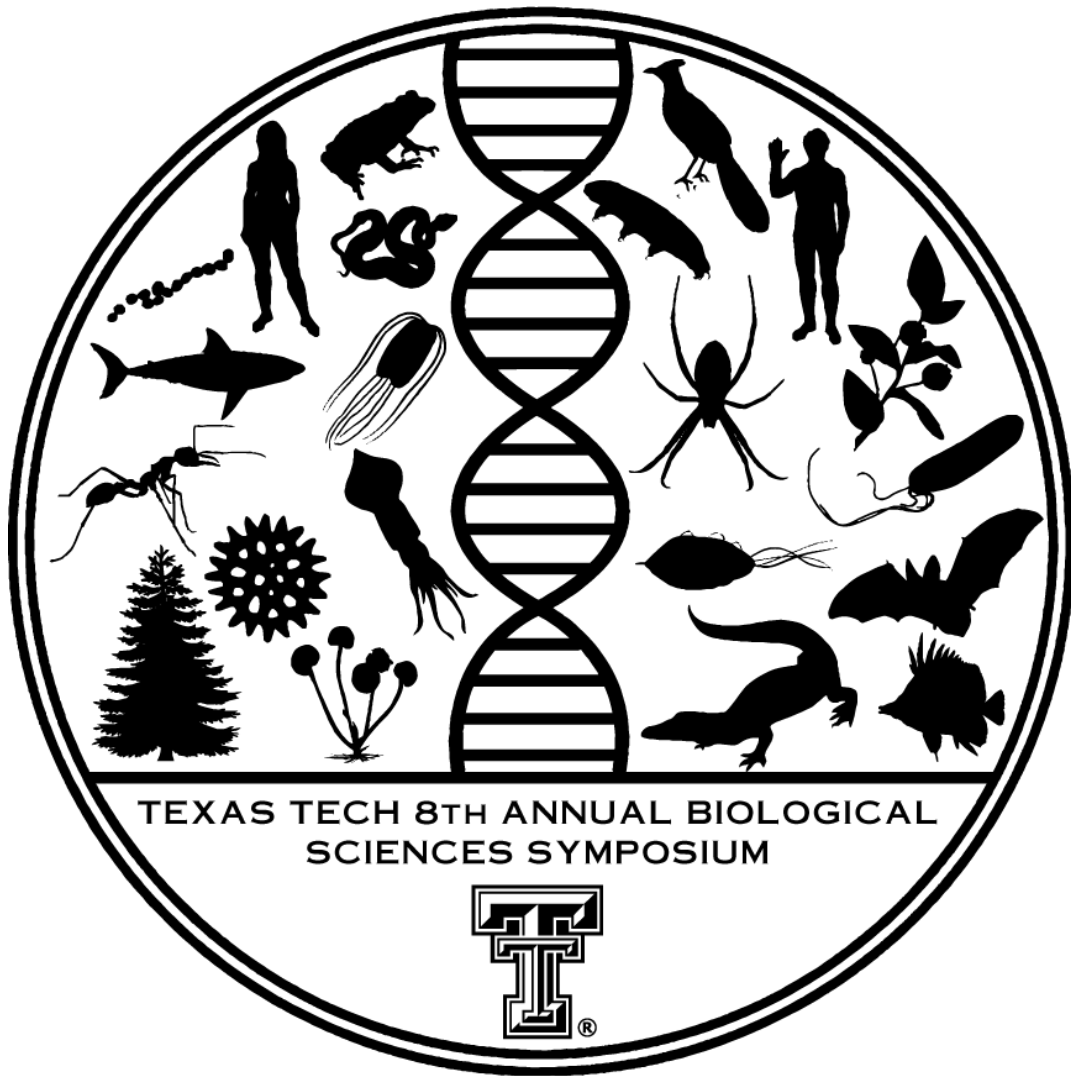


8th TEXAS TECH ANNUAL BIOLOGICAL SCIENCES  
SYMPOSIUM (TTABSS)



DEPARTMENT OF BIOLOGICAL SCIENCES  
LUBBOCK, TEXAS  
APRIL 7-8, 2017



# Thank You TTABSS 2017 Sponsors!



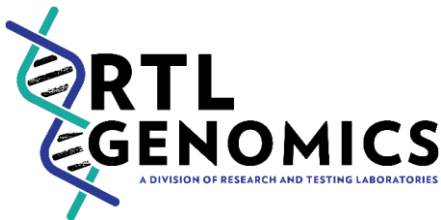
TEXAS TECH UNIVERSITY  
Department of  
Biological Sciences™



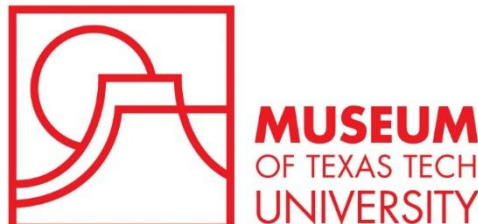
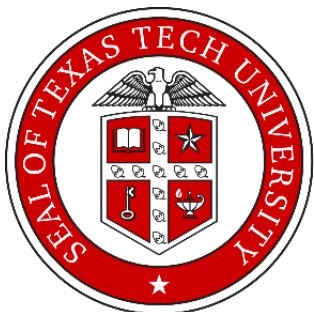
TEXAS TECH UNIVERSITY  
Department of Natural  
Resources Management™



TEXAS TECH UNIVERSITY  
Graduate School™



TEXAS TECH UNIVERSITY  
Office of the Vice President  
for Research™





Association of Biologists at  
Texas Tech University

## TABLE OF CONTENTS

WELCOME NOTE.....	2
ACKNOWLEDGMENTS.....	3-7
TTUAB OFFICERS & COMMITTEES.....	8
LOCAL RESTAURANTS .....	9
PROGRAM AT A GLANCE.....	10-11
MAP OF EVENT LOCATION.....	12
COMPLETE DAILY SCHEDULE.....	13-26
FRIDAY, APRIL 7.....	13-18
UNDERGRADUATE POSTERS.....	14-15
GRADUATE POSTERS.....	15-18
SATURDAY, APRIL 8.....	19-26
ABSTRACTS.....	27-56
POSTERS.....	27-48
UNDERGRADUATE POSTERS.....	27-34
GRADUATE POSTERS.....	34-48
UNDERGRADUATE.....	48-50
CELL & MOLECULAR BIOLOGY.....	51-55
ECOLOGY.....	55-61
EVOLUTIONARY BIOLOGY.....	61-64
MICROBIOLOGY.....	65-67
MUSEUM SCIENCE.....	68-69
NATURAL RESOURCES MANAGEMENT CONSERVATION.....	69-71
PROPOSAL.....	72-77
TOXICOLOGY.....	77-79
AUTHOR INDEX BY ABSTRACT NUMBER.....	80-81
THANK YOU NOTE.....	82
NOTES.....	83-85



**Welcome Note:**

It is with great pleasure we welcome everyone to the 8<sup>th</sup> Texas Tech Annual Biological Sciences Symposium (TTABSS), which is held this year of 2017, on April 7<sup>th</sup> and 8<sup>th</sup>. This year, the Biological Sciences Symposium is hosted at the Helen DeVitt Jones Sculpture Court at the Museum of Texas Tech University in Lubbock, Texas. Since the first TTABSS in 2009, the Association of Biologists at Texas Tech University (TTUAB) and the Department of Biological Sciences have planned this annual symposium. Three graduate student organizations, Association of Biologists at Texas Tech (TTUAB), Association of Natural Resource Scientists (ANRS), and Tech American Society for Microbiology (Tech ASM), have worked closely with both Departments of Biological Sciences and Natural Resource Management to make this symposium possible.

Our goal as a scientific community is to provide a platform to share scientific findings, explore the diverse world of Biological Sciences by exchanging ideas among peers, and gain experiences from academic advisors. TTABSS helps us achieve this.

This year, the symposium has a total of 160 undergraduate, graduate and faculty participants from 13 academic institutions. Our program will have 95 research presentations that include 39 poster presentations and 4 concurrent oral sessions. In addition, we would like to announce our two distinguished guest speakers, Dr. Matt Chumchal and Dr. Dan Riskin. They are both renowned scientists in their respective fields. Dr. Matt Chumchal is from Texas Christian University, and Dr. Dan Riskin is from the TV show, Daily Planet, and University of Toronto Mississauga. We are excited to have such incredible plenary speakers donate their time and support for our event.

As Co-Presidents of TTUAB and Chair of the TTABSS committee, we would like to thank all the members of the local TTABSS committee for their hard work and dedication. Thank you to our advisors for their advice and suggestions on organizing the program, and to our event sponsors and vendors who have helped us with the costs of TTABSS 2017. We would like to express our deepest gratitude to all of you for your participation and contribution in making this year's event a continued success, and for the development of a better conference for future years.

Wish you all a productive and enjoyable experience!

Best,

Amanda Starr and Emma Brookover  
Co-Presidents, TTUAB

Emily Wright  
Local Committee Chair, TTABSS 2017



## **EVENT HOSTS**

The Association of Biologists at Texas Tech University (TTUAB)  
Department of Biological Sciences, Texas Tech University (DBS)  
Museum of Texas Tech University (MoTTU)  
American Society of Microbiology (ASM), TTU Chapter  
Department of Natural Resources Management, Texas Tech University (NRM)  
The Graduate School at Texas Tech University  
Association of Natural Resource Scientists at TTU (ANRS)  
Student Government Association at Texas Tech University (SGA)

## **EVENT COLLABORATORS**

CISER/HHMI at Texas Tech University  
The Institute for Environmental and Human Health (TIEHH)  
Museum Heritage Student Association (MHSA)  
Vice President of Research  
Division of Institutional Diversity, Equity & Community  
Engagement (DIDECE)

## **PARTICIPATING INSTITUTIONS**

Texas Tech University  
Hardin-Simmons University  
McMurry University  
Museum of Texas Tech University  
Texas Tech Health Science Center  
Texas Tech University Climate Science Center  
University of Arkansas- Fort Smith  
Baylor University  
University of Toronto Mississauga  
Discovery Canada  
Wayland Baptist University  
Texas Woman's University  
University of Texas at Arlington  
University of Texas Rio Grande Valley  
West Texas A&M University  
All Saints Episcopal School  
Texas Christian University



## PLENARY SPEAKERS



Dr. Matt Chumchal is an Associate Professor of Biology at Texas Christian University. He is an ecologist interested in the interactions between ecological and human systems. Since earning a PhD in 2007 at the University of Oklahoma, his research has primarily focused on mercury contamination in the environment. Recent areas of interest include the trophic transfer of mercury in food webs and factors that lead to spatial variation in the mercury contamination of organisms at a variety of scales. He has used both experimental and field survey approaches to study mercury contamination in wetlands, lakes, rivers, estuaries and the Gulf of Mexico. His lab works with a wide variety of aquatic organisms including plankton, macroinvertebrates, fish, and turtles.



Dr. Dan Riskin is a biologist turned TV personality for Animal Planet and Discovery Channel Canada. He received a Doctorate from Cornell University and did post-doc work at Boston and Brown University working on the biomechanics of bats. During his post-doc, he helped out with the TV show called “Monsters Inside of Me” talking about the disturbing, yet fascinating world of parasites. He then accepted a position as an Assistant Professor at the City University of New York. In 2011, he left academia and became a full-time TV co-host on Daily Planet. Today, he is busy discussing science on several TV shows and in his book “Mother Nature is trying to Kill You”, being an Adjunct Professor for the University of Toronto Mississauga, and researching biomechanics of small mammals.



## A SPECIAL NOTE

With the blessings of his wife, Heather Whitlaw, the Department of Natural Resources Management and the Association of Natural Resource Scientists; since 2012, the award for the Natural Resource Management and Conservation category has been named the:

### *Warren B. Ballard Memorial Award*

With the permission of his wife and family, Department of Biological Sciences, TTUAB and Tech ASM proudly names the microbiology award in honor and fond memory of Dr. Bilimoria, professor of microbiology and virology at Texas Tech University for 35 years, who also mentored almost 20 graduate students.

This award would stimulate interest and discover the strength of aspiring students in the field of microbiology.

### *Shan L. Bilimoria Memorial Graduate Student Award*



## ACKNOWLEDGMENTS

*If not for the support from the following individuals, TTABSS 2017 would not have been possible.*

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

Robert Duncan - Chancellor, TTU  
Lawrence Schovanec - Interim President, TTU  
Michael Galyean - Interim Provost and Senior Vice President, TTU  
Guy Loneragan - Vice President for Research, TTU  
Mark Sheridan- Dean of Graduate School, TTU  
Michael San Francisco- Dean of Honors College, TTU  
W. Brent Lindquist – Dean, College of Arts & Sciences, TTU  
Clifford Fedler- Associate Dean of Graduate School, TTU  
John Zak – Associate Dean of Research, Interim Chair, Biological Sciences, TTU  
Lou Densmore – Full Professor, Graduate Student Advisor, Biological Sciences, TTU  
Ron Chesser – Full Professor, TTUAB Faculty Advisor, Biological Sciences, TTU  
Lauren Gollahon – Associate Professor, Biological Sciences, TTU  
Mark Wallace – Chair, Natural Resources Management, TTU  
Richard E. Zartman – Chair, Plant & Soil Sciences, TTU  
Todd Anderson – Chair, The Institute of Environmental and Human Health, TTU  
Tobin Brannan - Museum of Texas Tech University  
Julie Isom- Associate Director, TTU/HHMI (CISER)  
Lanita Ladd – Business Manager, Biological Sciences, TTU  
Pat Moore – Senior Office Assistant, Biological Sciences, TTU  
Lisa Dion – Lead Account Processor, Biological Sciences, TTU  
Stephanie Eggeling – Senior Business Assistant, Biological Sciences, TTU  
Kunyu Li – IT Support, Biological Sciences, TTU  
Chris Long – Unit Manager, Biology Building, TTU  
Jennifer Smith – Unit Manager, Biology Greenhouse, TTU  
Vina Khan – Specialist II, Dept. of Biological Sciences, TTU  
Carol Espinosa – Senior Business Assistant, Biological Sciences, TTU  
Jacqueline Miralles-Salazar – Senior Technician, Biological Sciences, TTU  
Raquel Miranda – Admin Business Assistant

### **Judges**

Robert Bradley – Biological Sciences, TTU  
Caleb Phillips – Biological Sciences, TTU  
Nabarun Gosh - Department of Life Earth and Environmental Sciences, West Texas A&M University  
Michael Dini – Biological Sciences, TTU  
Lou Densmore – Biological Sciences, TTU  
Rhonda Boros – Biological Sciences, TTU  
Kendra Phelps – Biological Sciences, TTU  
John Zak – Biological Sciences, TTU  
Nicté Ordoñez Garza – Biological Sciences, TTU  
Richard Stevens – Department of Natural Resources Management, TTU  
Ruth Serra-Morena – Biological Sciences, TTU  
Craig Tipton – Biological Sciences, TTU  
Brandon Gross – Biological Sciences, TTU  
Brian Sanderson – Biological Sciences, TTU  
Juan Pablo Carrera Estupiñan – Biological Sciences, TTU  
Joel Brant – Biological Sciences, McMurry University  
Mike Vanderwege – Biological Sciences, TTU  
Kenneth Schmidt – Biological Sciences, TTU  
Julie Parlos – Instructure, All Saints Episcopal





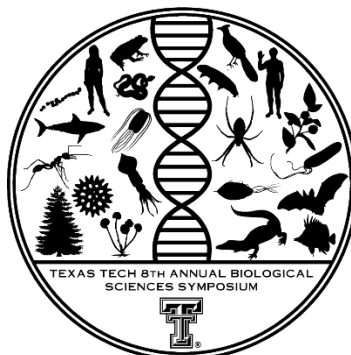
Dan Riskin – Discovery Canada  
Chiquito Crasto – Center for Biotechnology and Genomics, TTU  
Masoud Zabet Moghaddam – Center for Biotechnology and Genomics, TTU  
Susan San-Francisco – Center for Biotechnology and Genomics, TTU  
Kameswara Rao Kottapalli – Center for Biotechnology and Genomics, TTU  
Ezinne Osuji – Biological Sciences, TTU  
Beth Rodgers – Biological Sciences, TTU  
Daniela Viveros – Biological Sciences, TTU  
Nikhil Menon – Biological Sciences, TTU  
Kelsey Thompson – Biological Sciences, TTU  
Kathryn Watson – Biological Sciences, TTU  
Laramie Lindsey – Biological Sciences, TTU  
Jeff Clerc – Biological Sciences, TTU  
Matt Chumchal – Biological Sciences, Texas Christian University  
Natasja van Gestel – Texas Tech Climate Science Center, TTU  
Karina Alvina – Biological Sciences, TTU  
Matthew Barnes – Department of Natural Resources Management, TTU  
Catherine Wakeman – Biological Sciences, TTU

#### **Moderators**

Laramie Lindsey – Biological Sciences, TTU  
Kayla Bounds - Biological Sciences, TTU/TTUHSC  
Nardana Esmaeili - Biological Sciences, TTU  
Taylor Soniat - Biological Sciences, TTU  
Whitney Watson - Biological Sciences, TTU  
John Stuhler - Biological Sciences, TTU  
Macy Madden - Biological Sciences, TTU  
Erin Bohlender - Biological Sciences, TTU  
Jenny Korstian - Biological Sciences, TTU  
Kathryn Watson - Biological Sciences, TTU  
Anuradha Dhingra - Biological Sciences, TTU

#### **Thanks to the following businesses and individuals for their contributions:**

TTU Graduate School	Puttin' on the Ritz	Pam Hellman
TIEHH	Texas Tech Libraries	Erika Densmore
Julie Isom	Texas Tech Athletics Dept.	Amazon
Thermo Fisher Scientific	Texas Tech University Press	



*The 2017 TTABSS logo was produced exclusively for the Association of Biologists at Texas Tech University by Mr. Mark A. Lee*



# ASSOCIATION OF BIOLOGISTS AT TEXAS TECH UNIVERSITY

## Faculty Advisor/Department of Biological Sciences Interim Chair

Dr. John Zak

### Faculty Co-Advisors

Dr. Ron Chesser

Dr. Lou Densmore

Dr. Robert Bradley

### TTUAB BOARD OF DIRECTORS

#### Co-Presidents

Emma K. Brookover

Amanda Starr

#### Vice President

Jenny Korstian

#### Treasurer

Daniela Arenas-Viveros

#### Secretary

Laura Blanco-Berdugo

#### Board Members

Laramie Lindsey

Brandon Gross

Caroline Shuster

Christine Prater

Rita Quiñones De Magalhães

Nardana Esmacili

Drake Smith

#### Local Committee

Chairperson

*Emily A. Wright*

Registration

*Daniela Arenas-Viveros*

Silent Auction

*Betzaida Rivera-Rivera*

Abstract & Program Book

*Taylor J. Soniat*

Public Relations

*Oscar Sandate*

IT/Website

*Shengjian Jiang*



## LOCAL RESTAURANTS

### SHORT DRIVING DISTANCE (within 2 miles)

<b>Name</b>		<b>Phone</b>
Blue Sky Texas Burgers	3216 4 <sup>th</sup> St (Right Across from Museum)	(806) 368-0750
Jumbo Joe's Burgers	3310 4 <sup>th</sup> St (Right Across from Museum)	(806) 747-7900
Rosa's Cafe	4407 4 <sup>th</sup> St	(806) 785-5334
Sonic	4401 4 <sup>th</sup> St	(806) 771-0117
McDonald's	5201 4 <sup>th</sup> St	(806) 791-7701
Chick-Fil-A	312 University Ave	(806) 744-1564
Panda Express	313 University Ave	(806) 744-1999
Chili's Grill & Bar	607 University Avenue	(806) 744-2025
Cricket's Grill	2412 Broadway	(806) 744-4677
Firehouse Subs	411 University Avenue	(806) 747-9600
Jimmy John's	2413 Broadway Avenue	(806) 740-0002
Little Panda	1221 University Avenue	(806) 722-0888
Mesquites Sports Grill	2419 Broadway	(806) 744-9277
One Guy's Pizza	1101 University Avenue	(806) 747-1226
Raising Canes Chicken	907 University Avenue	(806) 744-8552
Rocky LaRues	2420 Broadway #B	(806) 747-6366
Ruby Tequila's	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 Sandwich	1021 University Avenue	(806) 472-9424

### DRIVING DISTANCE (INSIDE LOOP 289)

<b>Name</b>	<b>Address</b>	<b>Phone</b>
Arby's	2422 19th Street, Suite 6037	(806) 744-2535
Burger King	2405 19th Street	(806) 762-2282
Fuzzy's Taco Shop	2102 Broadway	(806) 740-8226
Josie's Authentic Mexican Food	2332 19th Street	(806) 796-0192
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
Schlotzsky'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



# 8<sup>th</sup> Texas Tech Annual Biological Sciences Symposium

## April 7-8, 2017

**Venue:**  
**Museum of Texas Tech University**  
**3301 4th Street**  
**Lubbock, TX 79415**

### PROGRAM AT A GLANCE

#### Friday, April 7<sup>th</sup>

- 4:30 pm – 5:00 pm** Poster Set-up and Registration, Museum of Texas Tech University (heavy hors d' oeuvres will be served)
- 5:00 pm – 5:15 pm** TTABSS 2017 kick off by Dr. Guy Loneragan, Vice President of Research, TTU
- 5:30 pm – 6:30 pm** Plenary Talk, Dr. Matt Chumchal, Texas Christian University- Auditorium
- “An environmental problem hidden in plain sight: small man-made ponds, emergent insects and mercury contamination of biota in the Great Plains”
- 6:30 pm – 8:30 pm** Poster Session, Judging, and Vendor Show
- 8:30 pm – 9:00 pm** Poster Takedown

#### Saturday, April 8<sup>th</sup>

- 7:30 am – 8:30 am** Registration and Breakfast, Museum of Texas Tech University
- 8:15 am – 8:30 am** Welcoming by Dr. John Zak, Associate Dean for Research, College Arts and Sciences, TTU



**9:00 am – 10:00 am** Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium

**10:00 am – 10:15 am** Coffee Break

**10:15 am – 12:00 pm** Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium

**12:00 pm – 1:30 pm** Lunch break (On Your Own)

**1:30 pm – 3:00 pm** Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium

**3:00 pm – 4:00 pm** Plenary Talk, Dr. Dan Riskin, Discovery Canada-Auditorium

“Some Thoughts on Science Communication, and the Story of a Botfly named Georgia”

**4:00 pm – 5:00 pm** Self-Guided Tour of Museum of Texas Tech University (optional)

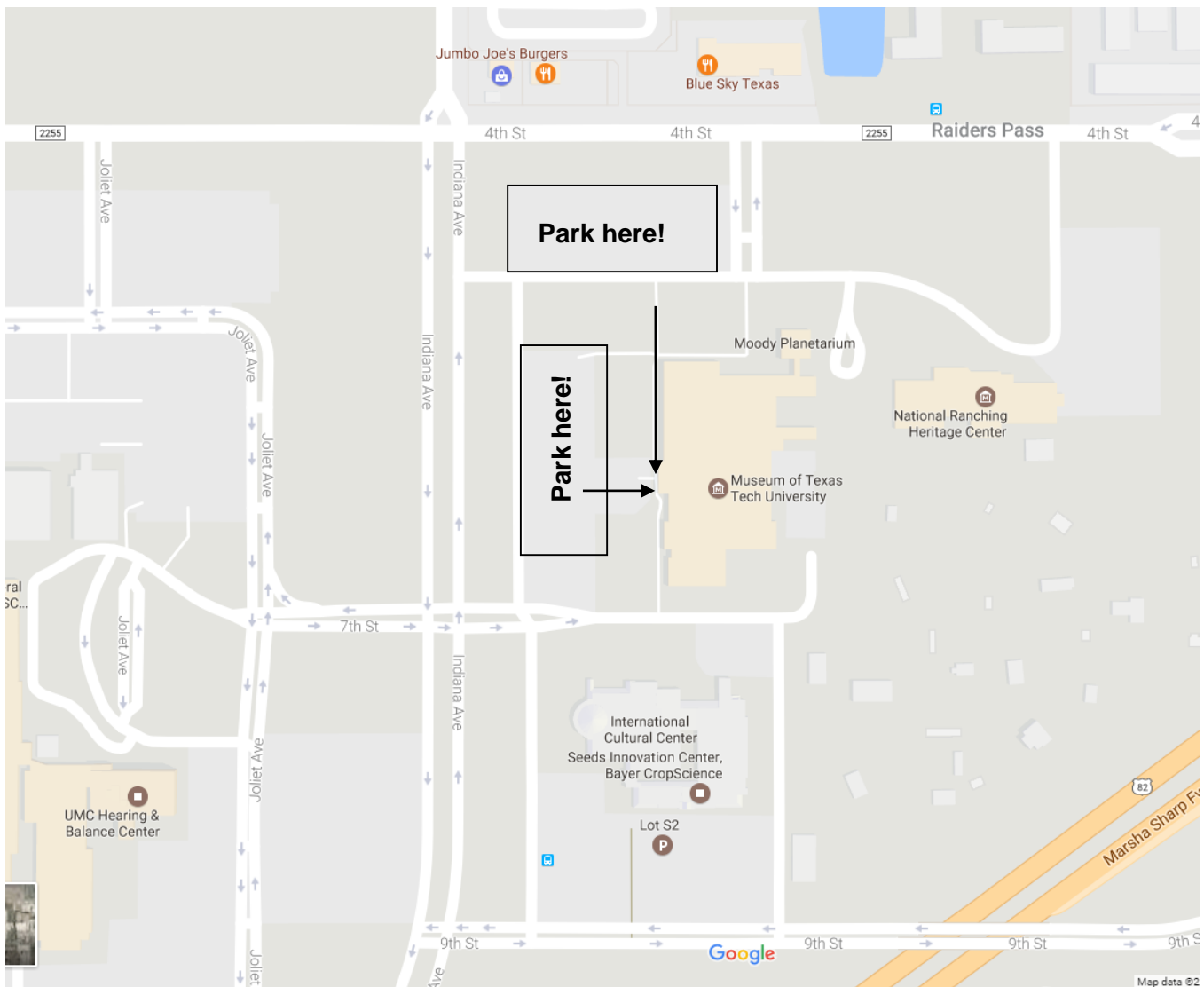
**6:00pm – 9:00 pm** Awards Banquet and Dinner, Sculpture, Museum of Texas Tech University



