



TEXAS TECH  
ANNUAL BIOLOGICAL  
SCIENCES SYMPOSIUM

Texas Tech University  
Department of Biological Sciences  
Lubbock, Texas  
February 5-7, 2010

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Keynote address by  
John Zak, Ph.D.  
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Texas Tech Annual Biological Science Symposium  
Jones AT&T Stadium, Club Level  
Lubbock, Texas  
February 6, 2010

## **Special Acknowledgements**

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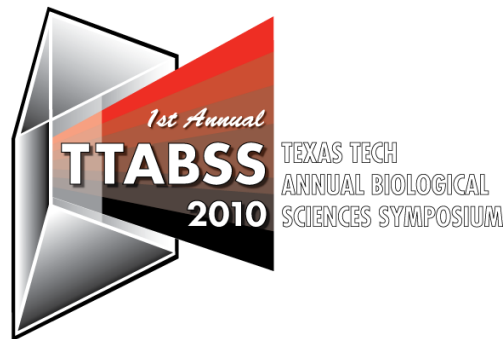
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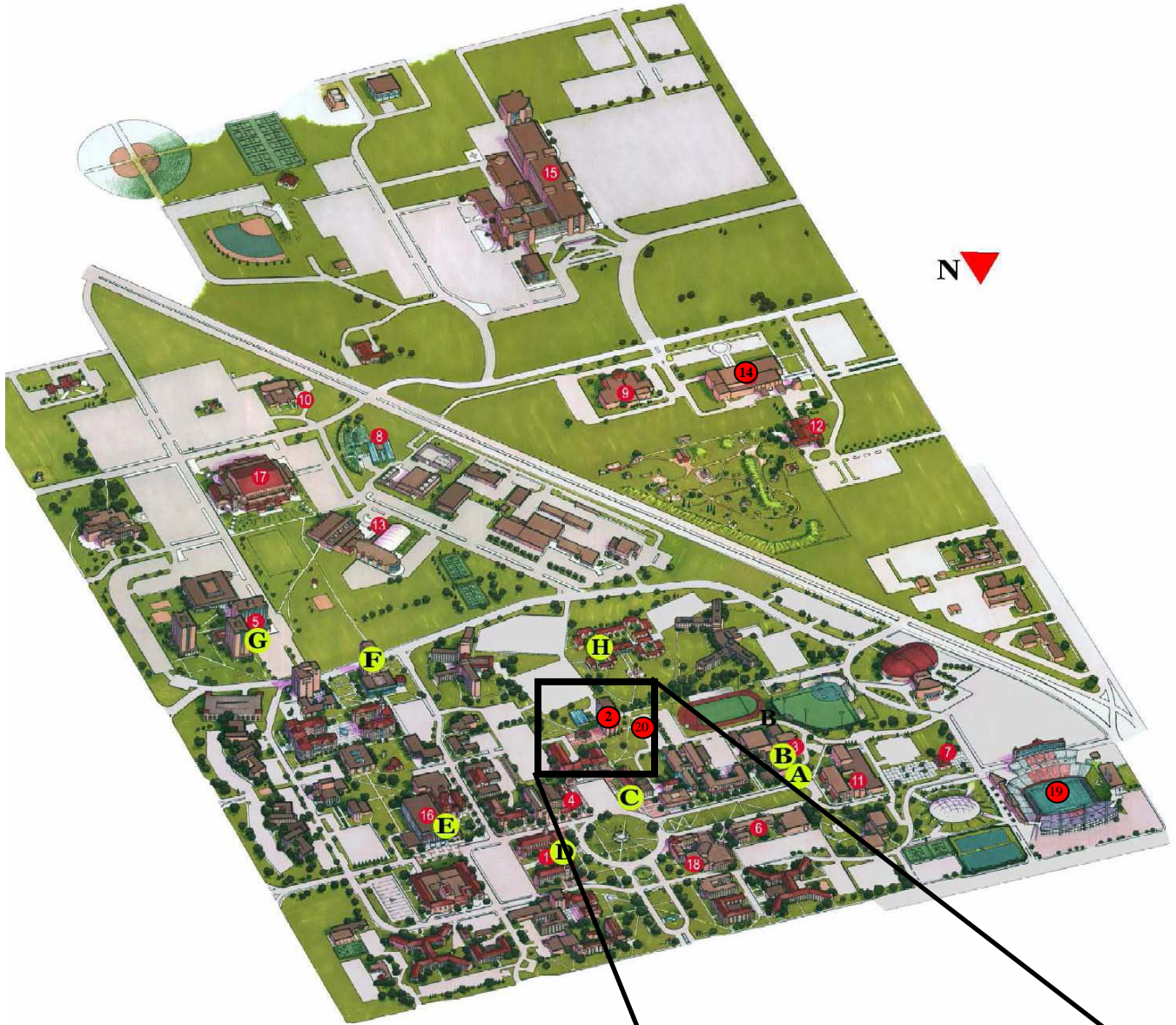
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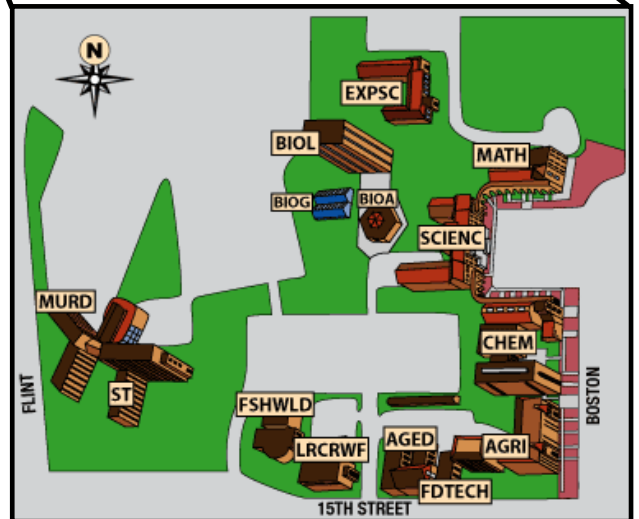
# Texas Tech University Campus Map



- 2** Biological Sciences Building
- 14** Texas Tech Museum (Natural Sciences Research Laboratory)
- 19** Jones AT&T Stadium
- 20** Experimental Sciences Building

**BIOL-** Biological Sciences Building

**EXPSC-** Experimental Sciences Building



**TEXAS TECH ANNUAL BIOLOGISTS SCIENCES SYMPOSIUM  
1<sup>ST</sup> ANNUAL MEETING  
5-7 FEBRUARY 2010  
TEXAS TECH UNIVERSITY, LUBBOCK, TEXAS**

**Schedule of Events**

<b>Friday, 5 February</b>	
<b>5:00pm – 8:00pm</b>	<b>Registration, EXPSC Lobby</b>
<b>5:00pm – 8:00pm</b>	<b>Vendor Show, Welcoming Reception, EXPSC Lobby</b>
<b>Saturday, 6 February</b>	
<b>8:00am – 8:30am</b>	<b>Continental Breakfast- Biology Lobby</b>
<b>8:30am – 9:00am</b>	<b>Welcome- BIOL 100</b>
<b>9:00am – 10:30am</b>	<b>Presentation Sessions- BIOL 101, BIOL 106, EXPSC 120</b>
<b>10:30am – 10:45am</b>	<b>Break- Biology Lobby</b>
<b>10:45am – 12:15pm</b>	<b>Presentation Sessions- BIOL 101, BIOL 106, EXPSC 120</b>
<b>12:15pm – 1:45pm</b>	<b>Lunch on your own</b>
<b>1:45pm – 3:00pm</b>	<b>Presentation Sessions- BIOL 101, BIOL 106</b>
<b>3:00pm – 3:15pm</b>	<b>Break- Biology Lobby</b>
<b>3:15pm – 5:15pm</b>	<b>Presentation Sessions- BIOL 101, BIOL 106</b>
<b>5:20pm</b>	<b>Closing Remarks- BIOL 100</b>
<b>7:00pm – 9:00pm</b>	<b>Banquet- Club Level, Jones AT&amp;T Stadium</b>
<b>Sunday, 7 February</b>	
<b>10:00am-12:00pm</b>	<b>Natural Sciences Research Laboratory Tour Courtesy of Heath Garner, Museum of Texas Tech University</b>



<b>Saturday AM</b>	<b>I. PROPOSAL</b> Room Biology 101	<b>II. ECOLOGY/CONSERVATION</b> Room Experimental Sciences 120	<b>III. MICROBIOLOGY</b> Room Biology 106
9:00	1- ASSESSING WATERSHED CONTROLS ON ODONATE DISTRIBUTION. <b>Steven D. Collins</b> and Nancy E. McIntyre	7- PATTERNS OF DISTRIBUTION OF THE ENDEMIC MAMMALS IN ECUADOR. <b>Juan P. Carrera-E.</b> and Hugo Mantilla-Meluk	13- THE DIFFERENTIAL CHITIN SYNTHASE ACTIVITY OF <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> AS A VIRULENCE FACTOR IN THE INFECTION OF AMPHIBIANS. <b>Adam M. Lord</b> and Michael San Francisco
9:15	2- AN AXIOMATIC THEORY FOR STOCHASTIC EVOLUTION IN MULTIPLE TRAITS WITH IMPLICATIONS FOR VARIATION IN HERITABILITY IN DIFFERENT ENVIRONMENTS. <b>John R. Harting</b>	8- A PREDICTIVE MODEL OF NON-VOLANT SMALL MAMMAL ASSEMBLAGES IN EASTERN PARAGUAY ATLANTIC FOREST REMNANTS. <b>Noé U. de la Sancha</b> and Richard E. Strauss	14- INVESTIGATING THE ROLE OF DNASE IN THE PATHOGENICITY CAUSED BY <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> IN AMPHIBIANS. <b>Priyanka Maiti</b> and Michael. J. San Francisco
9:30	3- ECOLOGICAL SERVICES PROVIDED BY INSECTIVOROUS BATS IN PALEOTROPICAL RAINFOREST AND AGROFOREST SYSTEMS: A FUNCTIONAL DIVERSITY STUDY. <b>Chun Chia Huang</b> and Tigga Kingston	9- EFFECT OF FEMALE BODY SIZE ON FITNESS IN DAMSELFLIES. <b>Kelly S. Baker</b> and Nancy E. McIntyre <sup>9</sup>	15- EXTRACELLULAR NUCLEASE DNSH IN AEROMONAS STRAIN. <b>Roopa Pulijala</b>
9:45	4- HETEROSPECIFIC INFORMATION TRANSFER OF ALARM CALLS IN GREY DUIKER ( <i>SYLVICAPRA GRIMMIA</i> ). <b>Amy M. Kuczynski</b> and Kenneth A. Schmidt	10- FUNCTION OF POISON SAC PROTEINS FROM QUEEN RED IMPORTED FIRE ANTS (FORMICIDAE: <i>SOLENOPSIS INVICTA</i> ). <b>Stephanie A. Lockwood</b> , Mohammed Fokar, and Richard J. Deslippe	16- HANTAVIRUS NATURAL RESERVOIR ABUNDANCE, SEROEPIDEMIOLOGY AND ARARAQUARA HANTAVIRUS AMONG WILD RODENTS IN SOUTHEASTERN BRAZIL. <b>Gilberto Sabino-Santos Jr.</b> , Felipe G. M. Maia, Glauciane G. Figueiredo, Alex M. Machado, Jorge Salazar-Bravo and Luiz T. M. Figueiredo
10:00	5- REDUCED NIMA RELATED KINASE 2 (NEK2) EXPRESSION LEVEL ENHANCES PACLITAXEL SENSITIVITY IN THE BREAST CANCER CELLS. <b>Jaehyung Lee</b> and Lauren Gollahon	11- CHOERONYCTERINE BATS AS A MODEL TO STUDY GLOBAL CLIMATE CHANGE AMONG MAMMALS. <b>Hugo Mantilla-Meluk</b>	17- MOLECULAR RESPONSES OF AN AMPHIBIAN PATHOGEN <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> UPON EXPOSURE TO THYROID HORMONE. <b>Jose C. Thekkiniath</b> , Mithun R. Pasham, Mohammed Fokar, and Michael J D. San Francisco
10:15	6- GENETIC REQUIREMENTS FOR STABILITY OF RAV1 TRANSCRIPT ENCODING A TRANSCRIPTION FACTOR THAT POSITIVELY REGULATES ABA SIGNALING. <b>Amandeep Mittal</b> , Qingjun Luo, and Chris D. Rock	12- GENETIC AND STABLE ISOTOPE ANALYSIS OF A POTENTIALLY NOVEL COLONY OF <i>TADARIDA BRASILIENSIS</i> MEXICANA IN WEST TEXAS. <b>Jennifer J. Miller</b> , Raymond S. Matlack, and Brenda E. Rodgers	
10:30	Break Biology Lobby	Break Biology Lobby	Break Biology Lobby

