

**4<sup>TH</sup> TEXAS TECH ANNUAL BIOLOGICAL SCIENCES  
SYMPOSIUM (TTABSS)**

**TEXAS TECH UNIVERSITY DEPARTMENT  
OF BIOLOGICAL SCIENCES LUBBOCK,  
TEXAS  
MARCH 22-23, 2013**

## SPECIAL THANKS TO OUR EVENT SPONSORS



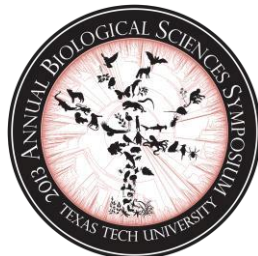
## EVENT CONTRIBUTORS



**PEARSON**

KEY SCIENTIFIC PRODUCTS

**AND EVENT PARTICIPANTS**  
**FISHER SCIENTIFIC**  
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**INTEGRATED DNA TECHNOLOGIES**



*The 2013 TTABSS Logo was produced exclusively for the Association of Biologists at Texas Tech University by  
María Ordóñez-Garza.*

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## WELCOME NOTE

*Welcome to the 4<sup>th</sup> Texas Tech Annual Biological Sciences Symposium –TTABSS 2013. This year the symposium has 140 participants, from eight academic institutions. Seventy-nine participants are graduate and undergraduate students presenting the results of their research. We count with the participation of our distinguished guest speaker, Dr. Richard Stevens. He is a renowned alumnus from Texas Tech University and is presenting part of his research on community ecology of Mojave rodents, including aspects of their phylogenetic structure, spatio-environmental gradients and meta-community dynamics.*

*The themes presented at the symposium cover a wide spectrum of scientific findings, and the diversity of subjects reflects the time and effort of academic advisors, students, and institutions.*

*On behalf of the Organizing Committee of TTABSS 2013, I would like to thank all participants for their incredible involvement to our annual event. I appreciate the enormous efforts of the scientific advisors, session organizers, supporters and hardworking organizing committee members to bring this grand program together. I want to express my deepest gratitude to all of you who have come to this symposium and prepared to share your work and time with others. We will work harder to carry this symposium and the future work of TTUAB forward in the forthcoming years.*

*Wish you all a productive and enjoyable stay!*

*Nicté Ordóñez-Garza  
Local committee chairperson  
President TTUAB 2012-2013*

## **ACKNOWLEDGEMENTS**

### **EVENT HOSTS**

The Association of Biologists at Texas Tech University (TTUAB)  
Department of Biological Sciences  
Museum of Texas Tech University  
American Society of Microbiology (ASM)- TTU Student Chapter  
Department of Natural Resources Management  
The Graduate School at Texas Tech University

**EVENT COLLABORATORS** Association of  
Natural Resource Scientists (ANRS) Department of  
Plant and Soil Science  
Howard Hughes Medical Institute/CISER  
The Institute for Environmental and Human Health (TIEHH)

### **PARTICIPATING UNIVERSITIES/INSTITUTIONS**

Louisiana State University  
Midland College  
McMurry University  
Texas Tech University Health Sciences Center  
University of Florida  
University of St. Thomas  
West Texas A&M University

### **A SPECIAL NOTE**

With the blessings of his wife, Heather Whitlaw, the Department of Natural Resources Management, and the Association of Natural Resource Scientists, the award for the Natural Resource Management & Conservation category was named in 2012 the  
*Warren B. Ballard Memorial Award.*

## ACKNOWLEDGMENTS

If not for the support from the following individuals, TTABSS would not have been possible.

### **TTU ADMINISTRATORS & DEPARTMENT OF BIOLOGICAL SCIENCES STAFF**

Dr. Lou Densmore – Chair, Department of Biological Sciences, TTU  
Mr. David Dorsett – Unit Manager, Experimental Sciences Building, TTU  
Ms. Judy Edwards – Business Manager, Department of Biological Sciences, TTU  
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Dr. Nicky Ladkin – Vice chair Museum Science, Museum of TTU  
Dr. Cameron Saffell – Assistant Director for operations, Museum of TTU

### **POSTER & ORAL PRESENTATION JUDGES**

Dr. Ximena Bernal – Department of Biological Sciences, TTU  
Dr. Robert Bradley – Department of Biological Sciences, TTU  
Dr. Joel Brant – Department of Biology, McMurry University  
Dr. Boyd Butler – Department of Biological Sciences, TTU  
Dr. Deborah Carr – Department of Biological Sciences, TTU  
Mr. Jian Chen – Department of Biological Sciences, TTU  
Dr. Arun Ghosh – Department of Life, Earth & Environmental Sciences, West Texas A&M University  
Dr. Lauren Gollahon – Department of Biological Sciences, TTU  
Dr. Scott Holaday – Department of Biological Sciences, TTU  
Dr. Fan Jia – Department of Biological Sciences, TTU  
Dr. Stephanie Lockwood – Department of Biological Sciences, TTU  
Dr. Paul Mangum – Biology Department, Midland College  
Dr. Nancy McIntyre – Department of Biological Sciences, TTU  
Dr. Amandeep Mittal – Department of Biological Sciences, TTU  
Dr. Matthew Olson – Department of Biological Sciences, TTU  
Dr. Caleb Phillips – Department of Biological Sciences, TTU  
Dr. Bill Resetarits – Department of Biological Sciences, TTU  
Dr. Maria Sagot – Department of Biological Sciences, TTU  
Ms. Juliana Senawi – Department of Biological Sciences, TTU  
Dr. Alon Silberbush – Department of Biological Sciences, TTU  
Dr. Richard Stevens – Department of Biological Sciences, Louisiana State University  
Dr. Rich Strauss – Department of Biological Sciences, TTU  
Dr. Li Wang – Department of Biological Sciences, TTU

Dr. Natasja Van Gestel – Department of Biological Sciences, TTU  
Dr. Zhixin Xie – Department of Biological Sciences, TTU  
Ms. Wei Xu – Department of Biological Sciences, TTU  
Dr. John Zak – Department of Biological Sciences, TTU

**MODERATORS**

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Mr. Lucas Heintzman – Department of Biological Sciences, TTU  
Ms. Amanda Hicks – Department of Biological Sciences, TTU  
Mr. Joe Chun Chia Huang – Department of Biological Sciences, TTU  
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Ms. Courtney Thomason – Department of Biological Sciences, TTU  
Ms. Lizz Waring – Department of Biological Sciences, TTU

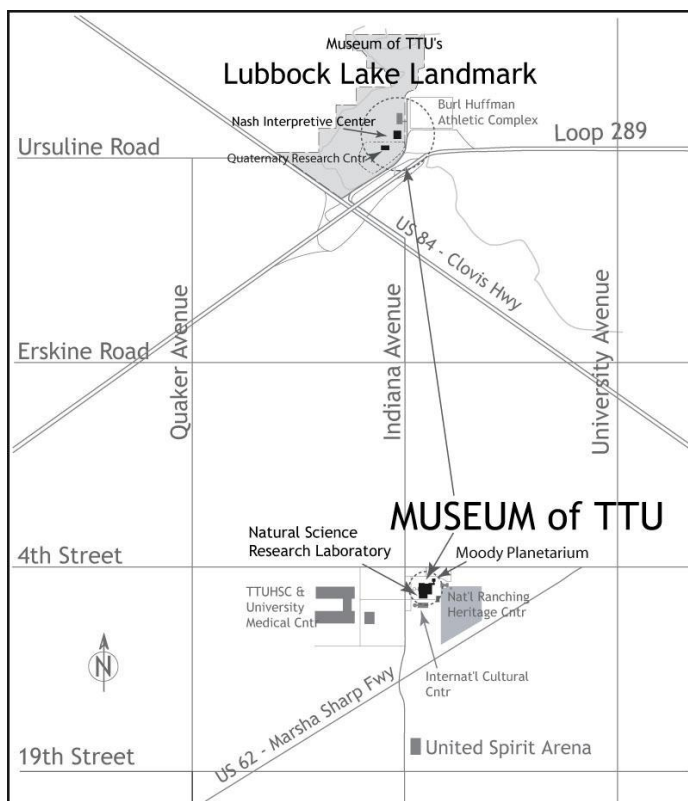
## EVENT LOCATIONS

# HELEN DEVITT JONES AUDITORIUM & SCULPTURE COURT AT THE MUSEUM OF TEXAS TECH UNIVERSITY VENDOR SHOW FRIDAY MARCH 22<sup>ND</sup>, 2013

The main Museum complex is located on the **SE corner of 4th Street and Indiana Avenue (3301 4th Street)**, across from the TTU Health Sciences Center and UMC Hospital. Free public parking is available in 4th Street and Indiana Avenue lots.

### DIRECTIONS

- **From the south on US 84 (Slaton Hwy)**, travel north (becomes Avenue Q) to 4th Street, turn left (west) to Indiana Avenue.
- **From Interstate 27**, take the 4th Street exit, travel west to Indiana Avenue.
- **From the northwest on US 84 (Clovis Hwy)**, travel east to Indiana Avenue and turn right (south) for approximately 1 mile to 4th Street.
- **From the southwest on Marsha Sharp Fwy (US 62)**, exit onto Quaker Avenue north, travel north to 4th Street, then turn right (east).

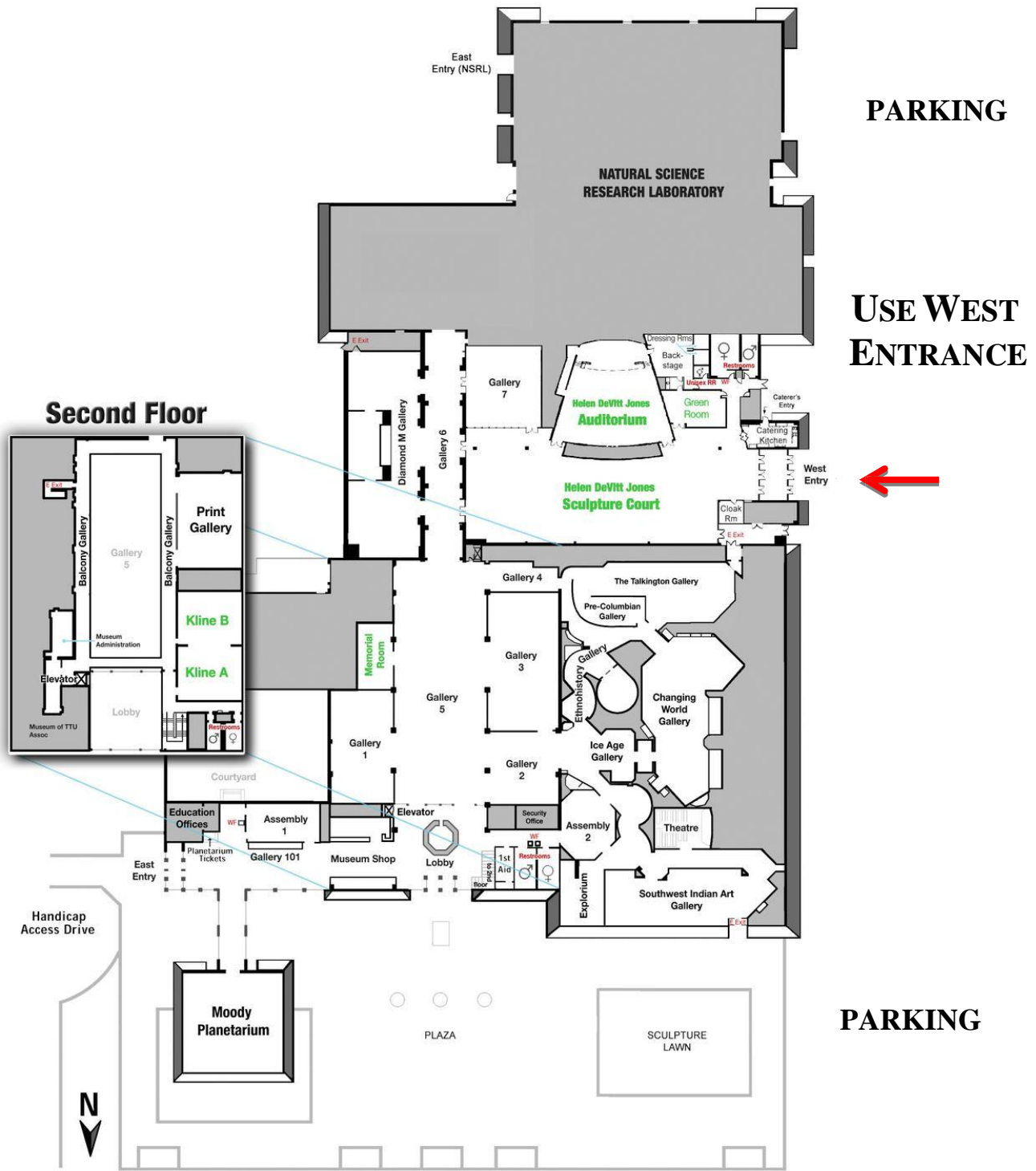


### ADDRESS

3301 Fourth Street  
Box 43191, Lubbock, Texas 79409-3191  
After hours recording and voice mail at  
806.742.2490



# MUSEUM OF TEXAS TECH UNIVERSITY





## LOCAL RESTAURANTS

### ON CAMPUS

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

### WALKING DISTANCE (EAST OF CAMPUS)

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

### SHORT DRIVING DISTANCE (INSIDE LOOP 289)

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

# ASSOCIATION OF BIOLOGISTS AT TEXAS TECH UNIVERSITY

## FACULTY ADVISOR/DEPARTMENT OF BIOLOGICAL SCIENCES CHAIR

Dr. Lou Densmore

## FACULTY CO-ADVISOR

Dr. María Sagot

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Waring

## LOCAL COMMITTEE

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Nicté Ordóñez-Garza

### Poster Competition

Saranya Ganapathy

### Abstract Program

Adam Ferguson

### Registration

Emma K. Roberts

### Social Committee chair

Megan Corley-Keith

### Judge Solicitation and Review

Dr. María Sagot

### Silent Auction

Diana Vargas

### Breaks

Juan Pablo Carrera

### Website

Kenneth D. W. Griffith

### Vendor Solicitation

Soumya M. Sundaram & local committee

**TEXAS TECH ANNUAL BIOLOGICAL SCIENCES SYMPOSIUM 4TH  
ANNUAL MEETING  
22-23 MARCH 2013  
TEXAS TECH UNIVERSITY–LUBBOCK**

**PROGRAM AT A GLANCE**

**FRIDAY, 22 MARCH**

- 5:30 pm – 8:00 pm** Registration – Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University
- 6:00 pm – 9:00 pm** Opening Social & Vendor Show – Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University
- 6:30 pm – 7:30 pm** Poster Session – Helen Devitt Jones auditorium & sculpture court at Museum of Texas Tech University (Poster Hanging 5:30 – 6:00 pm)

**SATURDAY, 23 MARCH**

- 08:00 am – 11:30 am** Registration – BIOL Lobby
- 08:00 am – 08:20 am** Breakfast – BIOL Lobby
- 08:30 am – 08:45 am** Welcome – BIOL 101
- 08:45 am – 09:45 am** Oral Presentations – BIOL 101, BIOL 106, ESB 120
- 09:45 am – 10:15 am** Break – BIOL Lobby
- 10:15 am – 11:45 am** Oral Presentations – BIOL 101, BIOL 106, ESB 120
- 11:45 am – 01:15 pm** Lunch – On Your Own
- 01:15 pm – 02:30 pm** Oral Presentations – BIOL 101, BIOL 106, ESB 120
- 02:30 pm – 02:45 pm** Break – BIOL Lobby
- 02:45 pm – 04:00 pm** Oral Presentations – BIOL 101, BIOL 106, ESB 120
- 03:45 pm – 04:00 pm** Break – BIOL Lobby
- 04:00 pm – 05:00 pm** Plenary Presentation (Dr. Richard Stevens) – BIOL 101
- 05:00 pm – 06:00 pm** Collections & Exhibit Viewing – Museum of Texas Tech University
- 06:00 pm – 09:00 pm** Awards Banquet – Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University

# DETAILED SCHEDULE OF EVENTS

## FRIDAY, 22<sup>ND</sup> MARCH

### REGISTRATION 5:30 – 8:00 PM

*Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University*

### OPENING SOCIAL & VENDOR SHOW 6:00 – 9:00 PM

*Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University*

### POSTER SESSION 6:30 – 7:30 PM

*Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University*

- 1 – MOLECULAR POPULATION GENETICS OF CBF GENES IN BALSAM POPLAR (*P. balsamifera*)  
William J. Barnes\*, Mitra Menon, and Matt S. Olson
- 2 – POPULATION GENETICS STUDY OF THE HUMAN PTC TASTER ALLELE  
Amanda Lyles\*, and Paul Mangum
- 3 – ISLAND PHYLOGEOGRAPHY OF ERYX JACULUS, THE JAVELIN SAND BOA, IN THE AEGEAN SEA  
Elizabeth Mack\*, Stephanos A. Roussos, and Llewellyn D. Densmore
- 4 – A POPULATION GENETICS STUDY OF THE HUMAN PMCT118 VNTR ALLELE  
Benjamyn Ortiz\*, and Paul Mangum
- 5 – AN ACCELERATED PTC FINGERPRINT PROTOCOL  
April R. Smith\*, and Paul Mangum
- 6 – GLOBAL WARMING, INCREASED ALLERGY AND ASTHMA CASES IN TEXAS PANHANDLE AND AHPCO NANOTECHNOLOGY  
Michele Veloz\*, Monica Nuzum, and Nabarun Ghosh
- 7 – POPULATION GENETICS STUDY OF THE HUMAN MITOCHONDRIAL HYPER VARIABLE REGION 2  
Thomas Weathers\*, and Paul Mangum

**POSTER SESSION 6:00 – 9:00 PM**

*Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University*

- 8 – THERMAL TOLERANCE OF COMMON TEXAS ANTS (HYMENOPTERA: FORMICIDAE)  
Victoria C. Young\*, and Robin M. Verble-Pearson
- 9 – IDENTIFICATION AND CHARACTERIZATION OF HETEROCHROMATIN-ASSOCIATED SMALL INTERFERING RNAs IN COTTON (*GOSSYPIUM HIRSUTUM L.*)  
Christian P. Bezboruah\*, Forrest S. Bao, Arnab Ghosh, Gengxiang Jia, Frank Meulewaeter, Thea Wilkins, and Zhixin Xie
- 10 – SEARCH FOR PROXIMATE CUES OF POLYPHENISMS IN FACULTATIVELY PAEDOMORPHIC NEWTS  
Jason R. Bohenek\* and William J. Resetarits, Jr.
- 11 – MORPHOLOGICAL VARIATION IN THE FRINGE-LIPPED BAT *TRACHOPS CIRRHOSUS* (CHIROPTERA: PHYLLOSTOMIDAE): PRELIMINARY RESULTS  
Juan P. Carrera-E\*, and Carleton Phillips
- 12 – MOLECULAR DEVELOPMENT OF THE MID-STAGE ELONGATING COTTON FIBER  
Abhishek Dass\*, Amanda J. Sooter, Komal Kunder, Kameswara Rao Kottapalli, Susan San Francisco, Paxton Payton, and Masoud Zabet-Moghaddam
- 13 – DETECTION OF TELOMERASE BY A PLATE-BOUND MOLECULAR BEACON  
Patrick Dennis\*, and Lauren Gollahon
- 14 – PHYLOGEOGRAPHY AND THE ORIGIN OF FREE-RANGING ELK (*CERVUS ELAPHUS*) IN TEXAS  
Christopher D Dunn\*, Matt R Mauldin, and Robert D. Bradley
- 15 – WHAT INFORMATION DO GRAY TREEFROGS UTILIZE WHEN SELECTING AN OVIPOSITION SITE?  
Lauren L. Eveland\*, William J. Resetarits, Jr.
- 16 – INFLUENCE OF STRESSOR TOLERANCE AND REPRODUCTIVE MODE ON THE INVASIVE POTENTIAL OF THE NON-NATIVE SNAIL *BIOMPHALARIA GLABRATA*  
Meghan A. Funkhouser\*, Stephanie C. Plautz, and Christopher J. Salice

