboscis. Results indicate that the skin of túngara frogs in their dorsum consists of a thickened epidermis followed by a thick connective tissues while it is thinner in the treefrogs. In all species there is a high density of blood vessels around the nostrils. There is variation in the length of the proboscis of the midges, and have implications on site bite selection. Overall our results suggest that biting site preference of *Corethrella* midges is highly influenced by the properties of the anuran skin.

7 – INFLUENCE OF THE MENSTRUAL CYCLE PHASES ON EXERCISE-INDUCED BRONCHOSPASM AND ITS EFFECT ON ENDURANCE PERFORMANCE

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This thesis proposal aims to determine the influence of the menstrual cycle on sex differences in exercise-induced bronchospasm (EIB) and exercise performance. Our primary aim is to test the hypothesis that estrogen and progesterone will be associated with the severity of EIB in women, such that women will experience greater EIB than men during the luteal phase of the menstrual cycle when estrogen and progesterone levels are highest, but no sex differences in EIB will be present during the early follicular phase when estrogen and progesterone levels are low. Our secondary aim will test the hypothesis that exercise performance will be lower during the luteal phase as compared to the follicular phase of the menstrual cycle in women with EIB. Participants (12 men and 12 women, 18-25 years old) with a history of EIB will perform an exercise protocol consisting of treadmill exercise at 60% HR_{max} for 5 minutes followed by exercise at 95% HR_{max} until volitional fatigue. Women will complete the protocol once during the early follicular phase and luteal phase of the menstrual cycle. Spirometry will be used to test pulmonary function before and after exercise (1, 5, 10, 15, and 30 minutes into recovery). A >10% drop in forced expired volume in 1 second will be used to indicate the presence of EIB. Other measurements will include pulmonary gas exchange to estimate exercise efficiency, time to exhaustion to assess endurance performance, and blood collection in women to associate EIB with plasma levels of hormones and inflammatory markers.

8 – SPECTROSCOPIC STUDIES OF THE DIMERIZATION OF ATP-BINDING CASSETTE (ABC) NUCLEOTIDE-BINDING DOMAINS (NBDs)

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ABC export proteins include multidrug resistance pumps that catalyze the efflux of chemotherapeutic agents out of cancer cells, preventing their intracellular accumulation and cytotoxic effect. The molecular mechanism of ABC protein is not well understood. As a starting effort in our plan to address how different part of ABC proteins move during the transport cycle, we performed experiment on isolated bacterial NBDs using Luminescence Resonance Energy Transfer (LRET) and tryptophan quenching, to determine the ATP dependence on NBD dimerization. As a model, we used *M. jannaschii* NBD MJ0796. Under non-hydrolysis conditions, tryptophan quenching and LRET experiments showed similar apparent affinity for ATP, in 10-30 μ M range. A mutation that abolishes ATPase activity increases the apparent affinity for ATP approximately 10 folds. Under conditions of ATP hydrolysis, in presence of Mg²⁺-ATP, the decrease in LRET indicates that there was an increase in the proportion of NBDs in the monomeric form. The results show: 1) The feasibility of LRET studies to determine dimerization of ABC protein NBDs, 2) The use of LRET to determine distances between subunits with Angstrom resolution, and 3) That ATP-induced dimerization is a transient phenomenon. This work was supported by grants from CPRIT (RP101073) and NIH (R01 GM79629 and 3R01 GM079629-03S1).

9 – WATER-USE STRATEGIES OF OAKS (*QUERCUS*, *FAGACEAE*) FOUND IN THE SKY ISLAND SYSTEM OF THE DAVIS MOUNTAINS, TEXAS, USA

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Global climate change has raised concerns about future shifts species distributions and the consequences of those changes. The sky island ecosystems of the southwest United States are expected to see hotter, more arid climates in the future. The Davis Mountains, Texas are the focus of this study. Increased length and severity of droughts in these regions may result in habitat loss and a decrease in biodiversity. Physiological traits, including leaf mass per area, leaf life span, leaf water potential (MPa), gas exchange characteristics, and vulnerability to xylem cavitation; will be measured for 5 oak species located within The Nature Conservancy's Davis Mountains Preserve. These traits help define a water-use strategy demonstrated by the plant. The species include *Quercus emoryi*, *Q. gambelii*, *Q. gravesii*, *Q. grisea* and *Q. hypoleucoides*. A total of 45 trees were tagged at paired sites at two elevations (4 sites total). A suite of environmental variables including soil water potential, soil water content, temperature and humidity will be measured at each study site. This study is a comparative study of physiological traits between species occurring at differing environmental gradients, but will be analyzed in conjunction with existing community occurrence data and climate data to determine how physiological characteristics influence species distributions and community structure. Information gained from this research will likely prove useful in future conservation efforts.

10 – REEVALUATION OF AFRICAN *MUS* IN BOTSWANA USING DNA, CYTOGENETICS, AND MORPHOLOGY

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Two species of *Mus* (Subgenus: *Nannomy* Peters, 1876) are thought to occur in the country of Botswana. *Mus setzeri* Petter, 1978 exists within a narrow strip in the northwestern portion of the country as well as a disjunct population in southern Botswana. *Mus indutus* (Thomas, 1910) has a countrywide distribution that extends into neighboring countries of Namibia, South Africa, and Zimbabwe. Using DNA sequences and cytogenetics, we document that a third species, *Mus minutoides* A. Smith, 1834 also occurs in Botswana. Two distinct lineages (5% divergent in cytochrome-*b* sequences) of *M. minutoides* and one lineage of *M. indutus* were collected from a single locality in the Koanaka Hills region, Ngamiland. Zoo-FISH with *Mus musculus* X chromosome paints and DAPI-banding revealed that these individuals of *M. minutoides* share the same sex-autosome translocation as *M. minutoides* from South Africa, indicating the presence of the translocation over a large geographic area or convergence; however data is lacking from other countries within this region to test these hypotheses. Currently, *M. minutoides* is known from the countries of South Africa, Mozambique, Zimbabwe, and Tanzania. Our data extend the species distributional range to northwestern Botswana, which indicates that this species might also be present in other regions of sub-Saharan Africa. Additionally, this research highlights the need for future work with African *Mus*.

11 – PHYLOGENETICS AND PHYLOGEOGRAPHY OF THE *HIPPOSIDEROS BICOLOR* (CHIROPTERA: HIPPOSIDERIDAE) COMPLEX BASED ON MITOCHONDRIAL DNA, MORPHOLOGY AND ECHOLOCATIONS

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Hipposideros bicolor Temminck, 1834 is a member of the *bicolor* species group, which encloses half of all named species in the genus *Hipposideros*, including representatives from Africa and Madagascar across southern Asia to Japan, and northern Australia. This study investigates the taxonomy of *H. bicolor* and its allies, to uncover the diversity and evolutionary relationship within this group. We examined the morphology, acoustic and genetic differences within currently recognized *H. bicolor* and some other morphologically similar species from Malaysia and Indonesia. We sequenced 1140 base pairs (bp) of cytochrome-b and 509 (bp) of NADH dehydrogenase subunit 2 gene for *H. ater*, *H. atrox*, *H. bicolor*, *H. cineraceus*, *H. doriae*, and *H. dyacorum*. Our analyses recovered three phylogroups within *H. bicolor* (Kimura 2 parameter distance value [K2P] = 3-7%), three phylogroups within *H. ater* (K2P = 8-17%), three phylogroups within *H. cineraceus* (K2P=5-7%) and a single phylogroup for *H. atrox*, *H. doriae* and *H. dyacorum* respectively. Discriminant function analysis of these specimens able to correctly classify all the *H. bicolor* clades at 79%, 3 clades within *H. ater* (two occur only in Borneo and one only in Java) at 90-100%, *H. atrox* at 100%, all the *H. cineraceus* clades at 71%, *H. doriae* at 100%, and *H. dyacorum* at 100%. Echolocation call analysis suggests that all the *H. bicolor* phylogroups echolocate at ~129-131 kHz. Herein we discuss the taxonomic implication of the *bicolor* species group based on multiple dataset that accounts for geographic variations and comparison to the type description.

12 – POPULATION GENETICS OF THE AMERICAN CROCODILE IN COIBA MARINE NATIONAL PARK, PANAMA

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The Coiba Marine National Park (CMNP) is made up of an archipelago of nine main islands and about 30 islets. These islands were part of the continental mainland (Gulf of Chiriqui) until they were separated at the end of the last glacial period during the Late Pleistocene. The population of *C. acutus* is widely distributed among the islands in CMNP and the Gulf of Chiriqui; and our null hypothesis assumes these populations are isolated with no gene flow among them. However, ecological and ethological observations describe *C. acutus* as an active colonizer through marine dispersion and are consistent with an alternative hypothesis that they belong to one cohesive population. Delineating populations as Evolutionarily Significant Units (ESUs) based on their genetic and geographic distribution is important especially when considering conservation and management actions. Therefore, the study of population structure of *C. acutus* is important in this context to devise an effective conservation strategy. Our study will address the following questions: 1) Are populations on CMNP and Gulf of Chiriqui ESUs or are they panmictic populations related by some level of gene flow? 2) What is the level of gene flow, if any, among

these populations? To address these questions, we are currently genetically characterizing these populations by amplifying ten polymorphic microsatellite loci. The genetic information obtained upon the completion of our study will be invaluable to devising an effective conservation plan for *C. acutus* within CMNP.