<b>Saturday AM</b>	<b>I. PROPOSAL</b> Room Biology 101	<b>II. ECOLOGY/CONSERVATION</b> Room Experimental Sciences 120	<b>IV. CELL/MOLECULAR BIOLOGY</b> Room Biology 106
10:45	18- SEQUENCE VARIATION OF MICRORNA BINDING SITES IN PLANTS. <b>Fangqian Ou-Yang</b> , Qing-Jun Luo, Casey R. Richardson, and Christopher D. Rock	24- SMALL MAMMAL ASSEMBLAGES FROM NATURAL AND MODIFIED HABITATS IN A CLOUD FOREST RESERVE, GUATEMALA. <b>Nicté Ordóñez-Garza</b> and Ana L. Grajeda	30- THE INFLUENCE OF ESTROGEN RECEPTORS ON THE TRANSCRIPTION AND EXPRESSION OF THE BREAST CANCER METASTASIS GENE 1 (BRMS1). <b>Hongtao Ma</b> and Lauren Gollahon
11:00	19- VOLANT VIRUSES: ARE CAVE-ROOSTING BATS AT GREATER RISK? <b>Kendra L. Phelps</b> , Akbar Zubaid, and Tigga Kingston	25- AN EVALUATION OF FECAL DNA PRESERVATION TECHNIQUES AND EFFECTS OF SAMPLE AGE AND DIET ON GENOTYPING SUCCESS. <b>Michael Panasci</b> , Warren Ballard, David Wester, Stewart Breck, David Rodriguez, Llewellyn Densmore, and Robert J. Baker	31- DETERMINING POPULATION GENETIC STRUCTURE OF <i>LYGUS HESPERUS</i> FROM TEXAS HIGH PLAINS USING SIMPLE SEQUENCE REPEAT MARKERS. <b>Ram B. Shrestha</b> , Megha N. Parajulee, Michael J. D. San Francisco, Lou D. Densmore, Richard E. Strauss, Mark D. Burrow, and A. Scott Holaday
11:15	20- ROLE AND MECHANISMS OF ACTION OF THYROID HORMONE DURING GONADAL SEX DIFFERENTIATION IN ZEBRAFISH ( <i>DANIO RARIO</i> ). <b>Prakash Sharma</b> and Reynaldo Patiño	26- BITE FORCE ANALYSIS OF RAINFOREST INSECTIVOROUS BATS. <b>Juliana Senawi</b> , Björn Siemers, Daniela Schmieder, Rosli Hashim, and Tigga Kingston	32- DEGRADATION OF HOST SPHINGOMYELIN IS ESSENTIAL FOR <i>LEISHMANIA</i> VIRULENCE <b>Ou Zhang</b> , Mattie C. Wilson, Wei Xu, Fong-Fu Hsu, John Turk, F. Matthew Kuhlmann, Yingwei Wang, Lynn Soong, Phillip Key, Stephen M. Beverley, and Kai Zhang
11:30	21- PROPOSAL FOR STUDYING THE PHYLOGEOGRAPHY OF <i>VIPERA AMMODYTES</i> ON THE CYCLADIC ISLANDS OF GREECE. <b>Stephen A. Roussos</b> and Llewellyn Densmore	27- THREE'S COMPANY: CO-INFECTION IN <i>PEROMYSCUS</i> . <b>Courtney A. Thomason</b>	
11:45	22- ECOLOGICAL EFFECTS OF AN INVASIVE ALGA, <i>PRYMNESIUM PARVUM</i> , ON AQUATIC COMMUNITIES. <b>Jamie G. Suski</b>	28- THE ROLE OF DAILY SOIL TEMPERATURE FLUCTUATIONS ON MICROBIAL AND NITROGEN DYNAMICS IN A CHIHUAHUAN DESERT CREOSOTE BUSH BAJADA. <b>Natasja C. van Gestel</b> , Stephen Cox, Richard E. Strauss, Dylan Schwilk, David T. Tissue, and John C. Zak	
12:00	23- COIBA RESEARCH AND EDUCATION PROJECT. <b>Miryam Vengas-Anaya</b> , Llewellyn Densmore D III, Oris Sanjur, and Eldredge Bermingham	29- DISTRIBUTION AND HABITAT SELECTION OF ENDANGERED WARM SPRINGS PUPFISH ( <i>CYPRINODON NEVADENSIS PECTORALIS</i> ) WITHIN A DESERT SPRING REFUGE. <b>Darrick S. Weissenfluh</b> , Gene R. Wilde, and Cristi R. Baldino	
12:15-1:45	Lunch on your own		

Saturday PM	V. SYSTEMATICS & EVOLUTIONARY BIOLOGY Room Biology 101	VI. PLANT BIOLOGY Room Biology 106	
1:45	33- EXTREME PARAPHYLY AND SPECIATION WITHIN A CRYPTIC SPECIES COMPLEX: BULLDOG BATS (CHIROPTERA: NOCTILIONIDAE) REVISITED. <u>Faisal A. Anwarali Khan</u> , C. Miguel Pinto, and Robert J. Baker	38- LINKING CARBOHYDRATE CONTENT AND GENE EXPRESSION FOR SEASONAL CARBOHYDRATE METABOLISM IN THE XYLEM (WOOD) OF <i>POPULUS</i> SPECIES. <b>Jayasri Alluvada</b>	
2:00	34- EXAMINING THE ROLE OF THE TRANSFERRIN-RECEPTOR 1 (TfR1) GENE AS THE HOST CELLULAR RECEPTOR FOR NORTH AMERICAN ARENAVIRUSES. <b>Sheri B. Ayers</b> and Robert D. Bradley	39- THE EFFECT OF NITROGEN AVAILABILITY ON PHOTOSYNTHESIS OF THE INVASIVE GRASS <i>PHALARIS ARUNDINACEA</i> . <b>Hasitha Guvvala</b> , Dr.A.S.Holaday	
2:15	35- DISTRIBUTION OF REPETITIVE ELEMENTS ON <i>DESMODUS ROTUNDUS</i> CHROMOSOMES. <b>Cibele G. Sotero-Caio</b> , LuAnn Scott, Holly A. Wichman , and Robert J. Baker	40- CO-REGULATION OF MIR842 AND MIR846 POLYCYSTRONIC MIRNAS ON THEIR TARGET GENE AT5G28520 IN RESPONSE TO ABA. <b>Fan Jia</b> , Gary R. Larson, Qing-Jun Luo, and Chris Rock	
2:30	36- MOLECULAR RELATIONSHIPS WITHIN THE NEOTOMINAE BASED ON COMBINED MITOCHONDRIAL AND NUCLEAR DNA SEQUENCES. <b>Megan S. Corley</b> , Roy N. Platt, Brian R. Amman, and Robert D. Bradley	41- THE ARABIDOPSIS ANKYRIN REPEAT-CONTAINING PROTEIN 2A IS AN ESSENTIAL MOLECULAR CHAPERONE FOR THE BIOGENESIS OF APX3 AND IT PLAYS AN IMPORTANT ROLE IN PLANT GROWTH AND DEVELOPMENT. <b>Sundaram Kuppu</b> , Guoxin Shen, and Hong Zhang	
2:45	37- GENETIC VARIATION AND PHENOTYPIC EVOLUTION IN THE LESSER ANTILLEAN TREE BAT ( <i>ARDOPS NICHOLLSI</i> ). <b>Roxanne J. Larsen</b> , Peter A. Larsen, Hugh H. Genoways, Gary G. Kwiecinski, Scott C. Pedersen, and Robert J. Baker	42- A FEEDBACK REGULATORY LOOP INVOLVING <i>PAP1/MYB75</i> AND MIR828/TAS4 IN RESPONSE TO SUGAR IN <i>ARABIDOPSIS</i> . <b>Qing-Jun Luo</b> , Hong-Liang Zhu, Fan Jia, and Chris Rock*	
3:00	Break Biology Lobby	Break Biology Lobby	Break Biology Lobby

<b>Saturday PM</b>	<b>V. SYSTEMATICS &amp; EVOLUTIONARY BIOLOGY</b> Room Biology 101	<b>VII. ANIMAL &amp; HUMAN PHYSIOLOGY</b> Room Biology 106	
3:15	43- MOLECULAR EVIDENCE FOR HYBRIDIZATION BETWEEN <i>NEOTOMA MICROPUS</i> AND <i>N. FLORIDANA</i> . <b>Matthew R. Mauldin</b> , Robert D. Bradley, J. Delton Hanson, and Robert J. Baker	50- POTENTIAL ROLE OF THE SYMPATHETIC NERVOUS SYSTEM IN MEDIATING THE CARDIOVASCULAR ACTIONS OF CRF-R2 RECEPTORS. <b>Richard A. Larson</b> and James A. Carr	
3:30	44- MIGRATION OF <i>ARTIBEUS JAMAICENSIS</i> AMONG THE U.S. VIRGIN ISLANDS. <b>Julie A. Parlos</b> , Gary G. Kwiecinski, and Robert J. Baker	51- EVIDENCE FOR EVOLUTIONARY REDUCTIONS IN BOTH THE LIGAND AND RECEPTOR THAT REGULATE RAPID SKIN DARKENING IN THE TEXAS TOAD, <i>BUFO SPECIOSUS</i> . <b>Sharanya Murali</b> , Bo Zhang, Anusha Kumar, Richard Larson, Cary Brown, James A. Carr	<b>VIII. OTHER</b> Room Biology 106
3:45	45- MORPHOMETRIC ASSESSMENT OF THE <i>MICRONYCTERIS MEGALOTIS</i> COMPLEX (CHIROPTERA: PHYLLOSTOMIDAE): SEARCHING FOR GEOGRAPHIC STRUCTURE. <b>Lizette Siles</b> and Robert J. Baker		56- INTRINSIC NEURONS CONTRIBUTE TO CRF INNERVATION OF THE ANURAN OPTIC TECTUM. <b>Bo Zhang</b> , Sharanya Murali, Richard Larson, Nafissa Ahmed, Omar Shoukfeh, Sarah Bulin, Nicholas Bergfeld, Jacob Lustgarten, James A. Carr
4:00	46- PRELIMINARY DATA ON THE PHYLOGEOGRAPHY OF THE THIRTEEN-LINED GROUND SQUIRREL ( <i>SPERMOPHILUS TRIDECEMLINEATUS</i> ). <b>Cody W. Thompson</b> and Robert D. Bradley		57- MIRPARA: A SVM-BASED SOFTWARE TOOL FOR PREDICTION OF MATURE MICRORNAS. <b>Yonggan Wu</b> , Haizhou Liu, Tianxian Li, Simon Rayner
	<b>IX. TOXICOLOGY</b> Room Biology 101	<b>X. UNDERGRADUATE</b> Room Biology 106	
4:15	47- CHERNOBYL LOW-DOSE RADIATION IS PROTECTIVE <i>IN-UTERO</i> : A MECHANISTIC INVESTIGATION USING RT-PCR. <b>Eric K. Howell</b> , Sergey P. Gaschak, Brenda E. Rodgers	52- GENETIC CHARACTERIZATION AND NATURAL HOST RELATIONSHIPS OF MULESHOE VIRUS IN NORTH TEXAS AND WESTERN OKLAHOMA. <b>Allie P. Clinton</b> , Robert D. Bradley, Mary Louise Milazzo, Charles F. Fulhorst	
4:30	48- A FIELD AND LABORATORY ASSESMENT OF THE EFFECTS OF MERCURY ON SNAKE BEHAVIOR. <b>David A. Kimberly</b>	53- ABSCISIC ACID REGULATES MICRORNA 842/846: IMPLICATIONS FOR PREDICTED TARGET GENE AT5G28520 FUNCTION AND MIRNA EVOLUTION. <b>Gary R. Larson</b> , Fan Jia, and Chris D. Rock	
4:45	49- MERCURY CONTAMINATION IN WETLANDS ASSOCIATED WITH COAL-FIRED POWER PLANTS. <b>Scott M. Weir</b> , Richard S. Halbrook, Don W. Sparling	54- MOLECULAR SYSTEMATICS OF <i>GEOMYS</i> BASED ON DNA SEQUENCES FROM THE PROTEIN CODING ALCOHOL DEHYDROGENASE GENE ( <i>ADH-1</i> ). <b>Erica Vargas</b> , Sheri B. Westerman, and Robert D. Bradley	
5:00	58- SEED NUTRIENT ANALYSIS FOR TWO TYPES OF <i>LITHOCARPUS</i> FRUITS: ACORNS AND ENCLOSED RECEPTACLE FRUITS (ER). Xi Chen, Chuck Cannon	55- INDUCING TRICLOSAN RESISTANCE. <b>Ashley Masters</b>	
7:00 -9:00	<b>Banquet</b> - Club Level, Jones AT&T Stadium		

## ABSTRACTS FOR PRESENTATIONS

1

### **ASSESSING WATERSHED CONTROLS ON ODONATE DISTRIBUTION**

Steven D. Collins<sup>1</sup> and Nancy E. McIntyre<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409-3131

Odonates (dragonflies and damselflies) are often used as indicators of habitat quality in permanent and ephemeral wetlands. Odonates have aquatic larvae sensitive to habitat quality, yet as aerial adults they may take advantage of widely dispersed habitats. However, little work has been done synthesizing distributional data to better understand the factors governing the biogeography of odonates. I propose to use distributional data from surveys coordinated by various state agencies to compare watershed characteristics of known locations to determine what environmental controls exist on odonate occurrence. Once the variables most correlated with species presence are determined, I propose to select watersheds from across physiographic provinces that have similar characteristics other than the variables of interest. Odonates will be surveyed from a random sample of these watershed "replicates" by collecting exuvia (exoskeleton shed upon adult emergence) several times throughout spring and early summer. These surveys will aid determination of the natural variability in odonate assemblages and the variability that can be correlated with environmental variables of interest. Local physical, chemical and biological stream characteristics will also be measured during the surveys, and these data will be used to test if local variables explain more variability than do regional (watershed-scale) ones. The objectives of this study are to better understand the habitat requirements for North American lotic odonates, to determine empirical thresholds limiting specific occupation of streams and rivers, and to construct predictive models that will be useful to watershed managers and state natural resource agencies.

2

### **AN AXIOMATIC THEORY FOR STOCHASTIC EVOLUTION IN MULTIPLE TRAITS WITH IMPLICATIONS FOR VARIATION IN HERITABILITY IN DIFFERENT ENVIRONMENTS**

John R Harting<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

In classical population genetics, we find many intentionally simplified models used to describe and analyze specific problems that occur in evolutionary theory. These early models are robust and continue to be used to great effect today; however, another approach to evolutionary model building which starts from a generalized concept of phenotype and uses only so-called 'axiomatic' assumptions can potentially provide a more unified view of evolution, including some processes which are hidden by the simplifying assumptions of classical models. The first such axiomatic theory described the exact mathematical method by which one could retrospectively calculate changes in the mean of a single phenotype in a closed population (Price, 1970). More recent work by Rice (2008) and Rice & Papadopoulos (2009) has extended this body of theory to include stochastic change in a single trait for both closed and open populations, respectively. Here, I propose a further extension of this theory to the case of stochastic change in multiple traits within a closed population. Some preliminary work has been done which already exposes a term that can be used to study the covariance between heritability and a variable environment. In a recent review by Charmantier & Garant (2005), multiple empirical examples of this relationship are discussed, but with little theoretical explanation. This study will examine these examples as a point of divergence for using the theory to ask questions about evolutionary mechanisms underlying this relationship.

3

### **ECOLOGICAL SERVICES PROVIDED BY INSECTIVOROUS BATS IN PALEOTROPICAL RAINFOREST AND AGROFOREST SYSTEMS: A FUNCTIONAL DIVERSITY STUDY**

Chun Chia Huang<sup>1</sup> and Tigger Kingston<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

Recent studies suggest that top-down control in complex food webs can be shaped by the existence of multiple predator effects. Although it has been demonstrated that consumption by insectivorous bats can influence insect herbivore abundance, there has been no consideration of the roles that specific foraging ensembles within diverse insectivorous bat assemblages may play. In Southeast Asia, where insectivorous bat diversity is among the highest in the world, rapid land-use change not only threatens overall bat diversity, but is changing local assemblage composition. *In this proposed work, I aim to i) document the variability in top-down effects of different functional groups (FGs), and ii) explore the consequences for ecosystem services in terms of pest control of functional diversity changes in local bat assemblages driven by anthropogenic land-use change.* The study will take place in and around Bukit Barisan Selatan National Park, Sumatra, Indonesia. I will conduct bat surveys in monocultural coffee farms, mixed coffee plantations, and the primary rainforest to understand how bat assemblages respond to different land management strategies. I will then assign all species into different FGs using experimental assessments of bat foraging behavior and flight performance. I will set enclosures to exclude different FGs of bats from targeted trees and will census the changes of arthropod density, diversity, and leaf damage. We expect our findings to improve our understanding of how top-down control by insectivorous bats varies within and between assemblages, the response of assemblage structure to land use, and increase our knowledge of autecology.