**POSTER SESSION 6:00 – 9:00 PM**

*Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University*

17 – MOLECULAR LANDSCAPE OF COTTON FIBER IN EARLY ELONGATION

Komal Ramesh Kunder\*, Abhishek Dass, Amanda J. Sooter, Masoud Zabet-Moghaddam, Kameswara R. Kottapalli, Paxton Payton, and Susan San Francisco

18 – PRIMING OF NATURAL KILLER CELLS FOLLOWING TRANSENDOTHELIAL MIGRATION MEDIATED BY SPECIFIC CYTOKINES AND CHEMOKINES

Sumit Mukherjee \*, Erin Brown, and William B. Butler

19 – ZONADHESIN - A SPERM PROTEIN INVOLVED IN SPECIES SPECIFIC BINDING TO THE ZONA PELLUCIDA

Archana Muthusubramanian\*, Emma K. Roberts, Robert Bradley and Daniel Hardy

20 – CFTR-GFP LOCALIZATION IN YEAST

Bala meenakshi Purna\*, and Ina L. Urbatsch

21 – CONSTRUCTION OF CYSTEINE MUTANTS TO MONITOR CONFORMATIONAL CHANGES IN P-GLYCOPROTEIN

Anukriti Singh\*, Leo Mok, and Ina L. Urbatsch

22 – MOLECULAR ANALYSIS OF LATE-STAGE FIBER DEVELOPMENT IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM*)

Amanda J Sooter\*, Komal Ramesh Kunder, Abhishek Dass, Kameswara R Kottapalli, Susan San Francisco, Masoud Zabet-Moghaddam, and Paxton Payton

23 – PREVALENCE OF *SALMONELLA ENTERICA*, *ESCHERICHIA COLI* O157:H7 AND NON-O157 SHIGA TOXIN-PRODUCING *E. COLI* IN BEEF CUTS SOLD AT RETAIL MARKETS IN COSTA RICA

Byron D. Chaves\* and Mindy M. Brashears

78 –THE TUMOR-SPECIFIC FUNCTIONS OF INOSINE

Drake Smith\*



**DETAILED SCHEDULE OF EVENTS**  
**SATURDAY, 23<sup>RD</sup> MARCH**

**REGISTRATION 8:30 – 11:30 AM**  
*Department of Biological Sciences, Biology building Lobby*

**CONTINENTAL BREAKFAST 8:00 – 8:25 AM**  
*Department of Biological Sciences, Biology building Lobby*

**WELCOME 8:30 – 8:45 AM**  
*Department of Biological Sciences, Biology building, Room 101*

	<b>CELL &amp; MOLECULAR BIOLOGY</b> Biology 101	<b>ECOLOGY</b> Biology 106	<b>EVOLUTIONARY BIOLOGY</b> Experimental Sciences 120
<b>8:45</b>	24– EVIDENCE FOR AN IMPORTANT ROLE OF MICRORNA-DIRECTED REGULATION OF GENE EXPRESSION IN DEVELOPING COTTON FIBER Arnab Ghosh*, Forrest S. Bao, Christian P. Bezboruah, Gengxiang Jia, Frank Meulewaeter, Thea Wilkins and Zhixin Xie	28– THE ROLE OF HABITAT SELECTION CUES OF AQUATIC COLEOPTERA IN A HABITAT CONTAGION SCENARIO Robert F. Bruner*, William J. Resetarits, Jr.	36– ACOUSTIC INTERACTIONS AND MATING BEHAVIOR OF FROG-BITING MIDGES (DIPTERA: CORETHRELLIDAE) Priyanka de Silva*, Brian Nutter and Ximena E. Bernal
<b>9:00</b>	25– THE INTERACTION OF ZSCAN4 WITH TRF1: EFFECTS ON REGULATION OF TELOMERE ELONGATION IN CANCER CELLS Kyungwoo Lee*, and Lauren Gollahon	29– THE PROBLEM WITH COUNTY-SCALE BIOLOGICAL INVENTORIES Steven D. Collins*, Nancy E. McIntyre	37– SHALLOW COALESCENCE TIMES FOR DIFFERENT SPECIES OF NEW WORLD ARENAVIRUSES Narayan P. Kandel*, and Jorge Salazar-Bravo

	<b>CELL &amp; MOLECULAR BIOLOGY</b> Biology 101	<b>ECOLOGY</b> Biology 106	<b>EVOLUTIONARY BIOLOGY</b> Experimental Sciences 120
<b>9:15</b>	26– COMBINING (HDACIS) AND (4-HPR) ACHIEVES SYNERGISTIC ACTIVITY AGAINST T CELL LYMPHOID MALIGNANCIES IN VITRO AND IN VIVO Monish Ram Makena*, Min H. Kang, Charles P. Reynold	30– THE REPRODUCTIVE PATTERNS OF THREE CAVE-ROOSTING BAT SPECIES (FAMILY: HIPPOSIDERIDAE) FROM A MALAYSIAN TROPICAL RAINFOREST Nurul Ain Elias*, R. Hashim and T. Kingston	38– A TOTAL EVIDENCE APPROACH TO RESOLVING AND DATING RADIATION WITHIN PEROMYSCUS Megan S. Corley-Keith*, Roy N. Platt, and Robert D. Bradley
<b>9:30</b>	27– THE GLUTATHIONE SYNTHESIS INHIBITOR BUTHIONINE SULFOXIMINE SYNERGIZED ANTI-MELANOMA ACTIVITY OF MELPHALAN AGAINST PRECLINICAL MODELS OF MULTIPLE MYLENOMA Ashujit Tagde <sup>1</sup> *, Hardeep Singh <sup>1</sup> , Min Kang <sup>1</sup> and C. Patrick Reynold	31– EFFECT OF ELEVATED TEMPERATURE AND SALINITY ON SWIMMING ENDURANCE OF THE WESTERN MOSQUITOFISH ( <i>GAMBUSIA AFFINIS</i> ) Collin R. Funkhouser* and David L. Rogowski	39– PHYLOGENETIC RELATIONSHIPS OF SOUTHERN AFRICAN RODENTS OF THE GENUS <i>GERBILLISCUS</i> (MURIDAE: GERBILLINAE) Molly M. McDonough*, Caleb D. Phillips, Josef Bryja, Kristofer M. Helgen, Duane A. Schlitter, Vladimír Mazoch, Radim Šumbera, Robert J. Baker
<b>9:45</b>	<b>BREAK</b> Biology Lobby		
	<b>PROPOSAL</b> Biology 101	<b>ECOLOGY</b> Biology 106	<b>EVOLUTIONARY BIOLOGY</b> Experimental Sciences 120
<b>10:15</b>	56– IMPACT OF THE MID-AEGEAN TRENCH IN SHAPING THE PHYLOGEOGRAPHIC PATTERNS OF KOTSCHY'S GECKO Ashish Bashyal*, and Llewellyn D. Densmore	32– HETEROSPECIFIC ALARM CALL RECOGNITION AND UTILI-ZATION IN TIME AND SPACE Amy M. Kuczynski*, and Kenneth A. Schmidt	40– GENETIC VARIATION IN COLD TOLERANCE AMONG NATURAL POPULATIONS OF BALSAM POPLAR ( <i>Populus balsamifera</i> ) Mitra Menon*, Matt S. Olson, and William Barnes
<b>10:30</b>	57– NEOPHILIA ACROSS AN URBAN-RURAL GRADIENT: THE CANE TOAD ( <i>RHINELLA MARINA</i> ) Sarah A. Candler*, Ximena E. Bernal	33– EFFECTS OF HABITAT SIZE AND ISOLATION ON COMMUNITY NESTEDNESS IN A DESERT RIVER SYSTEM Seiji Miyazono*, and Christopher M. Taylor	41– MOLECULAR PHYLOGEOGRAPHY OF THE LONG-NOSED VIPER ( <i>VIPERA AMMODYTES</i> ) IN THE CYCLADES, GREECE Stephanos A. Roussos*, and Llewellyn D. Densmore III

	<b>PROPOSAL</b> Biology 101	<b>ECOLOGY</b> Biology 106	<b>EVOLUTIONARY BIOLOGY</b> Experimental Sciences 120
<b>10:45</b>	58– THE INVOLVEMENT OF PROTEIN PHOSPHATASE 2A IN ABA SIGNALING PATHWAY Jian Chen*, Yinfeng Zhu, Rongbin Hu, and Hong Zhang	34– ANALYSIS OF THE BITE FORCE AND MECHANICAL DESIGN OF FEEDING MECHANISM OF THE MALAYSIAN INSECTIVOROUS BATS Juliana Senawi*, and Tigga Kingston	42– CHROMOSOMAL EVOLUTION AMONG LEAF-NOSED NECTARIVOROUS BATS: EVIDENCE FROM CHROMOSOME PAINTING (PHYLOSTOMIDAE: CHIROPTERA) Cibele G. Sotero-Caio*, Fengtang Yang, Marianne Volleth, Lauren S. Gollahon, Beiyuan Fu, William Cheng, Bee Ling Ng, and Robert J. Baker
<b>11:00</b>	59– MANAGEMENT OF MOSQUITO BORNE DISEASE RISK THROUGH SPATIALLY-EXPLICIT SIMULATION MODELING Daniel E. Dawson*, and Christopher J. Salice	35– AN EXPERIMENTAL APPROACH TO UNCOVERING THE CONSEQUENCES OF PARASITE CO-INFECTION IN <i>PEROMYSCUS</i> Courtney A. Thomason*, Amy B. Pedersen, and Richard E. Strauss	
<b>11:15</b>	60– ENVIRONMENTAL HETEROGENEITY AND INSECTIVOROUS BAT FORAGING ACTIVITY AND SPECIES RICHNESS AROUND TEXAS AGRICULTURAL AREAS AT A SPECIES-SPECIFIC SCALE Marina L. Fisher-Phelps*, and Tigga Kingston		<b>UNDERGRADUATE</b> Experimental Sciences 120 76– ANALYZING INDIRECT EFFECTS ON INVERTEBRATES FROM AN ALLELOPATHIC CHEMICAL RELEASE OF COMMON REED ( <i>PHRAGMITES AUSTRALIS</i> ) Sasha Soto*, Elizabeth Roesler, and David L. Rogowski
<b>11:30</b>	61– TRANSIENT EXPRESSION OF A MODIFIED VIRAL INSECTICIDE IN PLANTS Saranya Ganapathy*, Hong Zhang, and Shan L. Bilimoria		77– THE EFFECTS OF OCEAN ACIDIFICATION AND HYPOXIA ON ELEMENTAL INCORPORATION INTO THE OTOLITHS OF ESTUARINE FISH IN THE GULF OF MEXICO Joshua O. Willms*, Alexander Norton, Tiffany Hedrick-Hopper, Sandra Diamond-Tissue

11:45	<b>LUNCH</b>		
	<b>PROPOSAL</b> Biology 101	<b>TOXICOLOGY</b> Biology 106	<b>PLANT AND SOIL SCIENCE</b> Experimental Sciences 120
<b>1:15</b>	62- EFFECTS OF REDUCED TEMPERATURE VARIABILITY ON SOIL MICROBES IN ARID AND SEMI ARID ECOSYSTEMS Michael L. Hyndman*	69- CO-EXPOSURE TO LA SWEET CRUDE OIL AND DISPERSANT ALTERS GENOMIC DNA DAMAGE OCCURRENCE IN THE GULF KILLIFISH ( <i>FUNDULUS GRANDIS</i> ) Kaylyn E. Germ*, Song Tang, Charles A. Brown, Adam J. Kuhl, Fern Galvez, Christopher C. Green, Greg D. Mayer	48- MULTIDISCIPLINARY APPROACH TO INVESTIGATE THE EFFECTS OF DROUGHT STRESS ON COTTON FIBER QUALITY Zhuanzhuan Ma*, Nouredine Abidi, Eric Hequet, and Junping Chen
<b>1:30</b>	63- EXAMINATION OF FLOODING AS A MECHANISM FOR ALTERING GRAY TREEFROG DEVELOPMENT IN TEMPORARY PONDS Matthew R. Pintar*	70- EXAMINATION OF POLYCYCLIC AROMATIC HYDROCARBONS IN AN URBAN STORMWATER SYSTEM AND BIOACCUMULATION IN ODONATA Lucas J. Heintzman*, Scott M. Starr, Steve D. Collins, Todd A. Anderson, and Nancy E. McIntyre	49- EFFECT OF FIBER MATURITY ON FIBER LENGTH DISTRIBUTION AND YARN EVENNESS PROPERTIES Roji Manandhar*, Eric F. Hequet, Nouredine Abidi, Brendan Kelly, Randy K. Boman, and John Wanjura
<b>1:45</b>	64- ARE VEERIES AFRAID TO SING IN THE DARK: STRUCTURAL CHANGES TO VOCAL COMMUNICATION IN THE PRESENCE OF A PREDATOR Andrea L. Reinhardt*, and Kenneth A. Schmidt	71- CHAINED TO THE PAST: BIOTIC AND ABIOTIC CONDITIONS IN THE PARENTAL ENVIRONMENT ALTER OFFSPRING TOXICANT TOLERANCE Stephanie C. Plautz*, Meghan A. Funkhouser, Christopher J. Salice	50- UNDERSTANDING THE IMPACTS OF WATER QUALITY ON GLYPHOSATE EFFICACY IN THE TEXAS HIGH PLAINS M. R. Manuchehri*, P. A. Dotray, T. S. Morris, and J. W. Keeling
<b>2:00</b>	65- IDENTIFICATION OF A PLASMINOGEN BINDING PROTEIN, ENOLASE, FROM CULTURES OF THE AMPHIBIAN PATHOGEN <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> W. Shalika D. K. Silva*, and Michael J. D. San Francisco	72- INCREASED GROWTH INHIBITION OF BREAST CANCER CELLS BY COMBINATION OF 5-AZA 2'DEOXYCYTIDINE AND (-)-EPIGALLOCATECHIN GALLATE Tulika Tyagi*, Justin N. Treas, and Kamaleshwar P. Singh	51- HETEROLOGOUS EXPRESSION OF A RICE SUMO E3 LIGASE ENHANCES DROUGHT AND HEAT TOLERANCE IN TRANSGENIC COTTON Neelam Mishra*, John Burke, Paxton Payton, and Hong Zhang

	<b>PROPOSAL</b> Biology 101	<b>TOXICOLOGY</b> Biology 106	<b>PLANT AND SOIL SCIENCE</b> Experimental Sciences 120
<b>2:15</b>	66– EFFECTS OF WATER TEMPERATURE ON THE DEVELOPMENT AND SURVIVORSHIP OF THE FAMILIAR BLUET DAMSELFLY ( <i>ENALLAGMA CIVILE</i> ). Scott M. Starr*, Nancy E. McIntyre	73–EFFECTS OF FUNGICIDES AND PHARMACEUTICALS ON SHREDDING DETRIVORE RESPONSES UNDER VARYING TEMPERATURE REGIMES Morgan M. Willming*, and Jonathan D. Maul	52– CONSTITUTIVELY OVER-EXPRESSING A TOMATO FRUCTOKINASE GENE ( <i>LeFRK1</i> ) IN <i>GOSSYPIUM HIRSUTUM</i> L. ENHANCES SEED COTTON YIELD AND FIBER MASS UNDER BOTH WELL-WATERED AND DROUGHT STRESSED CONDITIONS Thiya Mukherjee*, Mariana Ivanova, Marisela Dagda, David Granot, and A. Scott Holaday
<b>2:30</b>		<b>BREAK</b> Biology Lobby	
<b>2:45</b>	67– CALIBRATION OF ALMANAC MODEL FOR SIMULATION GROWTH OF WW-B. DAHL OLD WORLD BLUESTEM Yedan “Victoria” Xiong*, and Charles West	74– POTENTIAL ENDOCRINE ACTIVITY OF PARTICULATE MATTER FROM BEEF CATTLE FEEDLOTS Kimberly J. Wooten*, Brett R. Blackwell, and Philip N. Smith	53– EVALUATION OF QUICKSPIN FOR YARN QUALITY AND DYE UPTAKE ASSESSMENTS Rajeev Rajbhandari*, Nouredine Abidi, Eric. Hequet, and Frank Meulewaeter
<b>3:00</b>	68– CYCLOPROPANE FATTY ACID SYNTHASE IN <i>LEISHMANIA</i> Wei Xu*, Fong-Fu Hsu, and Kai Zhang	75– EPIGALLOCATECHIN-3-GALLATE ABROGATES CYTOTOXICITY AND DNA DAMAGE INDUCED BY BENZO [A] PYRENE IN LUNG EPITHELIAL CELLS Wenbin Zhu*, and Weimin Gao	54– THRIPS (THYSANOPTERA: THIRIPIDAE) TOLERANCE AND FIELD PERFORMANCE OF COTTON ( <i>GOSSYPIUM HIRSUTUM</i> L.) BREEDING LINES AND CULTIVARS UNDER ORGANIC MANAGEMENT Dylan Q. Wann*, Jane K. Dever, Megha N. Parajulee, Mark D. Arnold, and Heather D. Flippin

	<b>PROPOSAL</b> Biology 101	<b>MICROBIOLOGY</b> Biology 106	<b>PLANT AND SOIL SCIENCE</b> Experimental Sciences 120
<b>3:15</b>	79- FACTORS INFLUENCING CHANGES IN VEERY ( <i>CATHARUS FUSCESCENS</i> ) SITE OCCUPANCY WITHIN A BREEDING SEASON Elizabeth A. Farley-Dawson*, and Kenneth A. Schmidt	43- VFR AFFECTS THE FORMATION OF BIOFILM IN <i>PSEUDOMONAS AERUGINOSA</i> Aysegul Balyimez*, Cecily Haley, Phat Tran, and Abdul Hamood	55- SEASONAL CHANGE EFFECTS ON PHOTOSYNTHESIS, NITROGEN METABOLISM, AND SOIL NITROGEN IN COMPETING INVASIVE PHALARIS AURUNDICACEAE AND NATIVE <i>CAREX STRICTA</i> Elizabeth F. Waring*, A. Scott Holaday
<b>3:30</b>		44- IMPACT OF EXTREME SOIL MOISTURE CHANGES AND DECREASED DAILY TEMPERATURE FLUCTUATIONS ON MICROBIAL COMMUNITY STRUCTURE Nirmala Dhungana*, Jennifer Moore-Kucera, Natasja van Gestel, Veronica Acosta-Martinez, and John Zak	<b>NATURAL RESOURCE MANAGEMENT CONSERVATION</b> Experimental Sciences 120 46- THE ECOLOGY AND POTENTIAL VALUE OF BAT COFFEE IN BIODIVERSITY CONSERVATION IN SOUTHWESTERN SUMATRA Joe Chun-Chia Huang*, Elly Rustali Jazdyk Meyner Nusalawo, and Tigga Kingston
<b>3:45</b>		45- THE PRESENCE OF EPIPOLYTHIODIOXOPIPERAZINE (ETP) TOXIN IN <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> Amanda M. Hicks*, and Michael J. San Francisco	47- EFFECT OF SURVEY NUMBER AND DURATION ON DETECTION PROBABILITY OF NORTHERN HARRIER ( <i>CIRCUS CYANEUS</i> ) Ben Skipper*, and Clint Boal