# EVENT LOCATION

**April 7-8, 2017**

**Helen DeVitt Jones Auditorium and Sculpture Court - Museum of Texas Tech University  
3301 4th Street  
Lubbock, TX 79415  
806-742-2490**





# DETAILED SCHEDULE OF EVENTS

## POSTER SESSION

### FRIDAY, APRIL 7<sup>th</sup>

#### Friday, April 7<sup>th</sup>

- 4:30 pm – 5:00 pm** Poster Set-up and Registration, Museum of Texas Tech University (heavy hors d' oeuvres will be served)
- 5:00 pm – 5:15 pm** TTABSS 2017 kick off by Dr. Guy Loneragan, Vice President of Research, TTU
- 5:30 pm – 6:30 pm** Plenary Talk, Dr. Matt Chumchal, Texas Christian University- Auditorium
- “An environmental problem hidden in plain sight: small man-made ponds, emergent insects and mercury contamination of biota in the Great Plains”
- 6:30 pm – 8:30 pm** Poster Session, Judging, and Vendor Show
- 8:30 pm – 9:00 pm** Poster Takedown



## **UNDERGRADUATE POSTERS**

**1. FISH ASSOCIATIONS WITH MILLEPORA SPP. (FIRE CORAL) IN THE MESOAMERICAN REEF IN UTILA, HONDURAS**

Sarah F. Cole<sup>1,2\*</sup>, Stephanie C. Randell<sup>2</sup>, Traesha R. Robertson<sup>3</sup>, Donna E. Hamilton<sup>4</sup>, and Stephanie A. Lockwood<sup>1</sup>

**2. BULLIES CD-1 RETIRED BREEDER MICE ARE RESILIENT TO CROSS-SENSITIZATION AMONG STRESS, ALCOHOL INTAKE, AND SALTY HIGH-FAT DIET PREFERENCE**

Josiah N Morales<sup>1\*</sup>, Aaron White<sup>2\*</sup>, Mayra Herrera-Gonzales<sup>3</sup>, Daniela P Derderian<sup>4</sup>

**3. IDENTIFYING THE GENETIC DIVERSITY OF *TRYPANOSOMA CRUZI* IN CHAGAS DISEASE VECTOR SPECIES IN SOUTHEAST TEXAS**

Patricia Feria<sup>1</sup> and Marcelo Pintos<sup>2\*</sup>

**4. DEGRADATION OF FEATHER COLORATION IN MUSEUM SPECIMENS OF THREE BIRD SPECIES OVER TIME**

Amanda K. Locke<sup>1\*</sup> and Erin Stukenholtz-Bohlender<sup>1</sup>

**5. TEMPORAL AND GEOGRAPHIC VARIATION OF MUSEUM RECORDS OF THREATENED BAT SPECIES FROM SOUTH AMERICA**

Sara Hamilton<sup>1\*</sup>, Jalissa Williams<sup>1\*</sup>, Cristina Ríos-Blanco<sup>1</sup> and Richard D. Stevens<sup>1,2</sup>

**6. CONCENTRATED CELL-FREE SUPERNATANT OF *LACTOBACILLUS* INHIBITS THE GROWTH OF DIFFERENT BACTERIAL PATHOGENS**

Sahar Mirza<sup>1\*</sup>, Kelsey Sprinkles<sup>2\*</sup>, Taylor Letbetter<sup>2</sup>, Nithya Mudaliar<sup>3</sup>, Gary Ventolini<sup>4</sup>, Natalia Schlabritz-Lutsevich<sup>4</sup>, and Abdul Hamood<sup>3</sup>

**7. BASELINE SURVEY OF TEXAS HORNED LIZARDS IN THE TEXAS PANHANDLE**

Sara A. van der Leek<sup>1\*</sup> and Andrew C. Kasner<sup>1</sup>

**8. FREQUENCIES AND SUBSTRATE ASSOCIATION OF EXCAVATING PORIFERANS IN UTILA, HONDURAS**

Collin M. Harvey<sup>1,2\*</sup>, Stephanie C. Randell<sup>2</sup>, Donna E. Hamilton<sup>4</sup>, Traesha R. Robertson<sup>3</sup>, and Stephanie A. Lockwood<sup>1</sup>

**9. MULTIPLE TOXIC BLOOMS OF GOLDEN ALGA OCCURRED IN THE LUBBOCK CANYON LAKES SYSTEM IN FALL OF 2016-- COULD THESE INSTANCES BE PREDICTIVE OF A LARGER BLOOM IN SPRING OF 2017?**

Lindsay D. Williams<sup>1\*</sup>, Reynaldo Patiño<sup>2</sup>





**10. PORIFERAN ASSOCIATION WITH WHITE AND YELLOW BAND CORAL DISEASES ON THE MESOAMERICAN REEF, UTILA, HONDURAS**

Andrea C. Edie<sup>1</sup>, MacKenzie L. Kroll<sup>1\*</sup>, Bobby A. Rodriguez<sup>1</sup>, Stephanie C. Randell<sup>2</sup>, Traesha R. Robertson<sup>3</sup>, Donna E. Hamilton<sup>4</sup>, Stephanie A. Lockwood<sup>1</sup>

**11. SEXUAL DIMORPHISM WITHIN THE WHITE-LINED BROAD-NOSED BAT (*PLATYRRHINUS LINEATUS*) USING SKULL MORPHOMETRICS**

Ashlyn N. Kildow<sup>1\*</sup>, John D. Stuhler<sup>1</sup>, and Richard D. Stevens<sup>1,2</sup>

**12. CONTRIBUTION OF THE CHOLINE BRANCH OF KENNEDY PATHWAY DURING THE SANDFLY TRANSMISSION STAGE OF LEISHMANIA MAJOR**

Brian C. Johnson<sup>1\*</sup>, Samrat Moitra<sup>1</sup> and Kai Zhang<sup>1</sup>

**13. ASSESSMENT OF SHORT-TERM WORKING MEMORY IN ALZHEIMER'S TRANSGENIC MICE**

Chelsea Limboy<sup>1\*</sup>, Breanna N. Harris<sup>1</sup>, Paul Soto<sup>2</sup>

**14. VALIDATION OF A SCOTOTAXIS ANXIETY TEST IN *XENOPUS LAEVIS***

Celina Pecos<sup>1\*</sup>, Kelsey Aguirre<sup>1</sup>, Boone Coleman<sup>1,2</sup>, Hannah Spiegel<sup>1</sup>, James A. Carr<sup>1</sup>, and Breanna N. Harris<sup>1</sup>

**GRADUATE POSTERS**

**15. CLIFF SWALLOWS (*PETROCHELIDON PYRRHONOTA*) PREFER TO NEST IN THE CENTER OF COLONIES**

Shelby Osborne<sup>1</sup>, Douglas Leasure<sup>1</sup>, Ragupathy Kannan<sup>1</sup>, and Steward Huang<sup>1</sup>

**16. METAGENOMIC STUDY OF POLYSTYRENE DEGRADATION BY MEALWORMS**

Anisha Navlekar<sup>1\*</sup>, Deborah Carr<sup>1</sup>

**17. STATISTICAL ANALYSIS OF BINOCULAR EYE GAZE TRAJECTORIES**

Pansujee V. Dissanayaka<sup>1</sup>, Jingyong Su<sup>1</sup> and Bijoy K. Ghosh<sup>1</sup>

**18. IN VIVO KINASE SUBSTRATE TAGGING, IDENTIFICATION AND QUANTIFICATION BY NANOTECHNOLOGY**

Fengqian Chen<sup>1</sup>

**19. PRELIMINARY INVESTIGATIONS OF LOSSES TO HERBIVORY IN A CARNIVOROUS PLANT**

Rachel N. Carmickle<sup>1\*</sup> and John D. Horner<sup>1</sup>



- 20. IMPACTS OF ANTHROPOGENIC PRESSURES ON THE CONTEMPORARY BIOGEOGRAPHY OF THREATENED CROCODYLIANS IN INDONESIA**  
Kyle J. Shaney<sup>1\*</sup>, Amir Hamidy<sup>2</sup>, Matthew Walsh<sup>1</sup>, Evy Arida<sup>2</sup>, Aisyah Arimbi<sup>3</sup>, and Eric N. Smith<sup>1</sup>
- 21. 3D TECHNOLOGIES: APPLICATIONS FOR DIGITIZING SMALL ANIMAL BONES FOR COMPARATIVE COLLECTIONS**  
Kathryn Faircloth<sup>1\*</sup> and Jessica Stepp<sup>1</sup>
- 22. EXTINCT GAZELLE-HORSE *NANNIPPUS PENINSULATUS* (MAMMALIA; EQUIDAE) FROM SCURRY COUNTY, TEXAS, WITH IMPLICATIONS FOR BIOCHRONOLOGY**  
John A. Moretti<sup>1\*</sup> and Eileen Johnson<sup>1</sup>
- 23. INFORMATIVE INDEX OF THE ALLERGENIC POLLEN AND FUNGI OF THE TEXAS PANHANDLE TO AID IN DIAGNOSIS OF ALLERGY AND ASTHMA**  
Nelofar Sherali<sup>1\*</sup>, Chandini Revanna<sup>2\*</sup>, Aubrey Howard<sup>1</sup>, Alyssa Coots<sup>1\*</sup>, Constantine Saadeh<sup>3</sup>, Jon Bennert<sup>4</sup>, Jeff Bennert<sup>4</sup>, and Nabarun Ghosh<sup>1</sup>
- 24. LASER PHOTO-STIMULATION OF PLANTS AND MICROBES ASSOCIATED WITH PLANTS, FOR BETTER PHYTOREMEDIATION OF HEAVY METAL CONTAMINATED SITES**  
Bigyan Rimal<sup>1\*</sup>, Jan W. Dobrowolski<sup>2</sup>, Deborah Carr<sup>1</sup>
- 25. NEXT SCIENCE INFLUENCES THE EXPRESSION OF CYTOKINES AND CHEMOKINES INVOLVED IN THE HOST RESPONSE TO INJURY IN WOUNDS INFECTED WITH *STAPHYLOCOCCUS AUREUS***  
Kayla Bounds<sup>1\*</sup>, Matt Myntti<sup>2</sup>, Jane A. Colmer-Hamood<sup>3,4</sup>, Randall Jeter<sup>1</sup>, and Abdul Hamood<sup>4,5</sup>
- 26. DNA TRANSPOSON ACTIVITY AND ASSOCIATED MUTATION RATES IN *MYOTIS* BATS**  
Nicole S. Paulat<sup>1\*</sup> and David A. Ray<sup>1</sup>
- 27. 3D GEOMETRIC MORPHOMETRICS APPLIED IN THE IDENTIFICATION OF A *CANIS* SPP. RECOVERED FROM A HISTORIC SITE IN WESTERN TEXAS**  
Lila S. Jones<sup>1\*</sup> and Eileen Johnson<sup>1</sup>
- 28. A FIRST PHYLOGENETIC APPRAISAL OF FOREST-DWELLING SKINKS OF THE GENUS *TYTTHOSCINCUS* FROM JAVA AND SUMATRA, INDONESIA**  
Panupong Thammachoti<sup>1\*</sup>, Utpal Smart<sup>1</sup>, Amir Hamidy<sup>2</sup>, Nia Kurniawan<sup>3</sup>, Irvan Sidik<sup>2</sup>, and Eric N. Smith<sup>1</sup>



**29. CHLORTETRACYCLINE IN WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) AND SUPERMARKET MEAT BY LIQUID CHROMATOGRAPHY TANDEM-MASS SPECTROMETRY**

Shanoy C. Anderson<sup>1\*</sup>, Subbiah Seenivasan<sup>1</sup>, Angella A. Gentles<sup>1</sup>, Paul Stonum<sup>2</sup>, Tiffanie A. Brooks<sup>2/3</sup> and Ernest E. Smith<sup>1</sup>

**30. REDUCTION IN DAILY SOIL TEMPERATURE RANGE INCREASE MICROBIAL COMMUNITY DYNAMICS IN A DRYLAND COTTON PRODUCTION SYSTEM IN WEST TEXAS**

Diana L. Vargas-Gutierrez<sup>1\*</sup>, John Zak<sup>1</sup>, Veronica Acosta-Martinez<sup>2</sup>, Bobbie McMichael<sup>1</sup>

**31. RECOMBINANT R2-PYOCIN CREAM IS EFFECTIVE IN TREATING *PSEUDOMONAS AERUGINOSA*-INFECTED WOUNDS**

Abdulaziz Y Alqahtani<sup>1\*</sup>, Nithya Mudaliar<sup>2</sup>, Dean Scholl<sup>3</sup>, Sharmila Dissanaiké<sup>4</sup>, Randal Jeter<sup>1</sup>, Jane Colmer-Hamood<sup>2,5</sup>, and Abdul Hamood<sup>2,4</sup>

**32. PHOSPHATIDYLCHOLINE BIOSYNTHESIS IN *LEISHMANIA MAJOR***

Samrat Moitra<sup>1\*</sup>, Mattie Pawlowicz<sup>2</sup>, Fong-Fu Hsu<sup>3</sup>, and Kai Zhang<sup>1</sup>

**33. TESTOSTERONE MAINTAINS SPERMATOGENESIS BY PREVENTING GERM CELL APOPTOSIS: IS TESTOSTERONE ACTING DIRECTLY ON GERM CELL MEMBRANE PROGESTERONE RECEPTORS?**

Arpita Talapatra<sup>1\*</sup>, Dibyendu Dutta<sup>2</sup>, Shuvalaxmi Dasgupta<sup>1</sup> and Nathaniel Mills<sup>1</sup>

**34. ESTIMATING REGIONAL CARRYING CAPACITIES ACROSS THE SOUTHERN HIGH PLAINS VISITED BY THE MID-CONTINENT POPULATION OF SANDHILL CRANES USING REMOTE SENSING TOOLS**

Kathryn J. Brautigam<sup>1\*</sup>, Blake A. Grisham<sup>1</sup>, William P. Johnson<sup>2</sup>, Daniel T. Raleigh<sup>1</sup>, Daniel P. Collins<sup>3</sup>, Shaun L. Oldenburger<sup>4</sup>, Jude R. Smith<sup>5</sup>, Nicole D. Athearn<sup>6</sup>, Warren C. Conway<sup>1</sup>

**35. GUT MICROBIOME ANALYSIS DURING PREGNANCY IN *TADARIDA BRASILIENSIS***

Oscar Sandate<sup>1\*</sup>, Matthew Fox<sup>1</sup>, Gregory Knox<sup>1</sup>, Marilyn Mathew<sup>1</sup>, Craig Tipton<sup>1</sup>, Caleb Phillips<sup>1,2</sup>

**36. THE CARBON BUDGETS OF CENTRAL TEXAS WOODLANDS IN THE CONTEXT OF CLIMATE CHANGE AND INDUSTRIAL ATMOSPHERIC CARBON DIOXIDE CONCENTRATIONS**

Tamura E. Dunbar<sup>\*</sup>, Mary Sides, Joseph D. White, Kyle Logan, Ariel Sorg, and Sunshyne Hendrix<sup>1</sup>

**37. INFLUENCE OF CLIMATE CHANGE, FRESHWATER INFLOWS, AND CHANGING LAND USE ON THE DISTRIBUTION OF DWARF SEAHORSE ON THE TEXAS COAST**

Elizabeth L. Roesler<sup>1\*</sup>, Matthew A. Barnes<sup>1</sup>, Timothy B. Grabowski<sup>2</sup>, Fernando Martinez-Andrade<sup>3</sup>, and Rachel Bittner<sup>1</sup>



### **38. WAPDAP – SOFTWARE THAT AUTOMATES PROTEOMICS DATA ANALYSIS PIPELINE**

Adnan Ahmed<sup>1\*</sup>, Masoud Zabet-Moghaddam<sup>1</sup> and Chiquito Crasto<sup>1</sup>

### **39. PIACAN: PATHWAY INTEGRATION AND ANALYSIS OF CANCER NETWORKS**

Adrian Quintana<sup>1\*</sup>, Chiquito J. Crasto<sup>1</sup>, Tommy Dang<sup>2</sup>, Vinh Nguyen<sup>2</sup>



## **DETAILED SCHEDULE OF EVENTS ORAL SESSIONS AND AWARDS BANQUET SATURDAY, APRIL 8<sup>th</sup>**

- 7:30 am – 8:30 am** Registration and Breakfast, Museum of Texas Tech University
- 8:15 am – 8:30 am** Welcoming by Dr. John Zak, Associate Dean for Research, College Arts and Sciences, TTU
- 9:00 am – 10:00 am** Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium
- 10:00 am – 10:15 am** Coffee Break
- 10:15 am – 12:00 pm** Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium
- 12:00 pm – 1:30 pm** Lunch Break (On Your Own)
- 1:30 pm – 3:00 pm** Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium
- 3:00 pm – 4:00 pm** Plenary Talk, Dr. Dan Riskin, Discovery Canada- Auditorium  
“Some Thoughts on Science Communication, and the Story of a Botfly named Georgia”
- 4:00 pm – 5:00 pm** Self-Guided Tour of Museum of Texas Tech University (optional)



**6:00pm – 9:00 pm** Awards Banquet and Dinner, Sculpture, Museum of Texas Tech University

### **AWARDS BANQUET**

**6:00pm – 6:30pm** Dinner Check-in

**6:00pm – 9:00pm** Silent Auction Hours (Cash, Credit Card, and Check accepted)

**6:00pm – 9:00pm** Open Bar

**6:30pm** Welcome, Amanda Starr and Emma Brookover, TTUAB Co-Presidents

**6:40pm** Dinner Buffet Opens

**7:45pm** Presentation of Awards  
Vendors, Sponsors, and Collaborators  
Participants  
Poster Presentations  
    Undergraduate, Dr. Lou Densmore, CISER  
    Graduate  
Oral Presentations  
    Undergraduate, Dr. Lou Densmore, CISER  
    Warren B. Ballard Memorial Award, Cristina Rios-Blanco, ANRS President  
    Shan L. Bilimoria Memorial Graduate Student Award, Ezinne Osuji, TechASM VP  
Museum Science  
Cell and Molecular Biology



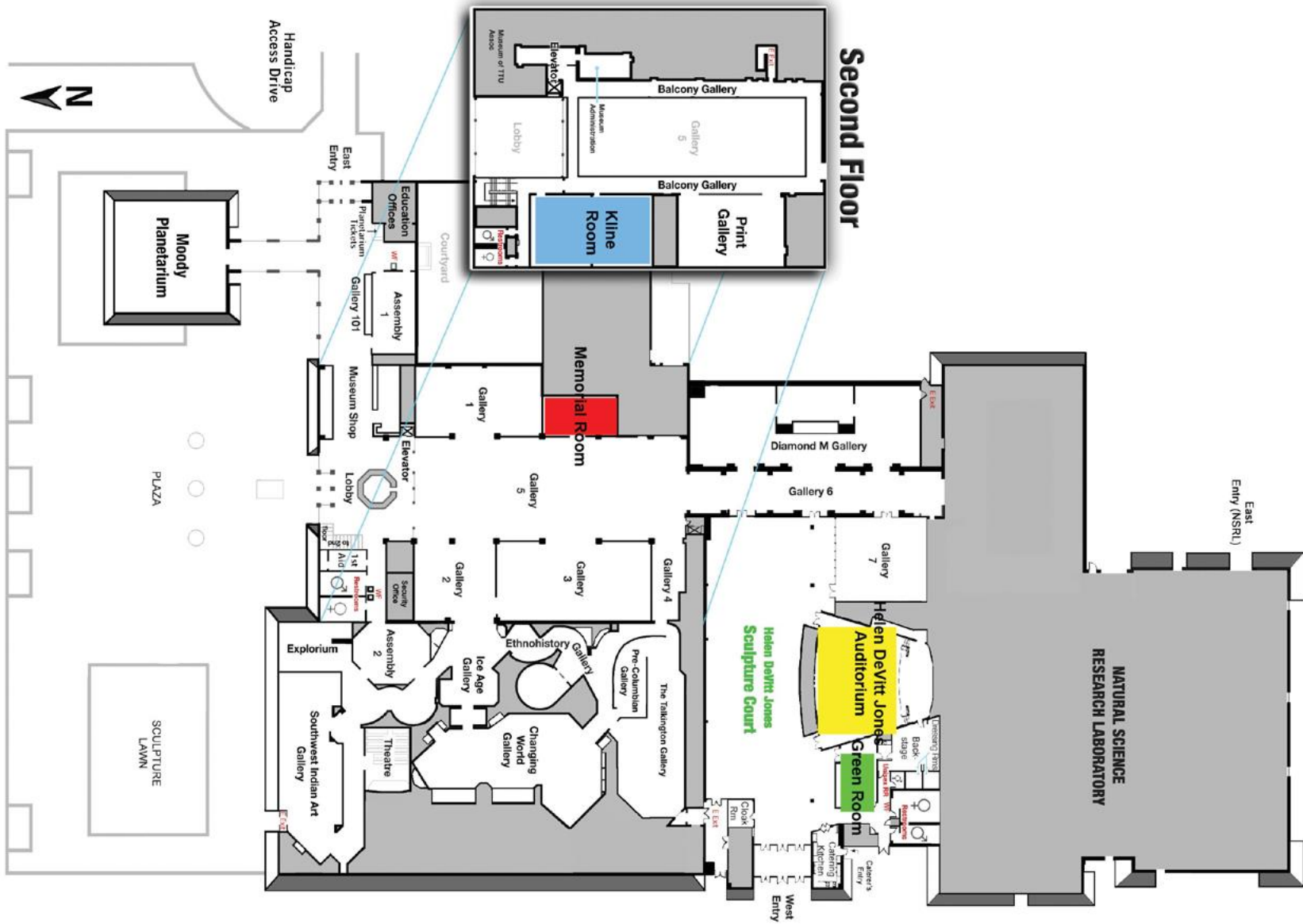
Ecology  
Evolutionary Biology  
Proposal  
Toxicology

8:45pm

Closing Remarks, Amanda Starr and Emma Brookover, TTUAB Co-Presidents



# Museum of Texas Tech University Interior Map







	NATURAL RESOURCES MANAGEMENT (Auditorium)	PROPOSALS (Green Room)	UNDERGRADUATE (Kline Room)	CELL & MOLECULAR BIOLOGY (Memorial Room)
9:00 AM	<b>HABITAT SELECTION BY WATERFOWL WINTERING AT ANAHUAC NATIONAL WILDLIFE REFUGE (78)</b> Tiffany C. Lane <sup>1*</sup> , Jena A. Moon <sup>2</sup> , Blake A. Grisham <sup>1</sup> , Doug M. Head <sup>2</sup> , David A. Haukos <sup>3</sup> , Warren C. Conway <sup>1</sup>	<b>HYPOXIA IN THE GULF OF MEXICO: LONG-TERM IMPACTS ON ATLANTIC CROAKER OTOLITHS (82)</b> Shengjian Jiang <sup>1*</sup>	<b>CYTOTOXIC AND APOPTOTIC EFFECTS OF CHAGA MUSHROOM (INONOTUS OBLIQUUS) ON CULTURED 4T1 MURINE BREAST CANCER CELLS (39)</b> Jake A. Brozek <sup>1*</sup> , Sarah Kelly <sup>1</sup> , Vianney Trujillo <sup>1</sup> , Trevor Burrow <sup>1</sup> , Gary O. Gray <sup>1</sup> , Adam J. Reinhart <sup>1</sup>	<b>CLONING AND CHARACTERIZATION OF THE W4 LOCUS OF MAIZE AND ITS ROLE IN VASCULAR DEVELOPMENT AND STRESS ADAPTATION (45)</b> Anuradha Dhingra <sup>1*</sup> and Chris Rock <sup>1</sup>
9:15 AM	<b>FEED BEHAVIORS AND PROPERTY DAMAGES OF SUS SCROFA (81)</b> Erin E. Ray <sup>1*</sup> , Steven J. Rosscoe <sup>2</sup> , Wendi K. Wolfram <sup>3</sup>	<b>SEASONAL FLEXIBILITY IN BODY COMPOSITION AND LIPID OXIDATIVE CAPACITY IN <i>TADARIDA BRASILIENSIS</i> (83)</b> Elizabeth J. Rogers <sup>1*</sup> , Amie S. Sommers <sup>1</sup> , and Liam P. McGuire <sup>1</sup>	<b>USING VHF RADIO TELEMETRY TO DETERMINE HOME RANGE AND HABITAT USE OF LADDER-BACKED WOODPECKERS (<i>PICOIDES SCALARIS</i>) IN THE TEXAS PANHANDLE (40)</b> Victoria K. Solis <sup>1*</sup> and Andrew C. Kasner <sup>1</sup>	<b>THE EFFECTS OF TECTAL NPY RECEPTORS ON FOOD INTAKE IN THE AFRICAN CLAWED FROG, <i>XENOPUS LAEVIS</i> (46)</b> Ranakul Islam <sup>1*</sup> and James A. Carr <sup>1</sup>
9:30 AM	<b>THE RATIO OF ORGANIC TO INORGANIC NITROGEN AFFECTS THE GROWTH OF ICHTHYOTOXIC GOLDEN ALGA (80)</b> Rakib H. Rashed <sup>1*</sup> , Lindsay D. Williams <sup>2</sup> , and Reynaldo Patiño <sup>3</sup>	<b>UNDERSTANDING THE EFFECTS OF HYPERGLYCEMIA ON SUBCORTICAL PROCESSING OF FEAR AND ANXIETY IN THE AFRICAN CLAWED FROG (<i>XENOPUS LAEVIS</i>) (84)</b> Nikhil Menon <sup>1*</sup> and James A. Carr <sup>1</sup>	<b>BULLIED C57BL/6J MICE DISPLAY CROSS-SENSITIZATION BETWEEN STRESS-INDUCED ALCOHOL DEPENDENCE AND SALTY HIGH-FAT DIET PREFERENCE: AVERSIVE SALTY HIGH FAT DIET BECOMES PALATABLE (41)</b> Mayra Gonzales <sup>1*</sup> , Josiah N. Morales <sup>1</sup> , Daniela P. Derderian DTB <sup>1</sup>	<b>CLASSIFICATION OF PROTEIN-LIGAND BINDING USING THEIR STRUCTURAL DISPERSION (47)</b> Galkande A.I.C. Premarathna <sup>1*</sup> , Leif Ellingson <sup>2</sup>
9:45 AM	<b>VELOCITY FAILS TO EXPLAIN SELECTION FOR LOW WIND POTENTIAL IN MIGRATING SWAINSON'S HAWKS (<i>BUTEO SWAINSONI</i>) (79)</b> Katheryn A. Watson <sup>1*</sup> , Clint W. Boal <sup>2</sup> , Laurie M. Groen <sup>1</sup> , and James D. Ray <sup>3</sup>	<b>NEST SITE OVERLAP OF NATIVE AND INVASIVE AVIAN SPECIES AT TEXAS TECH (88)</b> Erin E. Bohlender <sup>1*</sup> and Richard D. Stevens <sup>1,2</sup>	<b>USING GENOMICS AND BIOINFORMATICS TO DETERMINE THE ORIGIN AND PHYLOGENETIC SIGNIFICANCE OF THE ZONADHESIN GENE IN RODENTIA (42)</b> Emma K. Roberts <sup>1</sup> , Whitney N. Watson <sup>1*</sup> , Daniel M. Hardy <sup>2</sup> , and Robert D. Bradley <sup>1,3</sup>	<b>RECOGNITION AND INVOLVEMENT OF CONSERVED BH3 DOMAIN INTERACTING MEMBERS OF BCL2 SUPERFAMILY OF PROTEINS INVOLVED IN TESTICULAR GERM CELL APOPTOSIS (48)</b> Arpita Talapatra <sup>1*</sup> , Nathaniel Mills <sup>1</sup> , Brian Beck <sup>2</sup>
10:00 AM	COFFEE BREAK			