4

### **HETEROSPECIFIC INFORMATION TRANSFER OF ALARM CALLS IN GREY DUIKER (SYLVICAPRA GRIMMIA)**

Amy M. Kuczynski<sup>1</sup> and Kenneth A. Schmidt<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

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, that quantifies perceived predation risk over time and space. Grey duiker are small, nocturnal antelope found in sub-Saharan Africa. Grey 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 small playback study testing if grey duiker adjust their level of perceived predation risk in response to bushbuck alarm calls using giving-up-densities. The data show interesting trends as duiker perceived predation risk was higher during alarm playbacks than during controls at one of two sites and the percentage of unforaged trays was higher during alarm playbacks at both sites. 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.

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## **REDUCED NIMA RELATED KINASE 2 (NEK2) EXPRESSION LEVEL ENHANCES PACLITAXEL SENSITIVITY IN THE BREAST CANCER CELLS**

Jaehyung Lee<sup>1</sup>, Lauren Gollahon<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

While many clinical trials have shown that the taxane, paclitaxel (Taxol™), is a very powerful anticancer drug, paclitaxel is still controversial in its applicability for cancer treatment because of the resistance of tumor cells to its effects. Therefore, the purpose of this study is to determine whether the sensitivity of paclitaxel is improved with the addition of antisense oligonucleotides (ASO) against NIMA related kinase 2 (Nek2) in the breast cancer cells. Nek2, a serine/threonine kinase is a gene emerging as important to cancer development because of its regulatory role in mammalian cell mitosis. Moreover, abnormally increased Nek2 expression and activity levels are the main trait of various cancer cells. For these reasons, regulation of the Nek2 expression levels may prove important as a target for cancer treatment. Because many cancer cells have demonstrated resistance to anticancer drugs, more effective therapeutic treatments for cancer patients are necessary. ASO are able to inhibit cancer progression because they bind to and depress, the expression of genes targeted for their involvement in tumor development. We will investigate drug sensitivity by using plus ASOs targeted against Nek2 to treat breast cancer cells. MDA-MB-468 breast cancer cells transfected with Nek2 ASO will be treated with paclitaxel to evaluate cell proliferation, cell cycle distribution, and apoptosis. We expect that MDA-MB-468 cells treated together with Nek2 ASO and paclitaxel will show more synergistic results compared with either agent alone. This study will suggest that Nek2 ASO and paclitaxel combination treatment may improve the sensitivity of cancer cells.

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## **GENETIC REQUIREMENTS FOR STABILITY OF *RAV1* TRANSCRIPT ENCODING A TRANSCRIPTION FACTOR THAT POSITIVELY REGULATES ABA SIGNALING**

Amandeep Mittal<sup>1</sup>, Qingjun Luo<sup>1</sup>, Chris D. Rock<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

Abscisic acid (ABA) is a phytohormone produced in response to stress and functions in seed maturation, dormancy, and growth and development. RAV1 is a transcription factor that responds ABA positively. RAV1 is highly expressed and turned over transcript as shown previously by treating arabidopsis with cordycepin, a chemical that stops de novo RNA synthesis. Addition of cycloheximide (CHX), protein synthesis inhibitor to liquid-cultured seedlings leads to 16-fold RAV1 transcript accumulation within 3 hours. 6hours treatment reduces the transcript level to 9folds suggesting RAV1 post transcriptional degradation, but the key factors responsible for its instability are unknown. 5' Exoribonucleases (XRNs) and 3' exoribonucleases (the 'exosome') are the protein complexes that degrade heterogeneous nuclear RNA and aberrant transcripts through 'surveillance' mechanisms. RAV1 transcript accumulated 2-fold above wild type in *xrn2-1/xrn4-6* double mutant and nearly three-fold in *xrn3-3/xrn4-6* as detected by Northern blot and validated by qRT-PCR. These results suggest exoribonucleases are key factors involved in RAV1 post- transcriptional regulation. In future we propose to do 5' and 3' Rapid Amplification of cDNA Ends (RACE) in wild type and mutant plants. Treatment of *xrn* mutants with cordycepin followed by RACE will reveal the accumulation of chewed RAV1 products. Further, we are interested in finding the DNA binding targets of RAV1. We propose to do chromatin immunoprecipitation of RAV1 and hybridization of the bound DNA to whole genome tiling microarray (Chip-Chip assay). Results will lead us to know all the targets of RAV1 and help us understand its molecular mechanism of action in ABA signaling.

## **PATTERNS OF DISTRIBUTION OF THE ENDEMIC MAMMALS IN ECUADOR**

Juan P. Carrera-E.<sup>1</sup> and Hugo Mantilla-Meluk<sup>1</sup>

<sup>1</sup>Department of Biological Sciences and the Museum of Texas Tech University, Lubbock, TX

Ecuador is categorized as one of the megadiverse countries showing high level of endemism for several taxa. The most recent checklist of mammals recognized 382 species including 38 endemics. In spite of their importance, no formal analysis has been conducted on the historical and geographic determinants that explain endemic species distribution inside the Ecuadorian territory. The main goal for this study was to identify the geographic affinities among Ecuadorian endemic mammalian records and to analyze the spatial relationship between endemic sampling localities and the National System of Protected Areas (SNAP). We analyzed public and museum records collected from 1859-2004, housed in 24 museums abroad. Endemic records were georeferenced and mapped. A polygon layer representing eight bioregions in Ecuador was used to determine the ecogeographic origin of the samples. To verify the spatial relationship between endemic records and conservation areas, a polygon layer representing SNAP, was overlaid using ArcGIS 9.3. Of the 23,000 mammalian records analyzed, we recovered 409 endemic records, containing only 265 with confirmed localities in our samples. The majority of our endemic records were located in the Andean region; a sample bias is suggested by the presence of 99 records in areas surrounding Quito. The majority of endemic species are rodents and most of the records come from the highlands. Surprisingly, only 5 records, representing three species, were collected in currently identified conservation areas. In general, these results position the Andes as a main hotspot for endemic species which contrasts with the few protected areas in the region.

## **A PREDICTIVE MODEL OF NON-VOLANT SMALL MAMMAL ASSEMBLAGES IN EASTERN PARAGUAY ATLANTIC FOREST REMNANTS**

Noé U. de la Sancha<sup>1</sup> and Richard Strauss<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

The Atlantic Forest (AF) of South America, extending from northeastern Brazil to eastern Paraguay, is the second most diverse forest system in that continent, second to the Amazon. This forest system has experience dramatic deforestation and alteration throughout its extent. Although a great deal of research has been dedicated to the Brazilian forests on the effects few studies have focused on Paraguayan taxa. Unlike its Brazilian counterpart, the Paraguayan AF deforestation is a new phenomenon. In this study, 19 Brazilian studies on non-volant small mammals, focused on forest fragmentation, were used to develop a predictive model for number of species expected to be found in eastern Paraguay AF using 2008 GIS data. A bi-variable statistical function from the relationships between forest patch size, trapping effort, and number of species were developed and used to predict number of species. Species richness was calculated for 46,435 forest patches in Paraguay varying from 0.1ha to 95,758.1ha, using a standardized trapping effort value and the area of each of the Paraguayan forest remnants. Initial forest patch sizes were reduced in intervals from 5%-50% and expected number of species were recalculate. The number of expected species predicted did not change between initial and reduced fragments when these were smaller than 782ha. Meanwhile, fragments larger than 20,000ha showed the most variation on species richness between original and reduced areas. This study suggests that species loss is not proportional with percent of area loss, and species richness declines are most severe in large forest remnants.



**EFFECT OF FEMALE BODY SIZE ON FITNESS IN DAMSELFLIES**Kelly S. Baker<sup>1</sup> and Nancy E. McIntyre<sup>1</sup><sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

The southern Great Plains have been highly modified by human activity. In this area, the primary source of above-ground freshwater is contained within playas (intermittent wetlands). For aquatic and amphibious wildlife, water quality within playas may be affected by surrounding land use. Prior research has demonstrated that environmental variables affect the growth and development of an indicator group of playa animals (odonates, i.e., dragonflies and damselflies). The larvae of these amphibious insects sense habitat quality as they mature. If habitat quality is poor, the larvae can grow and develop faster in order to escape adverse conditions. Presumably, faster growth and development incur a tradeoff of smaller adult body size, which may then impact fitness. We captured 70 actively mating *Enallagma civile* females between June-September 2009 to determine what effect body size has on fitness in terms of egg load and larval survivorship. However, we could detect no significant correlation between body size (head capsule width) and number of eggs laid or with larval survivorship. It is possible that there was a confounding association with increasing date: time to hatch decreased as the summer progressed. Furthermore, there was high variation in the number of eggs laid and in larval hatching. Use of a different body size metric (e.g. mass or body length) and/or collection of a larger sample over a shorter period may help resolve these issues and reveal a relationship between female body size and fitness in damselflies.

**FUNCTION OF POISON SAC PROTEINS FROM QUEEN RED IMPORTED FIRE ANTS (FORMICIDAE: *SOLENOPSIS INVICTA*)**Stephanie A. Lockwood<sup>1</sup>, Mohammed Fokar<sup>2</sup>, and Richard J. Deslippe<sup>1</sup><sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409-3131<sup>2</sup>Center for Biotechnology, Texas Tech University, Lubbock, Texas 79409-3131

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 gland and dispersed over the body via the stinger along with an attraction pheromone. Two proteins were recently isolated from the poison gland of queens which proved to be unique but homologous to two of the four proteins stored in the poison gland of conspecific workers. Evidence also suggests that the proteins may inhibit bacterial and fungal growth. Research objectives are to establish protocols for 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. Two different expression systems were used with varying results, but still no functional protein has been obtained. New evidence, however, supports two suspected characteristics of these proteins. First, during bacterial expression trials, transformed bacteria grew at different rates depending upon which genes were involved in the transformation. Second, the size and composition of the amino acids of the poison sac proteins are consistent with cysteine-knot or knottin proteins, a class of proteins that are attractive for drug designs because of their stability. Should the queen proteins induce workers to kill sexual larvae, they could be exploited and developed into a potentially new and powerful tool to aid in the management of this ant.

## **CHOERONYCTERINE BATS AS A MODEL TO STUDY GLOBAL CLIMATE CHANGE AMONG MAMMALS**

Hugo Mantilla-Meluk<sup>1</sup>

<sup>1</sup>Texas Tech University

Global climate change continues to generate considerable political, public and academic interest and controversy. In this matter, mountain ecosystems have recently received considerable interest based on the understanding that climate change might have particularly serious irreversible impacts on physical and biological systems in these habitats. Within the Neotropical family of bats Phyllostomidae, bats in the tribe Choeronycterina are considered highland specialists. The high geographic partitioning documented for these three groups of bats as well as their ecological sensitivity made them a perfect model to study the effect of global warming on Neotropical highland ecosystems and to solve the fundamental question of: How can we determine to what extent the integrity of the “greater ecosystem” is being affected when the climate is changing? As a result of global warming, changes in ranges of elevational belts associated with the different mountain ecosystems have been observed and it is likely that the structure of highland mammalian assemblages is silently changing with the potential negative effect of extinction events accelerated by competition and niche displacement. Herein, a combined set of methodological approaches including morphometrics, genetics, and niche modeling are proposed to: 1) resolve the phylogenetic affinities among choeronycterine bats; 2) to analyze the geographic and ecological structure of its diversity; 3) to assess the effect of environmental complexity, particularly elevation gradients, on species richness and species composition, and 4) to generate predictive scenarios to understand the effect of global climate changes on richness and composition for this group of highland specialists.

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## **GENETIC AND STABLE ISOTOPE ANALYSIS OF A POTENTIALLY NOVEL COLONY OF *TADARIDA BRASILIENSIS MEXICANA* IN WEST TEXAS.**

Jennifer J. Miller<sup>1</sup>, Raymond S. Matlack<sup>2</sup>, and Brenda E. Rodgers<sup>1</sup>,

<sup>1</sup>Texas Tech University, <sup>2</sup>West Texas A&M University

The objective of this research is to evaluate the status of a colony of *Tadarida brasiliensis mexicana* (the Brazilian Free-Tailed Bat also known as the Mexican Free-Tailed Bat) in west Texas. Populations of *Tadarida brasiliensis mexicana* are thought to be migratory in the central and southwest regions of the United States, but a roosting location in west Texas has been observed to have year-round emergences. This behavior is contradictory to the published literature. Both genetic and stable isotope analysis will be employed to determine whether this roost supports a stationary colony or whether it is being used by a number of transient populations throughout the year. If a stationary colony of *Tadarida brasiliensis mexicana* is roosting in west Texas, it may be the first documentation of such behavior.

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## **THE DIFFERENTIAL CHITIN SYNTHASE ACTIVITY OF *BATRACHOCHYTRIUM DENDROBATIDIS* AS A VIRULENCE FACTOR IN THE INFECTION OF AMPHIBIANS**

Adam M. Lord<sup>1</sup> and Michael San Francisco

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

Chytridiomycosis, caused by *Batrachochytrium dendrobatidis*, has been deemed an emerging infectious disease by the CDC (4) and is currently threatening 30% of the world's 6285 known amphibian species (2). The asexual reproducing fungus has two life cycle stages, a motile, zoospore and a sessile zoosporangium. One major structural difference between the two forms of this pathogenic fungus is the presence of a chitin-rich cell wall in the reproductive sporangium and the absence of any chitin wall in the zoospore (1). *Bd* has 6 annotated chitin synthase enzymes in its genome and their activity can be quantified using a differential assay based on lectin binding to the chitin chains formed by the enzyme (3).

The linkage of the chytrid's development to its pathogenicity makes the chitin synthase enzyme a possible virulence factor in the development of chytridiomycosis and therefore a key enzyme activity to study. Preliminary studies in our lab and studies of other fungal pathogens show differential regulation of the various Chs enzymes that may provide clues as to methods to inhibit the pathogenesis of chytridiomycosis in amphibians. I propose that chitin synthase gene expression and CHS activity are differentially regulated in *Bd* during thallus/sporangial development in free-living biofilm state and in the animal host

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#### **INVESTIGATING THE ROLE OF DNASE IN THE PATHOGENICITY CAUSED BY *BATRACHOCHYTRIUM DENDROBATIDIS* IN AMPHIBIANS**

Priyanka Maiti<sup>1</sup> and Michael. J. San Francisco<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

The pathogen *Batrachochytrium dendrobatidis* (*Bd*) has been associated with amphibian declines in multiple continents, including western North America. In an attempt to identify the factors responsible for fungal pathogenicity, we have focused on enzymes involved in degradation of host-related proteins and nucleic acids. We have identified a powerful DNase activity in *Bd* that may play a role in pathogenicity. Here we show the presence of this activity using qualitative and quantitative methods. DNase tests were performed using methyl green DNA-containing plates and agarose gel electrophoresis. Studies are currently underway to study optimal conditions for this activity and to assess its role in the life history of the fungus.