**PLENARY PRESENTATION 4:00 – 5:00 PM**

*Department of Biological Sciences, Biology building Room 101.*

Dr. Richard Stevens

Department of Biological Sciences, Louisiana State University

“Comparative community ecology of Mojave Desert Rodents:  
phylogenetic structure, spatio-environmental gradients and metacommunity  
dynamics”

**COLLECTIONS AND EXHIBITS VIEW 5:00 – 6:00 PM**

*Museum of Texas Tech University*

**AWARDS BANQUET 6:00 – 9:00 PM**

*Helen Devitt Jones auditorium & sculpture court at the Museum of Texas Tech University*

## ABSTRACTS

### POSTER (UNDERGRADUATE)

#### 1- MOLECULAR POPULATION GENETICS OF CBF GENES IN BALSAM POPLAR (*P. BALSAMIFERA*)

William J. Barnes<sup>\*1</sup>, Mitra Menon<sup>1</sup>, and Matt S. Olson<sup>1</sup>

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

*Populus balsamifera* is one of most northern deciduous tree in North America, and has undergone a rapid range expansion due to the last glacial retreat. This resulted in the formation of 3 distinct regions of genetic diversity (Keller et al. 2010). Electrolyte leakage assays and other phenotypic studies on leaves have indicated a strong latitudinal gradient in cold tolerance. To investigate whether this pattern is due to plastic response or local adaptation, we examined the CBF gene pathway, which is known to be up-regulated under cold stress in poplars (Benedict et al. 2006). Using 32 individuals from the Northern and Southern extremes of the population, diversity estimates were calculated for all 6 CBF homologs. Nucleotide diversity estimates for CBF genes ranged from 0.0007 to 0.06, with CBF5 having the highest diversity, and CBF3 having the lowest. CBF2 had higher non-synonymous substitutions that might be indicative of positive selection. Divergence estimates using *P. deltoides*, indicate that CBF6 has significantly diverged. Our estimates of nucleotide diversity using CBF genes do not reiterate the observed pattern of latitudinal gradient in cold tolerance. Future work will investigate differential expression of CBF genes and other putative genes contributing to cold tolerance. This study is a pioneer in understanding the population genetics of cold tolerance in perennials.

#### 2- POPULATION GENETICS STUDY OF THE HUMAN PTC TASTER ALLELE

Amanda Lyle<sup>\*1</sup>, and Paul Mangum<sup>1</sup>

<sup>1</sup>Department of Biology, Midland College, Midland, Texas 79705

The ability to taste Phenylthiocarbamide (PTC) is a genetically dominant trait. A Single Nucleotide Polymorphic (SNP) marker for the gene of this trait has been used to screen the genotypes of DNA samples in a classroom demonstration. Over several years DNA samples were obtained from consenting adults and submitted to the Midland College DNA collection. In the past year self-identified race has also been collected with the DNA samples. These samples were screened and alleles of the PTC taster gene were identified. Analysis of allele frequencies and Hardy-Weinberg Equilibrium was conducted for the DNA population as a whole and within racial groups.

#### 3- ISLAND PHYLOGEOGRAPHY OF *ERYX JACULUS*, THE JAVELIN SAND BOA, IN THE AEGEAN SEA

Elizabeth Mack<sup>1\*</sup>, Stephanos A. Roussos<sup>2</sup>, and Llewellyn D. Densmore<sup>2</sup>

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

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

*Eryx jaculus* is a semi-fossorial sand boa which ranges from Morocco to Iran, including North Africa and several countries of the Balkan Peninsula. In the Aegean Sea, the main Cycladic island group (and its accompanying sand boa population) split from mainland Greece approximately 200,000 years ago. In contrast, the Dodecanese islands split from mainland Turkey much more recently, with the main land bridge breaking up around 20,000 years ago. In addition to these events, the Mid-Aegean Trench (MAT) formed 9-12 million years ago, separating the Aegean into eastern and western halves with corresponding fauna being of European and Asian origin. The complex paleogeography of these islands makes the Aegean an interesting site for phylogeographic studies. Despite a wide geographic distribution, very little is known about *E. jaculus* at the genetic level. This project's focus is to increase the understanding of the evolutionary history of the species by studying the genetic relationships of the populations that occur in



the Cycladic and Dodecanese archipelagos in the Aegean Sea. To determine the phylogenetic relationships of the sand boa populations, the mitochondrial cytochrome *b* gene will be amplified and sequenced, with analyses being performed to determine the relationships between both island groups and between each island group and the corresponding mainland populations. The results of this study will increase the understanding of the evolutionary history of *E. jaculus* populations in the Aegean and will facilitate other scientists looking to study this boa or taxa in similar systems for which there is little available information.

#### **4- A POPULATION GENETICS STUDY OF THE HUMAN PMCT118 VNTR ALLELE**

Benjamyn Ortiz<sup>\*1</sup>, and Paul Mangum<sup>1</sup>

<sup>1</sup>Department of Biology, Midland College, Midland, Texas 79705

The Variable Number Tandem Repeat (VNTR) PMCT118 is used in identification DNA fingerprinting. A protocol was developed for the resolution of this VNTR in the research laboratories at Midland College. DNA samples were obtained from consenting adults and submitted to the Midland College DNA collection along with a self-identified race. These samples were screened and alleles of the PMCT118 VNTR were identified. Analysis of allele frequencies and Hardy-Weinberg Equilibrium was conducted for the DNA population as a whole and within racial groups.

#### **5- AN ACCELERATED PTC FINGERPRINT PROTOCOL**

April R. Smith<sup>\*1</sup>, and Paul Mangum<sup>1</sup>

<sup>1</sup>Department of Biology, Midland College, Midland, Texas 79705

This research project was initiated to shorten the time required to produce a DNA fingerprint that can be used to accurately predict an individual's PTC taste phenotype. The accelerated protocol could then be used in teaching laboratories and for community outreach presentations. Experiments were conducted to determine the time limits required to shorten the standard protocol. The time required to complete the following steps of the protocol were decreased: DNA isolation from human cheek cells, PCR amplification of a 220 bp amplicon, restriction enzyme digestion of the 220 bp PCR amplicon and electrophoresis of the resulting fragments. The goal of the project was to shorten the time required to complete the standard protocol from a minimum of 4 – 6 hours to less than 2 hours using a standard thermocycler and new electrophoresis equipment.

#### **6- GLOBAL WARMING, INCREASED ALLERGY AND ASTHMA CASES IN TEXAS PANHANDLE AND AHPCO NANOTECHNOLOGY**

Michele Veloz<sup>1</sup>, Monica Nuzum<sup>1</sup>, and Nabarun Ghosh<sup>1</sup>

<sup>1</sup>Department of Life, Earth and Environmental Sciences, West Texas A&M University, Canyon, Texas 79015

Global warming exerts substantial effect on flora and fauna. Increasing greenhouse gasses causing accelerated pollinosis and fungal spore production, two major aeroallergens for asthma and allergies. Recently Amarillo-Globe-News reported on rate of Amarillo residents suffering from asthma has increased since 2007 and is twice that of Texas. We have been analyzing the daily aeroallergen by using the coated Melinex tape from the Burkard Volumetric Spore Trap. Exposed, stained Melinex tape was observed under a BX-40 Olympus microscope. 12 years aeroallergen data of Texas Panhandle revealed a gradual shift in aeroallergen index with the warmer climate and a shift in flowering seasons. We assessed an air purifier that uses Advanced Hydrated Photocatalytic Oxidation Technology for net reduction of bacteria, fungi, VOCs with the specific effect on Methicillin resistant *Staphylococcus aureus*, MRSA. A fiberglass chamber was built to evaluate the performance and safety of the air purifiers. Blood, Human cell culture and plant cells were exposed to the AO chamber and The UV chambers to compare the exposures. Images were captured with FITC, TRITC Filters with a BX40 Olympus Microscope. Experiments with Air Oasis air purifiers proved that negative ion purification system is a safe and

effective means of eradicating aeroallergens such as mold and microbes and VOCs from indoor air. Evaluations on safety measures showed no side effect on human cell cultures. Indoor aeroallergens such as, mold spores, airborne bacteria and animal dander reduced significantly on using the air purification units to improve indoor air quality and alleviating breathing ailments.

## **7- POPULATION GENETICS STUDY OF THE HUMAN MITOCHONDRIAL HYPER VARIABLE REGION 2**

Thomas Weathers<sup>\*1</sup>, and Paul Mangum<sup>1</sup>

<sup>1</sup>Department of Biology, Midland College, Midland, Texas 79705

The Hyper Variable Region 2 (HVR2) of mitochondrial DNA is a polymorphic marker on the mitochondrial chromosome. A protocol was developed for the resolution of this HVR2 in the research laboratories at Midland College. DNA samples were obtained from consenting adults and submitted to the Midland College DNA collection along with a self-identified race. These samples were screened and alleles of the HVR2 were identified. Analysis of allele frequencies and Hardy-Weinberg Equilibrium was conducted for the DNA population as a whole and within racial groups.

## **8- THERMAL TOLERANCE OF COMMON TEXAS ANTS (HYMENOPTERA: FORMICIDAE)**

Victoria C. Young<sup>1\*</sup>, and Robin M. Verble-Pearson<sup>1</sup>

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

Ants are nearly ubiquitous in terrestrial environments, occupying diverse habitats and ecological niches. In Texas alone, there are upwards of 200 species of ants. The critical thermal maximum of an organism is the hottest temperature at which it can perform a given function (e.g., foraging, respiring, etc.). Many ants already forage near their thermal maxima; thus, they may be particularly sensitive to warming climates. We examined the critical thermal maxima of common ant species in west Texas. Five workers from each colony were placed in thin plastic vials and submerged in a water bath. The temperature of the water bath was increased 1 degree C per minute until the ants lost the ability to right themselves. The temperature was recorded and plotted against body size. Temperatures were also compared among species and habitat types.

## **POSTER (GRADUATE)**

## **9- IDENTIFICATION AND CHARACTERIZATION OF HETEROCHROMATIN-ASSOCIATED SMALL INTERFERING RNAS IN COTTON (*GOSSYPIUM HIRSUTUM L.*)**

Christian P. Bezboruah<sup>1\*</sup>, Forrest S. Bao<sup>1</sup>, Arnab Ghosh<sup>1</sup>, Gengxiang Jia<sup>1</sup>, Frank Meulewaeter<sup>2</sup>, Thea Wilkins<sup>3</sup>, and Zhixin Xie<sup>1</sup>

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

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<sup>3</sup>Department of Plant and Soil Science, Texas Tech University, Lubbock, Texas 79409

Cotton is the primary renewable source of natural spinnable fiber. Although much effort has been directed to understand the mechanisms of fiber development, the role of DNA methylation in the regulation of fiber gene expression remains largely unknown. Small RNAs (sRNAs) have emerged as an essential regulatory component in both plants and animals. Heterochromatin-associated siRNAs (hc-siRNAs) are a class of 24-nucleotide (nt) endogenous siRNAs that arise from genomic repetitive sequences and function to direct DNA methylation through a process known as RNA-directed DNA methylation (RdDM). As with other sRNA pathways, hc-siRNAs are recruited into an Argonaute (AGO) protein-containing effector complex for their cellular function. In the model plant *Arabidopsis thaliana*, hc-siRNAs have been shown to silence the transcription of homologous repetitive sequences, such as transposable elements (TE) and 5S rDNA repeats by directing DNA methylation at cytosine primarily in CHH sequence context. The *Gossypium hirsutum* genome is much larger than that of the *Arabidopsis* and

contains a much higher proportion of repetitive sequences. Hc-siRNAs are therefore expected to play a much larger role in epigenetic regulation of genome expression in cotton. To explore the regulatory role of sRNA in cotton genome evolution and fiber development, we have initiated a sRNA deep sequencing effort in cotton using Illumina's sRNA-seq platform. Preliminary analysis revealed abundant hc-sRNAs with highly dynamic expression patterns across multiple tissue types and developmental stages. Data from further characterized of a subset of hc-siRNAs that are associated with known TE sequences in cotton will be presented.

## **10- SEARCH FOR PROXIMATE CUES OF POLYPHENISMS IN FACULTATIVELY PAEDOMORPHIC NEWTS**

Jason R. Bohenek<sup>1\*</sup>, and William J. Resetarits, Jr.<sup>1</sup>

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

Polyphenisms are an expression of two or more distinct phenotypes due to variation in the environment. They are hypothesized as important evolutionary mechanisms behind disruptive selection, which can lead to sympatric speciation. Facultative paedomorphic salamanders are polyphenic in that they either metamorphose into terrestrial adults or become sexually mature, aquatic paedomorphs. Environmental cues such as conspecific density and hydroperiod elicit development of different morphotypes from these polyphenic species. However, the proximate cues of how larval salamanders assess density and hydroperiod are unknown. It is unlikely that larval salamanders can assess conspecific density and hydroperiod directly, suggesting that they may cue in on some correlate of either or both. It is hypothesized that competitive interactions affect growth rates which influence morphotype. I plan to improve upon past mesocosm studies in order to determine the more proximate factors affecting facultative paedomorphosis. My objectives are to (1) remove competitive interactions by isolating individuals whilst retaining total conspecific density within mesocosms and (2) test for the presence of semiochemicals by isolating individuals with permeable barriers. If isolated individuals elicit a morphotype response during development, then it is improbable that competitive interactions are the pathway to polyphenism. With competition excluded, it is likely that semiochemicals (wastes or pheromones) are the proximate cues which larvae use to assess conspecific density and/or potential for future growth in that habitat (since density negatively correlates with growth). Understanding the proximate mechanisms behind polyphenisms can lead to great insight concerning life history evolution, population divergence and speciation.

## **11- MORPHOLOGICAL VARIATION IN THE FRINGE-LIPPED BAT *TRACHOPS CIRRHOSUS* (CHIROPTERA: PHYLLOSTOMIDAE): PRELIMINARY RESULTS**

Juan P. Carrera-E<sup>1\*</sup>, and Carleton J. Phillips<sup>1</sup>

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

The fringe-lipped bat *Trachops cirrhosus* (Chiroptera: Phyllostomidae) is distributed from southern Mexico to southern Brazil and Bolivia. Currently there are three recognized subspecies: *T. c. coffini* distributed from Nicaragua to southern Mexico, *T. c. cirrhosus*, distributed from Costa Rica to central Brazil, and *T. c. erdhardi* restricted to southern Brazil. The main objective of this study is to compare the three subspecies using morphological characters to test the species limits within *Trachops cirrhosus*. A total of 121 voucher specimens, representing the whole geographic distribution of *Trachops*, were characterized based on 17 measurements (16 cranial plus the forearm length) and compared using descriptive and multivariate statistics. Skull shape and size variation between sex and among the three subspecies were analyzed. Our analyses suggest that sexual dimorphism is not present in this species and that there is a geographic component influencing the morphological variation among *T. cirrhosus* populations.

## 12- MOLECULAR DEVELOPMENT OF THE MID-STAGE ELONGATING COTTON FIBER

Abhishek Dass<sup>1\*</sup>, Amanda J. Sooter<sup>1</sup>, Komal Kunder<sup>1</sup>, Kameswara Rao Kottapalli<sup>1</sup>, Susan San Francisco<sup>1</sup>, Paxton Payton<sup>2</sup>, and Masoud Zabet-Moghaddam<sup>1</sup>.

<sup>1</sup>Center for Biotechnology and Genomics, Texas Tech University, Lubbock, Texas 79409.

<sup>2</sup>USDA-ARS, Cropping Systems Research Lab, Lubbock, Texas 79415

Cotton fiber is one of the leading natural textile fibers and is the leading value added crop in the USA. The annual business revenue from the cotton industry exceeds \$120 billion. The growth of the cotton fiber is divided into four unique, yet overlapping stages; initiation, elongation, secondary wall biosynthesis and maturation. The quality of the cotton fiber quality is measured in terms of length and strength, which are primarily determined during elongation and secondary wall biosynthesis stages of growth. Here, we analyzed cotton fiber from Upland cotton cv. TM-1 (*Gossypium hirsutum*) at 11 and 17 days post-anthesis (DPA). Paired-end sequencing (Illumina MiSeq) generated 15 million reads from these two libraries and a unique cotton transcriptome database was created using the sequencing data from six stages fiber development (3, 5, 11, 17, 21, and 24 DPA), cotton community transcriptome and cotton D-genome. RNA-Seq analysis of 11 and 17 DPA tissues revealed 3391 differentially expressed transcripts. Annotation and putative gene functions were assigned to the contigs and known functions were mapped onto pathways using MapMan. Preliminary analysis showed differential expression of known marker genes for elongation (primarily down-regulated) and maturation (primarily up-regulated) along with a number of unknown genes. A shotgun proteomics analysis of the same tissues is being performed in parallel with expression studies to provide additional insight into the transition from elongation to maturation and aid in identifying unknown genes and possible roles in fiber quality. Current results on transcript and proteome data will be discussed at this meeting.

## 13- DETECTION OF TELOMERASE BY A PLATE-BOUND MOLECULAR BEACON

Patrick Dennis<sup>1\*</sup>, and Lauren Gollahon<sup>1</sup>

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

Telomerase is a ribonucleoprotein DNA polymerase that confers immortality to transformed cells through the maintenance of tandem, hexameric repeats at the ends of linear chromosomes and is associated with up to 90% of cancers. Since its expression in proliferating cancer cells facilitates the acquisition of genetic perturbations and consequently, malignant phenotypes, telomerase is considered an important biomarker for cancer identification and treatment. One goal of the investigations proposed herein is to further adapt the assay system by incorporation of a biotin-linked MB into the wells of micotitre plates coated with streptavidin. *In vitro* reconstituted telomerase as well as freshly prepared and frozen cell lysates may also be assayed in order to compare the utility of fixed MB to previous iterations. Since the *in vitro* concentration of these targets can be controlled, the detection sensitivity of biotin-SA linked MBs can be determined through construction of a standard calibration curve. Furthermore, by detecting telomerase molecules instead of measurements of enzyme activity, derivation of a standardized range for telomerase molecules that directly associates with stages of cancer progression is also proposed. Additionally, cancers with high telomerase activity are generally more aggressive in phenotype than those with less telomerase activity. Therefore, an assay that determines the molecules of telomerase that are present may represent a more efficient and direct measurement of a tumor's telomerase status since activity can be masked by multiple factors.