	EVOLUTIONARY BIOLOGY (Auditorium)	PROPOSALS (Green Room)	ECOLOGY (Kline Room)	CELL & MOLECULAR BIOLOGY (Memorial Room)
10:15 AM	<b>EVALUATING THE LINEAGE DIVERSIFICATION OF PEROMYSCUS USING A PHYLOGENOMIC APPROACH (62)</b> Laramie L. Lindsey <sup>1*</sup> , Roy N. Platt II <sup>1</sup> , Caleb D. Phillips <sup>1,2</sup> , David A. Ray <sup>1</sup> , and Robert D. Bradley <sup>1,2</sup>	<b>STEPS TO THE PHYLOGENETIC RESOLUTION OF SPECIES-RICH GENERA (85)</b> Michaela K. Halsey <sup>1,2*</sup> , Laura A. Blanco-Berdugo <sup>1</sup> , Nicole S. Paulat <sup>1</sup> , Roy N. Platt II <sup>1</sup> , Richard D. Stevens <sup>2</sup> and David A. Ray <sup>1</sup>	<b>CONSERVATION ASSESSMENT OF THE EGYPTIAN FRUIT BAT (ROUSETTUS AEGYPTIACUS): HUNTING EFFECTS AND ECOSYSTEM SERVICES IN SOUTHERN NIGERIA (54)</b> Benneth C. Obitte <sup>1*</sup> and Tigga Kingston <sup>1</sup>	<b>MOLECULAR MECHANISMS UNDERLYING DROUGHT STRESS ACCLIMATION IN TWO DIVERSE DROUGHT TOLERANT PEANUT GENOTYPES (49)</b> Ashwini Challa <sup>1*</sup> , Poornasree Kumar <sup>1</sup> , Pratibha Kottapalli <sup>1</sup> , Paxton Payton <sup>2</sup> , Kameswara Rao Kottapalli <sup>1</sup>
10:30 AM	<b>RESOLVING THE PHYLOGENETIC VARIATION IN PEROMYSCUS MANICULATUS; POSSIBLE EVIDENCE FOR MULTIPLE SPECIES (63)</b> James Q. Francis <sup>1*</sup> , Roy N. Platt II <sup>1</sup> , Caleb D. Phillips <sup>1,2</sup> , and Robert D. Bradley <sup>1,2</sup>	<b>THE INFLUENCE OF CATEGORICALLY DISTINCT STRESSORS ON ATTENTION TO VISUAL FOOD CUES (86)</b> Songhe Li <sup>1*</sup> , James. Carr <sup>1</sup>	<b>THE EFFECT OF WHISPER CALLS ON SETTLEMENT DECISIONS OF VEERIES (CATHARUS FUSCESCENS) (55)</b> William D. Fetzner <sup>1*</sup> , Kenneth A. Schmidt <sup>1</sup>	<b>MICRORNA REGULATION OF GENE EXPRESSION UNDER DROUGHT STRESS ACCLIMATION IN PEANUT ROOTS (50)</b> Poornasree Kumar <sup>1*</sup> , Ashwini Challa <sup>1</sup> , Pratibha Kottapalli <sup>1</sup> , Paxton Payton <sup>2</sup> , Kameswara Rao Kottapalli <sup>1</sup>
10:45 AM	<b>TECTAL CRF R1 RECEPTORS INHIBIT FOOD INTAKE (64)</b> C. Prater <sup>1*</sup> , B.N. Harris <sup>1</sup> , and J.A. Carr <sup>1</sup>	<b>ASSESSING THE POTENTIAL CONTRIBUTIONS OF THE MICROBIAL COMMUNITIES OCCURRING WITHIN CONCRETE TO ENVIRONMENTAL CARBON FLUXES (89)</b> Jordan I. T. Brown <sup>1*</sup> and Deborah L Carr <sup>1</sup>	<b>ARE ALL MOUNTAINS THE SAME? CHANGES IN SOUTH AMERICAN BAT DIVERSITY PATTERNS ALONG ENVIRONMENTAL GRADIENTS (56)</b> Cristina Ríos-Blanco <sup>1*</sup> and Richard D. Stevens <sup>1</sup>	<b>IDENTIFYING POST-TRANSLATIONALLY MODIFIED PROTEINS IN BREAST CANCER CELLS FOR INVESTIGATING THE MECHANISMS OF ACTION OF A POTENTIAL ANTI-CANCER DRUG (51)</b> Bilkis A. Mitu <sup>1*</sup> , Lauren S. Gollahon <sup>2</sup> , Susan K. San Francisco <sup>1</sup> , and Zabet M. Masoud <sup>1</sup>
11:00 AM	<b>HIDDEN BENEFITS AID THE EVOLUTION OF ALTRUISM IN SMALL POPULATIONS OF UNRELATED INDIVIDUALS (65)</b> Sarah E. Fumagalli <sup>1*</sup> and Sean H. Rice <sup>1</sup>	<b>ADDRESSING THREATS TO LANDSCAPE SUSTAINABILITY: USING LAND-USE AND CLIMATE CHANGE SCENARIOS TO MODEL FUTURE SPATIAL AND POPULATION ECOLOGY OF THE MID-CONTINENT POPULATION OF SANDHILL CRANE ON THE SOUTHERN HIGH PLAINS (90)</b> Kathryn J. Brautigam <sup>1*</sup>	<b>SOIL MICROBIAL COMMUNITY PHYSIOLOGICAL AND COMPOSITIONAL CHANGES IN BIODIESELS VS. PETRODIESEL CONTAMINATED SOILS (57)</b> Meijun Dong <sup>1*</sup> , Deborah L. Carr <sup>1</sup>	<b>TRANSGENIC COTTON CO-OVEREXPRESSION OsSIZ1 AND AVP1 SHOWS IMPROVED GROWTH AND DEVELOPMENT UNDER MULTIPLE-STRESS CONDITIONS (44)</b> Nardana Esmaili <sup>1*</sup> , Yifan Cai <sup>1</sup> , Paxton Payton <sup>2</sup> , Hong Zhang <sup>1</sup>



	EVOLUTIONARY BIOLOGY (Auditorium)	PROPOSALS (Green Room)	ECOLOGY (Kline Room)	
11:15 AM	<p><b>THE FIRST COMPLETE PHYLOGENY OF SOUTHEAST ASIAN TOADS (ANURA: BUFONIDAE) REVEALS A UNIQUE EVOLUTIONARY LINEAGE, A POLYTYPIC NEW ARBOREAL GENUS ENDEMIC TO SUMATRA (66)</b></p> <p>Goutam C. Sarker<sup>1*</sup>, Utpal Smart<sup>1</sup>, Michael B. Harvey<sup>2</sup>, Amir Hamidy<sup>3</sup>, Nia Kurniawan<sup>4</sup>, and Eric N. Smith<sup>1</sup></p>	<p><b>SOIL MICROBIAL DYNAMICS IN A LONG-TERM SUSTAINABLE COTTON FIELD FOR SEMI-ARID WEST TEXAS (87)</b></p> <p>Pablo Tovar-Ballen<sup>1*</sup>, Veronica Acosta-Martinez<sup>2</sup>, John Zak<sup>1</sup></p>	<p><b>MODELING OPTIMAL STOPOVER USE ACROSS VARIED THERMOREGULATORY CAPACITIES DURING MIGRATION (58)</b></p> <p>Jeff Clerc<sup>1*</sup>, Liam P. McGuire<sup>1</sup></p>	
11:30 AM	<p><b>PHYLOGENETIC RELATIONSHIPS BETWEEN THE MEMBERS OF THE GENUS NOTROPIS (FAMILY CYPRINIDAE) (67)</b></p> <p>Ryan R. Vazquez<sup>1*</sup>, Lou Densmore<sup>1</sup>, and Gene Wilde<sup>1</sup></p>		<p><b>PHENOTYPIC FLEXIBILITY IN BODY COMPOSITION OF INSECTIVOROUS BATS DURING THE SUMMER ACTIVE PERIOD (59)</b></p> <p>Amie S. Sommers<sup>1*</sup>, Elizabeth J. Rogers<sup>1</sup>, Liam P. McGuire<sup>1</sup></p>	
11:45 AM	<p><b>THE UTILITY OF ZONADHESIN IN EXAMINING A POTENTIAL REPRODUCTIVE ISOLATION MECHANISM IN RODENTS (68)</b></p> <p>Emma K. Roberts<sup>1*</sup>, Daniel M. Hardy<sup>2</sup>, and Robert D. Bradley<sup>1,3</sup></p>		<p><b>ARE BATS MORE EFFECTIVE POLLINATORS THAN INSECTS? POSSIBLY NOT IN SOUTH AFRICAN BAOBABS (53)</b></p> <p>Macy A. Madden<sup>1*</sup> and Tigga Kingston<sup>1</sup></p>	
12:00pm	LUNCH (On Your Own)			



	MICROBIOLOGY (Auditorium)	MUSEUM SCIENCE (Green Room)	ECOLOGY (Kline Room)	TOXICOLOGY (Memorial Room)
1:30 PM	<b>BLOOD FROM TRAUMA PATIENTS PRODUCES MAJOR SHIFTS IN PSEUDOMONAS AERUGINOSA TRANSCRIPTOME (69)</b> Moamen Elmassry <sup>1*</sup> , Nithya S. Mudaliar <sup>2</sup> , Rao Kottapalli <sup>3</sup> , Sharmila Dissanaik <sup>4</sup> , John A. Griswold <sup>4</sup> , Michael J. San Francisco <sup>5</sup> , Jane A. Colmer-Hamood <sup>2,6</sup> , and Abdul N. Hamood <sup>2,4</sup>	<b>ENGAGING COLLECTIONS MANAGEMENT WITH MOBILE TECHNOLOGY (74)</b> Taylor S. Ernst <sup>1*</sup>	<b>PATTERN OF MICROBIAL DEGRADATION OF ESTRONE AND TRICLOSAN MIXTURE AND ITS EFFECT ON SOIL MICROBIAL COMMUNITY (60)</b> Ezinne Adabaram Osuji <sup>1*</sup> , Deborah L. Carr <sup>1</sup>	<b>ELETROSPUN NANOFIBER MEMBRANES FOR PARTICULATE MATTER AIR POLLUTION CLEANUP (91)</b> Lihua Lou <sup>1*</sup> , Hongnan Zhang <sup>2</sup> , Seshadri Ramkumar <sup>1</sup> , Xiaohong Qin <sup>2</sup>
1:45 PM	<b>VIABILITY OF ANTIBIOTIC RESISTANT BACTERIA EMITTED FROM CATTLE FEEDYARDS IN AIRBORNE PARTICULATE MATTER (70)</b> Kelsey N. Thompson <sup>1*</sup> , Loren L. Hensley <sup>1</sup> , Kim J. Wooten <sup>1</sup> , Philip N. Smith <sup>1</sup> and Gregory D. Mayer <sup>1</sup>	<b>FIRST WORLD PROBLEMS: THE RISE OF NATURE DEFICIT DISORDER (75)</b> Bailee K. Roche <sup>1*</sup>	<b>ARE THERE GRASS FLAMMABILITY TRAITS? BIOMASS DIRVES GRASS FIRE BEHAVIOR, BUT CANOPY SPECIES-SPECIFIC ARCHITECTURE CAN CONTROL SURFACE HEATING (61)</b> Xiulin Gao <sup>1*</sup> and Dylan W. Schwillk <sup>2</sup>	<b>MODELING THE MOST ABUNDANT MOSQUITO SPECIES (<i>Aedes vexans</i> AND <i>Culex tarsalis</i>) IN LUBBOCK, TEXAS, UNITED STATES (92)</b> Steven T. Peper <sup>1*</sup> , Daniel E. Dawson <sup>1</sup> , Grant E. Sorensen <sup>1</sup> , Jordan Hunter <sup>1</sup> , Francis Loko <sup>1</sup> , Sadia Almas <sup>1</sup> , Kevan Athanasiou <sup>1</sup> , Anna G. Gibson <sup>1</sup> , Steven M. Presley <sup>1</sup>
2:00 PM	<b>BIOFILM FORMATION OF BATRACHOCHYTRIUM DENDROBATIDIS VM1 (71)</b> Shalika Silva <sup>1*</sup> , Lisa Atkins <sup>2</sup> , Uzma Qaisar <sup>3</sup> , and Michael San Francisco <sup>1</sup>	<b>PHOTO DOCUMENTATION PRESERVATION CONSERVATION (76)</b> Hanna Reed <sup>1*</sup>	<b>PATTERNS OF RODENT SPECIES CO-OCCURRENCE ON ROADS VERSUS FIELD HABITATS (52)</b> John Stuhler <sup>1*</sup> , Michaela Halsey <sup>1,2</sup> , Robert Bradley <sup>2,3</sup> , Neal Platt <sup>2</sup> , David Ray <sup>2</sup> , and Richard Stevens <sup>1,3</sup>	<b>THE UPTAKE OF SEVERAL SHORT AND LONG-CHAIN PERFLUORINATED COMPOUNDS (PFCS) BY CARROTS (<i>DAUCUS CAROTA</i>), RADISHES (<i>RAPHANUS SATIVUS</i>), ALFALFA (<i>MEDICAGO SATIVA</i>), AND TOMATO (<i>SOLANUM LYCOPERSICUM</i>) GROWN IN SOILS CONTAINING DIFFERENT ORGANIC CARBON CONTENTS (93)</b> Steven Lasee, Seenivasan Subbiah, William Thompson, Paxton Payton, & Todd A. Anderson
2:15 PM	<b>ESSENTIAL ROLES OF ERGOSTEROL AND SPHINGOLIPIDS IN THE SANDFLY TRANSMISSION STAGE OF LEISHMANIA MAJOR (72)</b> Samrat Moitra <sup>1*</sup> and Kai Zhang <sup>1</sup>	<b>ASSESSING LEVELS OF DNA AND RNA DEGRADATION IN FROZEN TISSUES ARCHIVED IN NATURAL HISTORY COLLECTIONS (77)</b> Taylor J. Soniat <sup>1*</sup> , Caleb D. Phillips <sup>1,2</sup> , Kathy MacDonald <sup>2</sup> , Jeremy E. Wilkinson <sup>3</sup> , and Robert D. Bradley <sup>1,2</sup>		<b>ANALYSIS OF ANIMAS WATERSHED SEDIMENT BACTERIAL COMMUNITIES AFTER THE GOLD KING MINE BREACH (94)</b> Kelsey N. Thompson <sup>1,2*</sup> , Jeremy E. Wilkinson <sup>1,2</sup> , Philip N. Smith <sup>1</sup> , and Gregory D. Mayer <sup>1,2</sup>
2:30 PM	<b>POTENTIAL SECRETED COMPOUNDS FROM BATRACHOCHYTRIUM DENDROBATIDIS WHEN EXPOSED TO STAPHYLOCOCCUS AUREUS AND ESCHERICHIA COLI (73)</b> Amanda M. Starr <sup>1*</sup> , Susan San Francisco <sup>2</sup> , and Michael J. San Francisco <sup>1</sup>			<b>EXTRACTION METHOD VALIDATION AND STABILITY OF NEONICOTINOIDS IN WATER (95)</b> Michelle M. McManus <sup>1*</sup> , Subbiah Seenivasan <sup>1</sup> , and Jaclyn E. Cañas-Carrell <sup>1</sup>
3:00 PM	<b>PLENARY TALK: "Some Thoughts on Science Communication, and the Story of a Botfly named Georgia"- Dr. Dan Riskin, Discovery Canada- Au+E22B17:E+A17:E23</b>			



# ABSTRACTS

## **POSTER (UNDERGRADUATE)**

### **1. FISH ASSOCIATIONS WITH MILLEPORA SPP. (FIRE CORAL) IN THE MESOAMERICAN REEF IN UTILA, HONDURAS**

Sarah F. Cole<sup>1,2\*</sup>, Stephanie C. Randell<sup>2</sup>, Traesha R. Robertson<sup>3</sup>, Donna E. Hamilton<sup>4</sup>, and Stephanie A. Lockwood<sup>1</sup>

<sup>1</sup>Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas 76708

<sup>2</sup>McLennan Community College, Waco, Texas, 76708

<sup>3</sup>College of Coastal Georgia, Brunswick, Georgia 31520

<sup>4</sup>University of North Texas-Dallas, Dallas, Texas 75241

Millepora species are an important reef builder that provides shelter and protection for small species of fish and juveniles. When touched the coral causes a painful stinging sensation that makes it less than hospitable. Although observations have been made between Millepora species and other species of coral, little has been recorded on fish association with Millepora species and why some species are not adversely affected by their defense mechanism. This study was conducted to access the fish species associated with Millepora on the Mesoamerican Reef in Utila, Honduras. Observations were made on depth of Millepora species observed, as well as species of Millepora, and fish species and their relation to the Millepora colonies. The most prevalent species of fish observed in relation to Millepora spp. were *Stegastes partitus* and *Stegastes planifrons*. As observed in previous studies, most of the species were small species in the adult life phase. Fish abundance was greater in shallower depths above twenty feet, possibly due to species limitations to depth and temperature or due to resource partitioning. Though not part of this study, several observations of Millepora species parasitizing common sea fans, *Gorgonia* species was observed. Field observations were also made of algal farms used by *Stegastes partitus* and *Stegastes planifrons* in close proximity to Millepora structures. This suggests that Millepora spp. may be used as boundary fences to deter other fish species. Further observations could be done to determine if there is a true correlation.

### **2. BULLIES CD-1 RETIRED BREEDER MICE ARE RESILIENT TO CROSS-SENSITIZATION AMONG STRESS, ALCOHOL INTAKE, AND SALTY HIGH-FAT DIET PREFERENCE**

Josiah N Morales<sup>1\*</sup>, Aaron White<sup>1\*</sup>, Mayra Herrera-Gonzales<sup>1</sup>, Daniela P Derderian<sup>1</sup>

<sup>1</sup>School of Mathematics and Sciences, Wayland Baptist University, Plainview, TX 79072

Stress-induced alcohol dependence cause long-term changes in reward pathways. Salty food intake can be rewarding but in excess it is harmful. We investigated if CD-1 retired breeder mice, previously used in CSDS, challenged with forced swim stress (FSS) or FSS followed by ethanol intake altered salty high-fat diet (HFD) preference. Male CD1 mice were subject to two salty HFD preference curves before and after either FSS or FSS followed by ethanol consumption. The two-food choice curves consisted of HFD 0.5g% of NaCl along with another HFD containing one out of seven different NaCl concentrations: 0.125, 0.25, 0.5, 1, 2, 4, or 8g% NaCl. FSS was performed for 6-min for



10-days and intermittent water-water (FSS-VEH, n=7) or ethanol-water (FSS-EtOH, n=8) exposure for 4-weeks. Consumption of HFD with increasing NaCl concentrations for FSS-VEH group during curve 1 was  $1.12 \pm 0.09$ ,  $0.99 \pm 0.07$ ,  $0.83 \pm 0.06$ ,  $0.88 \pm 0.04$ ,  $0.80 \pm 0.07$ ,  $0.32 \pm 0.07^*$ ,  $0.08 \pm 0.03^*$  g/20g b.w., respectively (\*p < 0.05) and  $1.11 \pm 0.17$ ,  $0.91 \pm 0.10$ ,  $0.44 \pm 0.05$ ,  $0.58 \pm 0.14$ ,  $0.31 \pm 0.08^*$ ,  $0.02 \pm 0.01^*$  g/20g b.w. for curve 2. The consumption of HFD 0.5g% NaCl during curves 1 and 2 were similar:  $1.05 \pm 0.09$ ,  $0.79 \pm 0.13$ ,  $0.84 \pm 0.11$ ,  $0.85 \pm 0.10$ ,  $1.00 \pm 0.11$ ,  $1.31 \pm 0.08$ , and  $1.39 \pm 0.04$  g/20g b.w. Both groups displayed similar preference for salty HFD in curves 1 and 2. Mice from both groups avoided HFD 4 and 8g% NaCl compared to HFD 0.5g% NaCl in both curves. Therefore, FSS and ethanol intake after FSS did not modify salty HFD preference in CD-1 retired breeder mice.

### 3. IDENTIFYING THE GENETIC DIVERSITY OF *TRYPANOSOMA CRUZI* IN CHAGAS DISEASE VECTOR SPECIES IN SOUTHEAST TEXAS

Patricia Feria<sup>1</sup> and Marcelo Pintos<sup>2\*</sup>

<sup>1</sup>Department of Biological Sciences, University of Texas Rio Grande Valley, Edinburg Texas 78539

Chagas disease (CD), also known as American trypanosomiasis, is becoming a public health concern in Texas. It is caused by the parasite *Trypanosoma cruzi*, which is mainly transmitted through Triatomine insects. CD currently affects millions of people in the American continent and it can be deadly if no treatment is provided. *T. cruzi* has been classified into six different lineages or Discrete Typing Units (DTUs). Each genetic group of *T. cruzi* can lead to different outcomes of the disease, such as cardiomyopathies or gastrointestinal complications. To date, there has not been many attempts to identify which DTUs are found in Southeast Texas, an area that is highly at risk for Chagas disease. The main goal of this research was to identify the DTUs that could be found in Southern Texas. We analyzed and compare the DNA sequence of Triatomine insects that were sent to our lab for different citizens using the insect's mitochondrial 16S rRNA gene. For DTU discrimination, we used a restriction fragment length polymorphism (RFLP) assay, based on the TcSC5D gene of the DNA samples of bugs that were *T. cruzi*-positive. From a total of 130 insects, 44 have been identified as *Triatoma gerstaeckeri*. The rest of the samples are still being identified using DNA sequence analysis. Regarding DTU identification, we used the samples infected with *T. cruzi* which were 85 out of 130 (65% infection rate). TcI and TcIV, both known to cause cardiovascular problems, were found in the tested samples. These results could be useful to inform health officials to make effective vector control. Moreover, since complications of this disease could be influenced by different groups of the parasite, our research can create awareness of possible symptoms among the population in Southeast Texas.

### 4. DEGRADATION OF FEATHER COLORATION IN MUSEUM SPECIMENS OF THREE BIRD SPECIES OVER TIME

Amanda K. Locke<sup>1\*</sup> and Erin Stukenholtz-Bohlender<sup>1</sup>

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

Plumage color of museum specimens can provide information for studies on molting patterns, age and/or gender characteristics and geographic variation. However, little is known about how plumage coloration can degrade over time and what colors (i.e., blue,



red, and green) are more susceptible to fading. We analyzed blue, red, and green feather pigmentation of male American Kestrel (*Falco sparverius*), Painted Bunting (*Passerina ciris*) and Northern Cardinal (*Cardinalis cardinalis*) specimens to determine whether or not plumage saturation fluctuated from the 1800s to present time. We scanned avian specimens with a flatbed scanner and used GNU Image Manipulation Software (GIMP), that detected red, green, and blue saturation levels in photos. We predict that color brightness within plumages will decrease over time, thus resulting in large differences between live individuals and older museum specimens. This decreased plumage saturation can result in inaccurate data collected from older specimens especially when comparing them to live ones. This study will help us better understand how plumage coloration can vary over time as well as help us determine how much caution should be taken when using data from older museum specimens.

## 5. TEMPORAL AND GEOGRAPHIC VARIATION OF MUSEUM RECORDS OF THREATENED BAT SPECIES FROM SOUTH AMERICA

Sara Hamilton\*<sup>1</sup>, Jalissa Williams\*<sup>1</sup>, Cristina Ríos-Blanco<sup>1</sup> and Richard D. Stevens<sup>1,2</sup>

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

<sup>2</sup> Museum of Texas Tech University

South America is a region known for its high biodiversity. However, anthropogenic transformation and climate change is expected to have an important effect on biodiversity. In 2016, thirteen South American bat species were listed by the International Union for Conservation of Nature (IUCN) as near threatened, vulnerable, or endangered. Field research focusing on threatened species is usually limited due to the sparse nature of populations from these species. However, museums across the United States contain many specimens from these species that could be used for research, but are often underutilized. Our goal was to determine the status of these species in museum collections and to see if we could find spatial and temporal trends in specimen collection for each species. We created a database using information from numerous museums, such as the Royal Ontario Museum and the American Museum of Natural History. We collected 931 records for 11 of the 13 listed species. *Leptonycteris curasoae* had the most records (567), and *Lonchorhina fernandesi* had only 6 records for the 46-year span. Due to the irregularity of specimen collection, temporal and spatial trends could not be determined for lesser known species (i.e., average of 1 record per year). Only three species were recorded more than once per year: *Chilonatalus micropus* (2.6), *L. curasoae* (12.3), and *Vampyrum spectrum* (2.2). To exemplify the disparity in records for endangered species, *Artibeus jamaicensis*, a common species in Central and South America has approximately 8,406 records, equivalent to 182.7 records per year. Over two-thirds of the specimens of our focal species were captured in Mexico, indicating geographic biases. Although there is a lack of consistent museum specimen collection for rare and endangered species, there is still importance in maintaining museum collections. If museum collections remain active and updated, we could better assess trends in species presence and abundance.