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#### **EXTRACELLULAR NUCLEASE DNSH IN *AEROMONAS* STRAIN**

Roopa Pulijala<sup>1</sup>, and Randall. M. Jeter<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

The genus *Aeromonas* consists of rod-shaped, facultatively anaerobic, nonspore-forming, Gram-negative bacteria. These are ubiquitous and natural inhabitants of aquatic environments. In Gram-negative bacteria, genetic transformation by donor DNA is decreased due to extracellular deoxyribonucleases (DNases). Extracellular DNase-encoding genes have been cloned in several Gram-negative bacteria, including *A. hydrophila*, *Escherichia coli*, *Serratia marcescens*, and *Vibrio cholerae*. In *S. marcescens*, inactivation of the extracellular nuclease NucA resulted in elevated levels of artificial transformation of plasmid DNA. In *Vibrio*, when the two genes encoding extracellular DNases Dns and Xds were inactivated, it increased natural transformation in these bacteria. In *A. hydrophila* JMP636, the nuclease gene *nucH* was studied for its role in artificial transformation. However, researchers did not find any change in a null mutant, indicating that multiple nucleases might be present and decrease transformation. We have isolated a highly transformable strain of *Aeromonas* designated strain 92. The *dnsH* gene of strain 92 was amplified, cloned in *E. coli*, and sequenced. The *dnsH* gene can be overexpressed in *E. coli* TOP10 host cells by induction with L-arabinose. Experiments are currently underway to overexpress the *dnsH* gene in *Aeromonas* strain 92 and to test the effect of this extracellular nuclease on natural transformation.

## **HANTAVIRUS NATURAL RESERVOIR ABUNDANCE, SEROEPIDEMIOLOGY AND ARARAQUARA HANTAVIRUS AMONG WILD RODENTS IN SOUTHEASTERN BRAZIL.**

Gilberto Sabino-Santos Jr<sup>1</sup>, Felipe G. M. Maia<sup>1</sup>, Glauciane G. Figueiredo<sup>1</sup>, Alex M. Machado<sup>1</sup>, Jorge Salazar-Bravo<sup>2</sup> and Luiz T. M. Figueiredo<sup>1</sup>.

<sup>1</sup>Center for Virological Research, School of Medicine in Ribeirao Preto, University of Sao Paulo, Brazil,

<sup>2</sup>Department of Biological Sciences, Texas Tech University, Lubbock, US.

Our aim was to associate abundance of wild rodents to hantavirus seroprevalence and to report a possible spillover species of Araraquara hantavirus (ARAV) among natural reservoirs in the northeastern region of Sao Paulo State (SE Brazil). Rodents were live-trapped in two 100-trap grids for 2–3 consecutive nights. Grids were separated by at least 800 m to represent individual populations. At least 800 m from the grids, a kill line with 100 Sherman traps was placed to collect animal organs for viral isolation in a BSL-3 laboratory. Captured rodents were identified by morphological characteristics, marked for recapture and had blood collected from the retro-orbital sinus. IgG antibodies against hantavirus were detected by an indirect ELISA using as antigen a nucleocapside recombinant protein of ARAV. A total of 592 animals were captured during 13 months (June 2008 to July 2009). ARAV were isolated from lung tissue of *Necromys lasiurus* and *Calomys tener*. The seroprevalence for the entire sample was 4.7%, whereas seroprevalence per species were as follow: *N. lasiurus* 10%; *Akodon* sp 1.28% and *C. tener* 0.97%; Hantavirus seroprevalence was slightly higher in the dry season (April to September). Our ongoing studies corroborate the hypothesis that hantaviruses are maintained in reservoir populations by seasonal persistence of chronically infected animals and suggest a spillover of species among natural reservoirs *N. lasiurus* to *C. tener* of ARAV in this region.

## **MOLECULAR RESPONSES OF AN AMPHIBIAN PATHOGEN BATRACHOCHYTRIUM DENDROBATIDIS UPON EXPOSURE TO THYROID HORMONE**

Jose C. Thekkiniath<sup>1</sup>, Mithun R. Pasham<sup>2</sup>, Mohammed Fokar<sup>2</sup> and Michael J D. San Francisco<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Center for Biotechnology and Genomics, Texas Tech University, Lubbock, Texas 79409

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 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 and protein profiling, we observed the expression of specific genes including chitin synthases, G proteins, proteases and adhesion factors in Bd exposed to TH. These studies suggest that TH might be an important factor in triggering virulence gene expression in Bd.

**SEQUENCE VARIATION OF MICRORNA BINDING SITES IN PLANTS**Fangqian Ou-Yang<sup>1</sup>, Qing-Jun Luo<sup>1</sup>, Casey R. Richardson<sup>1</sup>, and Christopher D. Rock<sup>1</sup><sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

We customized miRNA prediction program miRanda V2.0 and performed a comprehensive prediction for miRNA targets in *Arabidopsis thaliana*, *Oryza sativa* subsp. japonica and subsp. indica cDNAs. We predicted 760, 1910 and 1299 unique target transcripts for Arabidopsis, japonica and indica rice, respectively having high sequence homologies to known miRNAs in miRBase (<http://www.mirbase.org/index.shtml>). In japonica rice, miRNA target-binding sites (73%) were located in coding regions of genes, while 16% in 3'- untranslated regions (UTRs) and 11% in 5'-UTRs, whereas Arabidopsis targets bear 3% of binding sites in their 3'-UTRs and 5'-UTRs respectively. Interestingly, a high ratio (8:1) was found in japonica rice 5'- and 3'-UTRs regions targeted by non-conserved miRNAs (unique to rice) than those by conserved miRNA families found in all plants. This suggests a novel regulatory importance for non-conserved rice miRNAs acting on UTR regions, a situation more analogous to animal miRNAs than plants. Bioinformatic analysis showed that the average level of single nucleotide polymorphisms (SNPs) per site ( $\theta$ ) at miRNA binding sites in japonica and indica rice is 0, indicating that purifying selection is the evolutionary driving force that acts on them. In addition, evidence of selective sweep was found at both nucleic acid and protein levels in plant miRNA target sites by sequence alignments using CLUSTAL algorithm, reflecting a flexible but constant mechanism of recognition for miRNAs on their targets. Analysis of wild relatives of *O. sativa* and miRNA discovery in emerging genomes should provide insights into evolution and functional significance of newly emerged miRNA classes.

**VOLANT VIRUSES: ARE CAVE-ROOSTING BATS AT GREATER RISK?**Kendra L. Phelps<sup>1</sup>, Akbar Zubaid<sup>2</sup>, Tigga Kingston<sup>1</sup><sup>1</sup>Department of Biological Sciences, Texas Tech University, United States<sup>2</sup>School of Environmental & Natural Resource Sciences, Universiti Kebangsaan Malaysia, Malaysia

Within Peninsular Malaysia, limestone outcrop formations (karsts) are sources of high species diversity. Numerous insectivorous and Old World fruit bats are highly dependent upon caves within these formations, which provide stable microclimates suitable for roosting and rearing young, as well as, shelter from climatic events and predators. Bats are known to be natural reservoir hosts for numerous infectious diseases which may spread to human populations and domestic species. Within tropical caves, high host densities, coupled with high diversity of co-habiting hosts, present ideal conditions for virus transmission between individuals and between different species. Threats to karst formations, particularly commercial quarrying and logging operations, result in the loss of roosting and foraging sites. Such threats have detrimental effects on the viability of cave-roosting bat populations, and present a potential source of stress that may lead to a spillover event. Therefore, documenting ecological characteristics and infection rates of cave-roosting bat species across a landscape experiencing anthropogenic modification is crucial to understanding the relationship between anthropogenic activities and the emergence of zoonotic diseases. Previous initiatives have acted retroactively, attempting to control or eradicate host populations after a spillover event has occurred. Our objective is document the host-parasite relationship across a spectrum of landscape modification to facilitate in a proactive approach to predicting potential spillover events. Methods include comparison of virus and bat diversity data with landscape characteristics, analyzed with geographic information systems (GIS), to understand the correlation between ecological characteristics and viral loads of cave-roosting bat populations and landscape modification.

## **ROLE AND MECHANISMS OF ACTION OF THYROID HORMONE DURING GONADAL SEX DIFFERENTIATION IN ZEBRAFISH (*DANIO RARIO*)**

Prakash Sharma<sup>1</sup> and Reynaldo Patiño<sup>2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>U.S. Geological Survey Texas Cooperative Fish and Wildlife Research Unit, Texas Tech University, Lubbock, TX 79409.

Gonadal sex determination and differentiation in zebrafish does not seem to be controlled by sex chromosomes but by genes on the autosomes. During the process of gonadal sex differentiation, the gonads of all zebrafish larvae first develop as ovaries and, in presumptive males, later transform into testes. The timing and expression levels of some autosomal genes such as *cyp19a*, *Sox9b* (female-specific), *ff1d*, *AMH*, *Sox9a*, *Dmrt1* (male-specific) reportedly are important to determine gonadal sex in zebrafish. Based on previous observations that the induction of hyperthyroid condition in zebrafish larvae results in male-biased populations and accelerates the timing of puberty in males; and that hypothyroid condition in zebrafish larvae results in female-biased populations, the overarching hypothesis of this research proposal is that thyroid hormone plays a major role in the differentiation and development of the reproductive system of zebrafish. One specific objective of my dissertation is to confirm the regulation of sex ratio (sex determination) by thyroid hormone and to establish its mechanisms. To address this objective, newly hatched zebrafish larvae will be exposed for 60 days to thyroid hormone inhibitors or exogenous thyroid hormone to render them hypo- or hyperthyroid, respectively; and the effects on the reproductive system and expression of various genes will be examined. Specific endpoints to be measured include gonadal and thyroid histopathology, sex ratios, and developmental expression of *cyp19a*, *ff1d*, *AMH*, *Sox9a*, *ER $\alpha$* , *ER $\beta$ 1*, *ER $\beta$ 2*, *AR*, *TR $\alpha$* , *TR $\beta$* , and *FSH- $\beta$* . The results obtained will be compared against expectations based on the main study hypothesis.

## **PROPOSAL FOR STUDYING THE PHYLOGEOGRAPHY OF *VIPERA AMMODYTES* ON THE CYCLADIC ISLANDS OF GREECE**

Stephen A. Roussos<sup>1</sup> and Dr. Llewelyn Densmore<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

The Balkan Peninsula and the islands of the Aegean Sea are recognized as one of three refugial biodiversity centers, their more complex topography has contributed to producing some the highest levels of reptile biodiversity and endemism in Europe. After the Pleistocene glacial retreat and the 200m increase in the Aegean Sea level, most of the Cycladic Plateau became submerged, leaving only the higher elevations exposed and forming the archipelago of islands that we now call the Cyclades. These set of circumstances have combined to create unique ecosystems on these islands with specialized fauna. The primary objectives of this study are to use both morphological data and molecular markers to evaluate the genetics and corresponding taxonomy of populations of the Long-nosed viper (*Vipera ammodytes*) in the Cycladic islands. Recent studies have suggested that there have been four refugia for *V. ammodytes* in Greece alone (including one representing the Cyclades), and that each of these refugia corresponded to a different clade of *V. ammodytes* due to isolation over time. Our analyses will allow us to generate and test systematic hypotheses regarding how these populations are related to other clades that have been recognized across the Balkans. They will also allow us to assess the phylogeography of the Long-nosed vipers that inhabit the most topographically diverse portion of the species range. Finally, because endemic populations may be present on a number of different islands, we will be able to make recommendations regarding the status of these populations and their possible future conservation.

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## **ECOLOGICAL EFFECTS OF AN INVASIVE ALGA, *PRYMNESIUM PARVUM*, ON AQUATIC COMMUNITIES.**

Jamie G. Suski<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

*Prymnesium parvum*, or commonly known as Golden Algae (GA), is an invasive algal species that is euryhaline and eurythermal. Golden algae release toxins that have caused fish kills throughout the world. The first reported incident within the United States was the Pecos River, TX in 1985; currently, over 16 states have reported fish kills attributed to GA blooms. Although, this invasive species is relatively new there has been a reasonable amount of research on the toxicological effects on fish. However, there are little to no data available on the potential effects of the toxins to gastropods or amphibians, both important components of many aquatic systems. Perhaps, this is because mortalities of these animals are less obvious or the toxins do not affect them. My aim is to focus on understanding the effects of GA toxins on gastropods and amphibians. The ultimate goal is to explore direct and indirect effects of the toxins to individual species and how these effects may translate to community level disturbances.

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## **COIBA RESEARCH AND EDUCATION PROJECT**

Miryam Vengas-Anaya<sup>1,2,3</sup>, Llewellyn Densmore D III<sup>1</sup>, Oris Sanjur<sup>2</sup>, and Eldredge Bermingham<sup>2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409.

<sup>2</sup>Smithsonian Tropical Research Institute. Balboa, Ancón, Panamá, República de Panamá.

<sup>3</sup>Crocodile Specialist Group, Species Survival Commission, International Union for Conservation of Nature.

The Coiba project is a Texas Tech University, Smithsonian Tropical Research Institute (STRI), and Crocodile Specialist Group (IUCN-SSC-CSG) initiative supported by The National Secretariat for Science, Technology and Innovation of Panama (SENACYT) to create opportunities for field research at Coiba Marine National Park (CMNP) and to diffuse the knowledge globally. This project is divided into three steps. The first step is the study of *Crocodylus acutus* population structure and habitat use at CMNP using genetics and telemetry. This study offer opportunities to research ecological genetics, evolutionary ecology, and *in situ* biodiversity conservation and marine costal habitat management using *C. acutus* as a model. The second step focuses on education. We will offer courses in hunting and management of crocodiles during summer 2010 and 2011. The third step, distance education, aims to establish a global network where teachers, students, and researchers from TTU and around the world could do real time virtual studies with the data provided by the *C. acutus* telemetry project. We also plan to join the *C. acutus* telemetry project to the STRI long-term project on coral reefs monitoring, migratory patterns of large pelagic species in the eastern Pacific, shark fishing, marine reserves networks using internet platforms. The objective of this presentation is to motivate TTU Students and faculties to participate actively in the full development of this idea.