## 14- PHYLOGEOGEPGRAPHY AND THE ORIGIN OF FREE-RANKING ELK (*CERVUS ELAPHUS*) IN TEXAS

Christopher D Dunn<sup>1\*</sup>, Matt R Mauldin<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 Sciences Research Laboratory, Museum of Texas Tech University, Lubbock, Texas 79409

The historic range of *Cervus elaphus* included much of the western United States. Natural distributions decreased substantially in the twentieth century almost eliminating the Texas population. In the last 20

years, two herds of free-ranging elk have appeared in the Trans-Pecos region of Texas. It is not known if these two herds are the result of introduction from captive herds, or if they represent natural migrants from New Mexico and Colorado. The purpose of this study is to determine the origin and genetic affinities of *C. elaphus* in western Texas. Hair and ear samples from thirteen individuals will be used to generate genotypes for comparison to wild populations in New Mexico and Colorado. We propose to sequence the mitochondrial Cytochrome-*b* locus to generate haplotype networks to compare *C. elaphus* samples from Texas with those from New Mexico, and Colorado. In addition we will utilize a minimum of seven microsatellite loci to understand the phylogeography and genetic divergence of the various aforementioned populations, which will help determine the origin and the relatedness of the *C. elaphus* herds in Texas.

### **15- OBSERVING THE BEHAVIOR OF GRAY TREEFROGS TOWARDS PREDATOR AFFILIATED HABITATS WHEN SELECSTING A SITE FOR CALLING, AMPLEXUS, AND OVIPOSITION**

Lauren L. Eveland<sup>1\*</sup>, and William J. Resetarits, Jr.<sup>1</sup>

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

The selection of an oviposition site is an extremely crucial decision for amphibians that affects an individual's reproductive fitness. There have been numerous studies looking at abiotic and biotic factors that affect a female's choice of oviposition site. The majority of studies look at egg count to establish habitat choice but have not physically observed female behavior in selecting an oviposition site. I hypothesize that treefrogs have the ability to sense habitats housing predators without having to enter the water. In my proposed experiment I will be physically observing where gray treefrogs choose to call, initiate amplexus, and oviposit. I will be looking at all three activities to see if the males have an effect on female choice. With each of these behaviors I will look at the proximity of the frogs to the experimental tanks with predators present and absent. There are four different proximities I will use to measure the distance of individual treefrogs to the tanks. They are: treefrogs entering the water inside of the tank, individuals perching on the edge of the tank, remaining directly outside of the tank, or individuals have no contact with the tank. The observations will take place on nights with and without rainfall. This will be done to see if there is a difference between behaviors on high and low density nights. This study will provide the evidence to see the actual behaviors of gray treefrogs when they come in contact with habitats consisting of predators.

### **16- INFLUENCE OF STRESSOR TOLERANCE AND REPRODUCTIVE MODE ON THE INVASIVE POTENTIAL OF THE NON-NATIVE SNAIL *BIOMPHALARIA GLABRATA***

Meghan A. Funkhouser<sup>1\*</sup>, Stephanie C. Plautz<sup>1</sup>, and Christopher J. Salice<sup>1</sup>

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Like chemical contaminants, invasive species can be responsible for considerable damage to natural resources. Despite the fact that contaminants and non-native species may frequently co-occur, there has been little research on stress tolerance traits of potential invaders. We were interested in whether a non-native species displayed greater tolerance to environmental stressors than a native species with a similar life history and habitat requirement. We raised two, hermaphroditic freshwater pulmonate snail species, a native wild-caught snail (*Physa pomilia*) and a non-native snail from laboratory cultures (*Biomphalaria glabrata*), either singly or in groups to monitor species differences and the impact of reproductive mode (self-fertilization or outcrossing). While individual *B. glabrata* laid more egg masses per snail per day than snails housed with conspecifics, individual *P. pomilia* laid less than multiples. The offspring of *P. pomilia* were more tolerant than those of *B. glabrata* to salinity and cold, but less tolerant of cadmium, heat, and malathion ( $P \leq 0.05$ ). Offspring from self-fertilization were less tolerant of all stressors than offspring of outcrossed snails ( $P \leq 0.05$ ). Overall, native, wild *P. pomilia* did more poorly than the non-native *B. glabrata* when alone, as may happen in the colonization of a new area. The invasive potential of *B. glabrata* as compared to the native *P. pomilia* is seen by the shorter time to reproduction, greater

reproductive output, and greater tolerance to certain stressors. Also, data here suggest that chemical contamination may predispose certain habitats toward successful establishment of non-native species.

### **17- MOLECULAR LANDSCAPE OF COTTON FIBER IN EARLY ELONGATION**

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Cotton fibers are the dominant source of natural fibers used in the textile industry and contribute significantly to the world economy. Adverse environmental conditions negatively affect fiber characteristics, especially when the fibers are in the elongation phase of development. Improvement in the yield and quality of cotton fibers requires the identification of the molecular networks involved in fiber development. In this research, we have analyzed TM-1 cotton fibers in the early elongation phase, 3 and 5 days post-anthesis (DPA) using RNA-Seq, to identify the genes involved in the different pathways during this stage of fiber development. The *de novo* assembly of the raw reads with NGen identified 20,270 contigs in 3 DPA and 20,339 contigs in 5 DPA. A total of 3,177 transcripts were differentially expressed between 3 DPA and 5 DPA. Mercator annotations revealed several processes linked to fiber development. The up-regulated transcripts at 5 DPA belonged to processes that were involved in cell wall extension, hinting that the fibers at this stage are involved in loosening the cell wall in anticipation of the rapid fiber elongation beyond 5 DPA. In the future, we plan to combine this data with proteomic analysis on the same stages. This is the first report on the generation of a transcriptome and a proteome of the elongating cotton fibers using RNA-Seq. These databases form a significant source of information, and will contribute towards research on the improvement of cotton fiber characteristics.

### **18- PRIMING OF NATURAL KILLER CELLS FOLLOWING TRANSENDOTHELIAL MIGRATION MEDIATED BY SPECIFIC CYTOKINES AND CHEMOKINES**

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Natural Killer (NK) cells must undergo transendothelial migration to locate and kill cancer or virally infected cells. This process is mediated in part by chemokines and cytokines that once secreted at the site of inflammation or tumorigenesis, activate the vascular endothelial cells, thus creating a homing signal for the NK cells. We have observed that when NK cells undergo transendothelial through vascular endothelial cells that have been activated with specific cytokines (TNF- $\alpha$  and TGF- $\beta$ ) and the chemokine (SDF-1 $\alpha$ ), the NK cells become primed. This priming results in a more rapid response with respect to signaling downstream of the NK activation receptor, NKG2D and the integrin LFA-1. This priming effect also promotes a more rapid response by the actin and microtubule cytoskeletons during NK-mediated cytolytic activity. Taken together, transendothelial migration that is mediated by specific cytokines and chemokines serves as a priming mechanism for Natural Killer cells and thus leads to enhanced and more rapid cytotoxicity.

### **19- ZONADHESIN - A SPERM PROTEIN INVOLVED IN SPECIES SPECIFIC BINDING TO THE ZONA PELLUCIDA**

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Zonadhesin is a sperm protein that can bind to the zona pellucida in a species-specific manner. The precursor form of the protein is synthesized only in the testes and later, undergoes processing to produce the mature, active form in spermatozoa. We compared zonadhesin between *Mus musculus* testes and sperm after sequentially extracting them with Triton X-100 and SDS. In sperm, only a fraction of the protein came out with Triton X-100 and it required SDS to extract the protein completely. In contrast, majority of the protein came out with Triton X-100 in testes. From this observation, we hypothesize that zonadhesin gets compacted in a sub-cellular, particulate form once it becomes matured in sperm. The structure of zonadhesin differs from one species to another but is similar in species capable of interbreeding. To understand the evolutionary significance of zonadhesin, we selected rodents like the white footed mouse (*Peromyscus leucopus*) and deer mouse (*Peromyscus maniculatus*). We compared testes samples of *Peromyscus* with that of *Mus musculus* and they showed similarity in protein processing. Thus, this study will serve as a platform to analyze how zonadhesin has evolved in species capable of interbreeding.

## 20- CFTR-GFP LOCALIZATION IN YEAST

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Cystic fibrosis is a lethal genetic disease, caused by mutations in the Cystic Fibrosis Transmembrane Regulator (CFTR) chloride channel protein. To study CFTR, yeasts are suitable for large scale CFTR production because of economic biomass production. The first obstacle with any heterologous CFTR host is to achieve expression of mature, properly folded protein. Several studies on human CFTR expression in baker's yeast, *Saccharomyces cerevisiae* have shown that human CFTR does not traffic to the plasma membrane; instead it is retained in Endoplasmic Reticulum Associated Complexes (ERACs) and is subsequently degraded. We have expressed human CFTR in the brewer's yeast *Pichia pastoris* under the control of a strong inducible promoter (AOX1); however, CFTR purified from this yeast is not active. Consequently, we engineered a Green Fluorescent Protein (GFP) to the C-terminus of CFTR to facilitate localization studies by fluorescence microscopy. We found that CFTR is retained in large intracellular bodies. In contrast, CFTR expressed in *P. pastoris* under a weaker, constitutive promoter (GAP) shows spotted green fluorescence near or at the cell membrane surface suggesting that some CFTR traffics to the plasma membrane in *P. pastoris*, with some sub-plasma membrane clusters similar to ERAC accumulation. Interestingly, preliminary experiments using chemical chaperone glycerol suggest improved surface expression of CFTR in *P. pastoris*-GAP as well as *S. cerevisiae*, possibly as a result of relieving ERAC accumulation. These results show great potential for developing the *P. pastoris*-GAP system for CFTR over-production which will accelerate our investigation on CFTR and the treatment of cystic fibrosis.

## 21- CONSTRUCTION OF CYSTEINE MUTANTS TO MONITOR CONFORMATIONAL CHANGES IN P-GLYCOPROTEIN

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P-glycoprotein (Pgp) is a member of the ATP-binding cassette (ABC) superfamily of transmembrane proteins. Pgp is often found highly expressed in tumor cells and its ability to transport a wide variety of anticancer and chemotherapeutic drugs out of cell can result in multidrug resistance. As such, Pgp is also known as a multidrug resistance (MDR) protein. To better understand the structure-function relationship of Pgp during drug transport, our first goal was to create a cysteine-less mouse Pgp (CL-Pgp). Next,

cysteines were re-introduced back into Pgp at strategic locations using site-directed mutagenesis so that conformational changes during drug transport could later be monitored using biophysical methods. To improve the purification of the wild-type and mutant proteins, we inserted a FLAG epitope (DYKDDDDK) at the C-terminus of the protein. Plasmids encoding mutant constructs were transformed into yeast for functional analysis using drug resistance assays. We found that mutants containing one or two cysteines were active and expressed at levels similar to both the CL-Pgp and wild-type proteins. The tandem affinity purification using the FLAG epitope greatly improved the final purity of Pgp (>90%) and the yield was about 6 mg from a fermentor culture. Taken together, we have successfully created a highly expressed cysteine-less Pgp that with the addition of cysteines at strategic locations, has a high potential to become a very valuable tool with which to study Pgp conformational changes.

## **22- MOLECULAR ANALYSIS OF LATE-STAGE FIBER DEVELOPMENT IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM*)**

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Cotton is the world's most important textile and value-added crop. It plays a crucial role in the economy of Texas – supporting close to 50,000 jobs and supplying \$2 billion to the economy. Its role is even more evident in the state's "South Plains", which supplies approximately 10% of the world's cotton. Understanding molecular events associated with the developing fiber could provide candidate targets for genetic improvement, potentially leading to substantial crop enhancements, in terms of either yield or fiber quality or both, and signifying considerable economic ramifications for the industry. Late-stage (21 and 24 dpa) fiber samples of the TM1 cotton cultivar were subjected to transcriptomic analysis using RNA Sequencing technology (Illumina MiSeq). Using *de novo* assembly in NGen software, the sequence reads with a quality score greater than 30 (9.2 and 7.5 million reads from 21 and 24 dpa, respectively) were assembled into 23942 and 19750 contigs, respectively. RNA-Seq analysis using Array Star revealed 2928 differentially expressed transcripts. Differential expression was defined as those transcripts with 99% confidence and greater than 1.5-fold expression change between 21 and 24 dpa samples. MapMan software was employed to visualize expression profiles at the pathway level. This mapping revealed up-regulation of pectinesterases, pectin lyases, and chromatin remodeling factors, such as DNA methyltransferases and histone deacetylases; and down-regulation of components of cell-signaling. Additionally, changes indicative of dormancy, prior to final maturation appear to begin during this critical phase of fiber development. A complete analysis of this key transition in fiber development will be discussed.

## **23- PREVALENCE OF *SALMONELLA ENTERICA*, *ESCHERICHIA COLI* O157:H7 AND NON-O157 SHIGA TOXIN-PRODUCING *E. COLI* IN BEEF CUTS SOLD AT RETAIL MARKETS IN COSTA RICA**

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In Costa Rica, limited data on the presence of pathogenic bacteria in raw meat products exist. Consequently, this study sought to determine the prevalence of *Salmonella enterica* and seven different Shiga toxin-producing *Escherichia coli* serogroups in retail meat samples collected in urban and rural areas of Costa Rica. Seventy-seven establishments (57 urban, 20 rural) were visited. Three non-visceral beef cuts were purchased at every store and each piece was swabbed individually with a sterile sponge. A PCR protocol was used to assess the presence of *S. enterica* and STEC serogroups O26, O45, O103, O111, O121, O145, and O157. *S. enterica* prevalence was 1.7% (4/231), of which three samples were collected in urban settings and one in rural areas. STEC were deemed positive in 4.8% of the samples (11/231), six in urban stores and five in rural ones. Among the 11 STEC positive samples, 37 serogroup-



specific markers were detected and those for O45, O121, and O103 were the most prevalent, with frequencies of 11/37 (29.7%), 8/37 (21.6%), and 7/37 (18.9%), respectively. Both O26 and O145 serogroups were present at 16.2% (6/37). Serogroups O111 and O157 were not detected. These results may help prioritize food safety policies, interventions, and control measures in this country.

## **78- THE TUMOR-SPECIFIC FUNCTIONS OF INOSINE**

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Most solid tumors contain immunosuppressive concentrations of extracellular adenosine, which are thought to be the primary means for tumor cell immune evasion. Although the tumor-specific mechanisms of adenosine perfusion have been established in detail, the respective functions of adenosine metabolites have yet to be established. The primary byproduct of adenosine metabolism is inosine, which is known to have a wide range of biological activity. Although inosine production is required to maintain immunosuppressive concentrations of adenosine, the additional functions of inosine within the tumor microenvironment remain undetermined. The tumor-specific activity of inosine is investigated here with respect to adenosine, CD73, ADA, AMP deaminase, ADAR-1, Ino-RNA, and relative degree of hypoxia.

## **CELL & MOLECULAR BIOLOGY**

### **24- EVIDENCE FOR AN IMPORTANT ROLE OF MICRORNA-DIRECTED REGULATION OF GENE EXPRESSION IN DEVELOPING COTTON FIBER**

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Cotton is the most important renewable source of natural spinnable fiber. Developing cotton fibers, which are amongst the longest and fastest growing single-celled cellulose-rich trichomes in the plant kingdom, have also emerged as a unique single-celled platform for studying cellulose biosynthesis and cell wall biogenesis. Although much effort has been directed to understand the mechanisms underlying the fiber initiation and development, the regulatory controls of fiber development, including regulation of stage-specific gene expression, remain poorly understood. Small RNAs including microRNA (miRNA) and small interfering RNA (siRNA) are essential regulatory components in both plants and animals. miRNAs are 21-nucleotide (nt) small RNAs that negatively regulate gene expression post-transcriptionally by guiding target cleavage or translational repression through Argonaute (ago)-containing effector complexes. Research over the past decade has firmly established a role of miRNAs in fundamental biological processes such as pattern formation, developmental timing, and response to environmental stress in plants. To uncover the regulatory role of small RNA in cotton fiber development we have launched a small RNA expression profiling effort using Illumina's small RNA deep sequencing (sRNA-seq) platform in the allotetraploid cotton (*Gossypium hirsutum* L.). Preliminary analysis revealed abundant known plant miRNAs expressed in the developing fiber. We have also identified hundreds novel, lineage-specific candidate miRNAs in cotton. Intriguingly, some of these newly identified miRNAs exhibit either fiber-enriched or fiber-specific expression patterns, indicative of active miRNA-directed regulatory mechanisms operating in the developing fiber. Insights from computational prediction and experimental validation of the regulatory targets for these miRNAs will be presented.

### **25- THE INTERACTION OF ZSCAN4 WITH TRF1: EFFECTS ON REGULATION OF TELOMERE ELONGATION IN CANCER CELLS**

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Telomeres are repetitive sequences at the ends of chromosomes protected by DNA binding proteins of shelterin complex that form capping structures. One of these proteins, TRF1, plays a role in the regulation of telomere length through its interaction with other proteins in the shelterin complex. High levels of TRF1 expression have been shown to accelerate telomere shortening, whereas dominant-negative inhibition of TRF1 leads to telomere elongation. Recently, the newly identified Zinc finger and SCAN domain containing4 gene (ZSCAN4) plays a key role in genomic stability by regulating telomere elongation and was shown to co-localize with TRF1 foci. Here, we show that ZSCAN4 is a TRF1 association protein. We hypothesized that ZSCAN4 would affect levels of TRF1 expression and correspondingly control the function of TRF1 through negative regulation and dominant-negative inhibition. Using Co-immunoprecipitation, we demonstrate that ZSCAN4 binds with TRF1 *in vitro*. Pull-down assay results show that ZSCAN4 directly interacts with TRF1. The ZSCAN4 mediated cooperative binding of TRF1 to telomeric DNA has important implications for understanding the mechanism of telomere extension.

## **26- COMBINING HISTONE DEACETYLASE INHIBITORS (HDACIS) AND THE CYTOTOXIC RETINOID FENRETINIDE (4-HPR) ACHIEVES SYNERGISTIC ACTIVITY AGAINST T CELL LYMPHOID MALIGNANCIES *IN VITRO* AND *IN VIVO***

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T-cell lymphoid malignancies (TCLM) are a therapeutic challenge with dismal five-year survival rates. Histone deacetylase inhibitors (HDACIs), which interfere with the function of histone deacetylases and Fenretinide (4-HPR) a synthetic cytotoxic retinoid, have shown therapeutic activity in TCLM clinical trials as single agents. We sought to determine whether these two different classes of drugs with different mechanisms of action could achieve synergistic anti-cancer activity in preclinical models of TCLM *In vitro* Cytotoxicity was assessed by combining the two FDA approved HDACIs, vorinostat (0-3  $\mu$ M) and romidepsin (0-5nM) respectively with fenretinide (0-10  $\mu$ M) using the DIMSCAN assay. Synergy was quantified using CalcuSyn<sup>TM</sup> software. Mitochondrial depolarization was measured by using JC-1 staining, caspase activity and acetylation of histone H3 by immunoblotting, and apoptosis (DNA fragmentation) by TdT labeling (TUNEL). *In vivo* activity of HDACI+fenretinide + ketoconazole combination was investigated in a subcutaneous xenograft model. The combination of HDACIs and 4-HPR synergistically enhanced cytotoxicity *in vitro* and induced multi-log cell kills (combination index < 0.7) in all 13 cell lines tested. The combination achieved a significant increase in the loss of mitochondrial membrane potential ( $p < 0.01$ ), DNA fragmentation ( $p < 0.01$ ), cleavage of caspase-9, 3, 8, and PARP compared with single agents ( $p < 0.05$ ). The xenograft studies indicated a substantial tumor growth delay ( $p < 0.01$ ) in the combination group compared to other groups. Our data shows a clear synergy between the novel combination HDACi and 4-HPR in TCLM. We are currently investigating the mechanism of synergy and testing additional xenograft models to consolidate our observation.