13 – MORPHOMETRIC AND GENETIC VARIATION AMONG SIX MONOTYPIC GENERA OF THE SUBFAMILY PHYLLOSTOMINAE (CHIROPTERA: PHYLLOSTOMIDAE)

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The Subfamily Phyllostominae is widely distributed across the Neotropics, occurring from the southern United States southward to northern Argentina and Paraguay. The systematics and distribution of species in the subfamily have been reviewed previously by several authors based on morphometric (i.e. Wetterer et al. 2000) or genetic data (i.e. Baker et al. 2003). However, disagreements regarding the taxonomic status of some species and genera still exist. In the most recent revision, Williams and Genoways (2008) recognized 16 genera and 43 species, including nine monotypic genera and 12 species identified as endemic for South America. My project will focus on the 6 monotypic genera (*Chrotopterus*, *Macrophyllum*, *Phylloderma*, *Trachops*, *Trinicterys* and *Vampyrum*) broadly distributed among the Neotropics. The main goal of my study is to compare morphometric variation with previously generated genetic data using statistical and geographic approaches. This research will help to define the extent of morphological variation within these genera and will place this information in the context of genetic divergence and geographic distribution. This approach will help to identify and to assess the role of geographic barriers (i.e. rivers, mountains) in the origin and dispersal of these bats. The potential results should provide important insights into their respective evolutionary histories and into common diversification patterns of phyllostomine bats.

14 – FIRE SURVIVAL STRATEGIES OF OAKS IN THE TRANS PECOS MOUNTAINS

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Fire is a powerful disturbance across the world's ecosystems. A number of climate models have predicted changes in precipitation patterns and increasing temperatures in the future. Drier and warmer climate conditions will lead to increased fire activity in the American Southwest. Developing our understanding of fire survival strategies of Southwestern oaks will allow us to address potential changes in community composition locally, as well as address a gap in the global understanding of fire survival strategies. I propose to investigate tradeoffs in fire survival strategies, sprouting and non-sprouting, in the common oaks of the Trans Pecos Mountains. This will be achieved by comparing bark thickness versus investment in total nonstructural carbohydrate reserves for eight species (*Q. emoryi*, *Q. gambelii*, *Q. gravesii*, *Q. grisea*, *Q. hypoleucooides*, *Q. muehlenbergii*, *Q. pungens*, *Q. rugosa*) in three study sites: the Chisos Mountains, the Davis Mountains and the Guadalupe Mountains. I hypothesize that southwestern oaks invest in surviving fires and that there is a continuum of investment between bark thickness and total nonstructural carbohydrates; the relationship will be negative across mature trees, but may vary throughout a tree's lifespan. Acquiring a deeper understanding of fire survival strategies will facilitate better fire management practices on private and public land. Additionally, these strategies can be included with other functional traits when determining species success or failure under intensifying disturbance regimes.

15 – EAVESDROPPING BY BLACK-TAILED PRAIRIE DOGS (*CYNOMYS LUDOVICIANUS*) ON ACOUSTIC SIGNALS OF KILLDEER (*CHARADRIUS VOCIFERUS*)

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This project will examine the ability of prairie dogs to utilize the alarm signals of killdeer (*Charadrius vociferus*). Killdeer are sympatric with black-tailed prairie dogs through part of their range, often breeding on active colonies. They utilize alarm signals, both acoustic and visual, under perceived threat of predation. Prairie dogs also have a well-developed alarm system for a variety of predators. Since both species have numerous predators in common, it would be advantageous for prairie dogs to be able to utilize the calls of killdeer as an early warning system. If prairie dogs are able to extract pertinent information about predation from killdeer alarm calls, they should alter their activities accordingly (e.g. cease foraging, seek cover). To determine if this is the case, several prairie dog colonies in and around Lubbock, TX will be videotaped before, during, and after exposure to killdeer alarm calls. Recordings will be analyzed frame-by-frame, and several metrics will be recorded for each individual including total number of headraises, number of times a burrow is approached, number of foraging bouts, number of barks, and number of tail flicks. If the hypothesis is supported, foraging activities should decline during and immediately after alarm signals are given relative to before signaling whereas vigilance-related behaviors should increase. Conversely, if prairie dogs cannot or do not utilize killdeer alarms, rates of vigilance behaviors vs. foraging should remain comparable.

16 – PHOTOSYNTHETIC RESPONSE OF THE INVASIVE GRASS *PHALARIS ARUNDINACEA* AND THE NATIVE SEDGE *CAREX STRICTA* THAT IT REPLACES TO CLIMATE CHANGE AND NITROGEN AVAILABILITY

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Increasing temperature with climate change in combination with increased inputs of nitrogen from agricultural processes will increase the risk of invasion by exotics in already sensitive freshwater wetlands. Wetlands have high intrinsic value due to their ability to support high biodiversity, making efforts to prevent exotic invasion in wetlands paramount. The invasion of *Phalaris arundinacea* in wetlands inhabited by the native sedge, *Carex stricta*, is an ideal model system to study the effects of climate change and eutrophication on invasion from a physiological standpoint. This system can be easily studied under controlled environmental conditions to examine how the two species may differentially respond to alterations in present temperatures in the presence of enhanced N input. We have determined that *P. arundinacea* exhibits higher rates of photosynthesis, higher specific leaf areas, and great net carbon gain across a broad range of temperatures compared to *C. stricta*. Present research is addressing the following questions: (a) How do seasonal changes affect photosynthetic and respiratory potentials of each species under the current climatic conditions?; (b) How will increased temperatures affect leaf photosynthesis and respiration under different N treatments for each species?; (c) How will increased temperature affect the ecological process of invasion?; (d) What are the physiological bases for the responses to increased temperature and N? Answers to these questions can lead to better targeting of management practices for all invasive species who have an advantage in net carbon gain over native, less-aggressive species.

17 – THE INVOLVEMENT OF PROTEIN PHOSPHATASE 2A IN AUXIN TRANSPORT PATHWAY

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Posttranslational modification of proteins by phosphorylation is a universal mechanism for regulating diverse biological functions. Protein phosphatase 2A (PP2A), one of the major protein phosphatase, serves as a tumor suppresser in humans, indicating its role in maintaining cell homeostasis in animals. In plants, PP2A was found to be involved in plant responses to hormones such as auxin, abscisic acid (ABA), and ethylene. PP2A is an heterotrimeric enzyme consisting of a scaffolding subunit A, a regulatory subunit B, and a catalytic subunit C. Given that the regulatory subunit B is much more diversified than other subunits, it is understandable why B subunits might be responsible for selecting PP2A's various substrates. However, the exact role of PP2A in plant hormone signaling has yet to be determined. In order to study how PP2A is involved in auxin signaling, we over-expressed one B subunit gene in Arabidopsis and found that transgenic plants are insensitive to N-1-Naphthylphthalamic Acid (NPA) treatment, suggesting this B subunit gene is involved in auxin transport pathway. Also, the GUS staining pattern of this B subunit gene's promoter indicates that this B gene is highly expressed in vascular tissues of plant root, stem and leaf, as well as the apical meristem in the seedling, which thought to be where auxin is synthesized in plants. In addition, the overexpression plants showed slightly more sensitive to ABA at germination stage and post-germination growth. Overall, our work with this B subunit gene suggests that PP2A is indeed involved in auxin polar transport in plants.

18 – abh1 sgs3 DOUBLE MUTANT MANIFESTS NOVEL PHENOTYPES SUGGESTING AN INTERACTION BETWEEN mRNA PROCESSING AND POST TRANSCRIPTIONAL GENE SILENCING

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It has been shown that mRNA processing machinery interacts with post transcriptional gene silencing (PTGS) in plants. To gain more insights into the interaction, we generated a double mutant between ABA hypersensitive1 (abh1) and suppressor of gene silencing3 (sgs3). ABH1 encodes a cap-binding protein that is also involved in pre-mRNA splicing, RNA 3' end formation and RNA nuclear export. SGS3 encodes a plant-specific RNA binding protein that plays a crucial role in PTGS against foreign RNAs produced by viruses or sense-transgenes and generation of endogenous trans-acting siRNAs (ta-siRNAs). abh1 sgs3 double mutant manifests a series of enhanced phenotypes compared to the parental lines including enhanced ABA sensitivity, increased fused cotyledons, reduced flowering time, and most interestingly, it has altered silique shape and significantly reduced seed set. These results suggest that there is a gene interaction between ABH1 and SGS3 in controlling flowering time, gametophyte development and response to ABA during seed germination. Future work will focus on transcriptome profiling of mutant expression of non-coding RNAs, MIRNA genes, and select targets identified by meta-analysis of whole genome tiling array datasets. These results will help dissect the interaction between ABA signaling, mRNA processing machinery and PTGS during key steps of plant development such as germination, flowering and embryogenesis.

19 – ANTISENSE TRANSCRIPTION AND SMALL RNA REGULATION OF ARABIDOPSIS AUXIN RESPONSE FACTOR ARF12/22 GENES IN OVULES

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Widespread overlapping cis-natural antisense transcription (cis-NATs) has been observed reproducibly for 7-30% of eukaryotic genes in large-scale transcriptome studies, but its origins and significance are largely unknown. A clade of seven highly homologous and tightly linked plant-specific AUXIN-RESPONSE-FACTORS (ARF12/22) that have specific expression pattern in the female gametophyte and during embryogenesis, appear to have a cis-NATs for ARF14, and spawn predominantly 24 n.t. species of siRNAs. Computational meta-analysis of published whole genome tiling microarray transcriptome datasets showed sense and antisense transcripts are elevated in argonaute1 (ago1) hyponastic leaves1 (hyl1) mutants. ARF12/22 sense and ARF14 antisense expression were characterized in the siRNA biogenesis mutants and the post-transcriptional gene silencing (PTGS) mutants by real-time semi-quantitative reverse transcriptase PCR, by northern blot and by whole mount in situ hybridization of developing embryos. It was found that before ovule fertilization ARF14 sense expression was localized in punctate cytoplasmic foci of integumentary cells, whereas antisense ARF12/22 expression was localized to the nucleus of these cells and to a callose-rich boundary between peripheral endosperm and the sporophyte endothelium which was altered in *rdr6-15* and *sgs3-11* mutants. Our data support the hypothesis that RDR6/SGS3 and DCL3 are involved in synthesis and processing of natural-cis-siRNAs from the ARF14 sense-antisense gene pair which silence ARF12/22 expression in peripheral endosperm/endothelium, and integument domains of the ovule. The significance of this work is a better mechanistic understanding of gene silencing associated with mobile siRNAs and the potential functions of ARF12/22 genes in the gametophyte.