## 6. CONCENTRATED CELL-FREE SUPERNATANT OF *LACTOBACILLUS* INHIBITS THE GROWTH OF DIFFERENT BACTERIAL PATHOGENS

\*Sahar Mirza<sup>1</sup>, \*Kelsey Sprinkles<sup>2</sup>, Taylor Letbetter<sup>2</sup>, Nithya Mudaliar<sup>3</sup>, Gary Ventolini<sup>4</sup>, Natalia Schlabritz-Lutsevich<sup>4</sup>, and Abdul Hamood<sup>3</sup>



<sup>1</sup>Department of Animal and Food Sciences, TTU, Lubbock, TX; <sup>2</sup>Department of Biological Sciences, TTU, Lubbock, TX; <sup>3</sup>Department of Immunology and Molecular Microbiology, TTUHSC, Lubbock, TX; <sup>4</sup>Department of Obstetrics and Gynecology, TTUHSC, Odessa, TX

Chronic skin wounds, such as foot ulcers and neuropathic ulcers that occur in diabetics and venous leg ulcers and pressure ulcers that occur among bedridden individuals, especially geriatric patients, can be very difficult to heal. All of these wounds can become colonized with and then infected by various species of Gram-positive and Gram-negative opportunistic bacteria that form organized communities termed biofilms. Within the biofilm, the organisms are protected from environmental stresses, host immune responses, and antimicrobials. Lactobacilli, which are the major components in probiotic products, protect the vaginal environment from potentially harmful microorganisms through different mechanisms including the production of bacteriocins. We recently showed that *Lactobacillus gasseri* produces an extracellular antimicrobial factor that inhibits the growth of and biofilm development by *P. aeruginosa*. Using the zone of inhibition assay, we investigated the effect of this factor on the growth of other bacterial pathogens. The 20X concentrated cell-free supernatant (CCFS) of *L. gasseri* completely inhibited the growth of *Escherichia coli* and *Klebsiella oxytoca* and partially inhibited the growth of *Proteus mirabilis*, *Enterococcus faecalis*, *Staphylococcus aureus*, and *Gardnerella vaginalis*. We also tested the effect of CCFS from *L. plantarum*, *L. crispatus*, and *L. jensenii* on the growth of different *P. aeruginosa* isolates. All isolates were sensitive to *L. gasseri* CCFS. Only one *P. aeruginosa* strain was sensitive to *L. plantarum* and *L. crispatus* CCFS; however, no strains were sensitive to *L. jensenii* CCFS. These results suggest that CCFS from lactobacilli is a potential antimicrobial agent to treat infected wounds.

## 7. BASELINE SURVEY OF TEXAS HORNED LIZARDS IN THE TEXAS PANHANDLE

Sara A. van der Leek<sup>1\*</sup> and Andrew C. Kasner<sup>1</sup>

<sup>1</sup>School of Math and Science, Wayland Baptist University, Plainview, Texas 79072

This baseline survey was conducted May-Sept 2016 using pitfall traps and visual encounters to determine the presence and habitat associations of Texas horned lizards in Hale and Floyd counties, Texas. A total of 25 lizards were documented, including 12 visual encounters and 13 captures. Of the 13 captured, 4 were males and 9 were females, with an average snout-to-vent length = 55.8 mm (range = 21.8-85.3 mm). Percent cover was measured using the Daubenmire cover class method, and the average percent grass cover = 7.04%, forb cover = 4.60%, litter cover = 2.88%, and bare ground = 85.84% of 20x50-cm quadrats centered on lizard locations. The height of vegetation was measured using a Robel pole, and the average height = 2.56 cm. The percent cover and height were not different between males and females nor between adults and young. All lizards were <1 m from the nearest escape cover providing total visual concealment from overhead predators.

## 8. FREQUENCIES AND SUBSTRATE ASSOCIATION OF EXCAVATING PORIFERANS IN UTILA, HONDURAS

Collin M. Harvey<sup>1,2\*</sup>, Stephanie C. Randell<sup>2</sup>, Donna E. Hamilton<sup>4</sup>, Traesha R. Robertson<sup>3</sup>, and Stephanie A. Lockwood<sup>1</sup>

<sup>1</sup>Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas 76708





<sup>2</sup>McLennan Community College, Waco, Texas, 76708

<sup>3</sup>College of Coastal Georgia, Brunswick, Georgia 31520

<sup>4</sup>University of North Texas-Dallas, Dallas, Texas 75241

Excavating sponges are important competitors for space on the Mesoamerican Reef System (MRS). These sponges bore into the coral skeletons, and are able to outgrow and eventually overtake entire coral. Some research suggests that certain excavating sponge species show associations with particular types of corals. This study was conducted in order to assess frequencies of excavating sponges of the coral reefs in Utila, Honduras, as well as record substrate associations. Utila is a small island 18 miles north of mainland Honduras and is part of the MRS, which is the largest coral reef system in the Atlantic Ocean. Multiple dive sites surrounding the island were surveyed using the Randell-Robertson Survey Technique which called for the researchers to reach maximum depth then survey along a path parallel to the reef wall. When an excavating sponge was found along the survey path the depth was recorded. The sponge was then photographed with a meter stick to serve as a size reference. Throughout all dive sites the only excavating sponges found were *Cliona delitrix* and *Aka coralliphaga*. Of the two species, *C. delitrix* was encountered with much greater frequency (76%). This sponge is also prevalent on massive coral types (85%), colonizing them in greater proportion than in other coral types (9%), such as branching or foliose. These results corroborate evidence from research in other areas of the MRS. Further research could be gathered from multiple other sites along the MRS in order to reinforce boring sponge habitat associations.

## **9. MULTIPLE TOXIC BLOOMS OF GOLDEN ALGA OCCURRED IN THE LUBBOCK CANYON LAKES SYSTEM IN FALL OF 2016-- COULD THESE INSTANCES BE PREDICTIVE OF A LARGER BLOOM IN SPRING OF 2017?**

Lindsay D. Williams<sup>1\*</sup>, Reynaldo Patiño<sup>2</sup>

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

<sup>2</sup>U.S. Geological Survey, Texas Cooperative Fish and Wildlife Research Unit and Departments of Natural Resources Management and Biological Sciences, Texas Tech University, Lubbock, TX 79409

Golden alga (*Prymnesium parvum*) is a harmful algae species that is found all over the world. When golden alga blooms occur, they often result in fish kills. In fall 2016, there were at least two fish kills in the Lubbock Canyon Lake System occurring a month apart from each other. The first toxic bloom occurred around October 29; at this site there were an estimated 100-200 dead shad downstream of Lake 1 dam. Grab water samples were taken from the area and analyzed, and results confirmed the presence of golden alga at an average of 1,778 cells/mL. In December 2, we discovered another toxic bloom that resulted in an estimated 100-200 dead carp. Analyzes of water samples indicated golden alga presence at an average of 5,833 cells/mL just above Lake 1 dam and an average of 6,999 cells/mL below the dam. While these cell concentrations are lower than levels normally associated with toxicity, both were measured approximately 1-2 weeks after the fish kills occurred and it is possible that cell numbers had decreased from their peak values. The unusual frequency of mild bloom events last fall could indicate that conditions are favorable for a larger event this coming spring, the season of the year when golden alga blooms typically occur. We will continue monitoring the Lubbock Canyon Lakes



System for the presence of golden alga and the incidence of toxic blooms.

#### **10. PORIFERAN ASSOCIATION WITH WHITE AND YELLOW BAND CORAL DISEASES ON THE MESOAMERICAN REEF, UTILA, HONDURAS**

Andrea C. Edie<sup>1</sup>, MacKenzie L. Kroll<sup>1\*</sup>, Bobby A. Rodriguez<sup>1</sup>, Stephanie C. Randell<sup>2</sup>, Traesha R. Robertson<sup>3</sup>, Donna E. Hamilton<sup>4</sup>, Stephanie A. Lockwood<sup>1</sup>

<sup>1</sup>Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas 76708

<sup>2</sup>McLennan Community College, Waco, Texas, 76708

<sup>3</sup>College of Coastal Georgia, Brunswick, Georgia 31520

<sup>4</sup>University of North Texas-Dallas, Dallas, Texas 75241

The Mesoamerican reef is the second largest reef in the world, extending from the northern tip of the Yucatan Peninsula to the Honduran Bay Islands. In the Caribbean, the two diseases affecting *Orbicella* spp., *Montastraea cavernosa*, and *Acropora* spp. corals are white band disease and yellow band disease. White band disease affects *Acropora* spp., while yellow band affects *Orbicella* spp. and *Montastraea cavernosa*. Sponges are filter feeders, contributing to many processes in the ecosystem, including substrate deposition and nutrient/energy cycling. Although important for the ocean and potentially the reef, researchers suspect that sponges could be harboring harmful bacteria that cause coral disease. The relationship between sponge and coral species is unknown; therefore, looking at the possible associations between them could be a key factor in determining this relationship. Four dive sites, off the coast of Utila, Honduras, were surveyed twice using the Randell Robertson Marine Survey Technique and radial survey techniques. Data collected in the Mesoamerican reef in May 2016 revealed that *Orbicella annularis* was the most documented coral with yellow band disease, being 67% of recorded observations. Dark volcano sponge (*Svenzea zeai*) was observed the most around diseased coral, with branching vase sponge (*Callyspongia vaginalis*) being identified the second most. *Orbicella annularis*, *S. zeai*, and *C. vaginalis* may have been documented the most due to their extensive depth range. An association between diseased coral and sponges is suspected; however, further investigation of healthy and diseased coral could verify this suspected correlation.

#### **11. SEXUAL DIMORPHISM WITHIN THE WHITE-LINED BROAD-NOSED BAT (*PLATYRRHINUS LINEATUS*) USING SKULL MORPHOMETRICS**

Ashlyn N. Kildow<sup>1\*</sup>, John D. Stuhler<sup>1</sup>, and Richard D. Stevens<sup>1,2</sup>

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

<sup>2</sup>Museum of Texas Tech University, Lubbock, Texas 79415

Examining sexual dimorphism is important for understanding selective pressures that influence behavior or fitness of a species in a given environment. For example, the presence of sexual dimorphism may indicate differences in breeding preferences, diets, or energy expenditures facing a species. In bats, sexual dimorphism has been reported for many species, where females are consistently larger than males. We evaluated whether sexual dimorphism exists in the white-lined broad-nosed bat (*Platyrrhinus lineatus*), a species endemic to South America. We examined sixteen skull measurements (i.e., eight cranial, six dental, and two mandibular) from bats collected from two sites in eastern Paraguay (i.e., Reserva Natural del Bosque Mbaracayú and Yaguareté Forests). Measurements were made to the nearest 0.01 mm using digital



calipers. We predict sexual dimorphism in this species. If sexual dimorphism is present within *P. lineatus* it could suggest that natural selection is driving intersexual differences due to sexual selection, intraspecific competition, or differential costs of parental care.

## **12. CONTRIBUTION OF THE CHOLINE BRANCH OF KENNEDY PATHWAY DURING THE SANDFLY TRANSMISSION STAGE OF LEISHMANIA MAJOR**

Brian C. Johnson<sup>1\*</sup>, Samrat Moitra<sup>1</sup> and Kai Zhang<sup>1</sup>

<sup>1</sup>Texas Tech University, Department of Biology

Leishmania contain a diverse pool of phosphatidylcholine (PtC), the most abundant lipid in these parasites. Synthesis of PtC occurs via the choline branch of the Kennedy pathway (choline  $\rightarrow$  choline-phosphate  $\rightarrow$  CDP-choline  $\rightarrow$  PtC) and the N-methylation of phosphatidylethanolamine (PtE). A key enzyme of choline branch, choline-phosphate cytidyltransferase (CPCT) forms CDP-choline, an intermediate to generate PtC. CPCT-null parasites were fully viable and replicative in axenic cultures, yet exhibited severe growth defects under low nutrient conditions. Leishmania parasites reside in the sandfly midgut where they have to compete for nutrients with a number of bacteria and survive the action of bacterial toxins. To better understand the contribution of de novo PtC synthesis in *L. major* in the sandfly stage, we investigated the role of CPCT in parasite-bacteria interaction. We monitored parasite growth in the bacteria-Leishmania co-culture mimicking the condition in sandfly midgut. CPCT null mutants showed growth delays/defects during co-culture with certain bacteria, indicating Leishmania major parasites may need the choline branch during ethanolamine depletion, and to survive the competitive environment in sandfly midgut. Our results highlight the importance of exploring the parasite-bacteria interaction in sandfly transmission experiments.

## **13. ASSESSMENT OF SHORT-TERM WORKING MEMORY IN ALZHEIMER'S TRANSGENIC MICE**

Chelsea Limboy<sup>1\*</sup>, Breanna N. Harris<sup>1</sup>, Paul Soto<sup>2</sup>

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

<sup>2</sup> Department of Educational Psychology & Leadership, Texas Tech University, Lubbock, TX 79409

Alzheimer's Disease (AD) is a progressive neurodegenerative disease that results in the deterioration of cognitive functions. Currently approved medications produce unpleasant side effects and are minimally effective in treating the symptoms of AD and there is a need to develop more effective symptomatic treatments. The overall goal of this experiment is to establish short-term working memory testing regimens in AD transgenic mice that are sensitive to age-related neuropathology that could serve as a basis for evaluating potential therapeutics for AD-associated cognitive decline. The hypothesis is that the transgenic mice will develop increasing deficits in short-term memory over time compared to non-transgenic mice. The effect of continuous (five days per week for duration of study) and intermittent (three months of five days per week testing followed by three months without testing and so on) on the development of deficits will be evaluated. Double transgenic APP<sup>swe</sup>/PS1<sup>dE9</sup> mice are being tested in a delayed matching-to-position (DMTP) task (a task thought to measure short-term memory). In all mice, accuracy of performance declines as delay increases, but as of 55 weeks of age,



transgenic mice have yet to develop deficits in performance. Differences between the two genotypes may occur when AD neuropathology is more developed in later stages of the experiment.

#### **14. VALIDATION OF A SCOTOTAXIS ANXIETY TEST IN *XENOPUS LAEVIS***

Celina Pecos<sup>1</sup>, Kelsey Aguirre<sup>1</sup>, Boone Coleman<sup>1,2</sup>, Hannah Spiegel<sup>1</sup>, James A. Carr<sup>1</sup>, and Breanna N. Harris<sup>1</sup>

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

<sup>2</sup>Proactive Recruitment in Introductory Science and Mathematic

Anxiety disorders affect 42.5 million people each year but the exact mechanisms that contribute to the pathological state remain unclear. The behavioral responses and brain mechanisms associated with the anxious state are primal responses which can be seen across multiple taxa, including crustaceans, fish, and mammals. Anxiety can be defined as a time when the individual realizes there is no control over a certain situation, thus leading to an unpredictable outcome. Rodent anxiety tests rely on the fact that animals generally tend to spend time in dark vs. bright open spaces as the later can increase susceptibility to predation. Rodent tests tend to show both construct (e.g., does the test represent anxiety?) and predictive (e.g., can the model predict treatment/drug outcomes?) validity. Here, we aim to validate an anxiety assay, the scototaxis test, for use in African-Clawed Frogs (*Xenopus laevis*). To do this, we injected frogs with nothing, saline, fluoxetine (selective serotonin reuptake inhibitor), or desipramine (tricyclic antidepressant) and then recorded behavior. Based on previous behavioral data in rodents, when treated with an anxiolytic drug we expect frogs to be less anxious, measured by spending more time in the light compartments of the tank. The use of common drugs will help demonstrate both construct and predictive validity for this model. This research being conducted is of great importance because no amphibian anxiety models currently exist. Being able to measure anxiety in amphibians would enhance understanding of this behavioral state as several of the neuroendocrine underpinnings appear to be evolutionarily conserved, and having multiple animals models is crucial for mapping the development of these disease states. We expect to confirm light-dark behavioral testing as an anxiety model in amphibians, and can thus be applied collectively across species.

#### **POSTER (GRADUATE)**

#### **15. CLIFF SWALLOWS (*PETROCHELIDON PYRRHONOTA*) PREFER TO NEST IN THE CENTER OF COLONIES**

Shelby Osborne<sup>1</sup>, Douglas Leasure<sup>1</sup>, Ragupathy Kannan<sup>1</sup>, and Steward Huang<sup>1</sup>

<sup>1</sup>College of STEM, University of Arkansas-Fort Smith, Ft Smith AR 72913

Predator avoidance is a major factor influencing nest site selection in birds. Cliff Swallows are common colonial nesting birds in summer in North America. They construct oblong mud nests mainly under bridges and overpasses. Old nests from previous years are frequently enhanced and reused. Previous studies have documented snake predation in these colonies, with nests located at the edge being more vulnerable to predation than those at the center of the colonies. We tested the hypothesis that Cliff Swallows prefer



to nest more in the center of a colony than the edge, and predicted that if the hypothesis is true, then: 1. there will be more nests in the central compared to edge zones, 2. there will be more tiered or stacked nests in the central than in the edge zones, and, 3. central nests, due to frequent reuse, would have higher masses than edge nests. We conducted field work in the summer of 2016 at a bridge colony in Fort Smith (Sebastian Co.), Arkansas. All nests on both sides of the bridge were counted, removed, and weighed. The “center” of the colony was defined as the mid 50% of the length of the colony, and the “edge” was defined as 25% of the length on both sides of the colony. Our data strongly supported our hypothesis. All three of our predictions were met. There were more nests at the center than the edge; there was just one set of 4 stacked nests at the edge compared to eight sets of 2-6 stacked nests in the center; and finally, central nests were significantly heavier than edge nests. Our study shows that Cliff Swallows have a clear preference to nest in the center of colonies.

## **16. METAGENOMIC STUDY OF POLYSTYRENE DEGRADATION BY MEALWORMS**

Anisha Navlekar<sup>1\*</sup>, Deborah Carr<sup>1</sup>

<sup>1</sup>Texas Tech University, Lubbock, TX 79415

In the last 50 years, there has been a rapid increase in plastic usage in almost every sphere of life. Polystyrene (PS) or Styrofoam, as it's more commonly known, has been used in various products like cups and packing material and also as a raw material and solvent in the processing of polymers. Its uncontained production, constant daily usage and incorrect disposal have led to grave environmental problems including destruction of wildlife habitats, and bioaccumulation in food chains. Until very recently, it was assumed that polystyrene was non-biodegradable. A study conducted in 2015 showed the ability of meal worms to degrade polystyrene; the ability was attributed to their gut microbiome (Yang et al., 2015). The researchers concluded that the degradation must occur due to the secretion of enzymes by the gut micro-organisms. A metagenomic study focused on PS degradation and the gut microbiota has not been carried out to date.

Mealworms, at different instars, were subjected to a diet of only Styrofoam for a period of 2 weeks and subsequently dissected to obtain intact guts. DNA was extracted using the Qiagen AllPrep DNA/RNA kit and 16S Metagenomic sequencing was conducted to determine the abundances of different PS degrading microorganisms.

In this study we report on the metagenomic diversity and identification of the major as well as active species involved in the gut microbiota of mealworms with Styrofoam as their only food source compared to mealworms fed a normal diet. A change in diet reflects change in abundances of the microbial community (Ley et al., 2008) and the same was expected when the mealworm diet shifted from bran and oats to Styrofoam. Results from this study contribute to understanding of the functionality of this mixed community that enables it to degrade PS successfully. Applications for landfill management as well as plastic recycling, one of the most intractable problems of human society today are expected deliverables from this study.

## **17. STATISTICAL ANALYSIS OF BINOCULAR EYE GAZE TRAJECTORIES**

Pansujee V. Dissanayaka<sup>1</sup>, Jingyong Su<sup>1</sup> and Bijoy K. Ghosh<sup>1</sup>

<sup>1</sup>Department of Mathematics and Statistics, Texas Tech University, Lubbock, TX79409



Eye gaze trajectories explain how humans would search the visual space during natural exploration. Typically, eyes move to capture objects in the visual space and head follows towards objects in focus. Subsequently eyes move to stabilize focused objects against head movement, while occasionally exploring additional targets introduced in the visual space. It follows that the gaze trajectory alternates between saccades and fixation points. Using segmentation and clustering algorithm on trajectories of points on a 2-sphere, we analyze binocular eye movement trajectory to understand how the gaze shifts between saccades and focused regions, marked by a dense set of sub-trajectories. We propose a new clustering algorithm on eye sub-trajectories using a well-known geodesic distance metric on the sphere. We combine the eye gaze trajectory data with the head rotation velocity data to estimate when and where the gaze is compensating for the head movement. The sub-trajectory based clustered fixation regions, we obtain, has also been compared with other point based clusters (K-mean clusters) that are in the literature, and superiority of our proposed algorithm has been demonstrated.

## **18. IN VIVO KINASE SUBSTRATE TAGGING, IDENTIFICATION AND QUANTIFICATION BY NANOTECHNOLOGY**

Fengqian Chen<sup>1\*</sup>, Degeng Wang<sup>1</sup>

<sup>1</sup>The Institute of Environmental and Human Health (TIEHH), Texas Tech University, Lubbock, Texas

We are achieving a significant, but never-been-done, goal in cellular signaling research – in vivo kinase substrate tagging, identification and quantification. Our innovative strategy is to combine three techniques – nanoparticle delivery of the bulky ATP analogues A\*TP- $\gamma$ -S, CRISPR/Cas9 genome editing and the Shokat chemical-genetic method – to enable specific in vivo thiophosphate tagging of the substrates of the kinase of interest. The tag in turn serves as a handle for identification and quantification of both known and new substrates. The strategy has two major advantages: 1) CRISPR/Cas9 genome editing replacing ectopic expression of a mutant protein kinase in current Shokat chemical genetic method, i.e., the protein kinase gene remains in native genomic environment; and 2) in vivo tagging of native substrates in intact live cells replacing in vitro tagging of an artificially prepared substrate – the basis and the cause of limitations of most current kinase assays. This strategy thus should dramatically improve kinase substrate identification and activity quantification efforts. If successful, this approach can be readily applied to other protein kinases and cell lines, and will open up tremendous, previously impossible opportunities.

## **19. PRELIMINARY INVESTIGATIONS OF LOSSES TO HERBIVORY IN A CARNIVOROUS PLANT**

Rachel N. Carmickle<sup>1\*</sup> and John D. Horner<sup>1</sup>

<sup>1</sup>Department of Biology, Texas Christian University, Fort Worth, Texas 76129

Carnivorous plants inhabit nutrient-poor environments, and they supplement nutrient uptake by capturing and absorbing nutrients from prey, such as insects. Like other plants, carnivorous plants are subject to loss of nutrient-containing tissues to herbivores. Because they occur in low-nutrient environments, tissue loss to herbivory can be expected to have a particularly strong negative effect on carnivorous plants. However, herbivory in carnivorous plants has not been well studied. In this study, we quantified



tissue and nutrient losses sustained from herbivory by larvae of the specialist noctuid, *Exyra semicrocea*, in a population of pitcher plants, *Sarracenia alata*. We conducted field surveys, analyses of areal foliar damage, nutrient analyses, and feeding trials. In the study population, 83% ( $0.83 \pm 0.033$ ) (mean  $\pm$  SE) of pitchers were damaged by *E. semicrocea* (surveyed in June & September). On average, 15% of each pitcher was consumed. Mean foliar nitrogen concentration was 1.19%, resulting in a mean nitrogen loss to consumption of  $0.24 \pm 0.041$  mg per pitcher (N = 40). Mean foliar phosphorus concentration was 0.044%, resulting in a mean phosphorus loss per pitcher of  $0.0086 \pm 0.0015$  mg (N = 37). *Exyra* preferentially fed on upper-pitcher 'waxy' tissue (25% of waxy tissue damaged) rather than mid-pitcher 'hairy' tissue (4.0% of hairy tissue damaged). In preliminary feeding trials, 4th and 5th instar larvae consumed  $7.5 \pm 0.90$  cm<sup>2</sup>/day and  $7.8 \pm 1.0$  cm<sup>2</sup>/day, respectively. *Exyra* larvae were observed moving among pitchers. Based on consumption rates, estimated mean time spent feeding on a single pitcher was  $2.5 \pm 0.18$  days (N = 95). Current studies are evaluating the impact of herbivory on the fitness of these plants.

## 20. IMPACTS OF ANTHROPOGENIC PRESSURES ON THE CONTEMPORARY BIOGEOGRAPHY OF THREATENED CROCODILIANS IN INDONESIA

Kyle J. Shaney<sup>1\*</sup>, Amir Hamidy<sup>2</sup>, Matthew Walsh<sup>1</sup>, Evy Arida<sup>2</sup>, Aisyah Arimbi<sup>3</sup>, and Eric N. Smith<sup>1</sup>

<sup>1</sup>The Amphibian and Reptile Diversity Research Center and Department of Biology; University of Texas at Arlington; 501 S. Nedderman Drive; Arlington, TX 76010; USA

<sup>2</sup>Laboratory of Herpetology; Museum Zoologicum Bogoriense; Research Center for Biology, Indonesian Institute of Sciences–LIPI; Jl. Raya Jakarta Bogor km 46; Cibinong, West Java, 16911; Indonesia.

<sup>3</sup>Wildlife Conservation Society, Indonesia.