## **27- THE GLUTATHIONE SYNTHESIS INHIBITOR BUTHIONINE SULFOXIMINE SYNERGIZED ANTI-MYELOMA ACTIVITY OF MELPHALAN AGAINST PRECLINICAL MODELS OF MULTIPLE MYELOMA**

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Multiple myeloma (MM) is a hematological cancer causing nearly 10,000 deaths per year. It is commonly treated with the myeloablative doses of melphalan (L-PAM) + stem cell transplantation (SCT). Relapse after SCT is common. Glutathione (GSH) is an antioxidant that protects cells against xenobiotics. Enhanced GSH is one known mechanism of L-PAM resistance. Buthionine sulfoximine (BSO) inhibits synthesis of GSH. We investigated the potential for BSO to enhance activity of L-PAM against *in vitro*

and in vivo models of MM. Cytotoxicity was assessed using the DIMSCAN assay. Single-strand DNA (ssDNA) damage was measured by F7-26, apoptosis by TUNEL, mitochondrial depolarization by JC-1 staining and caspase activity by immunoblots. GSH was determined by HPLC. In vivo activity of BSO + L-PAM was investigated in the 3 xenograft models. BSO significantly depleted GSH ( $p < 0.05$ ), caused 2-4 logs enhancement of L-PAM cytotoxicity. Combination induced a significant increase in ssDNA damage ( $p < 0.01$ ), mitochondrial depolarization ( $p < 0.001$ ), DNA fragmentation ( $p < 0.001$ ), cleavage of caspase-9, caspase-3, and PARP ( $p < 0.05$ ), complete response (CR) in 21/25 mice, MCR in 6/25 mice, 2.25 fold increase ( $p < 0.001$ ) in the median EFS (49.5 days) as compared to L-PAM alone (22 days) and significantly enhanced ( $p < 0.01$ ) the percentage of apoptotic cells in vivo as compare to single agents and control. Depletion of GSH with BSO enhanced the activity of L-PAM in MM cell lines in vitro and in xenografts. Combining BSO with L-PAM warrants clinical testing in recurrent MM.

## **ECOLOGY**

### **28- THE ROLE OF HABITAT SELECTION CUES OF AQUATIC COLEOPTERA IN A HABITAT CONTAGION SCENARIO**

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Insects are a critical component of many communities. Habitat selection plays a role in the oviposition site choices made by these organisms; the quality of site will determine the future fitness of any offspring, which will in turn influence the structure of the community. However, how these organisms choose their habitat is not yet fully understood. By examining the incorporation of environmental stimuli into an organism's decision-making process, we can begin to construct a framework for predicting the habitat selection choices of these insects. We propose a study to test the hypothesis that different gradients of shade and concentrations of plant volatile chemicals will discourage colonization of aquatic beetle species, and that these cues will create an effect similar to a habitat contagion scenario. In two separate experiments, insects will be allowed to colonize an artificial mesocosm array that simulates their natural oviposition sites. One experiment will be composed of treatments of varying gradients of artificial and natural shading as well as gradients of extracts from local flora. The second experiment will use these cues to test if a contagion effect exists with either of these cues following the methodology used in previous research into aquatic insect habitat selection. While a wealth of research studying the impact of plant volatiles and other effects exists in the subject of host-plant selection with insects, these concepts have yet to be applied to habitat selection research with regards to aquatic insects.

### **29- THE PROBLEM WITH COUNTY-SCALE BIOLOGICAL INVENTORIES**

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The use of counties as an indication of species occurrence in many U.S. citizen science databases is often an artifact of imprecise historical data and early distribution cataloging. The value of these centralized databases is now being realized for developing species distribution models (SDMs), though modelers must be cautious, since as many as 80% of records may be only associated with county centroids and not more precise locality information. Associating species presence localities with the correct environmental attributes is important for SDMs, yet environmental conditions can vary substantially within a U.S. county, with greater variability associated with larger and mountainous counties. SDMs were developed in Maxent v3.3.3k using bioclimatic parameters derived from PRISM, a gridded climate dataset for the contiguous U.S., for 284 and 232 species of odonata (dragonflies and damselflies) and butterflies, respectively, using the OdonataCentral and Butterflies and Moths of North America citizen science databases. Having filtered each database to only include one species record per county, separate SDMs were developed and compared 1) using precise localities and 2) using corresponding county centroids. County centroid models overpredicted the areal extent of suitable habitat by 14% on average (range: -

68% to 368%). Larger sample sizes reduced the disparity. Quantifying the variance of environmental parameters across U.S. counties may permit county centroid data to be filtered and included when developing SDMs.

### **30- THE REPRODUCTIVE PATTERNS OF THREE CAVE-ROOSTING BAT SPECIES (FAMILY: HIPPOSIDERIDAE) FROM A MALAYSIAN TROPICAL RAINFOREST**

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High energetic and nutritional demands during pregnancy and lactation, force bat species inhabiting seasonal regions to breed when food is abundant. Failure to match parturition with food availability, may incur in high individual fitness costs. If such mismatch occurs repeatedly; it can lead to population declines. In this study, we determined reproductive patterns in three insectivorous cave-roosting bats: *Hipposideros bicolor* 142-kHz, *H. cervinus* and *H. diadema*. We also investigated the correlation between reproductive patterns and local climate. Bats were trapped in five consecutive nights per week, from February 2009 to October 2010, at Krau Wildlife Reserve, Malaysia. We also visited nearby caves once a month during the study period. Rainfall and temperature were recorded using HOBO Automated Weather Station. Female reproductive assessment was performed by observation and external palpation. The study area was characterized by two rainy seasons (first: April-May; second: October-November). We found that these hipposiderids species have a restricted seasonal monoestrus reproductive pattern. Pregnancy was detected only during the first wet season. The highest percentage of pregnant females was found before the peak of rainfall. These bats started giving birth in April. Lactation period for *H. diadema* and *H. bicolor* 142-kHz was correlated with the peak of the first rainy season, with, *H. diadema* showing the shortest period (three months). Meanwhile, *H. cervinus* had the highest percentage of lactating females after the peak of the first rainy season. In conclusion, we suggest that rainfall indirectly induce reproductive timing by affecting local temperature and the availability of food.

### **31- EFFECT OF ELEVATED TEMPERATURE AND SALINITY ON SWIMMING ENDURANCE OF THE WESTERN MOSQUITOFISH (*GAMBUSIA AFFINIS*)**

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Climate and anthropogenic changes are predicted to increase temperatures and salinities in aquatic systems. These changes may negatively affect a variety of aquatic species. By testing swimming performance one can assess the potential impacts of increased temperatures and salinity (specific conductance) on the physiology of exothermic organisms. We used the western mosquitofish, *Gambusia affinis*, as our study organism. Twenty fish were exposed to either, temperature (23, 26, 30°C) or specific conductance (900, 10,000, 17,000  $\mu\text{S}/\text{cm}^2$ ), and exercised individually in a flume at a water velocity of 0.2m/s. Time to exhaustion was recorded when the fish was no longer able to maintain its position in the water column and was ejected from the flume. Temperature had no significant effect on time to exhaustion, though specific conductance did ( $F_{1, 59}=4.4$ ,  $p=0.04$ ). At the higher and lower specific conductances (900 and 17,000 $\mu\text{S}/\text{cm}^2$ ) time to exhaustion was significantly less than the control at 10,000  $\mu\text{S}/\text{cm}^2$ . Sex had no effect on time to exhaustion for either the temperature or specific conductance trials.

These results showed consistent swimming performance of *G. affinis* across a seven degree range of temperature, but decreasing performance with elevated specific conductance (salinity). These tolerances may potentially provide *G. affinis* an advantage over less tolerant native species as climate continues to change and habitats are altered.

### **32- HETEROSPECIFIC ALARM CALL RECOGNITION AND UTILIZATION IN TIME AND SPACE**

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As prey move through a landscape and perform their daily activities they must also avoid their predators. Predation risk can vary spatially and temporally; thus information about predation risk is seldom perfect and this creates a challenge for prey. Information from the soundscape (i.e., alarm calls), about predation risk can provide an animal valuable information about predator location, so they can make more informed decisions and can potentially have extra time in which to make those decisions. If alarm calls are reliably associated with an increase in perceived predation risk, it behooves an individual to respond, given the high costs of not responding. This should be true of both conspecifics and heterospecifics that share predators. Gray duikers are small, nocturnal antelope that occur sympatrically and share the same predators as another antelope species, the bushbuck, which produce an alarm call or ‘bark’ when encountering or spotting a leopard. Optimal foraging theory provides a technique, called giving-up densities (GUDs), which can be used to quantify perceived predation risk over time and space. I conducted a playback experiment to test if gray duiker recognize and utilize bushbuck alarm calls in adjusting their perceived predation risk by collecting GUDs and traditional vigilance measures. GUDs were significantly lower while scan rate and percent time vigilant were significantly higher during alarm calls nights. While this approach is valuable to quantify an individual’s perceived predation risk, it is insufficient to reveal perceived risk at a larger spatial scale or follow changes in perceived predation risk temporally.

### **33- EFFECTS OF HABITAT SIZE AND ISOLATION ON COMMUNITY NESTEDNESS IN A DESERT RIVER SYSTEM**

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Habitat fragmentation is one of the major threats causing local and regional species extinctions in freshwater ecosystems. It is important to understand how habitat size and isolation affect species occupancy patterns to predict the potential sequence of extinctions due to fragmentation of the river continuum. We examined fish nested subset patterns in relation to habitat isolation and size in the Rio Grande and its tributaries in the Trans-Pecos region of Texas, USA. Our results indicated that fish assemblages showed significant nested subset patterns across our study sites, and the importance of habitat size and isolation on the nested subset patterns varied with spatial scale. Certain non-native fish taxa were idiosyncratic, reducing the strength of the nested subset pattern. Increasing the spatial scale of the study system likely resulted in an increased ability to detect dispersal limitation between the mainstream and its tributaries. Our results suggest that increased habitat fragmentation by the human activities can accelerate the regional extinction of certain native fish taxa and the dominance of ecologically tolerant, possibly nonnative fish taxa, leading to a decline in regional diversity.

### **34- ANALYSIS OF THE BITE FORCE AND MECHANICAL DESIGN OF FEEDING MECHANISM OF THE MALAYSIAN INSECTIVOROUS BATS**

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Malaysia’s rainforest are home to the greatest diversity of bats species in the Old World. This outstanding diversity is likely achieved through an intricate partitioning of the available resources within the habitat. Differences in food processing capabilities, particularly bite force, may further mediate resource portioning in species-rich assemblage. However experimental data documenting that biting ability (bite force) at the assemblage level is limited. Here, we examine the correlation between morphological

variation and bite force capacity of 37 species from six families of insectivorous bats from Krau Wildlife Reserve (KWR). We find that bite force correlates strongly with head and body dimensions. However we also find that bite force is predicted more strongly by head length, which exceeds all head dimensions (head height and head width) in predictive strength. In understanding the relationship between bite force and morphology, the mechanical advantage that generated from relevance morphology has also been considered. The explanation and consequences of these findings for structuring mechanism in monophagous assemblages are discussed.

### **35- AN EXPERIMENTAL APPROACH TO UNCOVERING THE CONSEQUENCES OF PARASITE CO-INFECTION IN *PEROMYSCUS***

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Infectious diseases are ubiquitous in nature and can be strong selective forces for the evolution of wild populations. In nature, hosts are commonly infected with multiple parasite species simultaneously, yet most research has focused on single parasite infections. We conducted a perturbation experiment designed to remove nematodes and disrupt the parasite community of a wild rodent host, *Peromyscus* mice, at Mountain Lake Biological Station (VA) to determine how interactions between co-infecting parasites impact mouse fitness and health. Nearly all captured mice (95%) were infected with parasites, and co-infection was very common, with 73% of mice infected by at least 2 parasite species. On average, mice were simultaneously infected with  $3.09 \pm 0.08$  SE parasite species. Nematode removal, via antihelmintic drug treatment, significantly reduced the burden of nematode infections, but unexpectedly also resulted in a reciprocal increase in non-target parasites, specifically coccidial protozoans. In addition, mice with low nematode burdens that were treated with the antihelmintic were recaptured significantly less than control mice with similar nematode burdens, suggesting a possible negative effect of treatment. In contrast, there was no effect of treatment on survival in mice with high nematode infection burdens. A similar, but reciprocal, interaction was found in treated mice with low burdens of the non-target parasites, coccidial protozoans; here antihelmintic treated mice were recaptured significantly longer than control mice. These unexpected results provide evidence that co-infecting parasites may be directly or indirectly interacting within the host, and that drug treatment could have unintended consequences for host survival because of these interactions.

## **EVOLUTIONARY BIOLOGY**

### **36- ACOUSTIC INTERACTIONS AND MATING BEHAVIOR OF FROG - BITING MIDGES (DIPTERA: CORETHRELLIDAE)**

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Swarming is the most common aggregation behavior shown by lower flies (Nematocera) when mating. Sound is the main communication channel in such mating swarms. Swarming has been observed in the wild and in laboratory colonies of mosquitoes (Culicidae) and phantom midges (Chaoboridae), but is assumed to be absent in frog-biting midges (Corethrellidae), their sister taxa. Corethrellidae is a monogeneric family that includes about 100 species of frog-biting midges (*Corethrella* spp). In contrast to mosquitoes, female frog-biting midges obtain a blood meal for egg development by eavesdropping on the mating calls of anurans. Here we describe the previously unknown mating behavior and the wing beat sounds potentially used in mating in frog-biting midges. We video recorded the mating behavior of individuals in a laboratory colony of *Corethrella appendiculata*. Contrary to previous speculations, we

find that frog-biting midges aggregate in mating swarms. We recorded the wing beat sounds of mating swarms of frog biting midges and individual flight tones using particle velocity microphone. Here we report the free flight recordings of naturally forming mating swarms and the individual flight tone frequencies of both sexes of frog-biting midges. We contrast our findings to the well known mating behaviors and the flight tones of mosquitoes. We ultimately begin to explore whether responding to acoustic mating signals has been co-opted over evolutionary time to exploit the communication system of anurans for foraging.

### **37- SHALLOW COALESCENCE TIMES FOR DIFFERENT SPECIES OF NEW WORLD ARENAVIRUSES**

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Arenaviruses are single stranded RNA viruses many of which are associated with zoonotic diseases. In the Americas, pathogenic species of New World Arenaviruses (NWA) cause hemorrhagic fevers with some reaching mortality rates above 30%. In most cases, viral transmission is thought to occur via contact with excreta of infected rodents. It has been hypothesized that NWA originated from the Old World Arenaviruses (OWA). The high genetic diversity within some worldwide strains (e.g., LCMV) of OWA has been attributed to the long and complex phylogeographic history of the reservoir rodent host in Europe. Given these factors, we hypothesize that NWA strains are much younger than their old world counterparts. We collected 35 to 43 partial sequences (nucleoprotein or glycoprotein or both genes) of Guanarito, Pirital, Machupo, and Junin viruses, originating from humans and rodents in South America between the time periods of 1958 to 2008. Following alignment, and once we discarded genetic recombination as a potential confounding factor we fit the best nucleotide substitution model, and estimated substitution rates and times to most recent common ancestor (TMRCA) with a Bayesian approximation in BEAST. We estimated the average rate of evolution to be 8.15E-04 substitution/site/year. Although very fast evolutionary rates are estimated for many RNA viruses, this is the first report we present here for NWA. In addition, coalescence times were estimated at 517 years, on average. These findings indicate that these viruses are probably recently emerging and have shallower coalescence time in the South America compared to OWA.

### **38- A TOTAL EVIDENCE APPROACH TO RESOLVING AND DATING RADIATIONS WITHIN PEROMYSCUS**

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Numerous studies have examined the subfamily Neotominae utilizing morphological, allozyme, or karyotypic data, as well as mitochondrial and nuclear DNA sequences. These studies have led to various taxonomic arrangements and numerous interpretations of relationships at the generic level most likely due to a rapid radiation event. Most interpretations as to how many genera should be recognized within the Neotominae center around the definition of *Peromyscus*. Do relationships within *Peromyscus* follow a *sensu stricto* interpretation where morphologically divergent taxa are recognized as genera following Carleton (1980, 1989) or a *sensu lato* interpretation in which *Peromyscus* contains multiple subgenera as proposed by Osgood (1909), Hooper (1968), Bradley et al. (2007), and Platt et al. (submitted)? Recent molecular data suggests that *Peromyscus (sensu stricto)* should be abandoned due to its paraphyletic nature and that the most logical solution would be to subsume all genera and subgenera formerly recognized within *Peromyscus (sensu lato)* excluding *Isthmomys*, to the species group level within a single genus (*Peromyscus*-Platt et al. submitted). We reanalyzed Carleton's 1980 dataset with more recent phylogenetic methods and combined the morphological data with genetic data to determine if a

total evidence approach provides better resolution for relationships within the Neotominae. In addition, the genetic data was used to determine divergences times for the genera recognized within *Peromyscus*.

### **39- PHYLOGENETIC RELATIONSHIPS OF SOUTHERN AFRICAN RODENTS OF THE GENUS *GERBILLISCUS* (MURIDAE: GERBILLINAE)**

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The murid rodent genus *Gerbilliscus* is widespread and abundant throughout sub-Saharan Africa. Several molecular and morphological studies have examined the evolutionary relationships of this genus in eastern and western Africa. However, to date no study has produced a complete phylogeny for the southern African forms. The most recent checklist for this group suggests that the genus contains at least six species in the southern Subregion. Herein, we estimate the number of species and the evolutionary relationships of the southern African *Gerbilliscus* using sequence data from mitochondrial cytochrome-*b* and cytochrome oxidase I, sequences from nuclear Y-chromosome markers, and nuclear AFLPs. Coalescent modeling indicates that the southern African forms originated from east Africa with a subsequent radiation into southern Africa at times that correspond to African savannah expansion during the Pleistocene. Our data also indicate that diversity within southern African *Gerbilliscus* is currently underrepresented and warrants specific taxonomic attention to accurately define species boundaries within this group and region.