20 – EXAMINATION OF 35S::ATMYB90 TRANSGENE SILENCING USING DICER LIKE KNOCKDOWN LINES IN *NICOTIANA TOBACCUM*.

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A series of 35S::AtMyb90 *N. tabaccum* transgenic lines were created, with several lines producing a purple phenotype due to plant-wide over-production of anthocyanin. One of the purple lines, Myb27F presents two distinct phenotypes that correlate with transgene dosage. Myb27F homozygotes appear to silence the 35S::AtMyb90 transgene, denoted by greening of the leaves in a pattern similar to systemic silencing. The Myb27F hemizygotes show no phenotypic signs of silencing. Analysis of mRNA levels by qRT-PCR reveals that AtMyb90 mRNA in the Myb27F homozygotes is dramatically reduced compared to that present in the Myb27F hemizygotes. It is also known that small RNA's for the coding region of the transgene are present only in the Myb27F homozygotes. To characterize silencing by small RNAs in *A. thaliana*, loss of function mutants of the silencing machinery in the pathway have been used e.g. (*dcl2*, *dcl3*, *dcl4*, *hyl1* and *drb4*). To explore the mechanisms by which the 35S::AtMyb90 transgene in *N. tabaccum* is silenced, transgenic tobacco lines containing Dicer-Like knockdowns (DCL2, DCL3, and DCL4) will be used. The knockdown lines were kindly provided by Barbara Baker's lab (USDA-ARS Albany California) and have been crossed with the Myb27F homozygous line, with a non-silencing AtMyb90 transgenic line Myb237G homozygous, and with wild type *N. tabaccum* SR1.

21 – COLIFORMS DETERMINATION IN MUNICIPAL DRINKING WATER, MAHENDRANAGAR, NEPAL

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Coliforms are indicator microorganisms of water pollution and their presence in drinking water is commonly referred as standard parameters to determine quality of potable water. The presence of coliforms in drinking water generally occurs due to contamination via fecal route since almost all coliforms microbes are inhabitants of the colons of human beings and others vertebrate hosts. They are also common causative agents of most of the water borne diseases. Between November 2006 to March 2007, we conducted a prospective study to determine the bacteriological quality of drinking water in Mahendranagar municipality, Nepal, using standard most probable number (MPN) method. Samples were obtained from number chosen at random from around the municipality. Our analyses show that over 64% of the samples were contaminated with coliforms and other pathogenic bacteria; in fact, the mean number of coliforms among total water samples at 95% confidence interval is 234 ± 86.6 per 100ml water (s.d.= 363.1). In addition to coliforms, other bacteria cultured or identified by biochemical methods included: *Escherichia coli*, *Proteus mirabilis*, *P. vulgaris*, *Salmonella typhi*, *S. paratyphi*, *Enterobater aerogenes*, *Klebsiella* spp, *Citrobacter* spp and *Shighella* spp. We conclude that the water samples in the Mahendranagar municipality were heavily contaminated with coliforms and other enteric pathogenic bacteria and thus, are not suitable for human without prior treatment.

22 – THE EFFECTS OF TRICLOSAN AND METHYLTRICLOSAN ON GENE EXPRESSION DURING EARLY EMBRYONIC DEVELOPMENT IN SOUTH AFRICAN CLAWED FROGS (*XENOPUS LAEVIS*)

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Triclosan (5-chloro-2-(2,4-dichlorophenoxy)phenol) is a bactericide used in many personal care products such as liquid detergents, liquid hand soaps, deodorants, cosmetics, creams, lotions, mouthwash, and toothpaste. Triclosan also can be added to fabrics, plastics, carpets, plastic kitchenware, and toys (Leiker, 2009). Methyltriclosan can be formed from triclosan via biological methylation at an unknown interval during waste water treatment. Methyltriclosan is more abundant in the environment, is more lipophilic than triclosan, and has greater potential to accumulate in fatty tissues (Leiker, 2009). The global decline of amphibian populations has raised awareness surrounding the possible effects of poor water quality. Triclosan and methyltriclosan have been reported in surface waters at concentrations of 0.40 µg/L and 0.04 µg/L, respectively (Leiker, 2009). Since metamorphosis and reproductive development (Shi, 2001) in amphibians is highly regulated by thyroid hormone (TH), and the structure of triclosan is similar to that of TH (Veldhoen, 2006), raises the possibility that triclosan or methyltriclosan may act on TH receptors to alter metamorphosis and reproductive development. In order to further elucidate these conjectures, it is imperative to understand the influence of triclosan and methyltriclosan on gene regulation. Furthermore, there are no studies to date examining the effects of methyltriclosan on anuran development and metamorphosis. Environmentally relevant concentrations of triclosan and methyltriclosan will be applied using standard FETAX protocols on the South African Clawed Frog, *Xenopus laevis*. RNA will be extracted and analyzed using

microarray gene expression techniques to determine the specific effects of triclosan and methyltriclosan on developing *Xenopus laevis*.

23 – CREATION AND ANALYSIS OF TRANSGENIC COTTON PLANTS EXPRESSING A SUMO (SMALL UBIQUITIN RELATED MODIFIER) E3 LIGASE SIZ1

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Abiotic stresses such as drought, salinity and extreme temperatures are serious threats to modern agriculture. These stresses lead to a series of morphological, physiological, biochemical and molecular changes in plants that adversely affect plant growth and productivity. High temperature stress adversely affects plants by causing membrane integrity loss, reactive oxygen species production, protein inactivation and denaturation, which ultimately leads to cell death. Plants show various thermal tolerance responses for better survival which include membrane compositional changes necessary for maintenance of functional integrity, activation of oxidative defense systems through ethylene and salicylic acid production and production of heat shock proteins necessary for cellular protection. Earlier researches indicate that high temperature induces conjugation of SUMO (small ubiquitin like modifier) to peptides, which is called sumoylation, probably a protective response to high temperatures stress. *SIZ1* is a SUMO E3 ligase that facilitates sumoylation of transcription factors like HSFs (heat shock transcription factors). Activation of heat shock transcription factors aid in the transient production of heat shock proteins (HSPs). HSPs are molecular chaperones that reduce protein denaturation, target denatured proteins to proteasome for destruction, facilitate protein folding necessary for protein maturation and renaturation, and regulate activity of HSFs to control HSP gene expression during thermotolerance acquisition. We speculate that if *SIZ1* gene is overexpressed in cotton plants, it might confer plants increased heat tolerance and thus benefit the west Texas farmers by minimizing loss in yield and productivity under high temperature conditions.

24 – THE ROLE OF SMALL RNAs IN ABIOTIC-STRESS RESPONSES IN PEANUT (*ARACHIS HYPOGAEA*)

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MicroRNAs (miRNAs) are an endogenous class of noncoding RNAs that are thought to play important roles in regulating gene expression in metazoans by targeting mRNAs for cleavage or translational repression. In plants, other than their developmental regulatory functions, little is known about their role in regulating gene expression under abiotic stress conditions. Through screening a diverse set of peanut genotypes from the U.S. peanut mini-core germplasm collection, we have identified two genotypes with contrasting stress response phenotypes: tolerant (Core Collection accession 041) and susceptible (Core Collection accession 166). These genotypes have subsequently been screened for physiological and yield response under water limiting conditions in crop year 2008 field trials. We hypothesize that the contrasting phenotypes are the result of underlying genetic differences between 041 and 166, and at least in part, due differences in the regulation of gene expression by small RNAs. Using these two contrasting genotypes, I propose to elucidate the regulatory mechanisms controlling these responses by identifying novel small RNAs for peanut and their expression patterns and specific gene targets.

25 – ENHANCING COTTON FIBER ELONGATION AND CELLULOSE SYNTHESIS BY MANIPULATING FRUCTOKINASE ACTIVITY

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The strength of the economically-important cotton “fiber” depends upon its cellulose content. Cellulose synthesis requires UDP-glucose that is produced from sucrose by sucrose synthase (SuSy). The other product of the SuSy-catalyzed reaction is fructose, which can inhibit SuSy. Our hypothesis was that enhancing the removal of fructose via phosphorylation by fructokinase would reduce SuSy inhibition and improve cellulose synthesis in cotton fiber. To test this hypothesis, we have developed transgenic cotton plants harbouring the fructokinase gene, *LeFRK1*, from tomato under the control of the 35S promoter. Six T1 plants for each of six transgenic lines and a control, null line were grown in a greenhouse to study the effects of enhanced fructokinase activity on fiber development. At least three lines had moderate and three had low expression of *LeFRK1* in leaves and in fibers at the stages of elongation and secondary wall synthesis. However, only one line had enhanced (three fold) extractable fructokinase activity in leaves, potentially due to post transcriptional modifications of *LeFRK1* transcripts or protein. Elongating fibers of four lines exhibited an enhancement in fructokinase activity from two to three fold, and this activity had remained the same for most lines by the secondary wall stage. There was improvement in seed cotton mass for one line of transgenic plants over-expressing *LeFRK1*. However, we will be having the fiber tested for length and strength properties. Our next experiment will test the hypothesis that elevated fructokinase activity will improve fiber development under drought conditions.

26 – CULTURE AND ISOLATION OF “NTAD GENE CLUSTER” PRODUCTS FOR FUNCTIONAL ANALYSIS IN ADDICTION AND RELAPSE

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In 2008, 22.2 million Americans were identified as suffering from substance dependence or abuse. Over sixty percent of those individuals completing a treatment program will relapse within six to twelve months; many within 90 days. As observational, genome wide association studies (GWAS) continue to investigate the role of genetics in craving, relapse and Substance Dependence Disorders (SDD), it is imperative to explore functional studies of target genes and their products. Interaction between the respective genes and gene products of the NCAM1, TTC12, ANKK1 and DRD2 (NTAD) cluster are associated with the dopaminergic, “reward” pathways in the brain. Their associations have been linked to several forms of SDD such as alcohol dependence, drug dependence and nicotine dependence in human populations. Initial findings of NTAD research indicate that sufficient concentrations of conserved NTAD neuropeptides are found within both human and rat hippocampi, yet gaps remain that delve into the functionality of this cluster. The experiments proposed herein will establish the primary cell culture of adult, rat hippocampal neurons to pursue functional studies of the NTAD gene cluster. The presence and relative quantity of gene product in rat hippocampi shall be determined, utilizing Western Blot and Enzyme-linked immunosorbent assay, or ELISA. These data will contribute to future, functional neuropeptide studies utilizing genotyping, gene expression studies, mass spectrometry and Spinning Disk Confocal microscopy.