The Greater Sunda Region of southeast Asia supports a myriad of economically and ecologically important species and is considered a biodiversity hotspot. However, human pressures are rapidly reshaping contemporary biogeography across the region. We conducted crocodile population surveys in Sumatra on Saltwater Crocodiles (*C. porosus*) and threatened False Gharials (*T. schlegelii*) and tested whether crocodile abundance and distribution are correlated with variation in human disturbance, fishing pressure, and habitat type. We then leveraged these data to model *T. schlegelii*'s remaining suitable habitat across southeast Asia. We find that *T. schlegelii* and *C. porosus* abundance is correlated with distance from human settlements and fish trapping pressure. Our data also expand the known range of *T. schlegelii* as we have documented this species in a new river system. We provide evidence that habitat alteration and interspecific competition with *C. porosus* may be synergistically, negatively affecting the abundance of *T. schlegelii*. We also find that *T. schlegelii*'s predicted remaining suitable habitat in Indonesia is largely limited to areas of low human activity. From these empirical and modeling approaches, we propose several key conservation priorities: (1) Further investigate the potential synergistic effects of *C. porosus* and land use change on *T. schlegelii*, (2) Eliminate the use of fish traps in remaining patches of *T. schlegelii* habitat, (3) Prioritize crocodile population surveys in remaining suitable habitat, particularly in remote areas, (4) Consider *T. schlegelii* as locally "Endangered" in Sumatra, (5) Expand existing reserves around the Lower Kampar River and Berbak National Park study areas.



## **21. 3D TECHNOLOGIES: APPLICATIONS FOR DIGITIZING SMALL ANIMAL BONES FOR COMPARATIVE COLLECTIONS**

Kathryn Faircloth<sup>1\*</sup> and Jessica Stepp<sup>1</sup>

<sup>1</sup> Museum of Texas Tech University, Texas Tech University, Lubbock, Texas 79409

Bone identification requires the use of comparative material, often housed in museums and laboratories, to identify animal bone remains. Identification issues arise when comparative material is fragile, rare, or unavailable for loan. Three skeletal elements from three different species have been created using photogrammetry and modeled using inexpensive software. These models have been evaluated by scholars with experience in bone identification to determine the usability of 3D models and 3D printed comparative material. 3D models, printed with high impact polystyrene, then have been sent to scholars for a second evaluation. Scholars have provided feedback through an electronic survey that evaluates the success of 3D printed bone remains for comparative analysis and the capacity of affordable 3D technology to create usable comparative material for bone identification. 3D modeling and 3D printing increases accessibility by allowing scholars to use digital 3D models and 3D printed replicas in lieu of handling the original material.

## **22. EXTINCT GAZELLE-HORSE *NANNIPPUS PENINSULATUS* (MAMMALIA; EQUIDAE) FROM SCURRY COUNTY, TEXAS, WITH IMPLICATIONS FOR BIOCHRONOLOGY**

John A. Moretti<sup>1\*</sup> and Eileen Johnson<sup>1</sup>

<sup>1</sup>Museum of Texas Tech University, Lubbock, 79409-3191

Excavations at Roland Springs Ranch Locality 1 (RSR-1) in Scurry County, Texas have produced skeletal remains representing a diverse assemblage of vertebrate life hypothesized to be early Pleistocene (~2.6-2.0 million years ago) in age. Remains of small, tridactyl equids are common in the stream sediments of RSR-1. As the most common large mammal in the RSR-1 fauna, understanding these diminutive horses is important to determining paleo-community composition. Further, identification of horse remains is biochronologically significant. Lacking numeric age determinations, placing the RSR-1 fauna in time is dependent upon faunal correlation. The RSR-1 small horse remains are identified as *Nannippus peninsulatus* based on a combination of cheek tooth crown height, enamel pattern form, and metapodial size. Highly cursorial with strongly hypsodont cheek teeth, *N. peninsulatus* is derived in its adaptations to open grassland. An enigmatic precursor, *N. beckensis*, is known only from the late Pliocene locality of Beck Ranch, also in Scurry County. The RSR-1 sample is distinguished from the slightly less advanced *N. beckensis* by increased crown height, absence of protostylids, and increased metapodial elongation. *Nannippus peninsulatus* is characteristic of the late Pliocene-early Pleistocene (Blancan Land Mammal Age) fauna of North America. The presence of *N. peninsulatus* at RSR-1 provides temporal separation from Beck Ranch, and indicates an age of less than ~3.5 million years ago that points towards the proposed early Pleistocene age for the fauna.

## **23. INFORMATIVE INDEX OF THE ALLERGENIC POLLEN AND FUNGI OF THE TEXAS PANHANDLE TO AID IN DIAGNOSIS OF ALLERGY AND ASTHMA**





Nelofar Sherali<sup>1\*</sup>, Chandini Revanna<sup>2\*</sup>, Aubrey Howard<sup>1</sup>, Alyssa Coots<sup>1</sup>, Constantine Saadeh<sup>3</sup>, Jon Bennert<sup>4</sup>, Jeff Bennert<sup>4</sup>, and Nabarun Ghosh<sup>1</sup>

<sup>1</sup>Center of Advanced Study in Aerobiology, Department of Life, Earth and Environmental Sciences, West Texas A&M University, Canyon, Texas

<sup>2</sup>Department of Environmental Health & Safety, Texas Tech University, Lubbock, Texas

<sup>3</sup>Allergy A.R.T.S., Amarillo, Texas, <sup>4</sup>R&D, Air Oasis, Amarillo, Texas

Airborne pollen and fungal spores are causative factors in respiratory allergy, asthma and other allergic diseases. Mold allergens are risk factors for bronchial asthma in patients suffering from allergic rhinitis. We have been analyzing the aeroallergens using a Burkard Volumetric Spore Trap. Recent reports (2007-11) suggest the occurrence of the mold related allergy cases are on the rise in the Texas Panhandle. A survey on asthma and allergic rhinitis showed that the rate of Amarillo residents suffering from asthma has increased since 2007 and is twice that of Texas. We determine the daily aeroallergen index using Melinex tape in the Spore Trap to find any possible correlation between the aeroallergen indices and incidence of asthma and allergic rhinitis cases. The Melinex tape was mounted on a slide, stained with safranin and images were captured using an Olympus BX-40 microscope attached to a DP-70 digital camera with ImagePro 6.0 software. The most significant aeroallergens recorded were the pollens, like grass pollen (Poaceae), Short Ragweed (*Ambrosia artemisiifolia*), Pine (*Pinus strobus*), Common Sunflower (*Helianthus annuus*), Hairy Sunflower (*Helianthus hirsutus*), Buffalo Bur (*Solanum rostratum*), Purple Nightshade (*Solanum elaeagnifolium*) and Lamb's Quarters (*Chenopodium album*). Major fungal species recorded were *Alternaria*, ascospores from Pezizales, *Drechslera*, *Stachybotrys*, *Cladosporium*, *Curvularia*, Teliospores of *Ustilago* sp. and *Pithomyces*. Our analysis of 17-year long aeroallergen data showed a gradual shift in aeroallergen index and change in flowering seasons with the warmer climate<sup>1</sup>. Our aeroallergen data is used by local TV channels and Allergy ARTS Clinic in Amarillo to aid in diagnosis.

#### **24. LASER PHOTO-STIMULATION OF PLANTS AND MICROBES ASSOCIATED WITH PLANTS, FOR BETTER PHYTOREMEDIATION OF HEAVY METAL CONTAMINATED SITES**

Bigyan Rimal<sup>1</sup>, Jan W. Dobrowolski<sup>2</sup>, Deborah Carr<sup>1</sup>

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

<sup>2</sup>AGH University of Science and Technology, Krakow, Poland

Empirically selected wavelengths and exposure times of low level lasers has resulted in immense possibilities of using plants for reclamation of degraded land masses and clean-up of contaminated water resources. Willow (*Salix viminalis*), which is one of the hyper-accumulator plants, used in the experiment, showed a remarkable increase in shooting and rooting, when the cuttings cultivated in hydroponic condition were photo-stimulated with low power lasers. Photo-stimulation with red beam Helium-Neon laser (power=20mW, wavelength= 660 nm) for 3 times at 10 seconds intervals after each 10 seconds irradiation followed by 3 times irradiation with blue beam Laser Diode (power=25mW, wavelength=514nm) for 3 seconds with 3 seconds pause after each irradiation was highly effective in increasing root and shoot growth. The increase in growth of plant parts, after laser irradiation, is attributed to an increase in the rate of adenosine triphosphate (ATP) production. The enhanced rate of energy production in plants and



microbes associated with plants make them able to adapt and clean up the sites that are highly contaminated with heavy metals and environmental pollutants.

## **25. NEXT SCIENCE INFLUENCES THE EXPRESSION OF CYTOKINES AND CHEMOKINES INVOLVED IN THE HOST RESPONSE TO INJURY IN WOUNDS INFECTED WITH *STAPHYLOCOCCUS AUREUS***

Kayla Bounds<sup>1</sup>, Matt Myntti<sup>2</sup>, Jane A. Colmer-Hamood<sup>3,4</sup>, Randall Jeter<sup>1</sup>, and Abdul Hamood<sup>4,5</sup>

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

<sup>2</sup>Next Science, Jacksonville, FL; Departments of <sup>3</sup>Medical Education, <sup>4</sup>Immunology and Molecular Microbiology, and <sup>5</sup>Surgery, Texas Tech University Health Sciences Center, Lubbock, TX

Chronic wounds, which include pressure ulcers and diabetic foot ulcers, affect approximately 6.5 million persons with a high annual cost. We recently showed that Next Science (NS) wound gel, a novel antimicrobial agent, inhibits *Staphylococcus aureus* infection of chronic wounds. Wound healing occurs through specific overlapping steps that are mediated by cytokines, chemokines, and growth factors (collectively, CKs). Therefore, NS may also promote wound healing by influencing the host immune response. Using the murine model of wound infection and RT<sup>2</sup> Profiler™ PCR Array Mouse Cytokines and Chemokines kit, we compared the level of expression of 21 genes for CKs involved in host response to injury between *S. aureus*-infected/mock-treated wounds and *S. aureus*-infected/NS-treated wounds. Skin tissues from infected and mock- or NS-treated wounds were excised at 1, 3, and 7 days post-infection/treatment, homogenized and total bacterial RNA was isolated from each sample. Compared with mock treatment of the infected wounds, NS treatment resulted in numerous alterations of CK gene expression including: 1) increased expression of *Spp1* at days 1, 3, and 7; 2) increased expression of *Gpi1* and *Vegfa* at day 3 only, and of *Ctf1* at day 7 only; 3) decreased expression of *Tnfsf11* (*Rankl* or *Trance*) at day 7; 4) decreased expression of *Il17f*, *Il17a*, *Il22*, *Ccl20*, and *Nodal* at day 1 followed by increased expression of all five genes at day 7; and 5) variable expression of *Bmp2*, *Bmp4*, *Bmp6*, and *Bmp7* over days 1, 3, and 7. As the products of these genes have been shown to play various roles in the response to injury and wound healing by recruiting cells to sites of infection, activating specific cells, and altering the microenvironment to promote healing, our results suggest that NS manipulates the host immune response within the *S. aureus*-infected wound throughout the different stages of healing.

## **26. DNA TRANSPOSON ACTIVITY AND ASSOCIATED MUTATION RATES IN MYOTIS BATS**

Nicole S. Paulat<sup>1</sup> and David A. Ray<sup>1</sup>

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

Transposable elements (TEs) are DNA sequences that mobilize through copy-and-paste or cut-and-paste mechanisms, expanding within a host genome. *Myotis* is one genus within vespertilionid bats which has experienced an unorthodox TE history. For example, their genomes are unique among mammals in containing many active DNA transposons, which continue to shape their genomic landscapes. Recent data suggests that, in addition to the indel mutations normally associated with TE activity, these genetic elements may also contribute to higher mutation rates via DNA repair mechanisms. DNA transposons preferentially insert near genes, and so transposon activity may be correlated with



mutation rate increases in regulatory regions and coding sequences. An analysis of transposon polymorphisms in nine *Myotis* species will reveal the extent of mutations in nearby genes that are associated with DNA repair after transposon insertions and excisions. These increased mutation rates could correlate to differences in orthologous genes between closely related *Myotis* species and contribute to our understanding of this exceptionally diverse clade.

### **27.3D GEOMETRIC MORPHOMETRICS APPLIED IN THE IDENTIFICATION OF A *CANIS* SPP. RECOVERED FROM A HISTORIC SITE IN WESTERN TEXAS**

Lila S. Jones<sup>1\*</sup> and Eileen Johnson<sup>1</sup>

Museum of Texas Tech University, Lubbock, Texas, 79409

Ongoing fieldwork at Whiskey Flats, a mid-18<sup>th</sup> century archaeological site on the Llano Estacado (Midland County, Texas), has produced a vertebrate assemblage of taxa native to the region and domesticated horse. A set of remains typical of coyote (*Canis latrans*) has been recovered along with the remains of a larger canid (*Canis* spp.) of a species that has not yet been identified. The larger canid is represented by an astragalus, proximal metacarpal, and axis that have the most potential for species identification, along with 12 non-diagnostic elements. Three species of canids may have been present at the time of deposition. Grey wolf (*C. lupus*) occurs in the region until extirpated in the early 20<sup>th</sup> century. Coyote is common regionally, both in the modern fauna and within late Quaternary faunas. And, the Comanche (known occupants of the site) and Apache (possible occupants) are known to have traveled with domestic dog (*C. domesticus*). The three species are closely related and present similar morphology, as well as overlapping size ranges, that can create a challenge in species identification. Making such distinctions however, is important for documenting faunal changes during any time period. Three-dimensional landmark-based morphometric analysis has been used as a method to determine if a species identification could be made. Principal component analysis (PCA) and analysis of variance (ANOVA) have been applied to the astragalus of comparative specimens of *C. lupus*, *C. latrans*, *C. domesticus*, and the unknown canid in an attempt to characterize quantitative variation. The method has proven useful in exploring the range of variation of the species in question. A larger sample, however, will be needed to make a definitive identification of the *Canis* spp.

### **28. A FIRST PHYLOGENETIC APPRAISAL OF FOREST-DWELLING SKINKS OF THE GENUS *TYTTHOSCINCUS* FROM JAVA AND SUMATRA, INDONESIA**

Panupong Thammachoti<sup>1\*</sup>, Utpal Smart<sup>1</sup>, Amir Hamidy<sup>2</sup>, Nia Kurniawan<sup>3</sup>, Irvan Sidik<sup>2</sup>, and Eric N. Smith<sup>1</sup>

<sup>1</sup>Amphibian and Reptile Diversity Research Center, Department of Biology, University of Texas at Arlington, Arlington, Texas 76019

<sup>2</sup>Museum Zoologicum Bogoriense, Indonesian Institute of Science, Widiasatwaloka Building, Jl. Raya Jakarta Bogor, Cibinong 16911, Indonesia.

<sup>3</sup>Department of Biology, Faculty of Mathematics and Science, Brawijaya University, Malang 65145, East Java, Indonesia.

The Greater Sunda Region encompasses the island of Borneo, Java and Sumatra and Peninsular Malaysia and is one amongst 25 of the world's biodiversity hotspots. Reptilian diversity currently remains poorly studied throughout the region, particularly in regards to



the forests of Java and Sumatra. Even though only one species of forest dwelling skink (*Tytthoscincus temmincki*) is currently known to occur in Java and Sumatra, based on our familiarity with the geography and faunal distribution patterns of the Greater Sunda islands, we surmised that the genus probably contained more hitherto undescribed taxonomy diversity. To confirm this, we collected forest dwelling skinks across a broad geographic range on the islands of Java and Sumatra, and conducted an integrative taxonomic assessment of the genus employing genetic and morphological approaches. We also included closely related species of the genus *Sphenomorphus* to clarify the systematic placement of *Tytthoscincus* in the larger context of southeast Asian skinks. For phylogenetic comparisons, we amplified four loci, including two mitochondrial genes (16S and ND4) and two nuclear genes (NGFB and R35) and concatenated the data for a Bayesian phylogenetic analysis. Molecular data reveal the presence of at least two additional *Tytthoscincus* lineages from the islands and our morphological results corroborate these findings. Our phylogenetic analyses also indicate that *Sphenomorphus vanhernei* from East Java should be transferred to *Tytthoscincus*. Given that *Tytthoscincus* are restricted to the highlands and these new species were collected from isolated montane forests, we believe that they are allopatric and endemic to relatively small, unfragmented mountainous. Overall, the phylogenetic relationships of *Tytthoscincus* skinks in Java and Sumatra indicate that Sunda Shelf skink diversity is still vastly underestimated and we advocate continued systematic studies in the region in an effort to alleviate this problem.

## **29. CHLORTETRACYCLINE IN WHITE-TAILED DEER (ODOCOILEUS VIRGINIANUS) AND SUPERMARKET MEAT BY LIQUID CHROMATOGRAPHY TANDEM-MASS SPECTROMETRY**

Shanoy C. Anderson<sup>\*1</sup>, Subbiah Seenivasan<sup>1</sup>, Angella A. Gentles<sup>1</sup>, Paul Stonum<sup>2</sup>, Tiffanie A. Brooks<sup>2/3</sup> and Ernest E. Smith<sup>1</sup>

<sup>1</sup>Department of Environmental Toxicology, Texas Tech University, Lubbock, Texas 79416

<sup>2</sup>Department of Animal Care Services, Texas Tech University, Lubbock, Texas 79409-3132

<sup>3</sup>Department of Animal and Food Sciences, Texas Tech University, Lubbock, Texas 79409-2141

A method for determining chlortetracycline residues in edible white-tailed deer tissues, using liquid chromatography with Heated Electrospray Ionization and mass spectrometry detection.

The procedure involved an extraction with EDTA-McIlvaine buffer at pH 4.0, followed by solid-phase extraction cleanup using a Hydrophilic-Lipophilic Balance (HLB) cartridge. The liquid chromatography analysis was performed with heated electrospray ionization and mass spectrometry detection. The limit of quantification for the method was 2.7 µg/kg and limit of detection was 0.8 µg/kg. The recovery values were greater than 78.5% for muscle, 65.1% for kidney, 63.1% for liver. The method has been successfully used for the quantification of chlortetracycline in white-tailed deer tissue samples.

## **30. REDUCTION IN DAILY SOIL TEMPERATURE RANGE INCREASE MICROBIAL COMMUNITY DYNAMICS IN A DRYLAND COTTON PRODUCTION SYSTEM IN WEST TEXAS**

Diana L. Vargas-Gutierrez<sup>1\*</sup>, John Zak<sup>1</sup>, Veronica Acosta-Martinez<sup>2</sup>, Bobbie McMichael<sup>1</sup>

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

<sup>2</sup>Wind erosion and water conservation unit, USDA-ARS, Lubbock, TX, 79415



Sustainability of agriculture in the Southern High Plains of West Texas faces challenges due to the variability that climate change is imposing on soil health, microbial dynamics, water use and plant productivity. Soil temperature is crucial for plant growth, and the ability of microorganism to carry out fundamental process. One component of soil temperature that have been shown to have a large impact on microbial activity in arid and semi-arid environments is the variation in Daily Temperature range ( $DTR_{soil}$ ). Thus, it is imperative to understand how temperature variability at the daily scale influences microbial communities and their roles in nutrient cycling, and carbon storage. We evaluated the impacts of modifying  $DTR_{soil}$  on microbial responses in dryland cotton in West Texas. For 2014-2015 growing season, 3 treatments were established: Control, Reduced  $DTR_{soil}$  using erosion blankets (shade), and Reduced  $DTR_{soil}$  using sorghum residue (stubble) to modify  $DTR_{soil}$ . Six replicates plots (3 x 4 m) with 4 rows in each treatment. Soil samples were collected monthly from each set of plots to evaluate edaphic parameters, nutrients levels (extractable  $NH_4^+$ -N and  $NO_3^-$ -N), and microbial structure and functional parameters. The stubble and shade reduced the  $DTR_{soil}$  by 6 °C on average at the soil surface and 2 °C at 15 cm during the hottest months. Microbial biomass carbon increased in stubble by 43 % on average irrespective of any changes to soil moisture while extractable nitrogen levels were higher under control plots in comparison with reduced  $DTR_{soil}$  plots indicating the reduction in  $DTR_{soil}$  regulated nutrient dynamics. The reduction in  $DTR_{soil}$  in these semi-arid systems positively affected the dynamics of microbial communities and their contributions to soil productivity. Understanding the role of  $DTR_{soil}$  will help cotton producers mitigate climate variability impacts and improve soil health leading to sustainable production in dryland cotton production system.

### **31. RECOMBINANT R2-PYOCIN CREAM IS EFFECTIVE IN TREATING *PSEUDOMONAS AERUGINOSA*-INFECTED WOUNDS**

Abdulaziz Y Alqahtani<sup>1\*</sup>, Nithya Mudaliar<sup>2</sup>, Dean Scholl<sup>3</sup>, Sharmila Dissanaiké<sup>4</sup>, Randal Jeter<sup>1</sup>, Jane Colmer-Hamood<sup>2,5</sup>, and Abdul Hamood<sup>2,4</sup>

<sup>1</sup>Department of Biological Sciences, TTU, Lubbock, TX; <sup>2</sup>Department of Immunology and Molecular Microbiology, TTUHSC, Lubbock, TX; <sup>3</sup>Avid Biotech, San Francisco, CA; <sup>4</sup>Department of Surgery, TTUHSC, Lubbock, TX; <sup>5</sup>Department of Medical Education, TTUHSC, Lubbock, TX

Due to the aging population combined with an increase in the incidence of diabetes and obesity plus rising healthcare costs, the treatment of chronic wounds has become a major burden to the healthcare system. Many chronic wounds are infected by organisms that establish biofilms in which the microbes are encased in a self-synthesized extracellular polymeric substance. Within chronic wounds, bacterial biofilms consist of diverse bacterial species including *Pseudomonas aeruginosa*. The multidrug resistance of *P. aeruginosa* combined with the high cost of producing new antibiotics necessitates the search for other potential therapies. One such therapy is the utilization of pyocins, which are narrow-spectrum antimicrobials produced by *P. aeruginosa* to eliminate other competing bacteria. *P. aeruginosa* produces three main types of pyocins, the R-, F-, and S-types. In this study, we examined the effectiveness of R2 pyocin in inhibiting *P. aeruginosa* biofilm formation. Using the pBAD/His expression system, we overexpressed the R2 structural gene from the arabinose-induced promoter pBAD. The recombinant R2 pyocin (rR2P) was purified using a standard protocol. SDS-PAGE confirmed the



purification of rR2P. Using the zone of inhibition assay, we identified several rR2P-sensitive *P. aeruginosa* clinical isolates. We then formulated rR2P in polyethylene glycol (PEG) to form a topical cream. In the *in vitro* wound biofilm model, rR2P inhibited biofilm development by the rR2P-sensitive clinical isolate CF69. We also utilized the murine model of wound infection to test the inhibitory effect of rR2P on the growth of *P. aeruginosa* within infected wounds. While untreated infected wounds contained about  $10^7$  CFU/gm of tissue, rR2P-treated wounds contained no bacteria. These results suggest that rR2P cream is potential topical application to effectively treat *P. aeruginosa*-infected chronic wounds.

### **32. PHOSPHATIDYLCHOLINE BIOSYNTHESIS IN *LEISHMANIA MAJOR***

Samrat Moitra<sup>1\*</sup>, Mattie Pawlowic<sup>2</sup>, Fong-Fu Hsu<sup>3</sup>, and Kai Zhang<sup>1</sup>

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

<sup>2</sup>Center for Tropical and Emerging Global Diseases, University of Georgia, Paul D. Coverdell Center, Athens, Georgia 30602, USA.

<sup>3</sup>Mass Spectrometry Resource, Department of Endocrinology, Diabetes, Metabolism, and Lipid Research, Washington University School of Medicine, St. Louis, MO, 63110

Phosphatidylcholine (PtC) is the most abundant group of lipids in many eukaryotes. *Leishmania* parasites contain a diverse pool of PtC that is enriched in ether phospholipids and unsaturated fatty acids. Synthesis of PtC occurs via the choline branch of the Kennedy pathway (choline  $\Rightarrow$  choline-phosphate  $\Rightarrow$  CDP-choline  $\Rightarrow$  PtC) and the N-methylation of phosphatidylethanolamine (PtE). To understand the role of *de novo* PtC synthesis in *L. major*, we investigated the choline-phosphate cytidylyltransferase (CPCT) which catalyzes the formation of CDP-choline from choline-phosphate and CTP. Although the CPCT-null mutants could not incorporate choline into PtC, they possessed a similar phospholipid composition as wild type parasites. These CPCT-null promastigotes were fully viable and replicative in regular medium, and showed a near-normal level of virulence in mice. These findings suggest that the ethanolamine branch of the Kennedy pathway alone is sufficient to compensate the loss of CPCT in culture. However, CPCT-null promastigotes exhibited severe growth defects under low nutrient conditions. CPCT may also play a role in promastigote-bacteria interaction which likely dictates *Leishmania* development in the sandfly. We are in the process of characterizing other Kennedy pathway enzymes to determine their roles in *Leishmania* life cycle and evaluate their potential as drug targets.

### **33. TESTOSTERONE MAINTAINS SPERMATOGENESIS BY PREVENTING GERM CELL APOPTOSIS: IS TESTOSTERONE ACTING DIRECTLY ON GERM CELL MEMBRANE PROGESTERONE RECEPTORS?**

Arpita Talapatra<sup>1\*</sup>, Dibyendu Dutta<sup>2</sup>, Shuvalaxmi Dasgupta<sup>1</sup> and Nathaniel Mills<sup>1</sup>

<sup>1</sup> Dept. of Biology, Texas Woman's University, Denton, Texas.

<sup>2</sup> Department of Professional Sciences, Middle Tennessee State University, Murfreesboro, TN.