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## **SMALL MAMMAL ASSEMBLAGES FROM NATURAL AND MODIFIED HABITATS IN A CLOUD FOREST RESERVE, GUATEMALA.**

Nicté Ordóñez-Garza<sup>1,2</sup>, and Ana L. Grajeda<sup>2</sup>.

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Centro de Estudios Conservacionistas, Universidad de San Carlos de Guatemala, Avenida. Reforma 0-63 zona 10, Ciudad de Guatemala.

Small mammal abundance and species richness were assessed in the Biotopo del Quetzal and its buffer zone in Baja Verapaz, Guatemala. Samplings were made in three different habitat types: mature and

second growth cloud forests and farm lands (across an anthropogenic disturbance gradient). Bats were mist-netted at understory and sub-canopy levels. Non-volant mammals were captured with Sherman, snap Museum Special, Tomahawk, and Pitfall traps at different vertical stratus of the forest and at ground level, respectively. Fifteen phyllostomid bat and 11 non-volant small mammal species were collected. Abundance and species richness of phyllostomid bats assemblages were similar among all habitats sampled. For non-volant small mammals, abundance was significantly different between structurally complex environments and crop fields. Differences on abundance and species richness of these small mammal assemblages were attributed to variations on the dispersion capacity and life history of each group. Forested habitats presented higher bat capture proportion in the sub-canopy than understory level. Three non-volant small mammal and one bat species may be vulnerable to habitat loss: *Peromyscus grandis*, *Tylomys nudicaudus*, *Reithrodontomys microdon* and *Micronycteris microtis*.

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### **AN EVALUATION OF FECAL DNA PRESERVATION TECHNIQUES AND EFFECTS OF SAMPLE AGE AND DIET ON GENOTYPING SUCCESS**

Michael Panasci<sup>1</sup>, Warren Ballard<sup>1</sup>, David Wester<sup>1</sup>, Stewart Breck<sup>2</sup>, David Rodriguez<sup>3</sup>, Llewellyn Densmore<sup>3</sup>, Robert Baker<sup>3</sup>

<sup>1</sup>Department of Natural Resources Management, Texas Tech University, Lubbock, TX 79409

<sup>2</sup>USDA, APHIS, Wildlife Services, National Wildlife Research Center, Fort Collins, CO 8052

<sup>3</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

**Abstract:** Although biologists increasingly utilize fecal DNA, optimal collection protocols are not yet established. We evaluated 3 factors that influence microsatellite genotyping of fecal DNA extracted from coyote (*Canis latrans*) scats: age, preservative, and diet content. We used the multiple tubes approach to generate consensus genotypes and recorded errors in replicate amplifications. Samples were subjected to 3 age and 3 preservation treatments. Ethanol and DET buffer performed similarly, and both were superior to lysis buffer. Samples collected at 5 and 10 days yielded poorer quality DNA than samples collected on day 1. We tested the influence of diet by using scats consisting of insect, mammalian, or juniper (*Juniperus* spp.) remains. Scats comprised of juniper were most reliably genotyped when preserved in DET buffer. Mammal-based scats were most reliable when stored in EtOH. Scats comprised of insects did not differ between preservatives. We recommend the collection of scats < 5 days old, ethanol preservation for scats of obligate carnivores, and DET buffer preservation for animals with plant-derived diets. Our study provides important methodology for studies utilizing fecal DNA analyses.

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### **BITE FORCE ANALYSIS OF RAINFOREST INSECTIVOROUS BATS**

Juliana Senawi<sup>1,2</sup>, Björn Siemers<sup>3</sup>, Daniela Schmieder<sup>3</sup>, Rosli Hashim<sup>4</sup> and Tigga Kingston<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409, USA

<sup>2</sup>Institute of Environmental Development (LESTARI), Universiti Kebangsaan Malaysia, 43600 Selangor, Malaysia

<sup>3</sup>Max Planck Institute for Ornithology, Seewiesen, Germany

<sup>4</sup>Institute of Biological Sciences, University of Malaya, Kuala Lumpur, Malaysia

Malaysia's rainforests are home to the greatest diversity of bat species in the Old World with over 70 species recorded at a single location, Krau Wildlife Reserve, Pahang. This outstanding diversity is likely achieved through an intricate partitioning of the available resources within the habitat. In insectivorous bat assemblages, niche partitioning of food resources is effected in large part by physical and sensory access to the insect prey base. Differences in wing morphology and echolocation signal design among species influence access to particular foraging habitats and the ability to detect or capture prey within them. Differences in food processing capabilities, particularly bite force, may further mediate resource partitioning in species-rich assemblages. However, experimental data documenting biting ability (bite



force) at the assemblage level are limited. Here, we examine the relationship between bite force and  $CM^3$  and forearm length of 30 species from six families of insectivorous bats from Krau Wildlife Reserve and surrounding areas. There was a highly significant relationship between bite force and forearm length and  $CM^3$  at the assemblage level (i.e., across all species), and within families. The consequences of these findings for structuring mechanisms in species-rich monophagous assemblages are discussed

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### **THREE'S COMPANY: CO-INFECTION IN *PEROMYSCUS* MICE**

Courtney A. Thomason<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

There is a direct relationship between the habitat in which an animal lives and the impact of parasites and pathogens upon the animal such that organisms living in disturbed habitat tend to experience more severe effects from infection. Most emerging infectious disease threats are associated with some form of anthropogenic disturbance. It is known that parasites tend to decrease immunocompetence of their hosts, and parasitized animals are more likely to contract and subsequently transmit disease to other hosts. Most hosts experience multiple parasite co-infections that invoke immune responses aimed at clearing specific parasites, often resulting in diminished immune system affectivity overall. The purpose of this study was to explore the effects of parasite co-infection on *Peromyscus* immunocompetence because co-infection by different types of parasites can potentially result in hierarchical trophic-level interactions. Eight intestinal and one blood-borne parasite (*Bartonella*) were identified. We found that parasite species were distributed randomly among the mouse population, and subadult mice had significantly higher parasite diversity than adult mice (53.32%,  $P=0.04115$ ). There was an inverse effect of *Bartonella* infection on neutrophil:lymphocyte (N:L) ratios (a measure of immune stress), where the presence of *Bartonella* seemed to cause a decrease in circulating lymphocytes as compared to mice with no *Bartonella* infection. Also, interesting co-infection patterns emerged with *Bartonella*-cestode co-infection occurring at a higher rate and *Bartonella*-coccidian co-infection occurring at a lower rate than expected compared to a null model. Finally, this data represent the first known instance of *Bartonella* infection at this elevation at Mountain Lake Biological Station.

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### **THE ROLE OF DAILY SOIL TEMPERATURE FLUCTUATIONS ON MICROBIAL AND NITROGEN DYNAMICS IN A CHIHUAHUAN DESERT CREOSOTE BUSH BAJADA.**

Natasja C. van Gestel<sup>1</sup>, Stephen Cox<sup>1</sup>, Rich E. Strauss<sup>1</sup>, Dylan Schwilk<sup>1</sup>, David T. Tissue<sup>1,2</sup>, and John C. Zak<sup>1</sup>

<sup>1</sup>Texas Tech University, Department of Biological Sciences, Lubbock, TX

<sup>2</sup>University of Western Sydney, Centre for Plant and Food Science, Richmond, Australia

During the 20<sup>th</sup> century, mean global surface temperatures had risen by 0.74 °C. Analyses showed that this was partly due to daily minimum temperatures increasing to a greater degree than maximum temperatures. Greater amounts of water vapor in the atmosphere, can, in cloud form, act to dampen temperature extremes by both reducing daytime solar radiation received by the soil surface and increasing downward longwave radiation at night. Most climate change studies focus on studying the effects of elevated [CO<sub>2</sub>], increased temperatures and altered precipitation regime. This is the first study to mimic the effects of increased atmospheric water vapor to elucidate the importance of reduced soil temperature fluctuations on soil microbial and nutrient dynamics. We suspended white polyethylene shade cloth (50% reduction) onto a raised (15 cm) PVC frame in a creosote bush bajada in the Chihuahuan Desert at Big Bend National Park. Our design allowed airflow over the soil surface to minimize alterations to the boundary layer and allowed precipitation to reach the soil surface. Soils beneath the shade cloth were generally warmer at nighttime, while cooler or similar to the unshaded (control) plots during the daytime. The resulting decrease in daily soil temperature fluctuations in summer increased microbial biomass C

and N and reduced soil available N. As of yet, plants have not shown a physiological response to changes in available soil N levels. Plants showed strong stomatal control of photosynthesis, and thus, were more greatly affected by plant water status than to changes in soil temperatures and soil nutrient levels.

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### **DISTRIBUTION AND HABITAT SELECTION OF ENDANGERED WARM SPRINGS PUPFISH (*CYPRINODON NEVADENSIS PECTORALIS*) WITHIN A DESERT SPRING REFUGE.**

Darrick S. Weissenfluh<sup>1,2</sup>, Gene R. Wilde<sup>1</sup>, Cristi R. Baldino<sup>2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>U.S. Fish and Wildlife Service, Ash Meadows National Wildlife Refuge, Amargosa Valley, Nevada 89020

The Warm Springs Complex (WSC) is one of four management units within Ash Meadows National Wildlife Refuge (AMNWR). It contains five low-discharge warm spring systems with individual flows ranging from 0.000113 to 0.000198 cubic meters per second (cms) and spring-source water temperatures ranging from 28° to 34°C. School Springs is one component of the WSC. This spring has undergone dramatic anthropogenic transformation since 1969, when the Bureau of Land Management (BLM) increased pool habitat in an effort to preserve the endemic, federally-listed (1970) Warm Springs pupfish, *Cyprinodon nevadensis pectoralis*. In 1983, four additional concrete ponds were constructed at School Springs to further increase water volume available to Warm Springs pupfish. During the summer of 2008, AMNWR completed rehabilitation of the School Springs refuge: the large concrete ponds were removed and a “naturalized” channel consisting of pools, runs, and riffles was created. There were three primary goals of the restoration: (1) eradicate three aquatic invasive species; (2) improve suitable habitat for the endangered Warm Springs pupfish and three endemic invertebrates which only occupy the WSC; and (3) test hypotheses concerning endemic fish habitat selection and distribution inherent in the design of the refuge. Preliminary results indicate most Warm Springs pupfish (>80%) occupy pool habitat, but they may be distributed throughout the system from spring orifice to wash despite extreme diel temperature fluctuations (>15°C) in parts of the stream.

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### **THE INFLUENCE OF ESTROGEN RECEPTORS ON THE TRANSCRIPTION AND EXPRESSION OF THE BREAST CANCER METASTASIS GENE 1 (BRMS1)**

Hongtao Ma,<sup>1</sup> Lauren Gollahon<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

Estrogen is well known to play a major role in the development and progression of breast cancer. Estrogen functions through the estrogen receptor (ER) in target cells. Two types of estrogen receptors exist. One is nuclear estrogen receptor (nER), which is a member of the nuclear hormone family of intracellular receptors, including ER $\alpha$  and ER $\beta$ . The other is the estrogen G protein coupled receptor GPR30. Studies have shown that aberrant ER signaling leads to abnormal cellular proliferation and survival. However, less is known about the association between the ER and metastasis in breast cancers. Breast cancer metastasis suppressor 1 (BRMS1) is a gene that is known to suppress metastasis in several solid tumors without affecting the growth of the primary tumor. In this study, the regulation of BRMS1 by ER subtypes will be investigated. This will be accomplished through two Specific Aims: 1) ER $\alpha$ , ER $\beta$  and GPR30 will be activated by their respective agonist PPT, DPN, and G-1. 2) ER $\alpha$ , ER $\beta$  and GPR30 will be knocked down using siRNA. Analyses will be performed using by real-time PCR and Western blot. Additionally, an invasion assay and a wound-healing assay will be used to assess breast cancer cell invasion capability and mobility. Successful completion of this study will give us a better understanding of the role that ER subtypes have in breast cancer metastasis.

## DETERMINING POPULATION GENETIC STRUCTURE OF *LYGUS HESPERUS* FROM TEXAS HIGH PLAINS USING SIMPLE SEQUENCE REPEAT MARKERS

Ram B. Shrestha<sup>1</sup>, Megha N. Parajulee<sup>2</sup>, Michael J. D. San Francisco<sup>1</sup>, Lou D. Densmore<sup>1</sup>, Rich E. Strauss<sup>1</sup>, Mark D. Burrow<sup>2</sup>, and A. Scott Holaday<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Texas AgriLife Research, Lubbock, Texas 79403

*Lygus hesperus* (Hemiptera: Miridae) are the most damaging pests of cotton in the United States. Lacking reliable molecular markers, *L. hesperus* genetic diversity information is not available for Texas High Plains (THP). Simple Sequence Repeat (SSR) markers were developed by sequencing a microsatellite-enriched genomic DNA library. Ten SSR markers were characterized, and published in the National Center for Biotechnology Information database. *L. hesperus* population genetic structure in THP was determined using six selected SSR markers. Samples (n=48 per location) collected from four locations in THP were genotyped by polymerase chain reaction and polyacrylamide gel electrophoresis. This study showed that SSR markers are useful for determination of *L. hesperus* intraspecific genetic diversity. Within the 153-mile geographic sampling range, *L. hesperus* were genetically differentiated into two populations: northern and southern population clusters. The AMOVA revealed 11.3% genetic variation was due to among population genetic differences. It is hypothesized that variations in ecological factors along the 623-foot north-south elevation gradient, such as host, habitat, and climate, induce *L. hesperus* genetic differentiation. A larger-scale landscape genetics study is planned to determine the relationships between the ecological parameters and *L. hesperus* genetic diversity.

## DEGRADATION OF HOST SPHINGOMYELIN IS ESSENTIAL FOR *LEISHMANIA VIRULENCE*

Ou Zhang<sup>1</sup>, Mattie C. Wilson<sup>1</sup>, Wei Xu<sup>1</sup>, Fong-Fu Hsu<sup>2</sup>, John Turk<sup>2</sup>, F. Matthew Kuhlmann<sup>2</sup>, Yingwei Wang<sup>3</sup>, Lynn Soong<sup>3</sup>, Phillip Key<sup>4</sup>, Stephen M. Beverley<sup>4</sup>, and Kai Zhang<sup>1\*</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409, USA.

<sup>2</sup>Department of Internal Medicine, Washington University School of Medicine, 660 S. Euclid Ave., Saint Louis, MO 63110, USA.

<sup>3</sup>Department of Microbiology and Immunology, Department of Pathology, The University of Texas Medical Branch, Galveston, TX 77555, USA

<sup>4</sup>Department of Molecular Microbiology, Washington University School of Medicine, 660 S. Euclid Ave., Saint Louis, MO 63110, USA.