27 – A SURVEY OF THE ACTIVITY PATTERNS OF MEDIUM TO LARGE MAMMALS IN THE SOUTHERN ROLLING PLAINS OF TEXAS

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Texas is a state known for biological diversity in both plant and animal life. This diversity is evident in the medium to large mammals that most Texans are familiar with. This study presents a survey of medium to large mammals on the Southern Rolling Plains of Texas using noninvasive methods. Camera traps were put out on two properties in Jones and Callahan counties, Texas, for a duration of ten months (March- December 2010). Each of the trap sites were scent baited and monitored weekly. A total of 301 animals were photographed including armadillo, bobcat, coyote, eastern fox squirrel, feral hog, opossum, raccoon, white tailed deer, and striped skunk. These data were used to characterize activity patterns in medium to large mammals in the Southern Rolling Plains of Texas. Linear regressions were used to show correlation and effect of day and night captures, moon phase, and seasonal changes.

28 – ASSOCIATIONS BETWEEN ADULT FEMALE BODY SIZE AND FITNESS IN ODONATES

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Odonates (dragonflies and damselflies) vary intraspecifically in body size due to both genetics and environmental variables (e.g. surrounding land use, food availability, and photoperiod). These size differences are hypothesized to impact fitness. The most ubiquitous yet one of the least-studied odonate species on the Southern High Plains of Texas is the damselfly *Enallagma civile*. Until now, no study has examined the effects of size differences on female *E. civile* fitness, and few have documented reproductive life history information. Between June 2009 and June 2010, we captured 530 actively mating *Enallagma civile* females in the field. Although roughly only a fourth of captured females subsequently laid eggs in the lab, among those that did, clutch size averaged 280.45 (range of 1-1047 eggs/female), and overall there was a high mean hatch success rate of 75.80%. Pearson correlations and t-tests revealed that female body size (head capsule width, a non-labile trait in adults) was significantly associated with various fitness metrics. Egg-laying females had larger head capsule widths than did non-egg laying females, and moreover, females laying >500 eggs were larger than those laying <500 eggs. Hatch success was positively associated with clutch size and egg length, and negatively related to hatch duration. Most of these conclusions correspond to our initial hypotheses; the unexpected findings provide interesting areas for future research.

29 – EFFECT OF REDUCED DAILY SOIL TEMPERATURE VARIABILITY ON A SOIL MICROBIAL COMMUNITY IN THE CHIHUAHUAN DESERT

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Recent climate models predict that night-time warming will increase significantly in arid systems leading to decreases in daily temperature range (DTR). The effects of a reduction in DTR_{soil} occur by altering ecosystem functions through effects on microbial activity, biomass production and biodiversity. To investigate the role of DTR_{soil} in regulating microbial community structure and function, we set up a manipulation study in the Chihuahuan Desert, at Big Bend National Park within a creosotebush bajada in 2006. Erosion control blankets were used to reduce DTR_{soil} from 2006-2008 in five 3x3m plots. We altered the design in 2009 by suspending polyethylene

shade cloth on a PVC frame 13cm above the soil surface minimizing alterations to the boundary layer and added five more plots with the new design, while five unshaded plots continued to serve as controls. Shading reduced soil temperature variation by 6.6°C on the surface and by 2.9°C at 15cm depth compared to that of controls. The decrease in DTR_{soil} significantly increased microbial biomass carbon and nitrogen (up to 90% and up to 70% respectively) while reducing soil free nitrogen (NO₃-N by 24%) during late summer of 2010. Similarly, soil CO₂ flux increased by 38-61%, and FAME analysis showed significantly increased saprophytic fungal composition (up 50%) in the reduced DTR_{soil} plots compared to controls. Current DTR_{soil} may account for the lower microbial activity associated with desert soils. Moreover, as DTR_{soil} decreases in these systems with climate change, the contribution of deserts to global carbon flux may actually increase from present proportions.

30 – REPRODUCTIVE PHENOLOGY OF INSECTIVOROUS BATS IN MALAYSIA: IMPLICATIONS FOR CLIMATE CHANGE

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The high energetic and nutritional demands of pregnancy and lactation in bats are presumed to require that species in seasonal habitats breed when food availability is greatest. Failure to match parturition with food availability could incur individual fitness costs and, should mismatches occur repeatedly, lead to population declines. In this study, we determine whether insectivorous bats synchronize reproductive activity with insect availability, and if insect availability correlates with local climate variables (temperature and rainfall). The study was conducted in lowland dipterocarp forest around Kuala Lompat Research Station at Krau Wildlife Reserve, Malaysia from February 2009 to January 2010. A HOBO Automated Weather Station was used to monitor the temperature and rainfall. Bats were trapped with four-bank harp traps in the forest understory for five nights each week, and once a month at a nearby cave. Females were assigned to five major reproductive categories by examination of the condition of mammary glands, pubic nipples and abdominal palpation. Two light traps were run simultaneously to the bat trapping in order to correlate the presence of insects as its food source. The analysis is still in progress but initial results suggest that insect abundance is influenced by rainfall and that lactation is timed to coincide with the period of maximum insect biomass. Thus it appears that Malaysian insectivorous bats synchronize breeding with insect availability, which is in turn determined by local climate seasonality. Our findings are discussed in context of climate change projections for Malaysia.

31 – CHARACTERIZATION OF THE ABIOTIC NICHE OF THE AMERICAN HOG-NOSED SKUNK (*CONEPATUS LEUCONOTUS*) USING ECOLOGICAL NICHE MODELING: PAST AND PRESENT VIEWPOINTS

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Spatially distributed occurrence records have been used to infer factors limiting an animal's distribution since the early 1900s. However, recent advances in GIS technologies and increasing availability of broad scale environmental data sets/museum records have led to the rapid development of new methodologies for understanding this fundamental question. One such

methodology, coined ecological niche modeling (ENM), allows researchers to create predictive maps of a species fundamental niche across both space and time. Using 131 vouchered museum specimens and 19 bioclimatic variables in the programs GARP and MaxEnt, we developed predictive models of the abiotic niche of the American hog-nosed skunk (*Conepatus leuconotus*) under present (1950 – 2004) and past (Last Glacial Maximum ~20,000 ybp and Last Interglacial ~135,000 ybp) environmental conditions. The present distribution of this species was best predicted using a subset of 8 bioclimatic variables, including minimum temperature of the coldest month and precipitation of wettest month. The predicted distribution of the Last Glacial Maximum is characterized by a southern contraction into north-central Mexico, a pattern consistent with cooler temperatures of this geologic period. Suitable environmental space of the Last Interglacial is similar to the present, except for the lack of suitable conditions in west-central Texas and east-central New Mexico. Differences between present and past distributions have allowed us to identify four potential Pleistocene refugia for *C. leuconotus* which we plan to subsequently examine using a phylogenetic framework. These ecological niche models provide a window into the ecological and evolutionary processes limiting the geographic distribution of *C. leuconotus*.

32 – PHYLOGENETIC RELATIONSHIPS AND TRIBAL DIVERGENCE TIMES IN THE SUBFAMILY NEOTOMINAE

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The subfamily Neotominae is a diverse and widespread group of rodents; however, there is some controversy surrounding the phylogenetic relationships within this group. There have been multiple studies that have examined this subfamily utilizing morphological, allozyme, or karyotypic data, as well as mitochondrial and nuclear DNA sequences, which have led to various taxonomic arrangements. More specifically, there have been several interpretations as to how many tribes should be recognized within this subfamily and the relationships of genera within each tribe. Previous studies provided support for 4 tribes: Baiomyini, Neotomini, Peromyscini, and Tylomyini. Some have suggested placement of *Ochrotomys* into a separate tribe (Ochrotomyini), whereas others have used Reithrodontomyini to represent the “old” Peromyscini. More recently, 5 tribes (Baiomyini, Neotomini, Ochrotomyini, Peromyscini, and Reithrodontomyini) have been recognized based on molecular data. The goals of this study are: 1) to develop a robust, multi-gene phylogeny to acquire higher resolution at the tribal level of the Neotominae and 2) to use coalescence theory to date tribal origins to test the hypothesis of rapid divergence over a short time frame. This study is the first to analyze combined mitochondrial and nuclear DNA sequences with representatives of all genera of neotomine-peromyscine rodents, including the Tylomyinae which historically have been placed in the subfamily Neotominae. Additionally, we have examined for the first time the molecular relationships of *Otonyctomys hatti*.

33 – MOLECULAR AND ECOLOGICAL EVALUATION OF HYBRIDIZATION IN TWO SPECIES OF WOODRATS (*NEOTOMA FLORIDANA* AND *N. MICROPUS*)

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The parapatric distributions of two species of woodrats (*N. floridana* and *N. micropus*) extend for over 2,200 kilometers, from the Gulf of Mexico to southeastern Colorado. The only reported contact zone between these two species is a small hybrid zone in western Oklahoma (Spencer 1968; Birney 1973; Bradley et al. unpublished data). We hypothesize that additional areas of sympatry, possibly resulting in hybridization, occur throughout the distribution borders. To test this hypothesis, two independent methods of estimation will be used to locate areas ecologically suitable for sympatry. A manual estimation method utilizing literature review, museum records, and geographic maps to estimate possible zones of sympatry has been used. A computational method of estimation utilizing Geographic Information Systems and Ecological Niche Modeling Software is in the preliminary stages of data collection. Collection trips have been made to multiple putative areas of sympatry, and genotypes of specimens are currently being established through the use of 4 molecular markers (1 maternally inherited [*Cytb*], 1 paternally inherited [Y-chromosome marker], and 2 biparentally inherited [*Fgb-17* and *Adh1-12*]). Molecular assays will be utilized to determine the full extent and directionality of the original hybrid zone, as well as any additional contact zones. After molecular analyses are complete, sampled areas will be classified as either positive or negative for evidence of hybridization. Accuracy and efficiency of both methods will be quantified and compared through statistical analyses. Results of this project will be used to advocate the most accurate and efficient method for detecting and examining hybrid zones.