Ethylene dimethane sulfonate (EDS) ablates Leydig cells and reducing serum testosterone to undetectable levels. Germ cells, lost by apoptosis are found in rat testicular tissue harvested at 7 and 10 days post-EDS. Regression of germinal epithelium is time dependent and correlated with decreased testicular weight. Apoptotic cells were identified by TUNEL staining and changes in gene expression were measured using RT



& qPCR. Significant differences of Bcl2 genes at 7 and 10 days were observed when compared to vehicle controls. Fas and FasL increased while caspases exhibited variable levels. We observed germ cell detachment from Sertoli cells that exhibited cytoskeletal disorganization.

Immunostaining indicated that androgen receptors (AR) are found in Sertoli cell nuclei, and myoid cell nuclei of the seminiferous tubule along with some staining in the stripped cytoplasm of spermatids, however, germ cells are reported not to have androgen receptors. Testosterone receptor (AR, NR3C4) and progesterone receptor (PR, NR3C3) are structurally similar and testosterone at double the progesterone concentration will compete with progesterone for progesterone receptor activation. We have initiated studies to find and characterize mRNAs for mPRs & membrane progesterone/adiponectin receptors (mPAQRs) by RT & qPCR. We find at least 5 mPRs mRNAs (*Paqr(s)*) expressed in testes but do not know the cells of origin since we are using total RNA from whole testes.

### **34. ESTIMATING REGIONAL CARRYING CAPACITIES ACROSS THE SOUTHERN HIGH PLAINS VISITED BY THE MID-CONTINENT POPULATION OF SANDHILL CRANES USING REMOTE SENSING TOOLS**

Kathryn J. Brautigam<sup>1\*</sup>, Blake A. Grisham<sup>1</sup>, William P. Johnson<sup>2</sup>, Daniel T. Raleigh<sup>1</sup>, Daniel P. Collins<sup>3</sup>, Shaun L. Oldenburger<sup>4</sup>, Jude R. Smith<sup>5</sup>, Nicole D. Athearn<sup>6</sup>, Warren C. Conway<sup>1</sup>

<sup>1</sup>Texas Tech University, Dept. Natural Resources Management, Lubbock, TX;

<sup>2</sup>USFWS-National Wildlife Refuge System, Canyon, TX;

<sup>3</sup>USFWS-Region Migratory Bird Office, Albuquerque, NM;

<sup>4</sup>Texas Parks and Wildlife Department, San Marcos, TX;

<sup>5</sup>Muleshoe National Wildlife Refuge, Muleshoe, TX;

<sup>6</sup>USFWS-Great Plains Landscape Conservation Cooperative, Norman, OK

Approximately 82% of the Mid-Continent Population (MCP) of sandhill cranes (*Antigone canadensis*) visit the Southern High Plains. The current landscape is a matrix of various crops, native rangelands, Conservation Reserve Program (CRP) lands, ephemeral playas, and pluvial-saline lakes. Our objective was to assess carrying capacities of each identified area of importance (AOI, region with visit duration  $\geq 40$  days by  $\geq 1$  crane) using remote sensing and Global Positioning System (GPS) tools. To gather location data, we utilized the most contemporary GPS-tagging materials and methodologies, and for analyses we used the BBMM package in Program R and several tools in ArcMap 10.3.1. We created Brownian Bridge Movement Model probability contours (home range contours) using data collected from GPS Platform Transmitting Terminals (PTT) attached to cranes captured during winters 2014/15 ( $n = 17$ ), 2015/16 ( $n = 10$ ) at various locations on the Southern High Plains. AOIs were created by overlaying and dissolving 95% contours, calculating mean centers, and creating a 20-kilometer buffer for each center point. Altogether, we identified and assessed 8 AOIs between 2014/15 and 2015/16 and calculated carrying capacities (CC) for each. We estimated CC using recent, known crane energy requirements, local crop-specific residuals, and average energy contents of the 3 main crop foods selected by cranes on the SHP (corn, grain sorghum, and winter wheat). Crop acreages were estimated for each AOI from 2014 and 2015 classification maps. Total Crane Energy Days (CED) of these 8 AOIs alone contain crop foods with enough energy needs for 5 (2014 crop season) to 6 (2015) times the size of the entire MCP for 120-day winter duration given current surface water and crop availability. While



it is not probable nor desirable for the entire population to overwinter in just these locations, we can use these results to monitor sandhill crane carrying capacities while ensuring that energy needs are met in the future.

### **35. GUT MICROBIOME ANALYSIS DURING PREGNANCY IN *TADARIDA BRASILIENSIS***

Oscar Sandate<sup>1\*</sup>, Matthew Fox<sup>1</sup>, Gregory Knox<sup>1</sup>, Marylin Mathew<sup>1</sup>, Craig Tipton<sup>1</sup>, Caleb Phillips<sup>1,2</sup>  
<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409. <sup>2</sup>Natural Science Research Laboratory at the Museum of Texas Tech University ([oscar.sandate@ttu.edu](mailto:oscar.sandate@ttu.edu))

The mammalian gut-microbiome is thought to be an influential component during pregnancy and lactation. Generally, the gut-microbiome is important for many processes including nutrient acquisition, nutrient storage, and cellular protection, among many others. All of these processes are important during pregnancy, but changes to microbiome community composition during pregnancy are not well understood. Microbiome changes are expected given the immunological modulation associated with pregnancy, but at the same time maintenance of community stability may be necessary for optimal functionality. Relative to other mammals, bats have unusually high energetic demands, shortened digestive tracts, and support fetuses that are a large proportion of mother's body mass. Because of the unique metabolic and pregnancy characteristics of bats, beneficial functions of microbiomes may be particularly important for bat reproductive success. In the current study we are investigating the host-microbiome relationship across pregnancy and lactation in Brazilian Free-tailed bats, *Tadarida brasiliensis*. We will use high-throughput 16s rDNA gene sequencing to understand bacterial community composition and restructuring during different pregnancy related stages. We will also integrate quantitative PCR and bomb calorimetry to understand how total bacterial abundance and energy extraction-efficiency changes throughout pregnancy and relates to community compositional changes. Finally, we will integrate histological analysis of intestinal sections to characterize how the size of the intestinal environment changes during pregnancy, a potential phenomenon that may regulate bacterial load during pregnancy. Results will provide new understanding about the host-microbiome relationship during pregnancy and its importance for reproductive success.

### **36. THE CARBON BUDGETS OF CENTRAL TEXAS WOODLANDS IN THE CONTEXT OF CLIMATE CHANGE AND INDUSTRIAL ATMOSPHERIC CARBON DIOXIDE CONCENTRATIONS**

Tamura E. Dunbar\*, Mary Sides, Joseph D. White, Kyle Logan, Ariel Sorg, and Sunshyne Hendrix<sup>1</sup>  
<sup>1</sup>Department of Biology, Baylor University, Waco, Texas 76798

Anthropogenic greenhouse gas emissions contribute to climate change. Climate change impacts plants within ecosystems; however, plant growth may mitigate climate change consequences. In southern and central Texas, recent woody plant abundance increased within ecosystems historically dominated by herbaceous species. This study investigates carbon budgets of aggrading woodlands in context of climate change and industrial carbon dioxide levels. Carbon storage was estimated for tree foliage, stem, litter, fine and coarse roots. Vine and shrub carbon were estimated. Photosynthesis and litter decomposition measurements estimated carbon flux into and out of woodland





ecosystems, respectively. Soil moisture was measured to evaluate water availability as a controlling mechanism of carbon storage between upland and riparian woodlands. A process model, Biome-BGC, assessed potential impacts of carbon dioxide and climate change on carbon sequestration. Modeling showed carbon dioxide concentrations and climate change impacted carbon sequestered in vegetation; these factors were not consistent across ecosystems and plant components.

### **37. INFLUENCE OF CLIMATE CHANGE, FRESHWATER INFLOWS, AND CHANGING LAND USE ON THE DISTRIBUTION OF DWARF SEAHORSE ON THE TEXAS COAST**

\*Elizabeth L. Roesler<sup>1</sup>, Matthew A. Barnes<sup>1</sup>, Timothy B. Grabowski<sup>2</sup>, Fernando Martinez-Andrade<sup>3</sup>, and Rachel Bittner<sup>1</sup>

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

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

<sup>3</sup>Texas Parks and Wildlife Department, Coastal Fisheries Division, Corpus Christi, Texas 78412

Syngnathid fishes, such as seahorses and pipefishes, are in decline worldwide due to anthropogenic disturbances, primarily habitat loss or degradation due to changing climate and coastal development, and unsustainable exploitation. Dwarf Seahorse *Hippocampus zosterae* inhabits Texas bays, usually associated with seagrasses. The species is considered a candidate for federal protection primarily due to population declines in Florida, but virtually nothing else is known of their distribution, population status, or habitat requirements. Our objectives were to assess the distribution and habitat use of Dwarf Seahorse in Texas and identify threats to its persistence. We used data collected during the Texas Parks and Wildlife Coastal Fisheries Division's fishery-independent surveys to develop species distribution models (SDMs) evaluating environmental factors influencing the distribution of Dwarf Seahorse. We used WorldClim climate data, physicochemical data from NOAA, land cover data from the Texas Ecological Classification Project, and seagrass distribution data from the TPWD Seagrass Monitoring Workgroup were incorporated into the models as influential factors on Dwarf Seahorse distribution. Distance to the nearest public boat ramp was used as a proxy variable for physical anthropogenic disturbance of seagrass habitats. In addition to survey data from other sources, primarily the Fishes of Texas database, selected sites within the six major bay systems on the Texas coast were surveyed using seines and push nets to generate data to validate the SDMs. Understanding the factors influencing the current and future distribution of Dwarf Seahorse is an important first step towards determining the viability of the species in Texas waters.

### **38. WAPDAP – SOFTWARE THAT AUTOMATES PROTEOMICS DATA ANALYSIS PIPELINE**

Adnan Ahmed<sup>1</sup>, Masoud Zabet-Moghaddam<sup>1</sup> and Chiquito Crasto<sup>1</sup>

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

Post-experiment, data-analysis is critical to mass spectrometry based proteomics, especially in the assessing the large amounts of data that are produced. "BIG DATA" analysis is often a multi-step (time-consuming) process and involves the use of several suites of software each being executed in series. Proteomics-analyses processes are



also iterative and repetitive. They require manual interventions at every step of the analysis where the output from one process is the input into the next, downstream process. Some steps require several hours to complete, burdening users with time constraints. In this report, we describe one potential solution to the above. We have designed software called, WAPDAP (A Wrapper for an Automated Proteomics Data Analysis Pipeline), a “wrapper” programmed in the Python programming and scripting language. WAPDAP sequentially and automatically executes two key proteomics-based mass spectrometry data-analyses software, MaxQuant and Perseus. WAPDAP is accessible via the World Wide Web. A web interface allows the user to input MaxQuant and Perseus parameters. These parameters are then incorporated into the software. Output results are also available online through a browser.

### **39. PIACAN: PATHWAY INTEGRATION AND ANALYSIS OF CANCER NETWORKS**

Adrian Quintana<sup>1\*</sup>, Chiquito J. Crasto<sup>1</sup>, Tommy Dang<sup>2</sup>, Vinh Nguyen<sup>2</sup>

<sup>1</sup>Department of Biotechnology and Genomics, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>Department of Computer Science, Texas Tech University, Lubbock, Texas 79409

The purpose of this research is to use bioinformatics tools to identify key cancer genes which affect more than one type of cancers by merging biological pathways associated with cancer. These overlapping cancer genes are putatively key factors that lead to the development of secondary cancers after the initial primary cancer has spread to distant tissue. The first phase of the study involved the data mining of the 15 total cancer networks from the Kyoto Encyclopedia of Genes and Genomes (KEGG) via parsing Python scripts. The secondary phase was the incorporation of the mined data into Cytoscape for merging and statistical analysis. The third phase concluded with the visualization of the merged networks via the JavaScript library Data-Drive-Documents (D3). As a primary focus, our goal was to create an easily accessible system that would automatically detail the genomic similarities of each cancer pathway, and because of this, we created a publicly accessible website where the cumulative 15-network and merging software are hosted on free use. PIACAN is also developed as a knowledge dissemination tool. In its current iteration, the system links to cancer gene information in KEGG, GeneCards and Gene Ontology.

### **ORAL (UNDERGRADUATE)**

### **40. CYTOTOXIC AND APOPTOTIC EFFECTS OF CHAGA MUSHROOM (*INONOTUS OBLIQUUS*) ON CULTURED 4T1 MURINE BREAST CANCER CELLS**

Jake A. Brozek<sup>1</sup>, Sarah C. Kelly<sup>1</sup>, Vianney Trujillo<sup>1</sup>, Trevor Burrow<sup>1</sup>, Gary O. Gray<sup>1</sup>, Adam J. Reinhart<sup>1</sup>

<sup>1</sup>Wayland Baptist University

Previous studies in our lab have shown that extracts from several common herbs with anti-inflammatory activity have cellular components which are cytotoxic to cultured 4T1 murine breast cancer cells. In this study, extracts of *Inonotus obliquus*, or the Chaga mushroom, were prepared by refluxing powered Chaga in acetone (Soxhlet extraction, 1.5 hours). The extracts were distilled into ethanol, concentrated, and then fractioned via



Sephadex LH20 chromatography (50% ethanol mobile phase; eluate monitored at 280 nm). The resulting fractions were assayed for cytotoxicity to cultured 4T1 cells, and the fractions pooled based upon cytotoxicity. Pooled fractions with strong cytotoxicity were further separated via HPLC (C<sub>18</sub>, 75-100% methanol gradient over 40 min.). The HPLC peaks were collected, concentrated and again tested for cytotoxicity. Analysis of the physicochemical properties of the six collected peaks is ongoing. To determine if the observed cytotoxicity was due to apoptosis, we examined expression levels of proteins involved in the activation of cellular apoptotic pathways using Western blots. We investigated expression levels of caspases 3, 6, 8, 9, and 12, along with Cleaved forms of caspases 3 and 8 and PARP. Cleavage of caspases 3 and 8 as well as cleaved PARP were elevated upon treatments with Chaga extract, suggesting cell death is due to apoptosis.

#### **41. USING VHF RADIO TELEMETRY TO DETERMINE HOME RANGE AND HABITAT USE OF LADDER-BACKED WOODPECKERS (*PICOIDES SCALARIS*) IN THE TEXAS PANHANDLE**

Victoria K. Solis<sup>1</sup> and Andrew C. Kasner<sup>1</sup>

<sup>1</sup>School of Math and Sciences, Wayland Baptist University, Plainview, TX 79072

Ladder-backed Woodpeckers (*Picoides scalaris*) were tracked using VHF radio telemetry in Blanco Canyon, near Floydada, TX to determine home range and core area sizes of individuals, habitat associations, and tree species use for males and females. A total of 7 (4 female and 3 male) woodpeckers were tracked throughout the summer months from May-Aug 2016, resulting in 138 point locations (about 20 point locations per woodpecker). Average home range size for all 7 birds was 8.75 ha (3.37 – 13.42 ha). Average home range for females was 10.57 ha, and average home range for males was 6.32 ha. Home range sizes were not significantly different for males and females ( $T=1.91$ ,  $P=0.129$ ,  $df=4$ ). Average core area size for all birds was 0.11 ha (0.05 – 0.24 ha). Average core area for males was 0.13 ha, and average core area for females was 0.08 ha. Core area sizes were not significantly different for males and females ( $T=-0.76$ ,  $P=0.528$ ,  $df=2$ ). Plant species richness was higher at male point locations (average total richness=3.93) than female point locations (average total richness=3.05) ( $T=-4.40$ ,  $P=0.022$ ,  $df=3$ ). Male woodpeckers were located more often in areas with more mesophytic plant species near the riparian corridor, and females were present in xeric areas adjacent to the riparian corridor. Tree use by males and females reflected these associations, with females using mesquite (*Prosopis glandulosa*) and hackberry (*Celtis occidentalis*) more often, and males using elm (*Ulmus* sp.) and other mesophytic trees more often.

#### **42. BULLIED C57BL/6J MICE DISPLAY CROSS-SENSITIZATION BETWEEN STRESS-INDUCED ALCOHOL DEPENDENCE AND SALTY HIGH-FAT DIET PREFERENCE: AVERSIVE SALTY HIGH FAT DIET BECOMES PALATABLE**

Mayra Gonzales<sup>1\*</sup>, Josiah N. Morales<sup>1</sup>, Daniela P. Derderian DTB<sup>1</sup>

<sup>1</sup>Department of Biology, Wayland Baptist University, Plainview, TX 79072

Stress-induced alcohol intake triggers neuronal plasticity; however, it is unknown if it cross-sensitizes with natural rewards like salty high fat diet (HFD). We investigated if CSDS-induced ethanol intake affects salty HFD preference. Male C57BL/6J mice were



subjected to two salty HFD preference curve before and after CSDS-induced ethanol consumption. The two-food choice curves consisted of 0.5g% of NaCl along with another HFD containing one out of seven different NaCl concentrations: 0.125, 0.25, 0.5, 1, 2, 4, and 8g% NaCl. Consumption of HFD with increasing NaCl concentrations for CSDS-VEH group during curve 1 was  $1.13 \pm 0.24$ ,  $1.34 \pm 0.18^*$ ,  $1.08 \pm 0.12$ ,  $0.99 \pm 0.09$ ,  $0.44 \pm 0.10^*$ ,  $0.10 \pm 0.03^*$ ,  $0.02 \pm 0.01^*$  g/20g b.w., respectively (\* $p < 0.05$  0.5g% same curve) and  $1.05 \pm 0.10$ ,  $1.17 \pm 0.06^{* \#}$ ,  $0.56 \pm 0.10$ ,  $0.81 \pm 0.06$ ,  $0.73 \pm 0.9^{* \#}$ ,  $0.37 \pm 0.05^{\#}$ ,  $0.05 \pm 0.01^*$  g/20 g b.w., respectively for curve 2 ( $\#p < 0.05$  same diet, curve 1). The consumption of HFD 0.5 g% NaCl during curves 1 and 2 were similar:  $1.13 \pm 0.24$ ,  $0.54 \pm 0.15$ ,  $0.78 \pm 0.12$ ,  $0.74 \pm 0.08$ ,  $1.31 \pm 0.10$ ,  $1.53 \pm 0.05$ , and  $1.67 \pm 0.04$  g/20g b.w., respectively. CSDS-EtOH displayed similar pattern of salty HFD preference during curve 1; however, the preference for HFD 1 and 8g% NaCl were further enhanced in curve 2. Mice from both groups preferred HFD 0.25 and avoided HFD 2, 4 and 8g% NaCl compared to HFD 0.5 g% NaCl in both curves. CSDS enhanced HFD high in NaCl and CSDS-induced EtOH dependence further increased HFD high and very high in NaCl.

#### **43. USING GENOMICS AND BIOINFORMATICS TO DETERMINE THE ORIGIN AND PHYLOGENETIC SIGNIFICANCE OF THE ZONADHESIN GENE IN RODENTIA**

Emma K. Roberts<sup>1</sup>, Whitney N. Watson<sup>1\*</sup>, Daniel M. Hardy<sup>2</sup>, and Robert D. Bradley<sup>1,3</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Graduate School of Biomedical Sciences, Texas Tech University Health Sciences Center, <sup>3</sup>Natural Sciences Research Laboratory, Museum of Texas Tech University (whitney.watson@ttu.edu)

Zonadhesin (ZAN) is a multi-domain protein that is utilized in the binding of the egg's zona pellucida layer (ZP) to the spermatozoa. It has been suggested that this process may function in a species-specific fashion and thereby regulate hybridization between closely related species. However, to date, ZAN's role in species-specific interaction is poorly understood and viability of hybrid offspring between species is largely unknown. ZAN's structural domains have been studied in several domesticated mammalian taxa, but unfortunately wild rodent systems have been under-utilized in reproductive isolation studies. Rodents are an ideal group of taxa for examining the reproductive role of ZAN, as rodents are r-selected and evolve rapidly compared to other mammalian orders. This thereby generates a system where the genome evolves at a quicker rate due to short gestation times and a rapid population turnover. Currently, we are comparing conserved and variable regions of ZAN in representative species from five suborders of Rodentia to examine differential variability in the gene and determine if regions of this gene are phylogenetically informative in this group of mammals. Protein-coding DNA of ZAN was obtained from genetic databases for representatives from each suborder. Sequences from domains of interest were aligned and scored for statistical accuracy using various software programs. Levels of sequence differentiation are being used to assess the rate of molecular evolution and possible codon and nucleotide biases in this gene among this taxonomic group. Further, research on ZAN enhances our understanding of the mammalian reproductive system.



## **ORAL (GRADUATE)**

### **CELL & MOLECULAR BIOLOGY**

#### **44. TRANSGENIC COTTON CO-OVEREXPRESSING *OsSIZ1* AND *AVP1* SHOWS IMPROVED GROWTH AND DEVELOPMENT UNDER MULTIPLE-STRESS CONDITIONS**

Nardana Esmaili<sup>1\*</sup>, Yifan Cai<sup>1</sup>, Paxton Payton<sup>2</sup>, Hong Zhang<sup>1</sup>

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

<sup>2</sup> United States Department of Agriculture Cropping Systems Research Laboratory, Lubbock, TX 79415, USA

Abiotic stresses such as drought, salt, and excess heat result in huge agricultural losses annually. Genetic engineering was used to improve plant performance under environmental stress conditions. Previous studies with overexpression of the rice gene *OsSIZ1* or the Arabidopsis gene *AVP1* have shown that transgenic plants displayed substantially increased tolerance to various stresses. For examples, overexpression of *OsSIZ1* led to higher heat- and drought-tolerance in transgenic plants, and overexpression of *AVP1* improved drought and salt tolerance in transgenic plants. We hypothesized that co-overexpression of *OsSIZ1* and *AVP1* in cotton would simultaneously confer higher heat-, drought-, and salt-tolerance in transgenic cotton and thus reduce yield loss in field conditions. Therefore, we introduced both *AVP1* and *OsSIZ1* into cotton and conducted experiments to test the performance of the *AVP1/OsSIZ1* co-overexpressing cotton plants in greenhouse and field conditions. Our preliminary results showed that *AVP1/OsSIZ1* co-overexpressing plants displayed higher photosynthetic rates under combined stresses of salt and drought, as well as under combined stresses of heat and drought. Furthermore, field-grown *AVP1/OsSIZ1* co-overexpressing plants performed better in rain-fed conditions when compared to non-transgenic plants.

#### **45. CLONING AND CHARACTERIZATION OF THE *Wi4* LOCUS OF MAIZE AND ITS ROLE IN VASCULAR DEVELOPMENT AND STRESS ADAPTATION**

Anuradha Dhingra<sup>\*1</sup> and Chris Rock<sup>1</sup>

<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409-2122.

Plant cell wall play an important role in plant growth and development. Cellulose, the most abundant biopolymer, is a fundamental component of primary and secondary cell wall in plants. It is synthesized in the plasma membrane by a hexameric multi-subunit cellulose synthase complex (CSC). The CSC along with other factors is essential for oriented deposition of the cellulose microfibrils in the plant cell wall. In this study, we are characterizing *wilty4* with a view to clone it by map-based methods. *Wi4* is an EMS-induced dominant mutant of maize, which manifests a severe wilting phenotype under well-watered conditions. The leaves of the mutant fail to unfurl due to lack of turgor pressure at the five-leaf stage. In addition to this, the mutant shows reduced biomass, reduced growth and smaller (yet more abundant) vascular bundles/unit area as compared to its wild type sibling. The *Wi4* maps on the short arm of chromosome 5. Histochemical staining of the fresh internodes of *Wi4* with Calcafluor white suggests differences in the cellulose content in the *Wi4* vascular bundles. To further investigate the genes involved



we analyzed the differentially expressed genes from control and drought stress treatments of wild type sibling versus the *Wi4* leaf tissue by mRNA-Seq. Considering the genotype parameter, we could identify an excellent candidate gene mapping in the genomic interval around *Wi4*. *KORRIGAN* function is critical for the assembly of the cellulose-hemicellulose network and cytokinesis. It interacts with the CSC complex and encodes a membrane-bound endo-1-4-beta-D-glucanase which plays a vital role in cellulose synthesis and cell plate formation. The drought stress parameter provides a unique opportunity to gain insights into the interaction of genotype and environment mediating vascular development. Further analysis by complementation of the mutant with the candidate gene/s and resultant rescue of phenotype will enable us to decipher the cause of wilted phenotype.

#### **46. THE EFFECTS OF TECTAL NPY RECEPTORS ON FOOD INTAKE IN THE AFRICAN CLAWED FROG, *XENOPUS LAEVIS***

Ranakul Islam<sup>1\*</sup> and James A. Carr<sup>1</sup>

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

Studies across several taxonomic groups have found that under high predation risk situations, prey increase vigilance by reducing their foraging effort. These behavioral decisions increase immediate survival at the expense of decreased intake of food which may impose long-term costs on the individual's growth rate or reproductive output. In Anurans, the optic tectum (OT) rapidly inhibit food intake when a visual threat is present. Accumulating evidence indicates that neuropeptide Y (NPY), an abundant peptide neurotransmitter in the brain, acting on Y2 receptors, rapidly shuts off visual cues regarding prey, thereby decreasing food intake. Here we test the hypothesis that tectal NPY receptors modulate food intake in juvenile *Xenopus laevis*. We tested two predictions: 1) Does tectal NPY micro-injection decrease food intake? 2) Does a selective Y2 receptor antagonist alter food intake after tectal administration? *X. laevis* were administered NPY via bilateral tectal injection alone or in combination with respective Y2 (BIIE0246) receptor antagonists or vehicle. NPY at three doses failed to statistically alter food intake. Interestingly, BIIE0246 alone increased food intake. While activation of tectal Y2 receptors did not affect food intake, blocking these receptors dramatically increased food intake.

#### **47. CLASSIFICATION OF PROTEIN-LIGAND BINDING USING THEIR STRUCTURAL DISPERSION**

Galkande A.I.C. Premarathna<sup>1\*</sup>, Leif Ellingson<sup>2</sup>

<sup>1</sup>Department of Mathematics and Statistics, Texas Tech University, Lubbock Texas 79409.

<sup>2</sup>Department of Mathematics and Statistics, Texas Tech University, Lubbock Texas 79409.