### **40- GENETIC VARIATION IN COLD TOLERANCE AMONG NATURAL POPULATIONS OF BALSAM POPLAR (*POPULUS BALSAMIFERA*)**

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For species with wide geographical distribution, such as *Populus balsamifera*, it is important to disentangle the role of plasticity and adaptive response contributing to their ability to survive in wide range of environmental conditions. This study focused on understanding the mechanism of cold acclimation in annual tissues (leaves) of *Populus balsamifera* and identifying signals of local adaptation, if any. To address the first question we conducted electrolyte leakage assay and supercooling assay on 25 individuals each from the Northern and Southern range. Comparisons of LT50 and supercooling temperature revealed that leaves use cold tolerance as a mechanism to withstand cold stress. Using the phenotypic data we were able to demonstrate strong latitudinal and seasonal gradients in cold tolerance. To address the second question about adaptive response to selective pressures, we examined patterns of genetic variation in all 6 CBF homologs using 16 individuals from the Northern and Southern edge of the distribution. Our results indicate that CBF3 has much reduced levels of nucleotide diversity and CBF5 had the highest estimated nucleotide diversity. Surprisingly, CBF2 had higher non-synonymous polymorphic sites and hence might be indicative of balancing selection. Divergence estimates using *Populus deltoides* as an out-group were significant only for CBF6 at  $P < 0.05$ . Further work is underway to ascertain the role of CBF genes in cold tolerance. This study provides a valuable insight into the population genetics of cold tolerance genes in trees and hence is a basis for further investigation on the underlying genetics of cold tolerance in trees.



#### **41- MOLECULAR PHYLOGEOGRAPHY OF THE LONG-NOSED VIPER (*VIPERA AMMODYTES*) IN THE CYCLADES, GREECE**

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The Cyclades are a group of 220 land-bridge islands in the Aegean Sea that have undergone several fragmentation events correlated with the Pleistocene glaciations. The archipelago last separated from mainland Greece about 200 thousand years ago (Kya), forming one large island (~6,500 km<sup>2</sup>) in the middle of the Aegean that was isolated during the last Pleistocene glaciation. This large island further fragmented into 30 large islands and dozens of satellite islands over the last 16 Kya as the Aegean Sea rose 120 meters to its current level. *Vipera ammodytes*, the long-nosed viper, is a widespread species in the Balkans and is found on 15 of the Cycladic islands. To understand the evolutionary relationships these insular populations have between each other and their mainland conspecifics, I analyzed sequences of mitochondrial DNA fragments of the two control regions (CR1 & CR2) and the ribosomal gene 16S. Using Maximum Likelihood and Maximum Parsimony methods, I was able to reveal the phylogenetic structure found within the viper populations of the Cycladic archipelago and relate it to the paleogeography of the islands. This is the first study on the genetics of these insular populations, allowing us to understand the island phylogeography of the species. This system not only provides a model for the evolutionary effects of fragmentation on terrestrially bound island fauna, but also provides essential information for future conservation of these unique islands.

#### **42- CHROMOSOMAL EVOLUTION AMONG LEAF-NOSED NECTARIVOROUS BATS: EVIDENCE FROM CHROMOSOME PAINTING (PHYLLOSTOMIDAE: CHIROPTERA)**

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The family Phyllostomidae represents a lineage of Chiroptera marked by unprecedented morphological/ecological diversity among mammalian families and by extensive intergeneric chromosomal reorganization. There is still controversy regarding their systematic relationships due to morphological convergence among some groups. Their history of karyotypic change has yet to be elucidated. To help understand the evolutionary relationships within Phyllostomidae, chromosome paints were developed from *Macrotus californicus*, a species with a proposed basal karyotype. Looking for chromosomal signatures within two lineages of nectarivorous phyllostomids whose independent origins have been strongly supported by molecular phylogenies, we tested the potential importance of these paints as phylogenetic tools. By examining chromosomal homologies among two representatives of the subfamily Glossophaginae (*Glossophaga soricina* and *Anoura cultrata*) and one from the subfamily Lonchophyllinae (*Lonchophylla concava*), the hypothesis that chromosomal rearrangements documented the independent origins of the Glossophaginae and Lonchophyllinae could not be rejected. Corresponding human chromosomal segments were also identified in the species analyzed. Furthermore, two chromosomal signatures uniting *G. soricina* and *A. cultrata* were observed. In summary, the chromosome painting data revealed extensive chromosomal reorganization among *M. californicus* and nectarivorous phyllostomids, with *G. soricina* demonstrating the greatest number of conserved ancestral chromosomes. This data suggests that the evolution of nectar-feeding bats occurs primarily through the reshuffling of Evolutionary Conserved Units (ECUs). Robertsonian fusions/ fissions and inversions appear to be important modifiers of phyllostomid karyotypes, and autapomorphic traits are common within species. Thus, *M. californicus* chromosome paints will be a valuable tool for documenting the pattern of karyotypic evolution within Phyllostomidae.

## MICROBIOLOGY

### 43- VFR AFFECTS THE FORMATION OF BIOFILM IN *PSEUDOMONAS AERUGINOSA*

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*Pseudomonas aeruginosa* is a gram negative opportunistic pathogen that causes serious infections in immunocompromised hosts including cystic fibrosis patients, severely burned patients, and cancer patient undergoing chemotherapy. The production of *P. aeruginosa* virulence factors is regulated by several global regulators including the virulence factors regulator, Vfr. Among the different factors that contribute to the virulence of *P. aeruginosa* is its ability to form a biofilm, a community within which bacteria are attached to a surface or to each other. Biofilm development occurs in stages that require specific bacterial factors at each stage. During the initial (attachment) stage of biofilm formation, bacteria depend on both the flagellum mediated swimming motility and the pili-mediated twitching motility. In this study, we have showed that vfr affects the biofilm formation in *P.aeruginosa* in vitro and in vivo. We compared the development of biofilm on plastic coverslips and cellulose surfaces by PAO1 and PAO1Δvfr. Compared with PAO1, PAO1Δvfr produced significantly reduced biofilms on both surfaces. We then examined the development of biofilm in vivo using PAO1 and PAO1Δvfr and showed that PAO1Δvfr produced significantly reduced biofilm. To examine at which stage vfr affects the biofilm formation, we tested the effect of vfr on twitching and swimming motility. PAO1Δvfr was defective in twitching motility but not swimming when compared to PAO1.

### 44- IMPACT OF EXTREME SOIL MOISTURE CHANGES AND DECREASED DAILY TEMPERATURE FLUCTUATIONS ON MICROBIAL COMMUNITY STRUCTURE

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Reduction in daily temperature variability has been predicted as one of the side effects of climate change in many climate models and has been supported by different field studies. However, how the reduction in daily temperature range (DTR) affects belowground processes is poorly understood. To study microbial community response to the decrease in DTR of soil (DTR<sub>soil</sub>), a study was initiated in the Chihuahuan Desert at Big Bend NP in 2006 and is currently ongoing. Polyethylene shade cloths suspended above the soil surface (of ten 4X3m plots) could successfully reduce the DTR<sub>soil</sub> by 2-6°C in the shaded plots with increased daily minimum temperature and lower daily maximum temperature without a change in soil moisture status. The decrease in DTR<sub>soil</sub> increased the concentrations of total PLFA, Gram positive and Gram negative bacteria, and AM fungi significantly (P < 0.05). Higher number and concentration of PLFA was observed when conditions were drier. At 4% soil moisture total number of PLFA indicators detected was reduced by about 40% compared to the average soil moisture status of 1.5% and total PLFA concentration was reduced by more than 50%. The enzymes β-glucosidase, β-glucosaminidase, alkaline phosphatase and phosphodiesterase had significantly higher activities in the reduced DTR<sub>soil</sub> plots than in the control plots (P < 0.05). These results show that continuous reduction in DTR<sub>soil</sub> may increase the abundance of bacteria and AM fungi. Aside from potential changes to microbial community structure under conditions of reduced DTR<sub>soil</sub>, nutrient cycling rates could be increased due to higher enzyme activities.

#### **45- THE PRESENCE OF EPIPOLYTHIODIOXOPIPERAZINE (ETP) TOXIN IN *BATRACHOCHYTRIUM DENDROBATIDIS***

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The continual decline of amphibians worldwide has been partially attributed to the fungus *Batrachochytrium dendrobatidis* (*Bd*). This fungus causes inflammation and thickening of the keratinized layer of amphibian skin which disrupts the osmotic balance leading to cardiac arrest. The action by which *Bd* penetrates the skin and causes disease is unknown. When using a *Bd*-nematode model, *Bd* is capable of killing nematodes without apparent attachment or completion of its life cycle. This suggests that a secreted substance capable of killing the host is produced by the fungus. The epipolythiodioxopiperazine (ETP) class of toxins increases the virulence of fungi and is regulated by a 12 gene cluster. *Aspergillus* and *Gliocladium sp.* are fungal pathogens known to produce gliotoxin, an ETP toxin, through the production of core biosynthetic enzymes. We hypothesize that the presence and expression of core biosynthetic enzymes for gliotoxin in *Bd* would indicate that this fungus can produce ETP-class toxins. Using the comparative search algorithm BLAST, we have observed the presence of all twelve required genes in *Bd* needed to produce ETP toxins. By using reverse transcriptase-PCR and Quantitative PCR we have studied the expression of seven of the twelve genes. We are optimizing the *in vitro* conditions under which these genes are expressed in *Bd*. Mass Spectrometry techniques are being used to validate the presence of the ETP toxin in *Bd*. These studies will contribute to our understanding of the mechanism(s) by which *Bd* is able to kill amphibians and can also aid in understanding other pathogenic fungi.

#### **NATURAL RESOURCE MANAGEMENT AND CONSERVATION**

#### **46- THE ECOLOGY AND POTENTIAL VALUE OF BAT COFFEE IN BIODIVERSITY CONSERVATION IN SOUTHWESTERN SUMATRA**

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Bat-discarded coffee is a wildlife-associated product recently reported from coffee agriculture areas of southwestern Sumatra. Although bat coffee is well-known by local farmers, the ecology and the potential value of this bat-associated product in biodiversity conservation are not yet known. From 2011 November to 2012 July, we carried out camera trapping, mist netting, and transect line surveys in Bukit Barisan Selatan area to evaluate the use of coffee plantations by wild mammals and to identify the production of bat coffee beans. We also interviewed local farmers about their perception of wildlife and bat coffee. During the survey period, 32 mammal species, including ten phytophagous bat species and the endangered Asian elephant (*Elaphas maximus*) were recorded. Bat-discarded beans were found beneath day or night feeding roosts of 21 plant species. All the bats observed taking coffee belonged to the genus *Cynopterus*, the most abundant phytophagous bats in the study area. Based on interviews, farmers were more aware of the presence and impacts of elephants, tree squirrels, and foliage-, house-, and cavity-roosting bats, but less familiar with reptiles, amphibians, and other bats. The unequal awareness among groups probably can be explained by the differences in the interactions between farmers and animals as well as lack of knowledge provided by the formal education system. Some possible conservation strategies based upon our findings are discussed.

#### **47- EFFECT OF SURVEY NUMBER AND DURATION ON DETECTION PROBABILITY OF NORTHERN HARRIER (*CIRCUS CYANEUS*)**

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Demand for renewable energy continues to grow in the United States and wind energy is expected to meet much of the demand. Although carbon free, wind energy is not without environmental costs - typically manifest as collisions of volant species with rotor blades. As a response, regulatory agencies now encourage developers to survey for these species, particularly raptors, prior to and after establishment of wind energy facilities. Currently, there is much debate about the length and number of surveys required to effectively determine use of an area by raptors. We used point count data on Northern Harriers (*Circus cyaneus*) to explore how changes in duration and the number of surveys affects the detection probability of this species. Data were collected at 50 survey points at the Snake River Birds of Prey Area in Idaho in 2012. We surveyed for 20, 40, and 60 minutes and visited sites 2 and 3 times during 2012. Utilizing occupancy modeling, detection probabilities (95% CI) for 20, 40 and 60 minute surveys were 0.26 (0.12 – 0.47), 0.26 (0.20 – 0.34), and 0.31 (0.24 – 0.38) for surveys with three visits, respectively. For surveys with only two visits, detection probabilities (95% CI) were 0.16 (0.10 – 0.25), 0.25 (0.17 – 0.34), and 0.31 (0.23 – 0.41) for 20, 40, and 60 minute surveys, respectively. Although further analysis is warranted, our data suggest that when relatively few surveys are to be conducted, short duration surveys perform poorly at detecting individuals of this species.

## PLANT AND SOIL SCIENCE

### **48- MULTIDISCIPLINARY APPROACH TO INVESTIGATE THE EFFECTS OF DROUGHT STRESS ON COTTON FIBER QUALITY**

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Drought is a major environmental stress that reduces cotton yield and fiber quality in the State of Texas. Because of the inherent difficulties to study fiber tissue and the lack of markers to monitor the fiber development, little is known about the regulation of processes (traits) that are critical to the formation of high quality fiber and the association of these traits with drought tolerance in cotton (their performance under drought stress). Four cotton cultivars were planted in the field under three different irrigation levels, with three replicates per condition in both 2010 and 2011 growing seasons. On the day of flowering (0 dpa) individual flowers were tagged and developing bolls from at least 8-10 per plants per replicate per irrigation level were harvested at critical stages from 10 to 56 dpa. Mature fibers were hand-harvested at the end of growing season. Multidisciplinary approach was used to investigate the effects of drought stress on fiber development. To detect the effect of drought stress on the structural changes of fibers and to identify the timing of the transition from primary cell wall synthesis to the secondary cell wall deposition, Fourier Transform Infrared spectroscopy (FTIR) and Thermogravimetric Analysis (TGA) were used. The effects on fiber quality traits of mature fibers were determined by High Volume Instrument (HVI), Advanced Fiber Information System (AFIS), and image analysis of fiber cross-sections.

### **49- EFFECT OF FIBER MATURITY ON FIBER LENGTH DISTRIBUTION AND YARN EVENNESS PROPERTIES**

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Sixty four commercial bales of cotton were harvested from eight different locations of West Texas from 2008 through 2010. For each location, 4 bales were harvested with a picker harvester and 4 bales with a stripper harvester. Picker harvested cottons were ginned with a picker sequence while stripper harvested cottons were ginned with a stripper sequence. 2008 and 2009 cottons were less mature compared to 2010 cottons. Each bale produced was sampled and the lint was tested on both HVI and AFIS. Then, the lint was processed through our short staple spinning facility to produce carded and combed ring spun yarn (30Ne). The yarns produced were tested on Statimat DS and UT5. The results obtained show that most of the fibers removed during processing (opening, carding, combing) were short and very immature. Therefore, the common hypothesis of independence between fiber length and fiber maturity within-sample needs to be revisited. In most of the cases, HVI testing did not allow us to discriminate between the two harvesting methods while the AFIS did. AFIS provides crucial information that can supplement HVI data and could allow us to better predict yarn quality.

#### **50- UNDERSTANDING THE IMPACTS OF WATER QUALITY ON GLYPHOSATE EFFICACY IN THE TEXAS HIGH PLAINS**

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Water is the primary carrier used in most herbicide applications. The quality of water plays a critical role in the success or failure of herbicide treatments, especially for weak acid herbicides such as glyphosate. In an attempt to offset potential antagonism of herbicides due to poor water quality, some growers in the Texas High Plains are investing in reverse osmosis systems. Reverse osmosis is a filtration process that removes dissolved inorganic solids from water. The effects of water quality and ammonium sulfate on glyphosate efficacy were assessed in five field trials established near Lubbock, TX in 2012. Test plants included volunteer winter wheat (*Triticum aestivum* L.) and Palmer amaranth (*Amaranthus palmeri* S. Wats.). All trials were organized in a randomized complete block design with four replications. Five water samples, ranging in cation concentrations of 519-1,046 ppm, were selected from a collection of 23 wells across the Texas High Plains. The selected five sources plus a reverse osmosis water source were used as carriers for the following four herbicide treatments: glyphosate applied alone at 0.43 and 0.86 kg ae ha<sup>-1</sup> and glyphosate applied at 0.43 and 0.86 kg ae ha<sup>-1</sup> with dry ammonium sulfate at 20.37 g L<sup>-1</sup>. Injury was recorded at 14, 21, and 28 days after application. Differences in efficacy due to water source or a water source by glyphosate rate interaction were observed in three of the four field trials. Additionally, efficacy improved with increasing glyphosate rate and the presence of ammonium sulfate.

#### **51- HETEROLOGOUS EXPRESSION OF A RICE SUMO E3 LIGASE ENHANCES DROUGHT AND HEAT TOLERANCE IN TRANSGENIC COTTON**

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Abiotic stresses such as drought, salinity and extreme temperatures are major threats to agriculture. These stresses lead to a series of morphological, physiological and biochemical changes in plants that adversely affect plant growth and productivity. Drought and high temperature stress adversely affects plants by causing membrane integrity loss, reactive oxygen species production, protein inactivation and denaturation, which ultimately leads to cell death. Plants have inherent capacity to tolerate high temperatures for better survival which include production of heat shock proteins necessary for cellular protection. Earlier researches indicate that high temperature induces conjugation of SUMO (small ubiquitin like modifier) to peptides called sumoylation which is probably a protective response to heat stress. *SIZ1* is a SUMO E3 ligase that facilitates sumoylation of transcription factors like HSFs (heat shock transcription factors). Activation of HSFs increases their affinity for heat shock elements. These processes later aid in the transient production of heat shock proteins (HSPs). HSPs are molecular

chaperones that reduce protein denaturation, target denatured proteins to proteasome for destruction, facilitate protein folding necessary for protein maturation and renaturation, and regulate activity of HSFs to control HSP gene expression during thermotolerance acquisition. The SIZ1-dependent increase in SUMO-protein conjugate levels in response to drought also suggests a possible role of this E3 ligase in the stress response. We speculate that if *SIZ1* gene is overexpressed in cotton plants, it might confer plants increased drought and heat tolerance and thus benefit the west Texas farmers by minimizing loss in yield and productivity under high temperature conditions.

## **52- CONSTITUTIVELY OVEREXPRESSING A TOMATO FRUCTOKINASE GENE (*LeFRK1*) IN *GOSSYPIMUM HIRSUTUM* L. ENHANCES SEED COTTON YIELD AND FIBER MASS UNDER BOTH WELL-WATERED AND DROUGHT STRESSED CONDITIONS.**

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Yield of cotton “fiber” depends, in part, upon cellulose synthesis during development. UDP-glucose, primarily produced from sucrose by sucrose synthase (SuSy), is the substrate for cellulose synthesis. Fructose, the other product of this reaction, inhibits SuSy. Our hypothesis was that enhancing fructose removal by elevating fructokinase (FRK) activity would reduce SuSy inhibition, enhance cellulose synthesis, and lead to higher fiber yield under optimum and possibly drought-stressed conditions. We developed transgenic cotton plants transformed with a tomato fructokinase gene (*LeFRK1*) under the control of the CMV 35S promoter. Three lines with moderate to high expression of *LeFRK1* in leaves and developing fibers and a control, null line were well watered (mid-day leaf relative water contents [RWC] of 70-80%) or exposed to slowly-developing drought periods with bi-weekly recovery (RWC of 40-60%) during boll development. All transgenic lines had a higher seed cotton yield (30-60%) and fiber mass under both well-watered and drought conditions than did the null plants. However, only two of the lines had elevated FRK activity in developing fiber. Relative to the nulls, all transgenic lines had a significantly higher boll number whether well watered or in drought. Also, compared to the null plants, all transformed plants had 17-30% larger stem diameters. The increase in boll number and yield that did not always correlate with the FRK activity in developing fibers suggested that a relationship might exist between elevated FRK activity and xylem development that could improve water conduction to the developing bolls and leaves in well-watered and drought conditions.