34 – MORPHOLOGICAL COMPARISON BETWEEN INSULAR AND CONTINENTAL POPULATIONS OF *VIPERA AMMODYTES* (SQUAMATA: VIPERIDAE) IN GREECE

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The Cyclades are a group of Greek islands, in the Aegean Sea, that were formed because of rising sea levels following the glacial retreat in northern Europe, 20 KYA. Dwarfism is prevalent among the 13 known insular populations of the Long-nosed viper (*Vipera ammodytes*), each isolated on their respective island since a landbridge with another island was disconnected. This is the first study to analyze external morphology of the insular forms in comparison to their continental ancestors. Multivariate statistics were used to analyze size and shape between the groups, finding that the insular forms varied from the continental groups in both size and shape.

35 – Y-CHROMOSOME AND MITOCHONDRIAL SEQUENCES INDICATE GENETIC INTROGRESSION IN MORPHOLOGICALLY-DISTINCT GROUND SQUIRRELS (GENUS *SPERMOPHILUS*)

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Spermophilus mexicanus and *S. tridecemlineatus* are sister species that form a zone of sympatry across southeastern New Mexico and the Texas Panhandle. Though morphologically distinct, allozymic, karyotypic, and morphologic data indicate that the 2 species hybridize. In addition, laboratory crosses of parental types have produced F₁ offspring verifying the ability for hybridization to occur between the 2 species. Recently, Stangl et al. (in prep) documented several locations of possible hybridization in the southeastern portion of the Texas Panhandle. Initial morphological analyses confirmed the presence of hybrids; however, neither species were collected in sympatry and probably exist in parapatrically interdigitated populations throughout the putative zone of sympatry. To further investigate hybridization between these 2 species, we have obtained mitochondrial cytochrome-*b* (*Cytb*) sequences from nearly 250 individuals and have begun sequencing the Y-linked structural maintenance of chromosomes gene (*SmcY*). The *Cytb* data indicates a common mitochondrial genome for *S. mexicanus* and *S. tridecemlineatus* within the putative zone, as well as the immediate vicinity. These populations are genetically divergent from parental populations outside of the putative zone, which may indicate an ancient introgression event. Preliminary data from the *SmcY* gene shows species-specific haplotypes and appears useful in delimiting species. The *SmcY* data will provide useful phylogeographic information in these male-biased dispersal species, especially in light of a potential common mitochondrial genome. In conjunction with amplified fragment length polymorphisms (in progress), these two datasets will help provide answers in identifying hybrids, determining directionality of hybridization, and discovering the evolutionary history of these 2 taxa.

36 – PHYLOGENETIC RECONSTRUCTION OF *DERMANURA*: TESTING FOR CONGRUENCE AMONG MULTIPLE MOLECULAR MARKERS

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Morphological studies have failed to yield congruent resolution for the number of species within the genus *Dermanura* (Chiroptera: Phyllostomidae). Species delineated based on morphological characteristics have ranged from one to ten. Eleven statistically supported monophyletic species are recovered from the cytochrome-*b* gene tree. Because of the lack of congruence among previous methods, we selected the genetically defined monophyletic bat genus *Dermanura* to test the resolving power of three distinct molecular markers for distinguishing species groups. To identify species groups, our goal was to use the same morphologically identified specimens for each marker. Nuclear data were generated for two markers, amplified fragment length polymorphisms (AFLP) and cross-species amplified microsatellites, for comparison to the previously published cytochrome-*b* gene tree. The preliminary nuclear data sets are limited to fewer species than were present in the cytochrome-*b* gene tree, probably due to poor quality DNA. The AFLP phylogeny produced the same species groups whereas few monophyletic species groups were recovered in the microsatellite phylogeny. These contrasting results may be due to the discrepancy in the number of AFLP bands (i.e., 384) versus the number of microsatellite loci (i.e., six) among the two different molecular markers. Very little AFLP data has been generated and is thought to be due to poor quality DNA. Future research will increase

the number of cross-species amplified microsatellite loci and new DNA extractions will be used to produce a more informative AFLP phylogeny from high molecular weight DNA.

37 – THE IMPACTS OF NITROGEN UTILIZATION AND ALLOCATION STRATEGIES ON PHOTOSYNTHESIS FOR AN INVASIVE GRASS, *PHALARIS ARUNDINACEA*, IN COMPARISON TO THE NATIVE SEDGE, *CAREX STRICTA*

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Phalaris arundinacea (reed canary grass) is an invasive C₃ perennial grass of temperate/boreal wetland communities. It is more abundant in areas with high nitrogen (N) inputs. Our hypothesis is *P. arundinacea* gains a competitive advantage over *Carex stricta*, the native sedge it often displaces, with increased N, because it allocates more N to features that enhance net carbon gain than *C. stricta* does. To test this hypothesis, we are comparing the responses of photosynthetic parameters and leaf morphology to various N levels (0.1 to 33 mM N) for *P. arundinacea* and *C. stricta*. We grow the plants in a course medium whose N content is controlled by varying the nitrate and ammonium in standard Hoagland's solution. With an increase in the N concentration provided, we observed an increase in net CO₂ assimilation on an area basis (*A*), leaf area, and specific leaf area (SLA) for *P. arundinacea*, but the effect on chlorophyll content was not clear. For *C. stricta*, the highest *A*, SLA and the chlorophyll content was determined for plants supplied only 2.75 mM N, suggesting that higher N levels led to the plants becoming pot-bound. It appears that N level affects total carbon gain for *P. arundinacea* by affecting *A*, leaf area, and SLA, allowing it to rapidly attain its full height and shade *C. stricta*. These advantages of high nitrogen had made the *P. arundinacea* become more aggressive and invade the wetlands displacing the *C. stricta*.

38 – THE DIVERSITY AND ECOLOGICAL AND ECONOMIC SERVICES OF BATS IN A COFFEE-FOREST LANDSCAPE IN SOUTHWESTERN SUMATRA, INDONESIA

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Bukit Barisan Selatan National Park (BBSNP), Sumatra, Indonesia, is one of the most biologically diverse tropical rainforests in the world, but is threatened by increasing levels of encroachment for coffee agriculture. Due to the impossibility of protecting all forest, a recent paradigm suggests that agroecosystems outside protected areas should be included as harbors of biodiversity. To implement this paradigm is challenging. First, the biodiversity value of the agroecosystem needs to be identified. Second, habitat losses frequently bring farmers into conflict with wildlife, and their actions can compromise biodiversity management. It is essential that conflicts be resolved and the benefits of biodiversity realized. The goals of this project are to determine the value of coffee plantations adjacent to BBSNP to bat conservation, and, in turn, the ecological and economic services provided by bats to the coffee plantations. To achieve these goals, I will: 1) carry out trapping and acoustic surveys to assess the bat diversity that different coffee plantation types support; 2) set up enclosures to exclude bats from experimental trees and then quantify bats' pest-control effects by comparing arthropod assemblages and leaf damage of the enclosed trees with control trees; 3) estimate the potential economic value of a new bat-associated coffee product; and 4) interview coffee farmers to evaluate their perception of bats, and bats' services. The expected results will help us to understand the significance of coffee

agroecosystems in maintaining bat diversity in the target area, and to increase farmers' recognition of the benefits of biodiversity associated with them.

39 – LEAF TRAITS AND LITTER FLAMMABILITY: UNDERSTANDING MULTI-SPECIES MIXTURES

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Our work seeks to understand how individual plant leaf traits influence fire behavior at the community scale. Although it is recognized that plant species vary in their flammability, we currently lack a mechanistic understanding of how plant traits influence fire and of how mixtures of litter behave in a fire. As modified fire regimes and climate change shift the species composition of communities, a mechanistic perspective is especially important in order to understand and predict fire in potentially novel plant communities. This work addresses three questions: 1) How do 8 species common in Sierra Nevada mixed-conifer forest differ in their litter flammability?; 2) What leaf traits are associated with various flammability components?; and 3) Do individual species measurements predict multi-species combinations or are there non-additive effects? Leaf litter was collected in Sequoia and Kings Canyon National Parks, California, from 8 species common in mixed-conifer forest. Controlled flammability tests were performed both on reconstructed monospecific litter beds and on three-species mixed litter beds. We tested for non-additive effects in multi-species mixtures using the weighted mean of single-species measures for each flammability component as a null expectation for each mixture; departures from this null indicated non-additive effects. The eight species differed significantly in all flammability components, and species with higher scores on a particular measurement didn't necessarily have a high score on the others, indicating that different traits influence different aspects of flammability. Most flammability components show non-additive effects. Exceptions were heat and peak temperature, which exhibit a simple additive relationship.

40 – AN ASSESSMENT OF GENETIC STRUCTURE AND DIVERSITY AMONG SWIFT FOX POPULATIONS IN THE UNITED STATES

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Habitat fragmentation can influence genetic interchange between groups of individuals, resulting in differences in genetic diversity and structure across the distribution of a species. Studying the genetic composition of populations of a species can lend insight into our understanding of the influence of habitat fragmentation on population interactions. The Great Plains region of the United States is fragmented by natural and anthropogenic sources, yet the interaction between habitat fragmentation and genetic patterns has received limited study in this region. Swift fox (*Vulpes velox*) are native to the short and mixed grass ecosystems of the Great Plains, and are a model organism for studying patterns of gene flow, diversity and genetic structure in the region. We collected 589 swift fox samples throughout the species' distribution in the United States and analyzed these samples using a combination of 15 nuclear DNA microsatellite loci and the control region of mitochondrial genome. Analysis of genetic structure and diversity indicates varying patterns of genetic structure, diversity and interchange over current and historic time scales. We discuss the results of these analyses and present several potential hypotheses explaining the observed patterns, which will be tested as part of ongoing research examining the relationship between habitat fragmentation and genetic patterns in the Great Plains region.