It is known that a protein's biological function is in some way related to its physical structure. Many researchers have studied this relationship both for the entire backbone structures of proteins as well as their binding sites, which are where binding activity occurs. However, despite this research, it remains an open challenge to predict a protein's function from its structure. Main purpose of this research is to gain a better understanding of how structure relates to binding activity and to classify proteins according to function via structural information. First we performed the classification of binding site to the data



set arising from Ellingson and Zhang (2012) through the use of logistic regression. Then we approach the problem from the data set compiled by Kahraman et al (2007). There we calculated the covariance matrices of site's coordinates which uses the distance of each atom to the center of mass and calculate distance from an atom to the 1<sup>st</sup>, 2<sup>nd</sup> and 3<sup>rd</sup> principal axis. Then we obtained covariance matrices of these distances to serve as our data objects. Finally, we performed classification on these matrices using a variety of techniques, including nearest neighbor.

#### **48. RECOGNITION AND INVOLVEMENT OF CONSERVED BH3 DOMAIN INTERACTING MEMBERS OF BCL2 SUPERFAMILY OF PROTEINS INVOLVED IN TESTICULAR GERM CELL APOPTOSIS**

Arpita Talapatra<sup>1\*</sup>, Nathaniel Mills<sup>1</sup>, Brian Beck<sup>2</sup>

<sup>1</sup>Dept. of Biology, Texas Woman's University, Denton, Texas.

<sup>2</sup>Texas Advanced Computing Center, Univ. of Texas, Austin TX

Apoptosis, characterized by shrinkage of total cell volume, increased cell densities and compaction of cell organelles, is an important regulatory process during spermatogenesis. Male rats were injected with ethylene dimethane sulfonate (EDS) (75 mg/kg body weight) to selectively eliminate mature Leydig cells thus, ablating the source of testosterone. The TUNEL assay and analysis of gene expression modulated by testosterone was assessed 7 days post-EDS. To substantiate testosterone's role, separate groups received exogenous testosterone for either supplementation or replacement of testosterone post-EDS. Significant germ cell apoptosis in EDS-treated rats was observed by the TUNEL assay and testosterone replacement prevented the germ cell apoptosis. The levels of pro- and anti-apoptotic genes of the Bcl2 family in testes were determined by RT & qPCR after 7 & 10 days treatment. Members of the Bcl2 superfamily are actively involved in the apoptotic pathway controlling cytochrome C release from mitochondria. These proteins share a conserved  $\alpha$ -helical BCL-2 homology (BH) domains 1-4. The BH3-domain has been marked as the minimal death domains required to bind with other multi-domain Bcl2 members. A significant increase in pro-apoptotic *BAK-1*, *BAD*, *BAX*, *BIK*, *BMF* & *BOK* and anti-apoptotic *BclW*, *Bcl2*, *BclXL* and *Mcl1* genes in testes of EDS-treated rats was found. All members possessing the BH3-domain were found to be regulated by testosterone, whereas Bcl2L10 (no BH3 domain) remains unchanged. Bcl2L10 is known to form heterodimers with Bcl2 rendering anti-apoptotic activity.

In this study, we used bioinformatics & computational tools to target the sequence of specific domain of Bcl2L10 involved in interactions with Bcl2. Sequence alignment studies compared different interacting domains in the Bcl2 superfamily to help in understanding the molecular mechanism of germ cell apoptosis.

#### **49. MOLECULAR MECHANISMS UNDERLYING DROUGHT STRESS ACCLIMATION IN TWO DIVERSE DROUGHT TOLERANT PEANUT GENOTYPES**

Ashwini Challa<sup>1\*</sup>, Poornasree Kumar<sup>1</sup>, Pratibha Kottapalli<sup>1</sup>, Paxton Payton<sup>2</sup>, Kameswara Rao Kottapalli<sup>1</sup>

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

<sup>2</sup>USDA-ARS, Lubbock, Texas 79415



*Arachis hypogaea* L. (cultivated peanut) is the third most important oilseed and legume crop in the world. More than 70% of the peanut is cultivated in arid and semi-arid regions, where the plants are subjected to the seasonal drought of different durations and intensities. Drought stress is a condition which results when the water loss from the plant exceeds the ability of the plant roots to absorb water. Plants can endure drought stress by various adaptive mechanisms such as drought avoidance, drought tolerance, drought acclimation etc. Acclimation is a phenomenon where plants slowly adapt themselves to different cycles of drought stress. Our previous studies in peanut revealed varying drought acclimation responses in leaf and root tissues. In order to understand the molecular mechanisms underlying drought stress acclimation responses in different genotypes, C76-16 (highly drought tolerant national check runner variety) and COC-041 (moderately drought tolerant Spanish variety) were selected for this study. The leaf and root transcriptomes from samples collected during stress and recovery time points were sequenced using Illumina platform followed by bioinformatic analysis for the RNA-Seq studies. This study will help in better understanding of the drought tolerance mechanisms and breeding germplasm tolerant to stress.

## **50. MICRORNA REGULATION OF GENE EXPRESSION UNDER DROUGHT STRESS ACCLIMATION IN PEANUT ROOTS**

Poornasree Kumar<sup>1\*</sup>, Ashwini Challa<sup>1</sup>, Pratibha Kottapalli<sup>1</sup>, Paxton Payton<sup>2</sup>, Kameswara Rao Kottapalli<sup>1</sup>

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

<sup>2</sup>USDA-ARS, Lubbock, Texas 79415

Drought is one of the major devastating abiotic stress factors that affects crop productivity. Plants tend to develop mechanisms to combat these adverse conditions. Some of these mechanisms are post-transcriptionally regulated by short non-coding microRNA that directly modulate gene expression during stress. Aim of this study was to identify differentially expressed microRNAs and their targets which have a significant role in drought acclimation in C76-16 genotype. The mRNA and miRNA were isolated and transcriptome profiles were generated by Illumina sequencing on HiSeq2500 and MiSeq platforms. Differential expression analysis identified 3,679 mRNA contigs and 350 microRNAs in response to drought acclimation. mRNA and miRNA expression profiles were analyzed and were found to be inversely correlated. Cell wall degradation enzymes such as pectin lyase and invertase were found to be upregulated during drought acclimation in contrast to being downregulated during drought recovery. These enzymes are regulated by gma-miR218b-3p and osa-miR166e-3p respectively. Another important target, Squamosa promoter binding like protein (SPL), was found to be downregulated by bna-miR156a which helps in formation of drought stress memory leading to better drought acclimation. Integrated study of miRNA and mRNA expression profiles helped in identifying many such microRNA-target pairs involved in drought stress acclimation. This unique combinatorial study will help in successful identification of molecular mechanisms that will assist in breeding improved drought tolerance in peanut.

## **51. IDENTIFYING POST-TRANSLATIONALLY MODIFIED PROTEINS IN BREAST CANCER CELLS FOR INVESTIGATING THE MECHANISMS OF ACTION OF A POTENTIAL ANTI-CANCER DRUG**





Bilkis A. Mitu<sup>1\*</sup>, Lauren S. Gollahon<sup>2</sup>, Susan K. San Francisco<sup>1</sup>, and Zabet M. Masoud<sup>1</sup>  
<sup>1</sup>Center for Biotechnology and Genomics, Texas Tech University, Lubbock, Texas-79409  
<sup>2</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas-79409

Phosphorylation is one of the most commonly occurring post-translational modifications (PTM). Phosphorylation plays a key role in activation or deactivation of protein cellular function, degradation, cell growth and proliferation, intracellular signaling, etc. A fundamental understanding of regulatory pathways requires identification of protein phosphorylation states and perturbation in the phosphorylation process can cause uncontrolled cell growth and cell development. Elucidating the changes in phosphorylation status in breast cancers may help to identify key signaling pathways and proteins significant in diseases progression. Till now there is no specific biomarkers for breast cancer and phosphoproteins have been a prime candidate for cancer biomarker. So, understanding the targets of PTM could become exploitable in drug development strategies for cancer treatment. This preliminary study will lay the foundation for understanding the mechanism of action for this candidate drugs with potential anti-cancer properties, helping elucidate their biological targets.

## **ECOLOGY**

### **52. PATTERNS OF RODENT SPECIES CO-OCCURRENCE ON ROADS VERSUS FIELD HABITATS**

John Stuhler<sup>1\*</sup>, Michaela Halsey<sup>1,2</sup>, Robert Bradley<sup>2,3</sup>, Neal Platt<sup>2</sup>, David Ray<sup>2</sup>, and Richard Stevens<sup>1,3</sup>

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

<sup>2</sup>Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

<sup>3</sup>Museum of Texas Tech University, Lubbock, Texas 79415

Many factors, such as interspecific interactions (e.g., competition, facilitation) and environmental filters (e.g., climate, habitat), influence the structure of ecological communities. One approach for identifying mechanisms that underlie community assembly is to analyze species co-occurrence patterns. Moreover, examination of patterns of co-occurrence may be useful for identifying factors limiting the distribution of rare species. We analyzed co-occurrence patterns of 13 rodent species on unpaved county roads (i.e., a pervasive habitat feature in many ecosystems; n = 750 sites) and in field habitats (i.e., rangeland and agricultural fields; n = 35 sites) across the historical range of the Texas kangaroo rat (*Dipodomys elator*) in north-central Texas. Importantly, roads may differentially impact distribution and abundance of small mammal species (e.g., by increasing habitat fragmentation, serving as dispersal corridors, or providing foraging habitat) relative to field habitats. Such effects could alter patterns of co-occurrence among small mammal species. We predicted that, because roads may serve as dispersal corridors for many small mammals, there will be higher species richness and a larger number of segregations of small mammal species (e.g., *D. elator* co-occurring with a higher number of species) relative to adjacent field habitat. If true, this would suggest that dirt roads may be an important habitat feature for promoting biodiversity in this region. Results from this work should improve understanding of factors limiting distribution of *D. elator*, as well as inform management strategies for promoting biodiversity of small mammals in this region.



### **53. ARE BATS MORE EFFECTIVE POLLINATORS THAN INSECTS? POSSIBLY NOT IN SOUTH AFRICAN BAOBABS**

Macy A. Madden<sup>1\*</sup> and Tigga Kingston<sup>1</sup>

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

While it is commonly thought that the bats in bat-pollinated plants are more effective in their pollination role than their insect counterparts, there is no quantitative evidence. Large size confers the ability to carry greater pollen loads and fly greater nightly distances, thus potentially connecting more plants. Baobabs (*Adansonia digitata*) exhibit chiropterophilous flowers and are also likely pollinated by hawk moths. In South Africa, we created a hand pollination experiment to test the effect of pollinator characteristics on fruit and seed production. We manipulated pollen load (small vs. large), distance of donor tree from recipient (near vs. far), and donor diversity (one vs. four individual donors) in a factorial design such that there were eight treatment conditions. In addition, there were open flowers that were not hand pollinated, but available for natural pollinators and flowers that were excluded and received no pollen; 40-45 replicates of each treatment on 16 unique baobabs were completed. Only some of the later treatment's flowers were emasculated after half of the first 36 replicates failed. After some maturation, the number of seeds, mass of fruit, and size of the fruit were recorded. All measured variables were correlated with each other, so the number of seeds was used in analyses. There was no effect of treatment on the number of seeds (ANOVA,  $p > 0.5$ ), but there was an effect of emasculation and of individual recipient tree. Our results indicate that there is no difference between bat and hawkmoth pollinators in our hand pollination simulation, but pollen loads are likely overestimated. Additionally, in South Africa, there is little evidence for bat pollination unlike eastern and western African populations of baobabs. It is possible that in southern Africa, baobabs have adapted to a different pollinator—thought to be hawkmoth species. Future studies will build on this experiment to explore the pollinator-baobab relationship in eastern Africa.

### **54. CONSERVATION ASSESSMENT OF THE EGYPTIAN FRUIT BAT (*ROUSETTUS AEGYPTIACUS*): HUNTING EFFECTS AND ECOSYSTEM SERVICES IN SOUTHERN NIGERIA**

Benneth C. Obitte<sup>1\*</sup> and Tigga Kingston<sup>1</sup>

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

The Egyptian fruit bat (*Rousettus aegyptiacus*) plays an essential role in the pollination and seed dispersal of ecologically and economically important plants, but is persecuted as pest and hunted in much of its range. In west Africa, *R. aegyptiacus* is the only obligate cave roosting fruit bat, and the most abundant non-migratory fruit bat species, forming large colonies that are critical for local plant community dynamics. Unfortunately, this bat species is intensely hunted across southern Nigeria. In a preliminary survey of hunters in the region in 2016, 72% ( $n = 150$ ) of interviewees reported hunting bats at least once in the previous year, and most of these efforts occurred in caves, with offtakes reaching over 1500 individuals per day from a single cave. We seek to detail bat hunting dynamics, assess harvest sustainability, and collect ecosystem services data (dietary characterization) in localities where hunting is



reported across five states in southern Nigeria. We will survey all cave roosts of *R. aegyptiacus* within 7hrs walking distance of hunting communities for population parameters. We will also sample bats at the sub-canopy for dietary analysis. Hunting surveys will be conducted in all hunting communities and households employing open-ended and fixed response questions to obtain information on hunting offtake, frequency, behavior, educational status, economic plants, bat meat commodity network, and mitigatory preferences. Measures of hunting behavior will be modeled against demographic and socio-economic variables using a mixed effects logistic regression model. To assess the sustainability of hunting in the study localities, we will model bat counts against hunting intensities. The results of this study will provide critical data for conservation efforts, and provide first data on the species richness of fruit bats in this region of high endemism - an area rated as the largest bat diversity hotspots in Africa but, where little is known about bats.

## **55. THE EFFECT OF WHISPER CALLS ON SETTLEMENT DECISIONS OF VEERIES (*CATHARUS FUSCESCENS*)**

William D. Fetzner\*<sup>1</sup>, Kenneth A. Schmidt<sup>1</sup>

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

Emerging research has shown that many species of birds utilize low amplitude vocalizations (LAVs) in a variety of social interactions; however, the function of these vocalizations in shaping the spatial dynamics of individuals within breeding populations remains unexplored. To gain further understanding of the function of LAVs in this context, I will experimentally test the function of LAVs by documenting the settlement decisions of a migratory songbird (the veery; *Catharus fuscescens*) in a manipulated forest soundscape. Sites will be manipulated through the playback of previously recorded male songs with LAVs (i.e. whisper calls) embedded in them. I will use low or high rate (number of LAVs/minute) of whisper calls embedded in the playback songs. The time and place of both male and female settlement will be recorded throughout the breeding season. I hypothesize that males will settle farther away from high frequency whisper call sites until later in the breeding season than concurrently arriving females. This is the first experimental study to attempt to fill the gap in the literature on the function of whisper calls as an aggressive signal and its consequences on breeding settlement decisions.

## **56. ARE ALL MOUNTAINS THE SAME? CHANGES IN SOUTH AMERICAN BAT DIVERSITY PATTERNS ALONG ENVIRONMENTAL GRADIENTS**

Cristina Ríos-Blanco\*<sup>1</sup> and Richard D. Stevens<sup>1,2</sup>

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

<sup>2</sup>Museum of Texas Tech University

Biodiversity patterns are often related to environmental gradients. Typical approaches to understanding the relationship between biodiversity and environmental gradients evaluate changes in species richness. However, different aspects of biodiversity may elicit different patterns along the same gradient. Using other dimensions of biodiversity may provide a more comprehensive understanding of biodiversity along environmental gradients. However, biodiversity changes along one gradient may also vary with respect other gradients. For example, patterns of different dimensions of biodiversity along elevation gradients may change with latitude. Thus, it is important to consider whether



biodiversity patterns along one gradient could be affected by variation along another. We examined change in four dimensions (taxonomic, phylogenetic, functional and phenetic) of bat biodiversity across elevational gradients that differ based on their latitudinal position in South America. We characterized biodiversity of 16 bat metacommunities using 12 diversity indices. We determined significance of diversity indices by comparing our measurements against index values from random communities. To examine whether diversity changes were similar across metacommunities we used analysis of covariance. Most metacommunities exhibit a decrease in biodiversity towards higher elevations. Decreases are more evident in the taxonomic dimension. However, these changes depended upon latitude. Metacommunities at lower latitudes exhibit a more rapid decline in biodiversity relative to higher latitude metacommunities. Our results suggest that biodiversity patterns along elevational gradients cannot be generalized along latitudinal gradients. Biodiversity changes in the tropics are more related to shifts in dominance of phylogenetic and functional with increasing elevation. In contrast, elevational changes in biodiversity at higher latitudes are primarily explained by changes in taxonomic diversity.

## **57. SOIL MICROBIAL COMMUNITY PHYSIOLOGICAL AND COMPOSITIONAL CHANGES IN BIODIESELS VS. PETRODIESEL CONTAMINATED SOILS**

Meijun Dong<sup>1\*</sup>, Deborah L. Carr<sup>1</sup>

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

Biodiesel has been generally considered as a viable substitute for petroleum diesel, however its impact on soil microbial communities is still unclear. Soil microorganisms participate in many critical ecosystem processes, including nutrient mineralization, and formation and enhancement of soil structure. However, most studies only investigated soil microbial diversity at pre and post contamination level without testing the changes in between. This laboratory study compared the effects of petrodiesel and three types of biodiesel on soil microbial communities in three types of soil. Contaminated soil samples were investigated at day 0, day 7 and day 180 to determine the degradation rate of the contaminants and their effects on the composition and function of soil microbial communities. GC-FID was used to determine the degradation rate of contaminants while commercial Biolog EcoPlates™ were used to test the microbial community function based on carbon utilization. Soil microbial composition were addressed by 16s rRNA gene sequencing of V3-V4 region. Results suggested that biodiesels were not statistically different from petroleum diesel in terms of their adverse impacts on soil microbial communities. In conclusion, our results suggested that the chemical structure of biodiesels might determine whether they are environmentally benign, and that they should not be automatically considered as harmless substitutes for diesel.

## **58. MODELING OPTIMAL STOPOVER USE ACROSS VARIED THERMOREGULATORY CAPACITIES DURING MIGRATION**

Jeff Clerc<sup>1\*</sup>, Liam P. McGuire<sup>1</sup>

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

For many organisms, seasonal migration is an integral part of life history. Understanding the migration ecology and physiology of these organisms is necessary for assessing the adaptive values associated with varied migration strategies. Stopover behavior plays a



critical role in the overall migratory strategy of organisms, yet to date the overwhelming majority of research on stopover behavior has focused on migrants that are strict homeotherms. This focus on homeotherms has led to a gap in our understanding about the stopover behavior of heterothermic migrants. Heterothermic migrants turn thermoregulatory costs into energy savings by reducing the energetic demands of maintaining a stable internal body temperature during periods of rest. These energy savings during periods of rest lead to interesting questions about how stopover behavior is altered due to varied thermoregulatory capacities. We developed a model that compares the optimal habitat use of migratory bats exhibiting varied thermoregulatory capacities. We use our model to generate testable predictions about the relative influence of stopover conditions on resource availability and the subsequent effects of resource availability on a migrant's decision whether to forage or rest upon arrival to stopover. We demonstrate how the model generates predictions about the basic relationships between site quality and ambient temperature on resource abundance. Our model further generates predictions about the critical threshold whereby heterothermic and homeothermic migrants balance stopover habitat use. Specifically, we investigate the decision to forage or rest upon arrival at stopover between heterothermic migrants and homeothermic migrants to gain insights into how varied thermoregulatory capacities influence stopover strategies and ultimately migration success.

## **59. PHENOTYPIC FLEXIBILITY IN BODY COMPOSITION OF INSECTIVOROUS BATS DURING THE SUMMER ACTIVE PERIOD**

Amie S. Sommers<sup>1\*</sup>, Elizabeth J. Rogers<sup>1</sup>, Liam P. McGuire<sup>1</sup>

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

Organisms respond to variation in energy availability and demand by altering behavior, physiology, and morphology; collectively, known as phenotypic flexibility. We studied Brazilian free-tailed bats (*Tadarida brasiliensis*) to assess phenotypic flexibility driven by intrinsic and extrinsic energetic factors. *T. brasiliensis* are small, volant endotherms that experience wide variation in energetic demand. Crucially, males and females experience reproductive energy demands at different times of the annual cycle. Pregnancy and lactation occur during the summer while males undergo spermatogenesis over winter. Thus, females face both intrinsic (reproductive) and extrinsic (environmental) challenges in summer. Males cope with the same environmental variation as females, but experience little intrinsic variation in summer. We hypothesized overall lean mass would vary in response to energy demand. We predicted greater variance in females than males due to greater and more variable intrinsic energy demand during the summer active season. We used quantitative magnetic resonance to measure body composition (lean mass, fat mass, total body water) of adult *T. brasiliensis* during the summer active period. To provide context to changes in lean mass, we collected bats to measure individual organs, considering organs associated with digestion and exercise. Female total lean mass decreased from pregnancy to lactation, but did not change from lactation to post-lactation. There was little variation in lean mass of males over the summer. Organ composition analysis is ongoing. Our results suggest that intrinsic factors have a greater effect than extrinsic factors on the phenotype of *T. brasiliensis* during the summer season.

## **60. PATTERN OF MICROBIAL DEGRADATION OF ESTRONE AND TRICLOSAN**



## **MIXTURE AND ITS EFFECT ON SOIL MICROBIAL COMMUNITY**

Ezinne Adabaram Osuji<sup>1</sup>, Deborah L. Carr<sup>1</sup>

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

Pharmaceutical and personal care products (PPCPs) associated with land farming of municipal wastewater effluent may potentially persist in the soil and alter soil microbial community processes. Estrone (E1) and Triclosan, were examined for their potential to persist and disrupt soil microbial community function. Soil with decades-long exposure to these chemicals (conditioned soil) and naive soil that has not been previously exposed (unconditioned soil), was spiked with estrone, triclosan, a 1:1 mixture of estrone: triclosan, and incubated for 90 days in the dark at 27°C. Control samples consisting of unspiked conditioned and unconditioned soil were included in the analysis. We examined the community level physiological profile using BIOLOG® EcoPlate for the ability of their microflora to utilize ecologically relevant carbon sources. There was a significant increase in substrate activity and substrate richness in all treatments. Principal component analysis of the data showed the microbial community utilized different carbon substrates by day 90 whereas they had exhibited similar substrate utilization at day 0. Microbial degradation rates were compared over the 90 days incubation period using high performance liquid chromatography (HPLC). Estrone and Triclosan showed the same pattern of biological degradation in both conditioned and unconditioned soils. Half-lives were determined to range between 5.9-6.8 days for estrone treatments and 24.1-26.9 days for triclosan treatments. The rate of degradation of the estrone:triclosan mixture was the same as the individual compound. 16S metagenome analysis of the conditioned day 0-control soil and the conditioned day 90 control, E1, triclosan and the binary mixture was done. The result showed a decrease in species diversity between control at day 0 and other treatments at day 90 with establishment of unique OTUs in each treatment group at day 90. *Bacillus* sp. was the most dominant bacterium specie in all the day 90 treatments.

## **61. ARE THERE GRASS FLAMMABILITY TRAITS? BIOMASS DIRVES GRASS FIRE BEHAVIOR, BUT CANOPY SPECIES-SPECIFIC ARCHITECTURE CAN CONTROL SURFACE HEATING**

Xiulin Gao<sup>1\*</sup> and Dylan W. Schwilk<sup>1</sup>

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

Plants fuel wildfire and understanding how plant traits influence fire behavior is necessary for linking species ecology to prediction of fire hazard and effects. Previous plant flammability studies point to the potential complexity behind the simple term "flammability", but recently several authors have argued that it is helpful to narrow in on the important axes of variation in flammability. Schwilk (2015) suggested that there are two important flammability axes, which are presented by total heat release and maximum rate of heat release, in litter driven fire and this may be a general case across fuels. Grasslands are among the most fire prone ecosystems and fine grass fuels are extremely flammable. Variation in flammability driven by species traits in grasses has generally been assumed to be minor while biomass has been thought to play the main role.

We aimed to test the generality of the two-axis flammability model and to explore grass traits other than biomass that may control fire behavior in grass species. We sampled 8



grass species (8~15 pairs of individuals per species) in shortgrass steppe and mixed grasslands in Texas and New Mexico. We measured canopy traits and conducted burning trials of grass individuals. Principal component analysis (PCA) supported the hypothesis that variation in flammability across species and individuals was largely two-dimensional (first two PCA axes explained 82% of total variance) and these axes largely corresponded to total heat release and maximum rate of heat release. As expected, plant biomass was the first order control of flammability measures, especially on total heat release. However, grass architecture (ratio of biomass above 10cm to that below 10cm) had an additional effect on duration of heating which is an important fire behavior metric predicting soil heating and meristem survival. These results demonstrate the potential for species-specific variation in architecture to influence local fire effects in grasses.

## **EVOLUTIONARY BIOLOGY**

### **62. EVALUATING THE LINEAGE DIVERSIFICATION OF *PEROMYSCUS* USING A PHYLOGENOMIC APPROACH**

Laramie L. Lindsey<sup>1\*</sup>, Roy N. Platt II<sup>1</sup>, Caleb D. Phillips<sup>1,2</sup>, David A. Ray<sup>1</sup>, and Robert D. Bradley<sup>1,2</sup>  
<sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Natural Science Research Laboratory, Texas Tech University

Lineage diversification of a group of organisms often can be accompanied by morphological changes as seen in adaptive radiations. However, many new species that originate over a short period of time display low morphological variation as well as low levels of sequence divergence as measured by comparison of mitochondrial and nuclear genes. The genus, *Peromyscus*, represents such a scenario with approximately 70+ species arising in the last 5-6my. Over the years, evolutionary biologists and systematists have attempted to decipher species boundaries of *Peromyscus* through morphological and genetic analyses. However, the proposed evolutionary tree still contains unresolved relationships within Peromyscine subclades, reflecting the rapidly radiating characteristic of *Peromyscus*. Advances in sequencing through-put and computational biology have provided biologists the opportunity to utilize more comprehensive datasets including transcriptomic and whole exome approaches. We hypothesize that closely related species possess a suite of genetic differences primarily in genes characterized as reproductive, and distantly related species will have accumulated differences in genes more commonly associated with non-reproductive genes. For this study, liver and testes transcriptomes of four taxa within *Peromyscus* were analyzed. To identify genes with putative testes-specific functions, transcriptomes were compared to determine if genes or suites of genes had differentiating expression levels in testes versus liver transcriptomes. All testes transcriptomes for the four species expressed higher levels of similar genes when compared to liver transcriptomes. Furthermore, sequences were aligned for all testes genes expressed in the four Peromyscine lineages; and, gene trees were constructed for each gene. Several analyses were conducted to identify which genes are subjected to directional selection in independent *Peromyscus* lineages.