In eukaryote, sphingolipids (SLs) are important membrane components and powerful signaling molecules. In *Leishmania*, the major SL is inositol phosphorylceramide (IPC), which is common in yeast and Trypanosomatids but absent in mammals. In contrast, sphingomyelin, an abundant group of SLs in mammals, is not synthesized by *Leishmania*. In the promastigote stage *in vitro*, *Leishmania* use SL metabolism as a major pathway to produce ethanolamine (EtN), a metabolite essential for survival and differentiation from non-virulent procyclics to highly virulent metacyclics. To further probe SL metabolism, we identified a gene encoding a putative neutral sphingomyelinase (SMase) and/or IPC hydrolase (IPCcase), designated *ISCL* (Inositol phosphoSphingolipid phospholipase C-Like). Despite the lack of sphingomyelin synthesis, *L.* major promastigotes exhibited a potent SMase activity which was abolished upon deletion of *ISCL*, and increased following over-expression by episomal complementation. *ISCL*-dependent activity with sphingomyelin was about 20 fold greater than that seen with IPC. Null mutants of *ISCL* (*iscl*<sup>-</sup>) showed modest accumulation of IPC, but grew and differentiated normally *in vitro*. Interestingly, *iscl*<sup>-</sup> mutants did not induce lesion pathology in the susceptible BALB/c mice, yet persisted indefinitely at low levels at the site of infection. Notably, the acute virulence of *iscl*<sup>-</sup> was completely restored by the expression of *ISCL* or heterologous mammalian or fungal SMases, but not by

fungal proteins exhibiting only IPCase activity. Together, these findings strongly suggest the degradation of host-derived sphingomyelin plays a pivotal role in the proliferation of *Leishmania* in mammalian hosts and the manifestation of acute disease pathology.

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### **EXTREME PARAPHYLY AND SPECIATION WITHIN A CRYPTIC SPECIES COMPLEX: BULLDOG BATS (CHIROPTERA: NOCTILIONIDAE) REVISITED**

Faisal A. Anwarali Khan<sup>1</sup>, C. Miguel Pinto<sup>2</sup>, and Robert J. Baker<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Department of Mammalogy, American Museum of Natural History, New York, New York 10024

Assessing species' boundaries or phylogroups using multifaceted approaches from independent genetic markers would be an appropriate method to identify independent evolutionary units. Under this framework, intrageneric relationship and species limits within Bulldog bats, genus *Noctilio* with an emphasis on *Noctilio albiventris* were explored using 4 datasets: cytochrome-*b* (*cyt-b*), cytochrome *c* oxidase-I (COI), Amplified Fragment Length Polymorphisms (AFLPs), and morphology. We genetically analyzed 51 samples of *Noctilio* from two currently recognized species: *N. albiventris* and *N. leporinus*. In *cyt-b* and COI gene phylogenetic analyses, *N. albiventris* form a paraphyletic clade, containing the gigantic species *N. leporinus*. Moreover, 5 monophyletic clades were documented, 4 associated with *N. albiventris* with > 5% genetic distance and a single clade for *N. leporinus*. Clades within *N. albiventris* are morphologically indistinguishable but they mostly have different geographic distributions, matching with all the recognized subspecies in *N. albiventris*: *N. a. minor*, *N. a. affinis*, *N. a. albiventris*, and *N. a. cabrerai*. Although we recovered all the clades from mitochondrial DNA in AFLP analysis (nuclear DNA), there are two individuals from different clades that were positioned differently. These individuals are from Bolivia and Guyana. These localities lie in the periphery of the geographic range of subspecies suggesting that these sites may represent a contact zone with gene flow between different maternal lineages. Genetic divergences in the mitochondrial genes (>5%) that are congruent with geographic distribution, and the paraphyly of *N. albiventris* (*sensu lato*) suggest that currently recognized subspecies within *N. albiventris* should be recognized at the specific level.

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### **EXAMINING THE ROLE OF THE TRANSFERRIN-RECEPTOR 1 (TfR1) GENE AS THE HOST CELLULAR RECEPTOR FOR NORTH AMERICAN ARENAVIRUSES**

Sheri B. Ayers<sup>1</sup>, Robert D. Bradley<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas, 79409

<sup>2</sup>Natural Sciences Research Laboratory, Museum of Texas Tech University, Lubbock, Texas 79409

Viruses of the family Arenaviridae, genus *Arenavirus*, are rodent-borne viruses associated with hemorrhagic fevers in humans. The New World clade of arenaviruses is divided into South American clades A, B, C, and a North American clade. North American arenaviruses, hosted mostly by woodrats (genus *Neotoma*), are important zoonoses in the southwest United States and northern Mexico. Although North American arenaviruses often use a single principal host species, other species of woodrats as well as *Peromyscus californicus* have been shown to acquire the virus through interactions with a principal host, and the south-plains woodrat (*Neotoma micropus*) is known to host three divergent strains of arenaviruses. Recently, the transferrin-receptor 1 gene (TfR1) was identified as the cellular receptor used by clade B and North American arenaviruses, with amino acid residues 208-212 in the apical domain of the human TfR1 gene being implicated as the binding site for arenaviral entry. DNA sequences from the TfR1 genes were obtained from 14 species representing known virus-positive individuals, known negative individuals from host species, and outgroup species which do not carry an arenavirus. Amino acid sites homologous to human tyr-211 were conserved in every species that carried a North American

arenavirus, regardless of whether the individual was virus positive or negative. Additionally, *N. micropus*, which hosts three divergent strains, does not appear to have comparable diversity in the Tfr1 gene. These results suggest that although amino acids 208-212 are important for arenavirus entry, other ecological or genetic factors may play a role.

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### **DISTRIBUTION OF REPETITIVE ELEMENTS ON *DESMODUS ROTUNDUS* CHROMOSOMES**

Cibele G. Sotero-Caio<sup>1</sup>, LuAnn Scott<sup>2</sup>, Holly A. Wichman<sup>2</sup>, and Robert J. Baker<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Department of Biological Sciences, University of Idaho, Moscow, Idaho 83844

LINE-1 retrotransposons comprise a substantial portion of mammalian genomes and up to date they have been described to occur non-randomly along chromosomes, preferentially on G-band regions, as well as sex chromosomes. In bats, studies for the description of distributional patterns of LINES were performed in few species, and deviations of this general pattern have not yet been observed. In this work we describe an unusual pattern of distribution of Drot6b, a portion of a young LINE-1 element from the common vampire bat, *Desmodus rotundus*, and compare the results with the overall distribution of repetitive elements in this species. Drot6b hybridized to the centromeric region of every chromosome of *D. rotundus* and only one chromosomal pair presented an interstitial signal with the probe. The X chromosome presented a greater accumulation of this element, in accordance with data in other species. Our data document differences between the genome organization of *D. rotundus* compared to other bat species and provide further support for non-random removal of repetitive sequences along chromosomes of at least one bat species.

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### **MOLECULAR RELATIONSHIPS WITHIN THE NEOTOMINAE BASED ON COMBINED MITOCHONDRIAL AND NUCLEAR DNA SEQUENCES**

Megan S. Corley<sup>1</sup>, Roy N. Platt<sup>2</sup>, Brian R. Amman<sup>3</sup>, and Robert D. Bradley<sup>1,4</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409-3131

<sup>2</sup>Department of Biological Sciences, Mississippi State University, Mississippi State, MS 39762

<sup>3</sup>Center for Disease Control, Atlanta, GA 30333

<sup>4</sup>Natural Sciences Research Laboratory, Museum of Texas Tech University, Lubbock, TX 79409-3191

Phylogenetic relationships and taxonomy of the North American neotomine-peromyscine rodents have been controversial for many years. There have been various arguments regarding the number of tribes within this speciose group of rodents as well as the relationships of genera in each tribe. The goal of this study is to use molecular data to address the issue of how many tribes should be recognized within the Neotominae. Most studies provided support for 4 tribes: Baiomyini, Neotomini, Peromyscini, and Tylomyini, some have suggested the 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. Additionally, the controversial relationships of genera within each tribe have contributed to the various taxonomic arrangements. Combined mitochondrial and nuclear DNA sequences of 19 genera of neotomine-peromyscine rodents, including the cytochrome *b* gene, intron 7 of the  $\beta$ -fibrinogen gene, exon 6 of the dentin matrix protein 1 gene, intron 2 of the alcohol dehydrogenase gene, exon 1 of the interphotoreceptor retinoid-binding protein gene, and exon 10 of the growth hormone receptor gene were analyzed to create a phylogeny. Our preliminary data suggests that there may be 5 to 6 tribes that should be recognized within this subfamily of rodents.

### GENETIC VARIATION AND PHENOTYPIC EVOLUTION IN THE LESSER ANTILLEAN TREE BAT (*ARDOPS NICHOLLSI*)

Roxanne J. Larsen<sup>1</sup>, Peter A. Larsen<sup>1</sup>, Hugh H. Genoways<sup>2</sup>, Gary G. Kwiecinski<sup>3</sup>, Scott C. Pedersen<sup>4</sup>, and Robert J. Baker<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>University of Nebraska State Museum, Lincoln, Nebraska 68588

<sup>3</sup>Biology Department, The University of Scranton, Scranton, Pennsylvania 18510

<sup>4</sup>Department of Biology/Microbiology, South Dakota State University, Brookings, South Dakota 57006

Intraspecific phenotypic variation is a product of many forces and mechanisms, involving genetics and the environment. To better understand the processes underlying the tempo of phenotypic evolution in allopatry, we analyzed multiple molecular datasets from *Ardops nichollsi*, a recently evolved species of phyllostomid bat (i.e., the most recent common ancestor of the genus occurred ~ 1.8 million years ago). Despite its recent origin in the family Phyllostomidae, the only member of this monotypic genus is comprised of five subspecies: *A. n. montserratensis*, *A. n. annectens*, *A. n. nichollsi*, *A. n. koopmani* and *A. n. luciae*. The subspecies of this Caribbean endemic show morphological variation with respect to the islands they inhabit, while phylogenetic structure appears in the northern and southern subspecies. Previous morphometric, molecular, and genetic studies of *A. nichollsi* indicated the need for further investigation to better understand this multifaceted species complex. Thus the objectives of the current study are to test for congruence between mitochondrial and nuclear datasets and to examine the processes underlying evolution and subspeciation in an insular endemic. In the future, we will use morphometric, genetic and environmental datasets to elucidate important evolutionary questions regarding the tempo of phenotypic evolution in allopatric island populations.

### LINKING CARBOHYDRATE CONTENT AND GENE EXPRESSION FOR SEASONAL CARBOHYDRATE METABOLISM IN THE XYLEM (WOOD) OF *POPULUS* SPECIES

Jayasri Alluvada<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

Previous research demonstrated seasonal patterns in carbohydrate of xylem parenchyma cells in poplars grown under natural conditions, with starch being high in the late summer and low in the winter and during bud break and sucrose exhibiting the opposite pattern. Spatially, starch was found to be low during the summer in first-year twigs and in the new growth rings of older stems. These seasonal and spatial patterns are consistent with the need to regulate starch storage so that it does not compete with xylem growth and yet can serve as a reserve for bud growth in the spring. Since variations in the amount of these carbohydrates have been shown to correlate with levels of the enzymes associated with their metabolism, I am using the seasonal and spatial patterns to determine whether regulation of this metabolism involves changes in gene expression for the enzymes involved. I isolated RNA from xylem of the twigs of *P. balsamifera* grown outside of the greenhouse. A decline in starch in the spring was associated with a lower transcript level for a key enzyme in starch synthesis than when starch levels were high. A low sucrose content was preceded by a low transcript level for a key sucrose synthesis enzyme. Transcripts for sucrose synthase that degrades sucrose for growth processes of the vascular cambium were highest during the summer. However, the transcript level for  $\beta$ -amylase, an enzyme of starch degradation, was not always consistent with starch content. Study of spatial variation in transcript levels is planned.

## THE EFFECT OF NITROGEN AVAILABILITY ON PHOTOSYNTHESIS OF THE INVASIVE GRASS *PHALARIS ARUNDINACEA*

Hasitha Guvvala<sup>1</sup>, Dr.A.S.Holaday<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

*Phalaris arundinacea* is an invasive C<sub>3</sub>, perennial grass of temperate wetland communities in the northern hemisphere. Although native to North America, the introduction of varieties from European sources has led to rapidly-spreading populations. Most of the previous ecological studies have focused on morphological differences and changes in the community dynamics that may explain the invasive nature of *P. arundinacea*, but few physiological factors have been addressed. Given that *P. arundinacea* is more abundant in areas with high nitrogen inputs, the aim of my project is to compare the response of physiological factors associated with photosynthesis to various nitrogen levels for *P. arundinacea* and for a native sedge, *Carex stricta*, that it often displaces. I will be growing plants of both species in a course soil medium whose nitrogen content will be controlled by varying the nitrate and ammonium in a standard nutrient solution. I will measure the response to nitrogen for CO<sub>2</sub>-exchange parameters, such as CO<sub>2</sub> assimilation (*A*), for chlorophyll content, and specific leaf area (SLA). My preliminary research on *P. arundinacea* has shown that a three fold increase in the nitrogen concentration of the standard solution resulted in an increase in *A* by 18.3% relative to that at 11 mM. The effect on chlorophyll was mixed. 1.1 mM nitrogen reduced *A* and the total chlorophyll by 13.12 and 8%, respectively, compared to values at 11 mM. Further reductions in nitrogen are planned to determine how sensitive *P. arundinacea* photosynthesis is to low nitrogen.

## CO-REGULATION OF miR842 and miR846 polycistronic miRNAs ON THEIR target gene AT5G28520 in response to ABA

Fan Jia<sup>1</sup>, Gary R. Larson<sup>1</sup>, Qing-Jun Luo<sup>1</sup> and Chris Rock<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

MicroRNAs (miRNAs) are 21-nucleotide long endogenous small RNAs. They regulate gene expression through transcriptional and/or post-transcriptional gene silencing (TGS/PTGS). In animals, miRNA genes are largely encoded in polycistrons, while most plant miRNAs are transcribed from independent transcription units. However, it has been discovered recently that plants also have polycistronic transcripts containing different miRNAs. In our current study, two miRNAs, miR842 and miR846 from *Arabidopsis thaliana*, were found in a long transcript by 5'-RACE experiment in a mutant line CS815868. Semi-quantitative realtime PCR (qPCR) analysis revealed about 3-fold higher expression for the putative primary transcripts of miR842 and miR846, designated as At-pri-miRNA842-846, in the mutant than in wild type Col-0 seedlings. Interestingly, these two miRNAs were predicted to target a common gene, At5g28520, which was highly upregulated by 10 μM abscisic acid (ABA) treatment in Col-0 seedling roots. Furthermore, our qPCR results showed that both predicted pre-mi842 and pre-mi846 were down-regulated by ABA in a time-dependent manner. 5'-RACE experiment indicated a possible cleavage product of At5g28520 by mi846, consistent with expression data that suggests endonucleolytic cleavage events on At5g28520 transcripts. In conclusion, we propose that miR842 and miR846 are polycistronic miRNAs that co-regulate gene AT5G28520 in response to ABA.