41 – STARTING OFF ON THE RIGHT FOOT: EXPLORING LIFE HISTORY STRATEGIES AND SALT TOLERANCE IN SYMPATRIC FRESHWATER SNAILS

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Salinization of freshwater habitats is a global concern that can be mostly attributed to anthropogenic causes such as urban runoff, wastewater effluent and agricultural practices. In the present study, the effect of salinity was determined on two sympatric freshwater snail species, *Physa pomilia* and *Planorbella tenuis*. Egg masses, juvenile snails and their progeny were exposed to salinities ranging from 250 – 4000 $\mu\text{S}/\text{cm}$ for 14-days, 12-weeks and 14-days, respectively. The results of this experiment showed species-specific sensitivity to salt tolerance. Egg masses of *P. tenuis* showed delayed time-to-hatch with increasing salinity; *P. pomilia* showed a bimodal response, where snails at the lowest and the highest salinities hatched earlier than those exposed to moderate levels of salinity. Juvenile *P. tenuis* experienced increased mortality at 12-weeks in salinities $\geq 3000 \mu\text{S}/\text{cm}$; furthermore, as adults they had little to no reproduction. Juvenile *P. pomilia* again showed a bimodal response in survival and no difference in reproduction at any salinity. There was no effect of salinity on hatching success on progeny of either species. Overall, it appears that *P. tenuis* may be more sensitive to increased salinities; however, the two species may have differing life history strategies that allow them to respond to salt stress.

42 – CHARACTERIZATION OF PA2783: A MEMBER OF THE *PSEUDOMONAS AERUGINOSA* Vfr REGULON

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Pseudomonas aeruginosa is a gram-negative opportunistic pathogen that causes serious infections in immunocompromised hosts, including cystic fibrosis patients, severely burned patients, and cancer patients undergoing chemotherapy. The production of *P. aeruginosa* virulence factors is controlled by several global regulators including the virulence factor regulator Vfr. Vfr requires cAMP for its activation, and both are essential components of a complex global regulatory system that controls the production of multiple virulence factors in the *P. aeruginosa*. Besides the known Vfr-target genes, a previous microarray analysis identified numerous additional *P. aeruginosa* genes that are positively regulated by Vfr. Currently, most of these genes (or their products) are not characterized. We previously identified *P. aeruginosa* PA2783 as a gene whose expression is enhanced by Vfr. This study extends the analysis of PA2783. Examination of the genomic sequence of PAO1 revealed the presence of a second gene, PA2782. Computer analyses suggested that PA2782 and PA2783 constitute an operon. Transcriptional analysis using real-time qPCR and a PAO1 *vfr* deletion mutant revealed that, the expression of both genes is significantly lower in the absence of Vfr. Electrophoretic mobility shift assays were used to determine if Vfr binds to the PA2782 upstream region, the PA2782-PA2783 intergenic region, or both. In the presence of cAMP, recombinant Vfr (r-Vfr) produced two gel shift bands when incubated with the PA2782 upstream region. These results suggest that Vfr directly binds to the upstream region on the PA2782-PA2783 operon.

43 – FUNCTION AND ANTI-MICROBIAL ACTIVITY OF POISON SAC PROTEINS FROM QUEEN RED IMPORTED FIRE ANTS (FORMICIDAE: *SOLENOPSIS INVICTA*)

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Queens of the red imported fire ant, *Solenopsis invicta* Buren, produce a pheromone that induces workers to execute sexual larvae. Evidence suggests that the pheromone is proteinaceous, stored in the poison sac and dispersed over the body via the stinger along with an attraction pheromone. Two proteins were recently isolated from the poison sac of queens which proved to be unique but homologous to two of the four proteins stored in the poison sac of conspecific workers. Evidence also suggests that the proteins may inhibit bacterial and fungal growth. Research objectives are to establish protocols for protein expression of the queen proteins and the homologous worker proteins and test the proteins for anti-microbial and pheromonal activity. Protein expression has been much more challenging than anticipated and lessons learned will be shared. Three different expression systems were used with varying results. It was determined that the best expression protocol for RIFA poison sac protein uses pEXP1-DEST RIFA constructs transformed in SHuffle™ T7 Express *lysY* competent bacterial cells. For protein purification, high pressure liquid chromatography performed cation exchange chromatography using a Mono-S FLPC column on a BioCAD Vision Workstation. Preliminary data has shown that some of these proteins have some antimicrobial ability, because after 24 hours, expression culture growth rates were significantly different ($F_{4,49} = 23.06$; $P < 0.001$), and after 24 hours the *Sol i 2w* and *q* were significantly different from *Sol i 4w* and *q* ($t_{35} = -4.46$; $P < 0.001$).

44 – CHARACTERIZATION OF SODIUM/IODIDE TRANSPORT ACTIVITY IN THYROID AND EXTRATHYROIDAL TISSUES OF THE AFRICAN CLAWED FROG *XENOPUS LAEVIS* DURING METAMORPHOSIS

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Iodide (I^-) is required for thyroid hormone synthesis and I^- deficiency severely impacts development. I^- is transported into thyroid follicle cells by the sodium iodide symporter (NIS). Transport of I^- by the NIS can be disrupted by the military waste product perchlorate, which out-competes I^- for the NIS. Given that many tissues require TH during critical periods of development, even a brief exposure to perchlorate is sufficient to adversely affect development and growth. Previous data from our laboratory suggest that there is a dramatic decrease in the sensitivity of the to perchlorate during metamorphosis in the African-clawed frog *Xenopus laevis*. Presently, nothing is known about the physiological mechanisms underlying developmental changes in the sensitivity to perchlorate. We hypothesize that changes in the availability of I^- from non-thyroid I^- transporting tissues increases during development and that increased I^- delivery to the thyroid mitigates the adverse effect of perchlorate. To support this hypothesis, we first examined which tissues express the NIS gene based upon reverse-transcriptase PCR and 24 h [^{125}I] uptake studies in stage 58-60 *X. laevis* tadpoles. RT-PCR analysis revealed that the NIS was expressed in stomach and small intestine in addition to the thyroid gland. [^{125}I] uptake studies revealed that the greatest amount of uptake was observed in the thyroid stomach followed by the lung, kidney, skin and intestine. Current work is focused on determining changes in NIS gene expression in stomach during metamorphosis, to see if increased stomach I^- transport coincides with the decrease in sensitivity to perchlorate.

45 – ANALYSIS OF *BATRACHOCHYTRIUM DENDROBATIDIS* GENE EXPRESSION IN PLANKTONIC VERSUS BIOFILM LIFE CYCLE STAGES

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Batrachochytrium dendrobatidis (Bd) is the causative agent of chytridiomycosis which has recognized as the proximate reason for amphibian decline worldwide. In previous studies, we have shown the ability of Bd to form a biofilm. In order to characterize the genes involved in the biofilm formation, we selected those that are most commonly observed to play a role in biofilm formation in fungi. These genes are, GGDEF, EAL, Zap1, ADH3, CS1, CS2, Cps1p, that play roles in biosynthesis and hydrolysis of c-di-GMP, inhibition of extracellular matrix production, regulation of chitinous cell wall production, respectively. Expression profiles of the genes were compared using biofilm and planktonic cells, through reverse transcriptase polymerase chain reaction (RT-PCR), and quantitative real-time RT-PCR analyses. Expression of the 5.8S rRNA gene was used as an internal standard. The results indicated that Cps1p, ADH3, Zap1, CS1 and CS2 genes are highly expressed in the biofilm stage being up-regulated 12-fold, 10-fold, 5-fold and 3-fold respectively. These genes are promising targets to treat chytridiomycosis by disturbing the biofilm formation and therefore survival of the Bd.

46 – DEGRADATION OF HOST LIPIDS BY *LEISHMANIA*

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Leishmania are eukaryotic parasites responsible for a spectrum of devastating diseases known as leishmaniasis. To survive and multiply, they avidly acquire nutrients including lipids from the mammalian host. Some lipid metabolites also play important roles in parasite differentiation and virulence. Recently we have demonstrated that the degradation of mammalian host sphingomyelin by *L. major* is essential for parasite growth and the manifestation of pathology. In addition to sphingomyelin, *Leishmania* may utilize other host lipids, such as phospholipids and neutral lipids. To further understand the role of lipid metabolism in parasite-host interaction, it is important to identify and characterize the enzymes involved in the uptake and turnover of host lipids. Among a family of phospholipases, we identified a single, putative phospholipase A2 (PLA2) from the *Leishmania* genome. In animals, PLA2s catalyze the production of lysophospholipids and arachidonic acid, which are precursors of potent signaling molecules. To determine its function in *Leishmania*, null mutants of PLA2 were generated and characterized in the promastigote (extracellular form) and amastigote (intracellular form) stages. Results showed that *L. major* PLA2 is synthesized in the ER and secreted, with a low but detectable activity against platelet activating factor (a powerful activator of platelet aggregation and inflammation). Although PLA2 mutants infect bone marrow-derived macrophages normally, they exhibit attenuated virulence in mice. These data suggest that PLA2 facilitates the initial delivery of *Leishmania* parasites to mammalian macrophages. Future studies will elucidate the role of phospholipases in parasite growth and virulence.