## **53- EVALUATION OF QUICKSPIN FOR YARN QUALITY AND DYE UPTAKE ASSESSMENTS**

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The basic requirement of cotton breeding programs is to produce germplasm that is balanced in terms of fiber properties and that fits a market need. It is well documented that lower fiber maturity leads to poor yarn quality, dye uptake and an increased probability of the presence of color defects such as “shiny neps” (cluster of very low maturity fibers with low dye affinity). Assessing new germplasm for yarn quality and dye uptake is not always possible because of cost considerations, and also because it requires large quantities for raw fibers. In this study, cotton bales representing a wide range of fiber properties were selected. Knitted fabrics were produced from yarns spun on industrial size ring and rotor spinning equipments, as well as MDTA3 + Quickspin. Yarn quality, dye uptake and dye exhaustion kinetics of reactive blue 19 are compared.

#### **54- THRIPS (THYSANOPTERA: THIRIPIDAE) TOLERANCE AND FIELD PERFORMANCE OF COTTON (*GOSSYPIUM HIRSUTUM* L.) BREEDING LINES AND CULTIVARS UNDER ORGANIC MANAGEMENT**

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Thrips management is more problematic in organic systems where synthetic pesticide applications are prohibited. Additionally, organic growers are in need of commercial, non-transgenic cotton varieties that are adapted for the Texas High Plains, where over 98% of cotton is produced with transgenic varieties. Twelve advanced cotton breeding lines and 4 cultivars were therefore evaluated in an organically-managed field experiment to evaluate lines for field thrips tolerance and other agronomic characteristics. Evaluated parameters included visual thrips injury, boll morphology, leaf pubescence, lint yield, and commercial fiber quality. There were a number of differences for each parameter among genotypes and nearly all breeding lines performed comparably with the commercial standards. Lines that were originally selected for early-season cold tolerance all exhibited among the highest tolerance to thrips feeding injury. Most breeding lines displayed only minimal pubescence, but two lines had high levels of pubescence that would be undesirable for organic production. Line 07-7-1407CT appeared to exhibit an excellent combination of thrips tolerance, desirable boll morphology, and minimal pubescence and could be viable option for commercial organic production as a cultivar or for use as a parent line.

#### **55- SEASONAL CHANGE EFFECTS ON PHOTOSYNTHESIS, NITROGEN METABOLISM, AND SOIL NITROGEN IN COMPETING INVASIVE *Phalaris arundinacea* AND NATIVE *Carex stricta***

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*Phalaris arundinacea* invasion of wetlands containing *Carex stricta* is an ideal system to study the physiological basis for the effects of eutrophication on invasion. We investigated whether the species differ seasonally with respect to nitrogen assimilation and photosynthesis, and whether a relationship between seasonal changes in physiological processes and available soil nitrogen (N) existed. Leaf and soil samples and photosynthetic data were collected from *Phalaris*-dominated Site 1 and *Carex*-dominated Site 2 in north-central Indiana in 2011 and 2012. Soil NO<sub>3</sub><sup>-</sup> was significantly higher in Site 1, while soil NH<sub>4</sub><sup>+</sup> was consistent between sites with an increase in autumn in Site 2. *Phalaris* had more leaf nitrate reductase activity and higher leaf N than *Carex*. *Phalaris* had higher photosynthetic capacity than *Carex* across seasons and sites. *Phalaris* leaf N did not vary seasonally in both sites, consistent with the maintenance of a high photosynthetic capacity. Leaf N decreased after the spring for *Carex* corresponded with a decline in photosynthetic capacity, potentially giving *Phalaris* a competitive advantage late in the year. *Phalaris* appeared respond better to high NO<sub>3</sub><sup>-</sup>, the N availability in either site appeared to be sufficient for *Phalaris* to maintain higher leaf N and photosynthesis than *Carex*. We postulate that the higher photosynthetic rates for *Phalaris* may be partially due to the maintenance of a higher nitrate reductase activity in leaves compared to *Carex*.

#### **PROPOSAL**

#### **56- IMPACT OF THE MID-AEGEAN TRENCH IN SHAPING THE PHYLOGEOGRAPHIC PATTERNS OF KOTSCHY'S GECKO**

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The Aegean region comprises the adjacent Greek and Anatolian mainland and also the group of islands in the Aegean Sea. This region was part of a united landmass (known as 'Agäis') 23-12 Million Years Ago (MYA) which began to break apart between 12-8 MYA. One of the most interesting geological features





of this region is the Mid-Aegean Trench (MAT), which began to form at the end of Middle Miocene (12 MYA). The formation of the MAT has played a crucial role in shaping the biogeographical patterns in many reptile species in the Aegean including Kotschy's geckos (*Mediodactylus kotschyi*). Kotschy's gecko is a small semidiurnal gecko widely distributed across numerous Aegean islands, and vicariance has been suggested to have played a prominent role in shaping their phylogeographic history, which started about 10 MYA. The main objectives of this study are to elucidate the impact of the MAT in shaping the phylogeography of *M. kotschyi*, and to assess the genetic differentiation among their various island and mainland populations. To accomplish afore mentioned objectives, samples of *M. kotschyi* (tissue or blood), will be collected from some 30 islands in the Aegean. Two mitochondrial DNA genes will be amplified for all the samples and phylogenetic analyses will be conducted based on Maximum Parsimony, Maximum Likelihood, and Bayesian Inference methods. The findings from this study are expected to help fill the gaps that exist for insular populations of this gecko by providing information on various aspects of their phylogeography.

### **57- NEOPHILIA ACROSS AN URBAN-RURAL GRADIENT: THE CANE TOAD (*RHINELLA MARINA*)**

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For species moving into new environments, locating and utilizing unfamiliar resources is crucial for survival. Within its introduced range, the cane toad (*Rhinella marina*) has been successful across rural and urban landscapes, persisting in habitats once thought unsuitable for them. Given that animals inhabiting urban habitats are confronted with novel feeding opportunities, individuals in those areas are expected to be more neophilic compared to individuals in rural populations. Previous studies have emphasized comparisons among species in their native and invasive ranges. There has, however, been no work investigating the neophilic responses to novel prey in urban and rural habitats. In this study, we propose to investigate the responses of cane toads to novel prey items inhabiting urban versus rural populations in their invasive range near Belle Glade, Florida. In a preliminary study of response to novel colored food items, we found that cane toads hesitate, but still consume novel colored mealworms. Amphibians worldwide are experiencing population declines, while the cane toad is expanding its range in several areas. Understanding the mechanisms of their successful invasions could provide insight into their ability to outcompete native species and move into new areas. This study also emphasizes the role of learning in amphibians faced with novel resources that they must exploit in order to survive.

### **58- THE INVOLVEMENT OF PROTEIN PHOSPHATASE 2A IN ABA SIGNALING PATHWAY**

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Posttranslational modification of protein by phosphorylation is a universal mechanism for regulating diverse biological functions. Protein phosphatase 2A (PP2A) serves as a tumor suppresser in humans. In plants, PP2A was found to be involved in plant response to hormones such as auxin, abscisic acid (ABA), and ethylene. PP2A is a heterotrimeric enzyme consisting of a scaffolding subunit A, a regulatory subunit B, and a catalytic subunit C. Given that the regulatory subunit B is much more diverse than A and C subunits, it is understandable why B subunits might be responsible for the diverse functions of PP2A. However, the exact role of each B subunit of PP2A in plant hormone signaling has yet to be determined. In order to study how PP2A is involved in ABA signaling pathway, we knock-down the expression level of one B subunit gene with artificial microRNA in Arabidopsis and found that transgenic plants are sensitive to ABA treatment at germination stage, suggesting that this B subunit gene is involved in ABA signaling pathway. In addition, this gene is quickly down-regulated at mRNA level when treated with ABA at seedlings stage. Also, the GUS staining pattern of this B subunit gene's promoter indicates that this B gene is highly expressed in vascular tissues of root, stem and leaf, as well as in the emerging lateral

roots, suggesting its positive role in plant development. Overall, our work with this B subunit gene suggests that PP2A is indeed involved in ABA signaling pathway in plants.

### **59- MANAGEMENT OF MOSQUITO-BORNE DISEASE RISK THROUGH SPATIALLY-EXPLICIT SIMULATION MODELING**

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Insect disease-vector and human populations are spatially heterogeneous across a landscape. Disease risk to humans from such vectors is, therefore, also spatially heterogeneous. To mitigate disease risk, spatially explicit modeling of insect populations and disease dynamics can be employed to help public health officials improve insect-control measures. However, few efforts have been made to model the impact of habitat variability and pest-control measures on disease risk in a spatially-explicit manner. We propose to develop a spatially-explicit model of the disease risk posed by Western Equine Encephalitis (WEE), an infectious disease vectored by the mosquito species, *Culex tarsalis*. The model will explicitly incorporate the impacts of mosquito-control measures, as well as habitat specific features important to mosquitoes. We propose to accomplish this in 3 main phases. In the first phase, we will develop models of population growth (under varying environmental and mosquito-control conditions) and dispersal for *C. tarsalis* via laboratory and field studies, respectively, and adapt models of disease transmission for WEE. In the second stage, we will integrate these models into a GIS environment, where we will model disease risk as a function of the overlap between mosquito populations and human populations in a hypothetical landscape. Lastly, we will transition the hypothetical landscape to a real environment using Lubbock, TX as a test case. The final product of this research will be a probabilistic, GIS-based tool that will enable public health officials to make better informed decisions when trying to mitigate disease risk posed by mosquito-borne pathogens such as WEE.

### **60- ENVIRONMENTAL HETEROGENEITY AND COMPLEXITY WILL PREDICT INSECTIVOROUS BAT FORAGING ACTIVITY AND SPECIES RICHNESS AROUND TEXAS AGRICULTURAL AREAS AT A SPECIES-SPECIFIC SCALE**

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Thirty-seven percent of all potential US crops are lost to insect pests each year; these economic losses cost the United States more than \$12 billion dollars a year. Promotion of natural pest predators may be a sustainable solution to pesticide problems. Bats are a dominant feature of many ecosystems, with over 1250 species worldwide and nearly 70% of those being insectivores, bats play a critical role in pest control. The estimated value of insectivorous bats to US agriculture is roughly \$22.9 billion per year, which is almost double the estimated value of other pest predators. Despite the overwhelming value of bats to agriculture, most research examining the promotion of natural pest control focuses on insect predators. The goal of my project is to examine the correlation between habitat heterogeneity and complexity with bat species abundance and richness in an agricultural landscape. The ultimate purpose is to provide evidence that higher habitat heterogeneity and complexity around agricultural fields will promote natural pest control by increasing bat activity and richness. I will use 10 km driving transects stratified randomly to sample bat diversity and activity. The stratified random approach was chosen because knowledge of bat habitat use is understudied in low density areas (such as croplands), consequently trying to further stratify by particularly land uses would impose preconceived biases that might lead to an unrepresentative sampling of bat activity. Pilot data suggests that acoustic point counts underestimate bat activity in low density areas relative to acoustic driving transects.

## **61- TRANSIENT EXPRESSION OF A MODIFIED VIRAL INSECTICIDE IN PLANTS**

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Insect pests are a serious threat to agricultural productivity. Use of chemical pesticides, the predominant control method thus far, has resulted in environmental damage, pest resurgence, and negative effects on non-target species. Genetically modified (GM) crops offer a promising alternative, and *Bacillus thuringiensis* toxin genes have played a major role in this respect. However, to overcome insect tolerance issues and to broaden the target range, it is critical to identify alternative insecticidal toxins working through novel mechanisms. Our group has identified a kinase gene from Chilo iridescent virus (CIV) that has insecticidal activity and designated it as *ISTK* (Iridovirus Serine/Threonine Kinase). This CIV toxin expressed in yeast systems induces 50% mortality in cotton aphids and 100% mortality in green peach aphids. Attempts to transform and express this gene in plants yielded viral kinase-specific RNA but no protein. Expression of foreign genes in plants is complicated by codon usage, mRNA instability, translational efficiency, and proteolytic degradation. In order to facilitate heterologous expression of this viral gene in plants, we will optimize *ISTK* codons based on codon usage in plant systems. We propose to test the hypothesis that over-expression of the optimized *ISTK* gene in plants will yield active and stable polypeptide in planta and this polypeptide will have aphidicidal activity.

## **62- EFFECTS OF REDUCED TEMPERATURE VARIABILITY ON SOIL MICROBES IN ARID AND SEMI ARID ECOSYSTEMS**

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Global climate change has the potential to alter our world in unprecedented ways. Arid and semi arid ecosystems are predicted to be among the most affected regions. While daily high temperatures will increase, climate studies show that the daily low temperatures will increase at a faster rate resulting in a reduction of the diurnal temperature range (DTR). Temperature plays a major role in the regulation of many biochemical processes carried out by soil microorganisms critical to the recycling of soil nutrients. Understanding the effect of the expected reduction of diurnal temperature range on soil organic biomass, CO<sub>2</sub> respiration, available soil nutrients, and soil enzyme activity (measured by way of carbon substrate activity and substrate richness) will help us anticipate the effects of global climate change in these regions. Shading 3 x 3m plots with solar shade cloth provided the desired reduction in DTR<sub>soil</sub>. Soil samples were taken in three-month intervals and CO<sub>2</sub> respiration data was recorded onsite every hour with automated equipment. Preliminary results indicate that a reduction in DTR<sub>soil</sub> has a positive effect on soil respiration and soil enzyme activity levels.

## **63- EXAMINATION OF FLOODING AS A MECHANISM FOR ALTERING GRAY TREEFROG DEVELOPMENT IN TEMPORARY PONDS**

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Gray treefrogs preferentially oviposit in fishless and predator-free ponds, but fishless ponds are often temporary and unstable environments reliant upon precipitation. Larval amphibians raised in ponds with shorter hydroperiods typically metamorphose earlier and at smaller sizes than those in ponds with longer hydroperiods, suggesting that frogs have the plasticity to survive in these variable environments. While earlier metamorphosis allows amphibians to survive pond drying, individuals with smaller metamorphosis sizes and times have reduced fecundity, mating success, and winter survival. The developmental rate of larval amphibians can be altered until a time in their development after which a trajectory has been set and cannot be changed. Large inputs of freshwater through heavy precipitation and flooding may revitalize drying ponds, but could also introduce predatory fish from nearby environments. I will examine gray treefrog development in artificial ponds that initially have a 60-day hydroperiod before being filled

in a simulated flood, after which the ponds will remain full. A control will never be flooded, completely drying after 60 days, and the three flood treatments will be filled after 16, 31, and 46 days. Caged fish will be added at the time of flooding to half of the ponds in each treatment. I hypothesize that ponds flooded earlier will produce larger frogs that have longer times to metamorphosis, those in ponds flooded after 46 days will have metamorph sizes and times similar to those in the ponds that were never flooded, and those with fish will develop faster than those without.

#### **64- ARE VEERIES AFRAID TO SING IN THE DARK: STRUCTURAL CHANGES TO VOCAL COMMUNICATION IN THE PRESENCE OF A PREDATOR**

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In Passerines, song serves as a vital component of communication, either to elicit a mate or defend a territory. In the presence of a predator, however, vocal communication can be detrimental, making a bird more susceptible to predation. The Veery, *Catharus fuscescens*, is a diurnal Passerine that showcases both a pronounced dawn and dusk chorus. The song structure of the Veery is extremely complex, exhibiting pronounced harmonics, making identifying location and distance to a bird difficult for a human observer. Research into Passerine dusk chorus, particularly as it relates to predation risk, is negligible. Previously, we have demonstrated that in the presence of a predator, the Barred Owl (*Strix varia*), there is a reduction in the number of Veery songs and the length at which dusk chorus extends post sunset. To expand upon this research, this proposal aims to identify fine scale vocal structural changes associated with Veery dusk chorus in the presence of a predator. It is hypothesized that at dusk, with diminished light conditions and a greater risk of perceived predation, the male Veery will modify his song structure to reduce detectability. To accomplish this, vocal recordings of Veery dusk chorus will be collected using active recording techniques. This experiment will also use audio stimuli, gray treefrog (*Hyla versicolor*) chorus and Barred Owl calls to simulate a control and predator, respectively. This study offers additional insight into dusk vocal communication, a vastly underrepresented field, as well as predator-prey interactions as they relate to vocal communication.

#### **65- IDENTIFICATION OF A PLASMINOGEN BINDING PROTEIN, ENOLASE, FROM CULTURES OF THE AMPHIBIAN PATHOGEN *BATRACHOCHYTRIUM DENDROBATIDIS***

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Chytridiomycosis, caused by the chytrid fungus *Batrachochytrium dendrobatidis* (*Bd*), is a disease that causes the death of the adult amphibians by interfering with critical skin functions including maintenance of fluid balance, electrolyte homeostasis and respiration all of which lead to cardiac arrest. The ability of the pathogen to interact with host components, including skin and extracellular matrix proteins is vital to invasion, colonization and pathogenicity. Following invasion of amphibian host cells, *Bd* zoospores transition into chitin walled reproductive sporangia. Interaction of cell surface-associated enolase with plasminogen, activating it to plasmin, facilitates colonization of the host. The protein has been observed in pathogenic fungi including *Candida albicans*, *Pneumocystis carinii* and *Paracoccidioides brasiliensis*. In order to study *Bd* enolase fungal cell wall proteins were extracted from isolated sporangia or zoospores by hot SDS and dithiothreitol treatment. Extracted wall proteins were separated on SDS PAGE and identified using LC-MS/MS. Enolase was identified from the wall fractions of *Bd* sporangia supporting the hypothesis that enolase may facilitate the host-pathogen interaction through plasminogen binding. The specific role of enolase in plasminogen binding and activation to plasmin resulting in fibrinolysis will be studied *in vitro*. Completion of this work will result in a reasonable understanding of the mechanism by which *Bd* establishes within amphibian host cells. This will also open new insights about treating chytridiomycosis while being the first study of the enolase in the pathogenicity of *Bd*.

## **66- EFFECTS OF WATER TEMPERATURE ON THE DEVELOPMENT AND SURVIVORSHIP OF THE FAMILIAR BLUET DAMSELFLY (*ENALLAGMA CIVILE*)**

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Weather patterns across the Southern High Plains of the USA have been experiencing longer durations of decreased precipitation and increases in temperature. With climate patterns for the region projected to increase in temperature and decrease in precipitation, it is expected that playas will be highly susceptible to climate change. Aquatic and semi-aquatic invertebrates are some of the dominant organisms inhabiting playas. These invertebrates require aquatic ecosystems for their juvenile life stages and live in or use aquatic ecosystems throughout their adulthood. Because of this, water parameters can greatly affect invertebrates. Here we propose a study of the effects of water temperature on the development and survivorship of the Familiar Bluet Damselfly (*Enallagma civile*), a common inhabitant of the playas of the Southern High Plains that serves as a model organism of simulated heating associated with climate change. Adult females in copula will be collected from the field and brought back to the laboratory and placed in oviposition chambers. Eggs will be reared under five temperature treatments based on current playa water temperatures and predicted temperature changes due to global warming. Daily observations of eggs (and later, nymphs) will be made. Percent and duration of survivorship of eggs and nymphs, time duration between molts, number of molts, and total body length and head capsule width after each molt will be measured for each individual. We predict that higher water temperature treatments will cause decreased survivorship, increased body size, and shorter development length of *Enallagma civile* until a lethal temperature is reached.