**THE ARABIDOPSIS ANKYRIN REPEAT-CONTAINING PROTEIN 2A IS AN ESSENTIAL MOLECULAR CHAPERONE FOR THE BIOGENESIS OF APX3 AND IT PLAYS AN IMPORTANT ROLE IN PLANT GROWTH AND DEVELOPMENT**

Sundaram Kuppu<sup>1</sup>, Guoxin Shen<sup>1</sup>, and Hong Zhang<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

Peroxisomes are eukaryotic organelle without its own genome; consequently all peroxisomal proteins are encoded by the nuclear genome, synthesized on free ribosomes, and post-translationally targeted to peroxisomes. The molecular mechanism of how matrix proteins are imported into peroxisomes is better understood, whereas the molecular mechanism of the biogenesis of peroxisomal membrane-bound proteins is less understood. The Arabidopsis ankyrin repeat-containing protein 2A (AKR2A) was found to interact with the peroxisomal membrane-bound ascorbate peroxidase 3 (APX3), and this interaction involves transmembrane domain plus a few basic amino acid residues at the c-terminus, that resembles the mPTS, a targeting signal for some peroxisomal membrane-bound proteins. The putative mPTS from APX3 can target green fluorescent protein (GFP) to peroxisomal membrane when fused to GFP. The specificity of the AKR2A-APX3 interaction hints at a possibility that AKR2A regulates APX3's biogenesis, because binding of AKR2A to APX3's mPTS could prevent APX3 from forming aggregates after biosynthesis from free ribosomes. Analysis of three *AKR2A* mutants indicates that AKR2A is required for APX3's stability in plant cell. Furthermore, reduced expression of *AKR2A* by using RNA interference technique also leads to reduced steady-state level of APX3 and significantly reduced APX3 targeting to peroxisomes in plant cells. In addition, *AKR2A* mutants display abnormal phenotypes and delayed flowering, indicating that AKR2A plays important roles in plant growth and development. AKR2A is an essential chaperon that binds specifically to the mPTS like sequence in a group of membrane-bound proteins and regulates the biogenesis of this group of membrane-bound proteins in plant cells.

**A FEEDBACK REGULATORY LOOP INVOLVING *PAP1/MYB75* AND *MIR828/TAS4* IN RESPONSE TO SUGAR IN ARABIDOPSIS**

Qing-Jun Luo<sup>1</sup>, Hong-Liang Zhu<sup>1</sup>, Fan Jia<sup>1</sup>, and Chris Rock<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX, USA 79409,

MiR828 in Arabidopsis triggers the cleavage for transcripts of Trans-Acting SiRNA Gene 4 (*TAS4*) and the production of *TAS4*-derived small interfering RNAs (siRNAs). One such siRNA, *TAS4*-siRNA81(-), targets the same subset of MYB transcription factors as miR828, including *PAP1/MYB75*, *PAP2/MYB90* and *MYB113* in the pathway for anthocyanin biosynthesis. We find that *PAP1*, *PAP2* and *TAS4* expression are induced specifically by exogenous sucrose treatment in Arabidopsis seedlings. The induction is attenuated in the ABA signaling pathway mutants, especially in *abi3-1* and *abi5-1* for *PAP1* or *PAP2*, while no such effect is observed for *TAS4*. Furthermore, *TAS4* expression is increased in *pap1-D*, a *PAP1* overexpressing line, while in a *tas4* knockout mutant, *PAP1* and *PAP2* transcripts become more abundant, indicating a feedback loop between *PAP1* and *TAS4*. Bioinformatic analysis reveals miR828 orthologues in dicots and gymnosperms and *TAS4* only in dicots. *PAP1/PAP2/MYB113* orthologues show that the peptide footprint of *TAS4*-siR81(-) binding site is dicot-specific. Taken together, these data suggest that regulation of anthocyanin biosynthesis by *TAS4* and miR828 in higher plants is evolutionarily significant and raise questions about the origins of *TAS4*/miR828.



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**MOLECULAR EVIDENCE FOR HYBRIDIZATION BETWEEN *NEOTOMA MICROPUS* AND *N. FLORIDANA***

Matthew R. Mauldin<sup>1</sup>, Robert D. Bradley<sup>1,2</sup>, J. Delton Hanson<sup>1</sup>, and Robert J. Baker<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409-3131

<sup>2</sup>Museum of Texas Tech University, Lubbock, TX 79409-3191

One hundred three individual woodrats were collected from a putative hybrid zone between *Neotoma floridana* and *N. micropus*. Three genetic markers, 1 mitochondrial (Cytochrome-*b* gene) and 2 nuclear (alcohol dehydrogenase, and beta fibrinogen) were used to develop a composite genotype for each individual to ascertain genetic identification of specimens and for detection of hybridization. Results indicated 13 individuals were identified as pure parental *N. micropus*, 85 as hybrids, and 5 as pure parental *N. floridana*. The genetic assays revealed a high frequency of hybridization (83%) and that hybrids were formed by bidirectional matings of the 2 parental types as well as matings involving hybrid individuals. Despite the lack of reproductive isolation (Biological Species Concept) within the narrow hybrid zone, the 2 species maintain their genetic integrity and are genetically isolated (Genetic Species Concept) outside of the hybrid zone and therefore appear to behave as species.

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**MIGRATION OF *ARTIBEUS JAMAICENSIS* AMONG THE U.S. VIRGIN ISLANDS**

Julie A. Parlos<sup>1</sup>, Gary G. Kwiecinski<sup>2</sup>, and Robert J. Baker<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Department of Biology, University of Scranton, Scranton, Pennsylvania 18510

*Artibeus jamaicensis* (Chiroptera: Phyllostomatidae: Stenodermatinae) is a wide-ranging frugivorous bat, inhabiting Central America, the Caribbean Islands, and South America west of the Andes. The subspecies *A. j. jamaicensis* is found throughout the Lesser Antilles and part of the Greater Antilles. To address questions regarding the migration of this species among the U.S. Virgin Islands specimens were collected from the three islands. Microsatellites developed in *A. jamaicensis* were amplified among collected specimens. These data were evaluated using the programs STRUCTURE and BAYESASS. STRUCTURE evaluates whether the specimens on the islands are genetically distinct and BAYESASS evaluates recent migration rates among populations. Preliminary data generated by STRUCTURE suggests that individuals on the island of St. Croix are more similar to one another, individuals of St. John are more similar to one another, and St. Thomas contains a mix of individuals representing the genetic populations predominantly observed on St. Croix and St. John. BAYESASS suggests migrants are most likely migrating to St. Thomas and St. John from St. Croix and that minimal migration is occurring between St. Thomas and St. John. The individuals collected among the three islands are not genetically distinct from one another. The genetic variation observed can be explained as sampling error, resulting from migration among and between the islands, rather than local adaptation. Identification of rare alleles can contribute to our understanding of the migratory patterns among these three islands as well as whether observed genetic similarities are the result of common ancestry.

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**MORPHOMETRIC ASSESSMENT OF THE *MICRONYCTERIS MEGALOTIS* COMPLEX (CHIROPTERA: PHYLLOSTOMIDAE): SEARCHING FOR GEOGRAPHIC STRUCTURE**

Lizette Siles<sup>1</sup> and Robert J. Baker<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79415, U.S.A.

The bat genus *Micronycteris* comprises ten insectivorous species that inhabit the Neotropical region of Central and South America. The taxonomy of this group is complex, the genus is usually divided into 2 informal groups based on venter coloration (pale or dark), and among the small dark venter

*Micronycteris*, two species have been described - *M. megalotis* and *M. microtis*-. However, consistent nonoverlapping characters to distinguish them are difficult to find, and several authors have stated that these may not represent two separate species. In this study, we used a set of cranial measurements of *M. megalotis* (49 specimens) and *M. microtis* (71 specimens) useful for explaining the variation in this group from across its distribution range. A Principal Component Analysis helped to distinguish which morphological variables explain most of the variation (length variables), and additionally it showed that the two species do not represent distinctive morphological groups. The collecting localities were mapped on layers containing environmental data, which allowed us to extract data on Precipitation, Elevation, and Temperature. These environmental variables were useful to perform a correlation analysis between morphological and environmental data. The correlation analysis suggests that Precipitation is an important variable that could be useful to explain the morphological variation in this group, with smaller bats present in dryer regions and the larger phenotypes usually in more humid areas.

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### **PRELIMINARY DATA ON THE PHYLOGEOGRAPHY OF THE THIRTEEN-LINED GROUND SQUIRREL (*SPERMOPHILUS TRIDECIMLINEATUS*)**

Cody W. Thompson<sup>1</sup> and Robert D. Bradley<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409-3131

<sup>2</sup>Natural Science Research Laboratory, Museum of Texas Tech University, Lubbock, Texas 79409-3191

The thirteen-lined ground squirrel (*Spermophilus tridecemlineatus*) consists of 10 recognized subspecies with a distribution covering much of the Great Plains of North America, extending from south-central Canada to central Texas and from eastern Utah to Ohio. Recent mitochondrial data (i.e., cytochrome-*b*) has shown phylogeographic structuring among some populations. However, a lack of differentiation among populations of *S. tridecemlineatus* and their southern congener, the Mexican ground squirrel (*S. mexicanus*), indicates the possibility of introgression, presumably as a result of hybridization. In fact, karyological and morphological data has indicated that these species hybridize readily in northern parts of Texas and eastern New Mexico. In addition, northern populations of *S. mexicanus* appear to be related more closely to *S. tridecemlineatus* than to southern populations of *S. mexicanus*. To further understand these relationships, this study will focus on the phylogeographic relationships within *S. tridecemlineatus*. Additional mitochondrial and nuclear data are being collected to further evaluate these relationships and the systematics of *S. tridecemlineatus*.

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### **CHERNOBYL LOW-DOSE RADIATION IS PROTECTIVE *IN-UTERO*: A MECHANISTIC INVESTIGATION USING RT-PCR**

Eric K. Howell<sup>1</sup>, Sergey P. Gaschak<sup>2</sup>, Brenda E. Rodgers<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>International Radioecology Laboratory, Slavutysh, Ukraine

Following the nuclear accident at the Chernobyl Nuclear Power Plant in April, 1986, fear of teratogenic effects from the radiation releases led to thousands of elective abortions in pregnant women from Ukraine and surrounding countries. Epidemiological, clinical, and biological studies have since aimed to elucidate the teratogenic effects of *in-utero* exposures to ionizing radiation. Recent data suggests that, depending on the dose absorbed, *in-utero* exposures to ionizing radiation are potentially protective with respect to a subsequent radiation exposure challenge dose. Our data support this radioadaptive response in a mouse model system and further demonstrates that the protective effect of the priming dose is retained throughout parturition and weaning, with the challenge dose occurring 15-18 days after birth. In offspring from mothers receiving a low-dose *in-utero* priming exposure of 13 cGy prior to a 2.4 Gy challenge dose, micronucleus frequencies were significantly lower than offspring from mothers receiving no priming dose. Although the compilation of data supporting radioadaptation is growing, the

mechanisms behind this phenomenon have yet to be completely elucidated, which is the focus of this study. Gene expression data is currently being characterized to evaluate specific pathways commonly involved in teratogenesis and radiation exposures including regulation of apoptosis, DNA repair mechanisms, oxidative stress metabolism, and immune response.

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### **A FIELD AND LABORATORY ASSESMENT OF THE EFFECTS OF MERCURY ON SNAKE BEHAVIOR**

David A. Kimberly<sup>1</sup>

<sup>1</sup>Texas Tech University, Department of Environmental Toxicology

Since the industrial revolution, mercury has increased in the atmosphere four fold. As a result, mercury has become one of the most studied contaminants worldwide. Although there is a wealth of data on mercury contamination, reptilian taxa are drastically understudied. The goal of this study was to compare exposed snakes from both field and laboratory settings to evaluate mercury's effects on behavior. Four performance tests including predatory strike response, righting response, sprint speed, and incline crawl were used. Four of the five components within the predatory strike response variable, which consisted of envenomation success, number of strikes, jaw walks, and prey handling time, were significantly different between contaminated and control sites. Additionally, laboratory exposed animals displayed slower sprint speeds and incline crawls than controls. This study suggests that snakes showing depressed performance behaviors may be experiencing adverse effects of mercury contamination.

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### **MERCURY CONTAMINATION IN WETLANDS ASSOCIATED WITH COAL-FIRED POWER PLANTS**

Scott M. Weir<sup>1,2</sup>, Richard S. Halbrook<sup>1</sup>, Don W. Sparling<sup>1</sup>

<sup>1</sup>Cooperative Wildlife Research Laboratory, Department of Zoology, Southern Illinois University, Carbondale, Illinois, 62901

<sup>2</sup>Current address: Department of Environmental Toxicology, The Institute of Environmental and Human Health, Texas Tech University, Lubbock, Texas, 79416

There have been contradictory reports of the relative proportion of mercury from coal-fired power plants that deposits locally. Our objective was to determine any local effect of coal-fired power plants on total mercury concentrations in wetland sediment and tadpole samples. Four power plants and 45 wetlands were selected for study. Total mercury concentrations were determined in 75 sediment samples (range: 8-82 ng/g dry weight) and 100 bullfrog (*Lithobates catesbeiana*) and green frog (*Lithobates clamitans*) tadpoles (range: 5-318 ng/g wet weight). Tadpole and sediment total mercury did not significantly vary by power plant or distance from the plant. Only one power plant had a significantly greater concentration of total mercury in sediment downwind compared to upwind wetlands. A similar (but non-significant) trend was found for tadpole total mercury surrounding the same plant. Tadpole total mercury was negatively correlated with both tadpole weight and total length. Tadpole and sediment total mercury concentrations were not significantly correlated with one another. The results of the current study suggest that coal-fired power plants are not significantly affecting mercury concentrations in surrounding wetlands.