47 – UTILIZING A VIRAL GENE TOWARDS GENERATING INSECT-RESISTANT *ARABIDOPSIS* AND COTTON

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A key factor determining agricultural productivity is yield reduction due to insect pests. Approximately 14% of US crops are lost to insect pests each year. Insect resistance and environmental damage due to chemical pesticides are of increasing public concern. This has led to renewed interest in biological approaches to pest control. The use of genetically modified crops is an effective pest management strategy in agriculture. Therefore, identification of novel insecticidal genes other than Bt toxins as plant-incorporated protectants is essential. Our research group is working on viral insecticidal toxins in the generation of insect-resistant transgenic plants. Chilo iridescent virus (CIV, family *Iridoviridae*) is the only virus known to induce mortality and metamorphic deformity in the cotton boll weevil. CIV also reduces aphid populations, but does not infect mammalian cells. We have identified and isolated the CIV gene responsible for insecticidal activity and have designated it *iridoptin*. Preliminary studies by our group showed that iridoptin is responsible for apoptotic blebbing and host shutoff in insect cell lines and induces mortality in the cotton aphid, *Aphis gossypii* Glover. We wanted to test our hypothesis that over-expression of the iridoptin gene in *Arabidopsis* and cotton would confer insect resistant phenotype in transgenic plants. We have created transgenic *Arabidopsis* and cotton plants that express iridoptin and we are studying these plants in greenhouse conditions. Most updated results will be presented at the TTABSS.

48 – PREDICTING SMALL-SCALE HOTSPOTS OF RED SNAPPER (*LUTJANUS CAMPECHANUS*) ABUNDANCE FROM LARGE-SCALE SPATIALLY REFERENCED DATA

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Large-scale low-resolution monitoring data are often used to provide regional-scale information about fish abundance. Understanding factors affecting areas of abundance is especially important in species such as Red snapper (*Lutjanus campechanus*) who experience overfishing and juvenile mortality due to bycatch. We used GIS maps generated by overlaying 20 years of large-scale low resolution abundance data for juvenile red snapper and interpolating an area of 124,000 sq km from about 200-300 data points using kriging. The objective of our study was to “ground truth” the maps created using this method by selecting 1.5km x 1.5 km areas predicted by the GIS analysis to have a high probability of being a “hotspot” of high snapper abundance or a “coldspot” of low snapper abundance. Data was collected during Fall 2007 (n=4), Summer 2008 (n=8), and Summer 2009(n=6). At each site we used traps and trawls to estimate snapper abundance and sidescan sonar to map bottom features (2007 and 2009 only). In all 3 years, higher snapper abundance was found in predicted hotspots than in predicted coldspots. Similarly, more features were found in predicted hotspots than in coldspots. The results of a regression analysis indicated that the number of features was the best predictor of juvenile snapper abundance. This study indicates that commonly collected large-scale low resolution monitoring data can be effectively used to predict juvenile snapper abundance on a smaller scale. It also suggests that the presence of large numbers of bottom features is important in juvenile snapper habitat selection.

49 – ROLE OF THYROID HORMONES IN GONADAL SEX DIFFERENTIATION OF ZEBRAFISH

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Our objective is to determine if the previously shown influence of thyroid hormones (TH) on gonadal sex differentiation of larval- juvenile zebrafish persists into sub-adult stages. Three-day postfertilization (dpf) larvae were reared for 30 days in control (reconstituted water), 100 ppm perchlorate, 0.15 and 0.3 mM methimazole, and 1 and 10 nM TH (T4) solutions. Perchlorate and methimazole are TH synthesis inhibitors. Standard length (SL), head depth, head length, pectoral fin length (PFL) and sex ratio were determined at 45 and 60 dpf. Sex ratios were biased toward male in the TH treatments and towards female in the perchlorate treatment at both sampling dates. Methimazole treatments biased sex ratios toward females only at 45 dpf. TH synthesis inhibitors trended to reduce, and T4 increased, PFL (corrected for SL) at both sampling dates. At 60 dpf, the only morphometric effect was a reduced SL in all treatments relative to control. In conclusion, TH dictates the direction of gonadal sex differentiation but, unlike their effect on development (PFL), the persistence of the effects of thyroid inhibitors on sex ratios differed between inhibitors. This differential response may be a useful tool for further study of the mechanisms of sex ratio regulation by TH.

50 – CAUSE-SPECIFIC MORTALITY OF MULE DEER (*ODOCOILEUS HEMIONUS*) FAWNS IN CENTRAL ARIZONA

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Neonatal mortality is a major factor driving desert mule deer (*Odocoileus hemionus*) population dynamics. The objective of our study was to determine specific causes and timing of mule deer adult and fawn mortalities in central Arizona. We captured 52 adult female desert mule deer in Gila County, Arizona in 2007 and 2008. We equipped pregnant females with vaginal implant transmitters to aid in capturing fawns quickly after birth. Survival analyses were performed with Program MARK (5.1) and models were compared with AICc (Akaike Information Criterion). Annual survival rate of adult females was 0.81. Of 49 adults, 7 died and 6 were killed by predators. We captured 44 desert mule deer fawns and annual fawn survival was 0.099. Predation was the major cause of mortality (64% of all mortalities). Fawn survival was lowest in the first month (0.442). Early survival (days 1–100) was 0.293. We recommend that predation be considered in mule deer population control strategies in central Arizona.

51 – INTRODUCTION AND ESTABLISHMENT OF THE EASTERN GRAY SQUIRREL (*SCIURUS CAROLINENSIS*) IN NOVA SCOTIA, CANADA.

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The Eastern gray squirrel, *Sciurus carolinensis*, is one of the most recognized and abundant sciurids in North America. Historically restricted to Eastern North America, gray squirrels are continuing to expand their geographic range westward. Human-sponsored introductions have also greatly facilitated the range extension of gray squirrels across North America and around the world, often resulting in significant negative impacts to the integrity of native ecosystems. Since the 1930s, apparently isolated sightings of Eastern gray squirrels in Nova Scotia, Canada have been attributed to captive releases or escapes. Despite reports of multiple introduction events over the past decades, many scientists believe the species has not become established in the province. However, our recent trapping efforts have demonstrated otherwise, and have resulted in the first (3) voucher specimens recorded for the province. These specimens provide first evidence that the Eastern gray squirrel is now present as a wild breeding mammal in Nova Scotia, Canada. Although the future ecological impact of the Eastern gray squirrel in Nova Scotia is unknown, it seems likely that this species will continue to expand its range and increase in abundance in the province in the decades ahead. We discuss the biological impacts of this highly adaptable species in non-native habitats.

52 – HETEROSPECIFIC ALARM CALL RECOGNITION AND UTILIZATION IN TIME AND SPACE

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One of the strongest selective pressures on an organism is predation. Due to this strong pressure, eavesdropping on heterospecific alarm calls may provide an animal additional information about the presence of potential predators. However, all of our current knowledge about heterospecific eavesdropping on alarm calls have used traditional vigilance measures (i.e., head raises or scan rate) as a measure of an individual's perceived predation risk. While these measurements are valuable, they are only able to provide information about perceived predation risk at a single moment in time and point in space. Optimal foraging theory provides a technique, called giving-up-densities, which can be used to quantify perceived predation risk over time and space. Gray duiker are small, nocturnal antelope found in sub-Saharan Africa. Gray duiker occur sympatrically and share the same predators as another antelope species, the bushbuck, which produce an alarm call specific to leopards. I conducted a playback experiment to test if gray duiker recognize and utilize heterospecific alarm calls in adjusting their perceived predation risk in times and space, collecting giving-up-densities and traditional vigilance measures. This research is crucial to determine if reaction to heterospecific alarm calls truly have ecological consequences. This study of heterospecific information transfer will also yield a greater understanding of the complexity of animal communication networks and increase our knowledge of how animals assess risk in their environment.

53 – POPULATION-LEVEL EFFECTS OF CO-INFECTION BY *BARTONELLA* AND INTESTINAL NEMATODES IN *PEROMYSCUS LEUCOPUS*

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Parasites are ubiquitous in nature, can have negative effects on the fitness of their host, and are strong selective forces for the dynamics of natural populations. In addition, recent evidence suggests that parasites can alter host immunity by reducing their ability to mount effective immune responses, which may also be crucial for the health of wild populations. However, much of this work has focused on single parasite infections, even though most hosts are infected with multiple parasites. The consequences of ‘co-infection’ may be very important for the immune response and health of the hosts, however we still know very little about how co-infections can affect host population dynamics. There is a suspected interaction between intestinal nematodes and *Bartonella*, a blood parasite, found in *Peromyscus* in the Appalachian Mountains. This interaction is thought to occur via the host immune system. A mark-recapture study of *Peromyscus* was conducted at Mountain Lake Biological Station in 2010. There are at least 8 common intestinal parasites known in this population, as well as 2 blood parasites. Co-infection is common in these populations, so mice were treated to remove intestinal nematodes to observe the effects on the parasite community. Blood samples were collected from all captured mice, and 85% of samples analyzed were infected with *Bartonella*. Treated individuals were recaptured significantly less over the course of the season than mice that received a control treatment, possibly as a result of interactive effects of nematode removal in conjunction with *Bartonella* infection.

54 – PUBLIC INFORMATION USE IN A GROUND-NESTING SONGBIRD COMMUNITY

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The territory a bird chooses to breed in can have large and direct effects on the bird’s fitness. Birds can use social cues emitted by other organisms to gather public information as an indicator of territory quality. Public information can accurately reveal territory quality by advertising the inhabitants’ reproductive success. I am studying the use of public information in the veery, *Catharus fuscescens*, and its effect on community assembly. I hypothesize that veery fledgling vocalizations produced during the post-breeding season are public information cues used by veeries and heterospecific ground-nesting songbirds for territory selection in subsequent breeding seasons. To test this, I played veery fledgling vocalizations and silent controls at plots during the post-breeding season in 2009. In 2010, response data (nest distances to nearest plot, nest counts at each plot, and settlement dates) was collected and treatments were replicated for data collection in summer 2011. Currently, results show that veeries are more likely to occupy treatment plots relative to control plots. Additionally, veeries settled at treatment plots one week earlier compared to control plots, but this trend is not significant. In contrast, heterospecifics were more likely to occupy and settle earlier at control plots relative to treatment plots. Current data suggest that veeries show a trend towards using public information to select breeding territories, while heterospecifics are not using public information as hypothesized. My study is

the first to address how public information influences community assembly by monitoring how heterospecifics respond to social cues when selecting their breeding territories.