## **67- CALIBRATION OF ALMANAC MODEL FOR SIMULATION GROWTH OF WW-B. DAHL OLD WORLD BLUESTEM**

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WW-B. Dahl Old World bluestem [*Bothriochla bladhii* (Retz) S.T. Blake] is one of the most promising warm-season perennial bunch grasses for use as forage in the Texas High Plains. WW-B. Dahl has drought tolerance under dryland conditions, and exhibits late-season flowering, which delays the decline in forage quality associated with reproductive development. It can also maintain excellent stands after 10 years without significant losses. Compared to other Old World bluestems (*Bothriochloa* spp.), WW-B. Dahl generally has higher concentrations of crude protein. The ALMANAC model has been used to simulate yields of several grass species under various environmental conditions. Yet, ALMANAC has not been applied to simulating growth of WW-B. Dahl. Developing digital image analysis (DIA) for high-speed monitoring of leaf area and canopy cover by taking periodic overhead images of the grass canopy would greatly reduce the labor requirement of measuring live (green) leaf area. The proposed research will test the accuracy of DIA for rapid measurement of leaf area, canopy cover and light interception, and its ability to distinguish between live and dead plant tissue. Successful application of DIA will aid in calibrating ALMANAC for simulation of growth and biomass yield of WW-B. Dahl under managed pastures conditions.

## **68- CYCLOPROPANE FATTY ACID SYNTHASE IN *LEISHMANIA***

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*Leishmania* parasites are vector-borne protozoans responsible for a spectrum of diseases (leishmaniasis) infecting 10-12 million people worldwide. With increased drug resistance and no safe vaccine available,

there is an urgent need to develop new drugs against these parasites. Studies in the fundamental mechanism of pathogenesis can often lead to better treatments. Interestingly, *Leishmania* parasites possess a rare phospholipid modification enzyme called cyclopropane fatty acid synthase (CFAS), which is not found in animals. CFAS catalyzes the transfer of a methyl group from S-adenosyl-methionine to an unsaturated fatty acid (usually olefinic acid), generating an unusual cyclopropane fatty acid. Functions of CFAS and cyclopropane fatty acid are not well understood. In *Leishmania*, CFAS is localized to the cytoplasmic side of plasma membrane. While the endogenous level of cyclopropane fatty acid is almost undetectable in wild type *Leishmania*, overexpression of CFAS results in a dramatic increase in the cyclopropanation of phosphatidylethanolamine (a major membrane lipid). Genetic inactivation of CFAS in *Leishmania mexicana* (*cfas*<sup>-</sup>) leads to more round cells in culture and a slower growth rate. In addition, the distribution of important virulence factors such as lipophosphoglycan was significantly altered in *cfas*<sup>-</sup> mutants, suggesting that cyclopropanation of membrane lipids play a role in the formation and organization of rafts. Nevertheless, *cfas*<sup>-</sup> mutants survived normally in macrophages and mice, indicating that CFAS is more important in the sandfly stage than in the mammalian stage. Future research will characterize the membrane permeability and osmolarity of *cfas*<sup>-</sup> mutants, as well as their transmissibility in sandflies.

#### **79 - FACTORS INFLUENCING CHANGES IN VEERY (*CATHARUS FUSCESCENS*) SITE OCCUPANCY WITHIN A BREEDING SEASON**

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Migratory birds select and occupy breeding territories before sufficient cues of quality are available. The ability to move up a gradient in territory quality during a breeding season may allow individuals to compensate for initially selecting a poor quality territory, and increase probability of successful reproduction. Within-season changes in site occupancy and territory movements remain poorly studied, but may have important consequences on population demography. We propose to investigate these processes within an on-going long-term study of Veeries (*Catharus fuscescens*) at the Cary Institute of Ecosystem Studies in Millbrook, New York. Data from previous manipulative experiments in this system showed significant spatial and inter-annual heterogeneity in abundance of rodents, the primary nest predators. However, spatial and temporal heterogeneity of other potential factors, such as food (arthropod) availability and microclimate, remain unexplored. Beginning in 2013, we will monitor microclimate, predator abundance, and sample leaf-litter arthropods throughout the breeding season to determine within season variation in the biotic and abiotic factors that may influence territory settlement and reproductive success. We predict occupancy rates will increase with favorable microclimates and food abundance, but decrease with predator abundance. Second, later occupied sites, based on nest initiation dates, should correlate more strongly with our metrics of site quality than earlier occupation. Lastly, we predict within season movement of individual birds (based on observation of uniquely marked individuals) should be up a gradient of habitat quality.

#### **TOXICOLOGY**

#### **69- CO-EXPOSURE TO LA SWEET CRUDE OIL AND DISPERSANT ALTERS GENOMIC DNA DAMAGE OCCURRENCE IN THE GULF KILLIFISH (*FUNDULUS GRANDIS*)**

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The BP-Deepwater Horizon oil well explosion in the Gulf of Mexico unleashed an unprecedented environmental disaster where more than 650 miles of Gulf coastline was littered with Louisiana Sweet Crude oil. The EPA allowed application of Corexit 9500, a surfactant designed to disperse and emulsify crude oil. Surfactant additives increase membrane permeability and biological uptake of exogenous compounds, including crude oil toxicants. Recent studies indicate that although visible traces of weathered crude oil have long been absent in the estuarine environments, particular toxic mutagens persist in organisms and sediments that were once co-exposed to oil and dispersant. We examined two genomic DNA coding sequences, cytochrome c oxidase-subunit1 and cystic fibrosis transmembrane conductance receptor for lesion analysis. Here we demonstrate that killifish, *Fundulus grandis*, exposed to crude oil and dispersant, generally have increased amounts of overt genetic damage compared to untreated killifish, after both mitochondrial and nuclear template analyses. However, no clear effects were apparent across salinity, weathering, or exposure-time gradients. In general, there were increased numbers of nuclear lesions after exposure to the dispersant, either singularly or in combination with crude oil. Additionally, mitochondrial DNA lesion formation was variable across salinity, weathering, and time, with the highest amounts of adducts forming in treatments containing dispersant. Adduct formation by environmental mutagens found in crude oil hinders replication accuracy and has the potential to go unrepaired. Our results indicate that there is overt DNA damage occurring after adult killifish are exposed to both crude oil, dispersant, and the combination of the two.

#### **70- EXAMINATION OF POLYCYCLIC AROMATIC HYDROCARBONS IN AN URBAN STORMWATER SYSTEM AND BIOACCUMULATION IN ODONATA**

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Polycyclic aromatic hydrocarbons (PAHs) are chemicals produced from fossil fuel combustion that are associated with urban runoff and can have teratogenic effects on aquatic and amphibious organisms. We investigated the occurrence of 15 PAHs within water samples and tissues of amphibious organisms (Odonata: dragonflies and damselflies, a flagship group of predatory wetland insects) from seven urban stormwater retention ponds along a runoff concentration gradient in Lubbock, Texas. PAH signatures from surface water samples were highly variable across sites and dates, with pyrene (in 27% of samples), benzo(ghi)-perylene (13%), and chrysene (12%) occurring most often. Adult Odonata PAH signatures were also variable but significantly different from corresponding surface water samples (suggesting bioaccumulation rather than passive chemical exposure), with flouranthene (90% of samples), naphthalene (75%), pyrene (75%), and benzo(k)flouranthene (60%) occurring most often. Research is ongoing to assess the influences of the amount of impervious surface surrounding each stormwater retention pond, the number of inflow points, and precipitation patterns on PAH concentrations in water and Odonata.

#### **71- CHAINED TO THE PAST: BIOTIC AND ABIOTIC CONDITIONS IN THE PARENTAL ENVIRONMENT ALTER OFFSPRING TOXICANT TOLERANCE**

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Parental effects are alterations in offspring phenotype resulting from the parental phenotype and/or environment that are not caused by changes in gene sequence. To better understand the impact that parental effects have on toxicant tolerance, we exposed egg masses and juvenile offspring of the freshwater snail *Biomphalaria glabrata* to cadmium and malathion. Parental snails were raised in either a diet regime, in which they were fed uncooked lettuce, fish food, cooked lettuce, or cooked lettuce plus fish food, or a predator cue regime, in which they were raised in predator cue or control water. Within the diet regime, half the snails were housed individually and half in groups of three snails per container to

evaluate the effects of self-fertilization. Malathion tolerance was greater in egg masses laid by outcrossing snails and varied with parental diet, but was not affected by parental predator cue exposure. Among juvenile offspring, malathion tolerance was greater in the offspring of outcrossing snails but was not affected by parental diet or predator cue exposure. Cadmium tolerance was greater in egg masses laid by outcrossing snails and predator-naïve snails, and varied with parental diet. Among juvenile offspring, cadmium tolerance was greater in the offspring of outcrossing and predator cue-exposed snails, and varied with parental diet. These results indicate that juvenile offspring toxicant tolerances can be heavily influenced by parental experience, but are not easily predictable from egg mass tolerance data. Additionally, results may depend on the specific toxicant and its mechanism of action and/or detoxification.

## **72- INCREASED GROWTH INHIBITION OF BREAST CANCER CELLS BY COMBINATION OF 5-AZA 2'DEOXYCYTIDINE AND (-)- EPIGALLOCATECHIN GALLATE**

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Breast cancer is the second leading cause of cancer mortality in US women. Both genetic and epigenetic modifications are involved in breast carcinogenesis. Deregulation of epigenetic mechanisms such as DNA methylation and histone tail modifications lead to aberrant gene expression (e.g. silencing of tumor suppressor gene) in breast cancer. Hypomethylating agent, 5-aza2'deoxyctidine (5-aza2'dC), used in acute myeloid leukemia has shown limited results in solid tumors. We hypothesized that extended treatment with combination of 5-aza2'dC with green tea polyphenol, EGCG, at non-toxic, low doses can improve breast cancer growth inhibition in vitro. MCF-7 breast cancer cells were treated with 5-aza2'dC (5 $\mu$ M), EGCG(50 $\mu$ M), EGCG+5-aza2'dC or DMSO (vehicle control) for 7days. Combination resulted in significantly ( $p < 0.05$ ) greater decrease in cell viability as compared to individual treatment, accompanied with slight, but statistically significant increase in G0/G1 cell cycle phase arrest. Real-time PCR data revealed that combination treatment lead to significantly greater ( $p < 0.05$ ) decrease in *CCND1*, *CCNE2* (G1/S specific cyclins), *Bcl2*, *survivin* (anti-apoptotic genes), *Wnt1* (oncogene), *VEGFA* (pro-angiogenic protein) and increase in *RASSF1A* (tumor suppressor gene) and *CDH1* (cellular adhesion/tumor suppressor gene) transcripts. Alteration in the transcript and/or protein expression of key epigenetic regulators, DNMT1, HDAC1, MBD4 indicated that combination treatment may have greater hypomethylating and transcription-activating ability as compared to individual treatment. Increase in DNA hypomethylation at was further confirmed by methylation specific RAPD-PCR. Significantly greater decrease in transcription-repressive histone H3K27trimethyl protein and neoplasm associated-p-Ac-H3(S11/K15) further confirmed the possibility of improving transcription-activation and tumor suppression potential by combination of EGCG and 5-aza2'deoxyctidine.

## **73- EFFECTS OF FUNGICIDES AND PHARMACUETICALS ON SHREDDING DETRITIVORE RESPONSES UNDER VARYING TEMPERATURE REGIMES**

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The presence of contaminants such as fungicides in aquatic environments may impact non-target bacterial and fungal communities and the invertebrate detritivores responsible for the decomposition of allochthonous organic matter. Additionally, in some aquatic systems daily water temperature fluctuations may influence these processes and alter contaminant toxicity, but such temperature fluctuations are rarely examined in conjunction with contaminants. In this study, *Hyalella azteca* served as a model shredding detritivore and organisms were exposed to fungicides of varying classes, the antimicrobial triclosan, and the antibiotic ciprofloxacin. Experiments were performed at a constant temperature (21°C), fluctuating temperature regime (20-26°C) based on field-collected data from the S. Llano River, TX, and a fluctuating temperature regime (22-27°C) adjusted based on possible climate change predictions.



Endpoints included organism growth and leaf processing. Generally, contaminant effects were greater than temperature effects for leaf shredding, and data suggest little effect on growth. This study provides information on the influence of realistic temperature variation on contaminant effects in aquatic systems, which is important for understanding how future alterations in temperature due to climate change may influence the assessment of ecological risk of contaminants.

#### **74- POTENTIAL ENDOCRINE ACTIVITY OF PARTICULATE MATTER FROM BEEF CATTLE FEEDLOTS**

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Over one third of the US beef supply passes through concentrated animal feeding operations, also known as feedlots, in the Southern High Plains. Feedlots hold a large number of cattle in a small space, creating large amounts of organic waste. Due to the arid nature of the Southern High Plains, waste has the potential to enter the environment as airborne particulate matter (PM). Included in the waste are both natural and synthetic hormones, administered to cattle to increase feed efficiency. It is unclear what effects hormones may have on the surrounding environment. For this study, airborne PM was collected from the downwind and upwind sides of five West Texas feedlots. Particulate matter samples were screened for potential androgenic and estrogenic activity using *in vitro* transcriptional activation assays. Concentrations of 17 $\alpha$ - and 17 $\beta$  estradiol, estrone, 17 $\alpha$ - and 17 $\beta$ -trenbolone, trendione, and melengestrol acetate were determined using LC-MS/MS. Androgenic activity *in vitro* was higher in downwind samples than in upwind samples, as hypothesized. Estrogenic activity *in vitro*, unexpectedly, was similar in upwind and downwind samples. *In vitro* results were supported by the LC-MS/MS data, as at least one estrogen was quantified in every PM sample. Further investigation is needed to determine the sources of these estrogens in the environment.

#### **75- EPIGALLOCATECHIN-3-GALLATE ABROGATES CYTOTOXICITY AND DNA DAMAGE INDUCED BY BENZO[A]PYRENE IN LUNG EPITHELIAL CELLS**

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Epigallocatechin-3-gallate (EGCG) is an active component isolated from green tea which has chemopreventive and anticancer properties. However, the molecular mechanisms of EGCG in these processes are still not very clear. The objective of the present study is to evaluate the potential protective effects of EGCG on benzo[a]pyrene (BaP)-induced cytotoxicity and DNA damage in BEAS-2B, a human normal lung epithelial cell. BEAS-2B cells were treated with vehicle control, BaP or BaP+EGCG for 24 hours. The cytotoxicity, cell cycle, benzo[a]pyrene diol epoxidation (BPDE)-DNA adducts, and mRNA expression levels of cytochrome P450 (CYPs) were determined by MTT assay, flow cytometry, HPLC, and qRT-PCR, respectively. BaP induced cell growth inhibition in a dose-dependent manner; while EGCG dose-dependently reversed this inhibition ( $P < 0.05$ ). The flow cytometry analysis showed that BaP caused significant G2/M phase arrest compared to controls, however, increased S phase and decreased G2/M phase were observed in cells co-treated with BaP and EGCG compared to BaP group ( $P < 0.05$ ). BaP-induced BPDE-DNA adducts were significantly reduced 80% by EGCG co-treatment. CYP1A1 and CYP1B1 expression levels analyzed by qRT-PCR dramatically increased after BaP exposure compared to controls (CYP1A1: 130.2-folds; CYP1B1: 6.0-folds;  $P < 0.001$ ). EGCG significantly reduced BaP-induced CYP1A1 and CYP1B1 expression (CYP1A1: 1.6-folds; CYP1B1: 1.2-folds; BaP vs. BaP+EGCG,  $P < 0.05$ ). On the other hand, CYP1A2 and CYP3A4 did not show any changes among the control, BaP-treated, and BaP and EGCG co-treated groups. In summary, BaP-induced adverse effects could be prevented by EGCG, suggesting a possible chemopreventive role for this natural polyphenol against the development of lung cancer.

## UNDERGRADUATE

### 76- ANALYZING INDIRECT EFFECTS ON INVERTEBRATES FROM AN ALLELOPATHIC CHEMICAL RELEASE OF COMMON REED (*PHRAGMITES AUSTRALIS*)

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Common reed (*Phragmites australis*) has invaded vast areas of Bitter Lake National Wildlife Refuge (BLNWR) in Roswell, New Mexico, which is home to a variety of endemic, threatened, and endangered species. *Phragmites* rapidly is becoming a world-wide problem for native vegetation communities. Little is known about the ecological effects of such a vigorous invasive plant species. Pecos assimineea (*Assiminea pecos*), a semi-terrestrial endangered snail, is potentially negatively impacted by this monotypic invasion. Research on *Phragmites* and *Assiminea* interactions is important for the management and conservation of this rare snail. It is known that *Phragmites australis* releases allelopathic chemicals that negatively affect other plants; leaching of these chemical has inhibited germination and growth of roots and shoots. Perhaps these allelopathic chemicals also negatively affect aquatic and semi-terrestrial invertebrates, resulting in avoidance and possible increased mortality. We are interested in the potential allelopathic effects of *Phragmites* on aquatic invertebrates. Samples of *Phragmites* (leaf and litter) will be dried, ground to a powder, and then soaked in water to extract potential allelopathic chemicals. We will expose the allelopathic extracts to the Phantom Cave snail (*Pyrgulopsis texana*) used as a surrogate for *Assiminea pecos* to record and analyze behavioral responses (e.g. avoidance). Various concentrations of *Phragmites* extracts from several sites at BLNWR will be tested. We expect greater snail avoidance with increased concentrations of *Phragmites* allelopathic extracts.

### 77- THE EFFECTS OF OCEAN ACIDIFICATION AND HYPOXIA ON ELEMENTAL INCORPORATION INTO THE OTOLITHS OF ESTUARINE FISH IN THE GULF OF MEXICO

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Otoliths are bones found in the ears of many fish species. As fish grow, they lay down layers of bone onto their otoliths at regular intervals. As this process takes place elements from the environment are incorporated into the rings of bone. By examining these elements, the location of fish over the span of their lifetimes can be followed. The integrity of this tracking method can be compromised by changes in water chemistry, such as the lowering of pH and dissolved oxygen concentration (dO). By 2100, surface ocean pH will be 0.4-0.5 units lower than preindustrial values and the dO of 'dead zones' in the Gulf of Mexico will be below 2 mg/L. While ocean acidification and hypoxia have been shown separately to affect elemental incorporation in marine organisms, both parameters have not been examined together in a controlled setting. The purpose of this study is to examine potential synergistic or antagonistic effects of simultaneously lowered pH and dO on otolith formation. Atlantic croaker, estuarine fish, play a key role in marine ecosystems. In this study Atlantic croaker will be placed into tanks with pH and oxygen levels lowered to the values projected for a dead zone in the Gulf of Mexico in 2100. Changes in elemental incorporation into otoliths based off of climate change scenarios will be used to modify current techniques so that they will be applicable for future studies on the geographical distribution of bony fish.

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