## POTENTIAL ROLE OF THE SYMPATHETIC NERVOUS SYSTEM IN MEDIATING THE CARDIOVASCULAR ACTIONS OF CRF-R2 RECEPTORS

Richard A. Larson<sup>1</sup> and James A. Carr<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

Stress is a physiological response that affects most organisms to some degree on a daily basis. Over time, an organism must learn how to adapt to stressful conditions. The hypothalamus-pituitary-adrenal axis (HPA) is important in the adaptation to stress and carries out its function through the hypothalamic hormone corticotropin-releasing factor (CRF), which controls the secretion of adrenocorticotropin from the anterior pituitary gland. Previous studies in mammals have shown that UCN-2, a selective CRF-R2 agonist, increases heart rate, but the degree to which the sympathetic nervous system (SNS) is involved in these effects is unknown. We conducted a series of in situ isometric experiments examining CRF-R2 regulation of heart rate, strength of contraction and blood pressure in the cane toad *Bufo marinus*. We found that the selective CRF-R2 agonist urocortin 2 (UCN-2), when administered peripherally, had no effect on heart rate or strength of contraction although the hypotensive agent sodium nitroprusside (SNP) significantly increased heart rate and decreased strength of contraction. Interestingly, both SNP and UCN-2 increased circulating levels of the catecholamines epinephrine and norepinephrine in anesthetized toads. Moreover, systemic administration of UCN-2 (20 ug) decreased blood pressure in anesthetized animals. We will also examine the effects of UCN-2 on isolated arterial ring preparations in vitro to examine whether UCN-2 has direct vasodilatory action on vascular smooth muscle. These experiments will allow us to have a better understanding of how CRF peptides affect cardiovascular function and SNS activity, which are related to an organism's stress response.

## EVIDENCE FOR EVOLUTIONARY REDUCTIONS IN BOTH THE LIGAND AND RECEPTOR THAT REGULATE RAPID SKIN DARKENING IN THE TEXAS TOAD, *BUFO SPECIOSUS*.

Sharanya Murali<sup>1</sup>, Bo Zhang<sup>1</sup>, Anusha Kumar<sup>1</sup>, Richard Larson<sup>1</sup>, Cary Brown<sup>1</sup>, James A. Carr<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas, 79409, USA

Two mechanisms regulate skin darkening in the South African clawed frog *Xenopus laevis*: a rapid response mediated by beta-adrenergic receptors on melanophores and a slower more sustained skin darkening resulting from MSH. Presumably these pathways have evolved as a response to predation, however it is unclear how these pathways operate in anuran species that would derive no benefit from the ability to mount a rapid melanophore response. *Bufo speciosus*, the Texas toad, is a desert adapted species that is nocturnal during the spring and summer but estivates underground the rest of the year. Compared to *X. laevis*, skin darkening is much slower and not as pronounced in *B. speciosus*. The dopamine neurotoxin 6-OHDA produced skin darkening in *B. speciosus* that amounted to 85% of the maximum achieved during long term dark adaptation. The dopamine receptor antagonist haloperidol had no effect while administration of the dopamine receptor agonist apomorphine significantly reduced skin darkening. Interestingly *B. speciosus* exhibited a strongly attenuated response to isoproterenol compared to *X. laevis*, and skin darkening in white adapted *Bufo* after transfer to a dark background was not affected by propranolol. To investigate the basis for the lack of response to beta-adrenergic agents, we examined differences in beta-adrenergic binding sites and skin catecholamine content between the two species. Skin from *X. laevis* had significantly more [3H]dihydroalprenolol binding sites as well as greater amounts of both dopamine and epinephrine compared to skin from *B. speciosus*. We conclude that *B. speciosus* appears to lack a mechanism for rapid skin darkening due to reductions in both the ligand and receptor controlling this response.

## GENETIC CHARACTERIZATION AND NATURAL HOST RELATIONSHIPS OF MULESHOE VIRUS IN NORTH TEXAS AND WESTERN OKLAHOMA

Allie P. Clinton<sup>1</sup>, Robert D. Bradley<sup>2</sup>, Mary Louise Milazzo<sup>3</sup>, Charles F. Fulhorst<sup>3</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas, 79409-3131

<sup>2</sup>Museum, Texas Tech University, Lubbock, Texas, 79409-3191

<sup>3</sup>Department of Pathology, University of Texas Medical Branch, Galveston, Texas, 77555-0609

Hantavirus pulmonary syndrome (HPS) is a rodent-borne zoonosis caused by certain members of the virus family *Bunyaviridae*, genus *Hantavirus*. Specific members of the rodent family Cricetidae are the principal hosts of the hantaviruses known to cause HPS. The etiological agents of HPS in North America are Bayou virus (BAYV), Black Creek Canal virus (BCCV), Choclo virus (CHOV), New York virus (NYV), and Sin Nombre virus (SNV). Other hantaviruses native to North America include Muleshoe virus (MULV). Our knowledge of the natural hosts relationships of this virus is limited to the detection of MULV RNA in two hispid cotton rats (*Sigmodon hispidus*) captured in 1995 in northern Texas. The purpose of this study was to extend our knowledge of the natural host relationships of MULV and define better the phylogenetic relationship of MULV to other hantaviruses. Four hundred twenty-six (426) cricetid rodents and 50 heteromyid rodents were captured in the summer of 2009 at 2 localities in northern Texas and 3 localities in western Oklahoma. Antibodies (IgG) to a hantavirus were found in blood samples from hispid cotton rats captured in Texas and white-footed mice (*Peromyscus leucopus*), a southern plains woodrat (*Neotoma micropus*), and hispid cotton rats captured in Oklahoma. The results of assays for hantavirus RNA in tissues from the antibody-positive rodents will be presented.

## ABSCISIC ACID REGULATES MICRORNA 842/846: IMPLICATIONS FOR PREDICTED TARGET GENE AT5G28520 FUNCTION AND MIRNA EVOLUTION

Gary R. Larson<sup>1</sup>, Fan Jia<sup>1</sup>, Chris D. Rock<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

The gene At5g28520 is a member of the jacalin/lectin family of plant-specific proteins whose functions are unknown. MicroRNAs (miRNAs) are a subclass of 21 n.t. eukaryotic riboregulators involved in post-transcriptional gene expression that are expressed from loci with extensive foldback secondary structures (hairpins) and their evolutionary origins are poorly understood. miR842/846 are tandem loci unique to Arabidopsis and have extensive homology to jacalin/lectin genes, suggesting a mechanism of evolution from a cognate target gene. We have shown by real-time PCR and RNA blotting that predicted miR842/846 target gene At5g28520 is strongly up-regulated by the plant hormone ABA in roots, which we hypothesize is due to negative regulation by miR842/846. Using 5' Rapid Amplification of cDNA Ends (RACE) we provide evidence of endonucleolytic cleavage by miR842/846 of At5g28520. We further show that miR842/846 primary transcripts are down-regulated by ABA, which provides functional evidence for the molecular mechanism of ABA regulation of At5g28520 by miR842/846. Further functional evidence comes from a T-DNA insertion allele adjacent to the miR842/846 locus (CS815868) that results in an increase in miR842/846 precursor expression and a decrease in At5g28520 expression. Our findings establish a system for testing jacalin/lectin function, elucidating the molecular mechanisms of ABA repression of miRNA842/846 expression, and gaining insights into the evolution of miRNAs.

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## **MOLECULAR SYSTEMATICS OF *GEOMYS* BASED ON DNA SEQUENCES FROM THE PROTEIN CODING THE ALCOHOL DEHYDROGENASE GENE (*ADH-1*)**

Erica Vargas<sup>1</sup>, Sheri B. Westerman<sup>1</sup>, and Robert D. Bradley<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Natural Science Research Laboratory, Museum of Texas Tech University, Lubbock, Texas 79409

Phylogenetic relationships among members of the genus *Geomys* have been difficult to discern because of the conservation of morphological characters presumably as the result of their fossorial lifestyle. Early studies of chromosomes and allozymes generated a few phylogenetic hypotheses, but most were hindered by taxon sampling or a low resolving power of characters and data due to homoplastic events. In recent years, DNA sequence data has been obtained from two mitochondrial genes (12S rRNA and cytochrome-*b*) and one nuclear gene (IRBP) and used to generate phylogenetic relationships for all members of the genus. In this study, we examine a second nuclear marker, the coding region of the alcohol dehydrogenase gene (*Adh-1*). Using a combination of molecular techniques and phylogenetic analyses, we were able to include many samples of *Geomys* and several samples of *Cratogeomys*, a sister genus. Although this study is preliminary – only eleven species examined, the data appears to be phylogenetically informative. However, more taxa or species of *Geomys* need to be further examined to have better resolution of the phylogenetic relationships.

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## **INDUCING TRICLOSAN RESISTANCE**

Ashley Masters<sup>1</sup>

<sup>1</sup>Midland College, Midland, Texas, 79705

Triclosan is an Antimicrobial agent used in a variety of personal hygiene products, plastic wares, and as a medical treatment for *Staphylococcus aureus*. The wide spread use of this compound has been linked to the low-level resistance in some bacteria. The purpose of this study is to establish if resistance can be induced in *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Bacillus cereus* and a wild type *Bacillus cereus* that had no previous exposure to Triclosan. Bacteria were cultured over sixty days, alternating between media containing Triclosan and media without triclosan. Beginning levels of resistance were noted for Triclosan and will be compared to resistance levels after the exposure period.

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## **INTRINSIC NEURONS CONTRIBUTE TO CRF INNERVATION OF THE ANURAN OPTIC TECTUM**

Bo Zhang<sup>1</sup>, Sharanya Murali<sup>1</sup>, Richard Larson<sup>1</sup>, Nafissa Ahmed<sup>1</sup>, Omar Shoukfeh<sup>1</sup>, Sarah Bulin<sup>1</sup>, Nicholas Bergfeld<sup>1</sup>, Jacob Lustgarten<sup>1</sup>, James A. Carr<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

The 41 amino acid peptide corticotropin-releasing factor inhibits visually guided feeding in anuran amphibians, but the targets for CRF action within sub-cortical visual pathways are unknown. We examined the distribution and origin of CRF immunoreactivity in the anuran optic tectum, a brain area at the interface of sensorimotor integration. CRF immunoreactive perikarya and fibers were observed in the optic tectum of three representative anuran amphibian species, the Texas toad *Bufo speciosus*, the South African clawed frog *Xenopus laevis*, and the Korean fire bellied toad *Bombina orientalis*. Intrinsic CRF-immunoreactive neurons were observed in tectal layer 8 in all species. These neurons were pyriform in shape, and had clearly stained projections directed laterally within layer 8 or directed vertically toward tectal layer 9. The optic tectum expressed mRNA for CRF, CRF R1 receptor, and urocortin-1. CRF was detected in toad optic tectum by radioimmunoassay, although tectal CRF content was considerably less than that of the hypothalamus and forebrain. The rank order for CRF content in toad brain as determined by radioimmunoassay was forebrain, hypothalamus>brainstem>optic tectum>>olfactory bulb. Unilateral

eye ablation did not affect CRF content of the contra lateral optic tectum. We conclude that neurons in the anuran optic tectum express mRNA for CRF and CRF R1 and that CRF immunoreactivity in the optic tectum arises from intrinsic CRF neurons.

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### **MIRPARA: A SVM-BASED SOFTWARE TOOL FOR PREDICTION OF MATURE MICRORNAS**

Yonggan Wu<sup>1,2,3,4</sup>, Haizhou Liu<sup>1</sup>, Tianxian Li<sup>3\*</sup>, Simon Rayner<sup>1\*</sup>

<sup>1</sup>Bioinformatics Group, State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Science, Wuhan, 430071, P.R. of China

<sup>2</sup>Graduate School, Chinese Academy of Sciences, Wuhan, 430071, P.R. of China

<sup>3</sup>State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, 430071, P.R. of China

<sup>4</sup>Department of Biological Science, Texas Tech University, Lubbock, Texas 79409

MicroRNAs (miRNAs) are a family of ~22-nucleotide small RNAs that can negatively or positively regulate gene expression at the post-transcriptional level. Identification of these molecules and their roles aids understanding of regulatory processes, but limited detection efficiency necessitates the use of automated prediction methods to complement experimental studies. However, the accuracy of computational methods is complicated by the variation of miRNA maturation pathways in different species. We have developed a software tool, miRPara, that can predict mature miRNA in a species specific manner. Our approach uses a support vector machine (SVM) to examine a comprehensive set of 77 different parameters related to the physical properties of the pre-miRNA and its miRNAs and which are related to the biogenesis process responsible for the generation of miRNAs. By applying parameter filtering we reduced this to four subsets of around 25 parameters specific to four different species models (*Overall*, *animal*, *plant* and *virus*) to achieve a significant improvement in speed without comprising accuracy. Our method achieves up to ~95% accuracy against a broad range of test sequences and an accuracy of ~75% against experimentally verified mature miRNAs predicted from long genome sequences, making it one of the fastest and most accurate methods available.

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### **SEED NUTRIENT ANALYSIS FOR TWO TYPES OF *LITHOCARPUS* FRUITS: ACORNS AND ENCLOSED RECEPTACLE FRUITS (ER)**

Xi Chen<sup>1</sup>, Chuck Cannon<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

<sup>2</sup>Chinese Academy of Sciences, Xishuangbanna Tropical Botanic Garden, Yunnan, P.R. China 666303

*Lithocarpus*, Fagaceae is one of the dominant tree genera in southeast Asia, particularly in Indo-China. Two distinct fruit types are found within the genus. "Acorn" fruits are similar to temperate oak fruit, with the seed enclosed by a thin exocarp or fruit wall. "Enclosed receptacle" or ER fruits generally have bigger seeds that are embedded in a thick, woody receptacle. Here, we test whether these morphological differences are correlated with phytochemical differences in the seed. Fruit samples representing both fruit types were collected in the Hengduan Mountains (China) in 2008. Four species were selected: *L. hancei*, *L. xylocarpus*, *L. truncatus*, and *L. craibianus*. The macronutrients and antifeedants level between two fruit types were quantified in the Human and Primates Nutrition and Ecology Lab (Dept. of Anthropology, Harvard University). For antifeedant analysis, Condensed Tannins (CT), Total Tannins Assayed by Radial Diffusion (RD), Non-detergent Fiber (NDF), Acid-Detergent Fiber (ADF) and Acid Lignin (AL) level were determined. For macronutrients, Crude Protein (CP), Crude Lipids and Free Simple Sugar (FSS) level were quantified. We found that seeds from ER fruits, with strong mechanical protection, contained lower concentrations of CT and fibers and higher concentrations of macronutrients than seeds from acorn fruits. Acorns fruits, because of their thin husks, invest in higher CT and fiber levels to enhance their chemical protection. These seeds are dispersed primarily by scatter-hoarding rodents. Previous research indicates that foraging behavior of these rodents are sensitive to seed size and degree of chemical protection. On Ailo Mt., *L. xylocarpus* (ER) and *L. hancei* (acorn) are co-dominant and sympatric. The coexistence of these closely related species is probably due to a trade-off in seed chemistry and fruit morphology, which causes a radically different response in seed-dispersal by rodents.





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