55 – AGO2 CLEAVAGES A PRE-MIRNA IN A RISC-LIKE MODE

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microRNAs (miRNAs) are a group of small RNAs that can negatively regulate the expression of proteins at post-transcriptional level. The maturation of miRNAs requires many critical enzyme complexes, one of them is Dicer. However, recent studies have shown that Dicer is not always required for miRNA processing; Argonaute 2 (AGO2) is an alternate protein that can cleave miRNAs precursors (pre-miRNAs) into mature miRNAs. Those miRNAs that are produced by AGO2 are called ago2-miRNAs. One of the most validated features of the ago2-miRNAs is that they are highly expressed in dicer-mutated samples and limited/no production from ago2-mutated models. Here, by comparing to the normal miRNAs, we found many unique features of ago-miRNAs. These include: 1) five more times of sRNAs were found from one single pre-miRNAs, and the number is length-sensitive; 2) Unlike normal miRNAs, both ~22-nt and ~26-nt were highly expressed among ago-miRNAs; 3) the start positions of ago-miRNAs in one pre-miRNAs are widely varies, which of normal miRNAs was pre-determined. We hypothesized a RISC-like cleavage mode is applied in ago-miRNAs production, and presented a novel AGO2 processing model to express the process.

56 – SPHINGOLIPID DEGRADATION IN *LEISHMANIA* VIRULENCE

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Leishmaniasis is a group of serious diseases caused by protozoan parasites of the genus *Leishmania*. These organisms alternate between flagellated promastigotes in the midgut of sandflies and non-flagellated amastigotes in the phagolysosome of mammalian macrophages. Current drugs are plagued with low efficacy and high toxicity, and no safe vaccine is available. To overcome these challenges, it is vital to develop new drugs and identify new molecular targets. A promising source of potential targets is the sphingolipid metabolism. In many eukaryotes, sphingolipids are critical membrane components and precursors for signaling molecules. *Leishmania* contains two abundant types of sphingolipids: inositol phosphoceramide (IPC) which is synthesized *de novo* by the parasites and sphingomyelin (SM) which is salvaged from the mammalian host. A single enzyme called ISCL (Inositol phosphoSphingolipid phospholipase C-Like protein) is responsible for the degradation of both parasite-derived IPC and host-derived SM. ISCL shows elevated expression and altered localization as promastigotes differentiate into amastigotes. Interestingly, null mutants of ISCL (*iscl*⁻) exhibit increased sensitivity to acidic pH as promastigotes and a complete loss of virulence as amastigotes. Therefore, sphingolipid degradation plays important roles in both the vectorial and mammalian stages of *Leishmania*. Future studies will elucidate the molecular mechanism by which ISCL contributes to parasite virulence, which will ultimately lead to the development of selective inhibitors against this enzyme.

57 – AN INTRINSIC CRF SIGNALING PATHWAYS IN THE OPTIC TECTUM

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Corticotropin-releasing factor (CRF) is a 41 amino acid peptide that is best known as the principle hypophysiotropic hormone regulating the pituitary-adrenal axis during stress. CRF also regulates many stress and anxiety related behaviors including food intake, and over-expression of CRF is thought to be the main causative agent in anxiety related eating disorders such as anorexia nervosa. Recent data collected in our lab using amphibian models indicate that in addition to affecting appetite, CRF may modulate visual sensory pathways involved in detecting and responding to food. Here we examine the hypothesis that CRF directly modulates sensorimotor processing in the optic tectum, the major site for integration of visually guided behavior in the amphibian brain. In the African clawed frog *Xenopus laevis*, RT-PCR revealed that cells in the tectum express mRNA for CRF and the CRF R1 receptor but not the CRF R2 receptor. Immunocytochemical analysis revealed that CRF neurons are interneurons located in tectal cell layers 6 and 8, with dendrites projecting to retinorecipient tectal layers. In vitro studies revealed that CRF is released from tectal neurons under depolarizing conditions. Receptor binding studies indicate that binding of radiolabeled CRF to tectal membranes can be displaced by the CRF R1 selective antagonist NBI 27914. We conclude that the optic tectum possesses a CRF signaling system that may be involved in modulating communication between sensory and motor pathways involved in food intake.

58 – MOLECULAR AND BIOCHEMICAL RESPONSES OF AN AMPHIBIAN PATHOGEN *BATRACHOCHYTRIUM DENDROBATIDIS* UPON EXPOSURE TO THYROID HORMONE

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Amphibians are disappearing worldwide at an increasing rate. One of the major contributing factors to amphibian decline is the chytrid fungus *Batrachochytrium dendrobatidis* (Bd), which infects the skin of metamorphosed amphibians. Infected animals suffer from hyperkeratosis where the epidermal layer of the animal thickens and may be sloughed. Microscopy of infected tissue has demonstrated the intracellular localization of fungal reproductive structures, sporangia. While we know that the fungus is capable of motility towards proteins, amino acids and specific hormones, we do not fully understand how the fungus detects the host or the molecular and biochemical responses of the fungus to the host. Thyroid hormone (TH) plays an essential role in amphibian metamorphosis. TH binds to cognate receptors leading to transcriptional activation of genes involved in the transition of tadpoles into young adults. Bd infects the keratinized mouthparts of tadpoles, but these infections are non-lethal. We hypothesize that the presence of Bd in tadpoles results in their exposure to TH inducing virulence gene expression in the fungus. Using quantitative PCR, we observed the expression of genes involved in cell wall biogenesis, and pathogenicity in Bd following exposure to TH. Using two-dimensional gel electrophoresis, we observed changes in the expression of proteins involved in cell polarity, G-protein signaling and survival under stress conditions in Bd. These studies suggest that TH might be an important factor in triggering virulence gene expression in Bd.

AUTHOR INDEX BY ABSTRACT NUMBER

A

Abdullah, M. 11
Acosta-Martinez, V. 29
Alcumbrac, O. 50
Altenberg, G. 8
Amman, B. 32
Anaya, M. 12
Anwarali Khan, F. 11
Armstrong, A. 1
Arner, A. 2
Artigas, P. 1

B

Baker, K. 28
Baker, R. 10, 11, 13, 36
Ballard, W. 40, 50
Balyimez, A. 42
Bashyal, A. 12
Beatty, L. 3
Bernal, X. 2, 3, 6
Bilimoria, S. 47
Bohara, M. 21
Bradley, R. 32, 33, 35
Brant, J. 27
Brewer, W. 4

C

Cariappa, C. 50
Carr, J. 22, 44, 57
Carrera-E., J. 13
Carty, N. 45
Chalise, P. 21
Chaudhari, N. 21
Chen, J. 17
Clinton, A. 5
Corley, M. 32
Cromie, M. 22

D

Dagda, M. 25
de Silva, P. 6
de Vos, Jr., J. 50
Densmore, L. 12, 34, 55
Deslippe, R. 43
Dhungana, G. 21
Dhungana, N. 29
Diamond, S. 48
Dimaki, M. 34

E

Elias, N. 30

F

Ferguson, A. 31
Fokar, M. 58

G

Gaetani, M. 14
Ganapathy, S. 47
Gonzales, J. 7
Graham, A. 53
Granot, D. 25
Griffith, K. 26
Guvvala, H. 37

H

Hamood, A. 42, 45
Hashim, R. 30
Haynie, M. 33
He, Zhiyu 16
Holaday, A. 16, 25, 37
Hopper, T. 48
Hu, R. 17
Huang, J. 38
Huynh, H. 51

I

Iñigo, M. 7
Ivanova, M. 25

J

Jaramillo, C. 6
Jazdzzyk, E. 38
Jia, F. 18
Jiang, Y. 19

K

Kandel, N. 21
Kandel, Y. 21
Kelly, J. 54
Kingston, T. 30, 38
Knowles, S. 53
Krausman, P. 50
Krishnan, S. 8
Kuczynski, A. 52

L

Lackey, R. 9
Layland, N. 20
Lewis, P. 10
Lockwood, S. 43

M

Maryanto, I. 11, 38
Mauldin, M. 33
McAlpine, D. 51
McDonough, M. 10
McIntyre, N. 28
Mishra, N. 23
Mitchell, E. 27
Mittal, M. 24
Mukherjee, T. 25
Murali, S. 44

N

Nusalawo, M. 38

O

O'Brien, C. 50

P

Parlos, J. 36
Pasham, M. 58
Patiño, R. 41, 49
Pawlowic, M. 46
Payton, P. 24
Pedersen, A. 53
Perry, G. 12
Peterson, A. 31
Phillips, C. 13
Platt, R. 32

Q

Qaisar, U. 45
Quiñones-Magalhães, R. 39

R

Rayner, S. 55
Rock, C. 18, 19
Rodgers, B. 26
Roussos, S. 34
Rowell, E. 33
Rumbaugh, K. 5
Rylander, K. 4

S

Salice, C. 41
Samanta, M. 19
San Francisco, M. 42, 45, 58
San Francisco, S. 58
Schmidt, K. 15, 52, 54
Schwalm, D. 40
Schwilk, D. 4, 39
Sharma, P. 49
Shen, G. 47
Silva, W. 45
Smith, E. 22, 44, 57
Sotero-Caio, C. 10
Stangl, Jr., F. 35
Strauss, R. 31, 53
Suski, J. 41

T

Tatman, N. 50
Thekkiniath, J. 58
Thies, M. 10
Thomason, C. 53
Thompson, C. 35
Thorington, Jr., R. 51
Tomovic, L. 34
Tswiio, M. 10

U**V**

van Gestel, N. 29
Velten, J. 20

W

Wages, M. 22, 44, 57
Waits, L. 40
Wallace, M. 50
Waring, E. 16
Watson, E. 15
Watters, C. 5
Wijaya, F. 11
Williams, G. 51
Wu, Y. 55

X

Xu, W. 56

Y**Z**

Zak, J. 29
Zhang, B. 57
Zhang, H. 17, 23, 47
Zhang, K. 46, 56
Zhang, O. 56
Zhu, Y. 17
Zoghbi, M. 8

NOTES