### **63. RESOLVING THE PHYLOGENETIC VARIATION IN *PEROMYSCUS MANICULATUS*; POSSIBLE EVIDENCE FOR MULTIPLE SPECIES**

James Q. Francis<sup>1\*</sup>, Roy N. Platt II<sup>1</sup>, Caleb D Phillips<sup>1,2</sup>, and Robert D. Bradley<sup>1,2</sup>



<sup>1</sup>Department of Biological Sciences, Texas Tech University, Lubbock, TX 79406, <sup>2</sup>Natural Science Research Laboratory at the Museum of Texas Tech University, Lubbock, TX 79406

*Peromyscus maniculatus* is one of the most commonly encountered small mammal species in North America. This taxon includes approximately 60 recognized subspecies, presumably a reflection of its adaptability to a wide variety of habitats and environmental conditions. Several studies have documented morphometric and genetic variation, however a wide-spread phylogenetic study that examines multiple populations across a broad scale environment is necessary to determine if genetic variation follows phylogeographic patterns of phenotypic variation. To investigate the relationship between geographic variation, morphotypes, genotypes, parsimony and likelihood analyses of the mitochondrial gene cytochrome-*b* (*Cytb*) were performed to determine the phylogenetic relationship of this species across the entire known geographic range of *P. maniculatus*. In addition, samples of closely related taxa were included assay taxonomic validity and phylogenetic relationship to *P. maniculatus*. Results indicated strongly supported clades of *P. maniculatus*, with each clade representing populations assignable to specific geographic areas. The topology of these clades indicates that the genetic variation within *P. maniculatus* can, in part, be defined by the geographic distribution of the species. With the preliminary data complete, the next step is to attempt to understand the genetic variation present in this wide ranging species by utilizing next generation sequencing to examine patterns of genetic isolation.

#### **64. TECTAL CRF R1 RECEPTORS INHIBIT FOOD INTAKE**

C. Prater<sup>1</sup>, B.N. Harris<sup>1</sup>, and J.A. Carr<sup>1</sup>

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

The optic tectum (OT) and superior colliculus (SC) rapidly inhibit food intake when a visual threat is present. Previous work from our laboratory indicates that CRF, acting on CRF R1 receptors, may play a role in tectally controlled inhibition of prey capture and food intake. Here we test the hypothesis that **tectal CRF neurons modulate food intake in juvenile *Xenopus laevis***. We tested five predictions: 1) Does tectal CRF injection decrease food intake? 2) Does a selective CRF R1 antagonist block CRF effects on feeding? 3) Does a selective CRF R1 antagonist block reactive stress-induced decrease in feeding? 4) Does eliminating tectal cells expressing CRF R1 increase feeding? 5) Does food deprivation increase food intake and, if so, can this be reversed with CRF? *X. laevis* were administered oCRF alone or in combination with the selective CRF R1 antagonist NBI 27914 or antagonist vehicle. Test agents were bilaterally injected into the tecta of juvenile *X. laevis*. CRF conjugated to the ribosomal toxin saporin (CRF-SAP) was administered to pharmacologically eliminate tectal cells expressing CRF R1. Q1) oCRF administered bilaterally into the tecta significantly reduced food intake compared to sham and saline injected juveniles. Q2) Injection of oCRF and antagonist vehicle significantly reduced food intake. Injection of NBI - 27914 and oCRF eliminated oCRF-induced decrease in food intake. Exposure to ether vapors (Q3) alone or with antagonist vehicle pre-treatment significantly decreased food consumption. Pre-treatment with NBI-27914 eliminated ether-induced feeding decrease (Q3). Neither CRF-SAP injection (2 wk) nor food deprivation (1 wk) caused a significant increase in food intake (Q4, Q5). Overall, we found support for questions 1-3 and conclude that activation of the tectal CRFR1 inhibits





food intake in *X. laevis*. Furthermore, tectal CRF R1 receptors appear to be involved in the reduction of food intake that occurs in response to a reactive stressor (ether vapors). However, elimination of tectal CRFR1 neurons did not increase feeding suggesting that this system may be more important for stress-related vs. baseline feeding.

## **65. HIDDEN BENEFITS AID THE EVOLUTION OF ALTRUISM IN SMALL POPULATIONS OF UNRELATED INDIVIDUALS**

Sarah E. Fumagalli<sup>1\*</sup> and Sean H. Rice<sup>1</sup>

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

Most models for the evolution of cooperation make highly restrictive assumptions. These models are therefore at best special cases, limited to the description of particular individual influences (e.g. genealogical relatedness) and to large population sizes. In addition, the majority of research has treated evolution as a deterministic, additive process – assigning fixed values to variables and precluding nonlinear effects. However, any general model of the evolution of cooperation must include the probability of interaction, variation in fitness and small population sizes. In this study, we model the evolution of altruism with stochastic variation and non-linear fitness effects in small populations of randomly assorted individuals. We found through mathematical modeling and *in silico* experiments that including nonlinearity and stochasticity allows for the inclusion of more diverse altruistic interactions (i.e. biofilms, lichens), plus the traditional cases. Altruism has traditionally been associated with kin selection and reciprocal altruism, even though a number of natural and experimental studies have shown that these models do not cast a wide enough evolutionary net to explain all possible cases. Our results demonstrate how altruism can readily evolve between related/ preferred individuals, but more importantly between random individuals in small populations.

## **66. THE FIRST COMPLETE PHYLOGENY OF SOUTHEAST ASIAN TOADS (ANURA: BUFONIDAE) REVEALS A UNIQUE EVOLUTIONARY LINEAGE, A POLYTYPIC NEW ARBOREAL GENUS ENDEMIC TO SUMATRA**

Goutam C. Sarker<sup>1\*</sup>, Utpal Smart<sup>1</sup>, Michael B. Harvey<sup>2</sup>, Amir Hamidy<sup>3</sup>, Nia Kurniawan<sup>4</sup>, and Eric N. Smith<sup>1</sup>

<sup>1</sup>Department of Biology and Amphibian and Reptile Diversity Research Center (ARDRC), The University of Texas at Arlington, Arlington, TX-76019

<sup>2</sup>Department of Biological Sciences, Broward College, 3501 S.W. Davie Road, Davie, FL 33314,

<sup>3</sup>Indonesian Institute of Sciences (LIPI), Cibinong, West Java, Indonesia 16912

<sup>4</sup>Brawijaya University, Malang, East Java, Indonesia 65145

We present the first study to examine the phylogenetic relationships between all extant Southeast Asian and East Asian toad genera (Amphibia: Bufonidae). Our molecular and morphological data identifies the presence a distinct evolutionary lineage, of a brand new and previously unknown genus, of toads endemic to the island of Sumatra. Our molecular data consists of two mitochondrial and two nuclear gene fragments. The small sized toads of the genus *Sigalegalephrynus* gen. nov. is distinguished from other toad genera of the region by outwardly projecting oval inner metacarpal tubercle in males, truncated toe tips with pads and the presence of more than one free phalanges in the first finger. This finding highlights the importance of comprehensive taxonomic sampling in phylogenetic



and evolutionary analyses of the region. It also warrants the conservation of the most rapidly disappearing tropical rainforests of Indonesia.

## **67. PHYLOGENETIC RELATIONSHIPS BETWEEN THE MEMBERS OF THE GENUS NOTROPIS (FAMILY CYPRINIDAE)**

Ryan R. Vazquez<sup>1\*</sup>, Lou Densmore<sup>1</sup>, and Gene Wilde<sup>1</sup>

*Notropis* is an ecologically diverse genus in the family Cyprinidae. The genus is speciose with over 91 species found from Mexico to Canada. Currently, there is not a complete phylogeny for the genus. Therefore, I propose to use data available on GenBank to perform the most complete phylogenetic analysis on the genus *Notropis*. I accumulated many different mitochondrial and nuclear sequences and performed phylogenetic analyses using maximum likelihood and Bayesian analyses. The gene trees show very different evolutionary relationships for the species in the genus *Notropis*. Many of the groupings within the phylogeny, however, aligned with many of the smaller published phylogenies of *Notropis*. More sequence data are needed to gain a better understanding for the evolutionary relationships between the members of *Notropis*.

## **68. THE UTILITY OF ZONADHESIN IN EXAMINING A POTENTIAL REPRODUCTIVE ISOLATION MECHANISM IN RODENTS**

Emma K. Roberts<sup>1</sup>, Daniel M. Hardy<sup>2</sup>, and Robert D. Bradley<sup>1,3</sup>,

<sup>1</sup>Department of Biological Sciences, Texas Tech University, <sup>2</sup>Graduate School of Biomedical Sciences, Texas Tech University Health Sciences Center, <sup>3</sup>Natural Science Research Laboratory, Museum of Texas Tech University

Species-specificity in mammals is crucial to maintain reproductive isolation boundaries and prevent interbreeding and dilution of the gene pool. It has been hypothesized that gamete recognition (sperm/egg compatibility) is one of the first steps in establishing post-mating isolating mechanisms. Gamete recognition is a known prezygotic isolation mechanism in certain invertebrates, but its significance in vertebrates, such as mammals, is not well established. One of the proteins crucial in this process is referred to as zonadhesin (ZAN), a rapidly evolving, sperm protein that mediates species-specific adhesion to the egg's zona pellucida. It has been suggested that the evolution of ZAN correlates with reproductive isolation in mammals and is an adaptive gene found only in certain internally fertilizing mammals. In addition, it has been concluded that intra-species differences are known to exist in human and pig ZAN and might be under strong selective pressures, and thus, evolution of those alternative transcripts of the gene might contribute to the process of speciation. Therefore, by examining the alternative transcripts and the protein-coding sequence of ZAN both between and within species, both closely and distantly related, we can determine the level of variability and conservation of the gene and further establish if the subsequent protein might be acting as a reproductive isolation barrier. To address this question, we examined genetic variability in multiple species of rodents including *Peromyscus*, *Ictidomys*, and *Sigmodon* in order to assess the extent of sequence variation across a 400 bp hyper-variable region of the gene. Currently, we are sequencing 4 species of *Peromyscus* (*leucopus*, *maniculatus*, *boylii*, and *attwateri*) to establish the magnitude of baseline variation of ZAN. In addition, these species possess different times of divergence and represent a broad genetic diversity of the genus.



## **MICROBIOLOGY**

### **69. BLOOD FROM TRAUMA PATIENTS PRODUCES MAJOR SHIFTS IN *PSEUDOMONAS AERUGINOSA* TRANSCRIPTOME**

Moamen Elmassry<sup>1\*</sup>, Nithya S. Mudaliar<sup>2</sup>, Rao Kottapalli<sup>3</sup>, Sharmila Dissanaik<sup>4</sup>, John A. Griswold<sup>4</sup>, Michael J. San Francisco<sup>5</sup>, Jane A. Colmer-Hamood<sup>2,6</sup>, and Abdul N. Hamood<sup>2,4</sup>

<sup>1</sup>Department of Biological Sciences, TTU, Lubbock, TX; <sup>2</sup>Department of Immunology and Molecular Microbiology, TTUHSC, Lubbock TX; <sup>3</sup>Center for Biotechnology Genomics, TTU; <sup>4</sup>Department of Surgery, TTUHSC; <sup>5</sup>Honors College, TTU; <sup>6</sup>Department of Medical Education, TTUHSC

Every year trauma accounts for 41 million emergency department visits across the United States. While massive bleeding and brain injury are the leading causes of early death after trauma, sepsis is the leading cause of death in the days and weeks after the initial injury. Sepsis is associated with different bacterial pathogens including *Pseudomonas aeruginosa*. Despite numerous studies, the pathogenesis of *P. aeruginosa* infection during trauma-induced sepsis has not been described. In this study, we examined the effect of trauma-induced changes in blood on the expression of *P. aeruginosa* genes. This was accomplished using our newly developed model system that enables us to grow *P. aeruginosa* directly in blood from either 8 male and female trauma patients ages 22-56 (TPs) who presented at University Medical Center or 7 male and female healthy volunteers (HVs). Transcriptomic analysis of the *P. aeruginosa* strain UCBPP-PA14 that was grown in blood from both TPs and HVs was done using RNA-seq technology. The Rockhopper 2 system was used for downstream analysis accompanied by orthogonal partial least square discriminant analysis (OPLS-DA). Compared with growth in blood from HVs, the growth of *P. aeruginosa* in blood from TPs significantly altered the expression of 149 genes, upregulating the expression of 39 genes and downregulating the expression of 110 others. Genes whose expression was significantly increased included *pscU* (type III secretion system), *PA14\_62100/PA14\_62110* (sulfur metabolism), *mdcA/mdcE* (malonate utilization), and *ygiW* (stress response). Those genes whose expression was significantly reduced included *estA* (virulence), *aaaA* (virulence), 23 genes of the type VI secretion system, and pyoverdine-producing genes. These results suggest that during systemic infection in trauma patients, and to adapt to the trauma-induced changes in blood, *P. aeruginosa* adjusts positively or negatively the expression of numerous genes.

### **70. VIABILITY OF ANTIBIOTIC RESISTANT BACTERIA EMITTED FROM CATTLE FEEDYARDS IN AIRBORNE PARTICULATE MATTER**

Kelsey N. Thompson<sup>1</sup>, Loren L. Hensley<sup>1</sup>, Kim J. Wooten<sup>1</sup>, Philip N. Smith<sup>1</sup> and Gregory D. Mayer<sup>1</sup>

<sup>1</sup>Department of Environmental Toxicology, Institute of Environmental and Human Health, Texas Tech University, Lubbock, Texas 79409

Bacteria have been using antibiotics and antibiotic resistance mechanisms as a mode of survival long before the current human health crisis. Different species of bacteria produce antibiotics as a mode combating competition for resources and space, thus these bacteria must have evolved an escape mechanism from their own toxins. However, in recent years the use of antibiotics in human health and agriculture has exponentially increased the



concentration of antibiotics in the environment, increasing selective pressures for the spread of antibiotic resistant bacteria. A recent investigation showed that particulate matter (PM) disseminated from cattle feedyards was a potential source of antibiotics in the environment. Additionally, an increase in antibiotic resistance genes was observed in bacterial communities on PM downwind of multiple feedyards. However, due to the use of DNA sequencing-based methods in the aforementioned study, it remained unclear whether bacteria on airborne PM were viable. In this study, we readily cultured several taxa of aerobic, microaerophilic, and anaerobic bacteria from airborne PM. Additionally, several isolates showed resistance to multiple antibiotic classes. These data support the growing evidence that feed-yard derived airborne PM can contribute to the dissemination of antibiotic resistant bacteria into the environment.

## **71. BIOFILM FORMATION OF *BATRACHOCHYTRIUM DENDROBATIDIS* VM1**

Shalika Silva<sup>1\*</sup>, Lisa Atkins<sup>2</sup>, Uzma Qaisar<sup>3</sup>, and Michael San Francisco<sup>1</sup>.

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

<sup>2</sup>Baylor College of Medicine, Houston, TX 77030

<sup>3</sup>University of Punjab, Pakistan

*Batrachochytrium dendrobatidis* (*Bd*) has been a major contributor to the global amphibian decline, causing chytridiomycosis with epidermal hyperplasia and hyperkeratosis in adults. The chytrid forms a “biofilm-like” structure when grown in nutrient rich media at room temperature. Therefore, we hypothesized that the chytrid forms a biofilm *in vitro*. The biofilm was studied using the crystal violet, scanning electron microscopy, epifluorescence microscopy and gas chromatography. Gene expression and protein analyses were done using quantitative PCR, and enzymatic assays. Cell density dependent biofilm formation was determined by crystal violet assays. Different microscopy showed that biofilm was mainly composed of sporangia which were covered with extracellular matrix (ECM) material. Epifluorescence imaging of the TexasRed conjugated concanavalin A stained *Bd* biofilms confirmed the presence of ECM. Gas chromatography analysis of the precipitated matrix material of 6-d old biofilm revealed the total carbohydrate content of 6.17% (wt/wt) with five relatively abundant monosaccharides, ribose, xylose, mannose, galactose and glucose, which accounted for 30.3%, 10.1%, 19.1%, 12%, and 23.4% respectively. Gene expression analysis showed higher expression of the genes, zinc responsive activator (*zap1*), polysaccharide synthase (*cps1*), alcohol dehydrogenase (*adh3*) and chitin synthase (*chs1*, *chs2*), being up-regulated 12-fold, 10-fold, 5-fold, and 3-fold, respectively in the biofilm-associated cells over planktonic zoospores. However, only the expression levels of *cps1* and *adh3* found to be significantly different ( $p = 0.0016$  and  $0.0104$  respectively). Enzyme assays of ADH3 further confirmed the higher expression of *adh3* in biofilm-associated cells. No activity was observed in the planktonic cells. Our findings provide the first evidence for the biofilm formation of *Bd*. This may provide new insights on chytrid survival in the environment in the absence of amphibian hosts.

## **72. ESSENTIAL ROLES OF ERGOSTEROL AND SPHINGOLIPIDS IN THE SANDFLY TRANSMISSION STAGE OF *LEISHMANIA MAJOR***

Samrat Moitra<sup>1\*</sup> and Kai Zhang<sup>1</sup>

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



*Leishmania* promastigotes reside in the sandfly midgut where they are exposed to a number of bacteria acquired by the sandfly during sugar meal feeding from plants and blood feeding from animal hosts. In order to replicate and develop to the infective metacyclic form, *Leishmania* promastigotes must resist bacterial toxins, compete for nutrients with sandfly gut microbiota, and adapt to osmo-changes during sugar and blood feeding. The goal of this project is to determine the roles of ergosterol and sphingolipids in *Leishmania*-bacteria interaction. These lipids are crucial in maintaining membrane integrity, mediating vesicular trafficking and regulating cell signaling. We hypothesize that ergosterol and sphingolipids protect *Leishmania* against certain bacterial toxins and help them adapt to starvation and osmolality change in sandfly midgut. *Pseudomonas aeruginosa* is one of many Gram negative opportunistic pathogens in the sandfly midgut, reported to be highly prevalent during blood feeding. To understand the role of endogenous ergosterol and sphingolipids in sandfly stage, we investigated the sensitivity of ergosterol and sphingolipid mutants against *Pseudomonas aeruginosa* conditioned medium and also osmotic stress. Ergosterol and sphingolipid null mutant *Leishmania* were hypersensitive to *Pseudomonas* toxins and highly susceptible to hyper and hypotonic osmotic stress. These findings suggest that depletion of ergosterol and sphingolipids makes *Leishmania* more susceptible to certain bacterial toxins, nutrient starvation along with osmotic stress encountered in sandfly midgut, thereby affecting transmission.

### **73.POTENTIAL SECRETED COMPOUNDS FROM *BATRACHOCHYTRIUM DENDROBATIDIS* WHEN EXPOSED TO *STAPHYLOCOCCUS AUREUS* AND *ESCHERICHIA COLI***

Amanda M. Starr<sup>1\*</sup>, Susan San Francisco<sup>2</sup>, and Michael J. San Francisco<sup>1</sup>

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

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

The decline of amphibians worldwide has been accredited to the fungus *Batrachochytrium dendrobatidis* (*Bd*). This fungus disrupts the osmotic balance of amphibian skin cells leading to cardiac arrest. The epidermis consists of a keratin rich layer, coated with mucous, antimicrobial peptides, immunoglobulins, and the microflora of the amphibian. Previous studies have shown that bacteria are capable of inhibiting growth of *Bd* through the production of antifungal substances. The interaction of *Bd* with commensal amphibian epidermal bacteria may increase the virulence of the fungus through the up-regulation of toxic compounds. Small molecules secreted by *Bd* were analyzed with mass spectrometry and Compound Discoverer 2.0. Numerous potential toxic compounds were identified. We will use thin layer chromatography coupled with additional diagnostic tools to confirm the identification of the most abundant secreted small molecules. Following this, we will test them against bacteria and nematodes for toxicity. These studies will contribute to our understanding of the mechanism(s) by which *Bd* is able to infect and kill amphibians and aid in the development of novel strategies for treating infections.



## **MUSEUM SCIENCE**

### **74. ENGAGING COLLECTIONS MANAGEMENT WITH MOBILE TECHNOLOGY**

Taylor S. Ernst<sup>1\*\*</sup>

<sup>1</sup>Department of Museum Science, Texas Tech University, Lubbock, Texas, 79415

The Collections Storage Wing (CSW) at the Museum of Texas Tech University holds a wide range of historical objects for the History Division in the Museum. CSW houses over 2,100 objects that vary from a 1957 Cadillac Coupe De Ville to a 19<sup>th</sup> century cash register. As part of the Museum's Life Safety Project that involves major renovations to the Museum, objects in CSW that are taller than 5'6" could not stay in their current location and had to be relocated elsewhere temporarily. To develop a collections move plan, objects first have been inventoried and had an up-to-date condition report completed. This task has involved the use of a host computer that holds the database, along with iPads on which inventory and condition reports were completed. The iPads directly deliver the inventory and condition reports to the host database that holds 90% of the actual objects found in CSW. Graduate students working with the Curator of History accomplished the work in CSW over a 12-week span.

### **75. FIRST WORLD PROBLEMS: THE RISE OF NATURE DEFICIT DISORDER**

Bailee K. Roche<sup>1\*</sup>

<sup>1</sup>Department of Museum Science, Texas Tech University, Lubbock, Texas 79409

First introduced in 2005 by Richard Louv in his book *Last Child in the Woods*, nature deficit disorder refers to the growing disconnect between children and nature. This growing gap correlates with increased occurrences of various medical and behavioral problems in children, including type 2 diabetes, obesity, and attention-deficit/hyperactivity disorder. This presentation analyzes current research on nature deficit disorder and its associated ills. It then recommends programs and interpretation methods that natural heritage sights and other types of museum institutions with outdoor components can use to combat the disorder, by getting children physically active, interacting with the natural environment, and learning at the same time.

### **76. PHOTO DOCUMENTATION PRESERVATION CONSERVATION**

Hanna Reed<sup>1\*</sup>

<sup>1</sup>Department of Museum Science, Texas Tech University, Lubbock, Texas 79409

For proper documentation records, photographs are a crucial component. All areas of research and collections rely on photographs for visual conformation of: location, damages, the item or person, physical out comes of research, and photo series of the work being conducted. Just like items in a collection, photographs for documentation need particular preservation conservation to maintain the documentation and research records. Photographs that were developed from the 20's to the late 80's are in particular need of conservation. By now they have either faded, have chemical damage, or distortion from not being properly stored over the years. Conservationist have tested and studied the proper way to bring life back to earlier photographs and how to properly store photograph to prolong their life span. Photographs are one of the newest media and the life timeline



of photographs is still unknown. The latest conservation standards for photographs is crucial for all ranges of research.

## **77. ASSESSING LEVELS OF DNA AND RNA DEGRADATION IN FROZEN TISSUES ARCHIVED IN NATURAL HISTORY COLLECTIONS**

Taylor J. Soniat<sup>1\*</sup>, Caleb D. Phillips<sup>1,2</sup>, Kathy MacDonald<sup>2</sup>, Jeremy E. Wilkinson<sup>3</sup>, and Robert D. Bradley<sup>1,2</sup>

<sup>1</sup>Department of Biology, Texas Tech University, <sup>2</sup>Natural Science Research Laboratory, Texas Tech University, <sup>3</sup>RTL Genomics, Lubbock, TX 79407

Frozen tissues archived in museum collections are a primary resource for researchers. They are used in a variety of disciplines, including phylogenomics, histology, and virology. Recently, liquid nitrogen freezers have been identified as best practices for long-term archival. Liquid nitrogen freezers allow tissues to be stored at a lower temperature, reducing the rate of nucleic acid degradation. Historically, many museums have relied on mechanical freezers that store tissues at  $-80^{\circ}\text{C}$ , whereas liquid nitrogen freezers maintain temperatures of  $-190^{\circ}\text{C}$ . The Natural Science Research Laboratory at the Museum of Texas Tech University recently obtained five liquid nitrogen freezers and staff members have been in the process of transferring the tissue collection from mechanical freezer storage into liquid nitrogen archival. The effects on sample integrity due to long-term storage at  $-80^{\circ}\text{C}$  is not well characterized. To address this, we obtained liver and muscle samples collected at various time intervals (1986, 1996, 2006, and 2016). We maintained a sample size of 25 for each time interval; with the exception of 1986, where only seven samples were available. The samples have been sent to RTL Genomics, where genomic DNA was robotically extracted, and a fragment analyzer is being used to assess the quality of the DNA. Statistical analyses will be performed to measure and compare the DNA quality from the different tissues, to see if any degradation has occurred in older samples.

## **NATURAL RESOURCES MANAGEMENT CONSERVATION**

### **78. HABITAT SELECTION BY WATERFOWL WINTERING AT ANAHUAC NATIONAL WILDLIFE REFUGE**

Tiffany C. Lane<sup>1\*</sup>, Jena A. Moon<sup>2</sup>, Blake A. Grisham<sup>1</sup>, Doug M. Head<sup>2</sup>, David A. Haukos<sup>3</sup>, Warren C. Conway<sup>1</sup>

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

<sup>2</sup>U.S. Fish and Wildlife Service - Region 2 Inventory and Monitoring Program, Winnie, TX, 77665

<sup>3</sup>U.S. Geological Survey - Kansas Cooperative Fish and Wildlife Research Unit, Manhattan, KS, 66502

Waterfowl conservation focuses on managing and conserving important habitats across their range. Past research aiming to describe resource selection often focused on single species to understand habitat selection by waterfowl. Understanding community-level responses is important because management efforts targeting selected habitat variables impacts multiple species, especially on wintering grounds where waterfowl communities aggregate around shared resources. Therefore, our goal was to assess habitat selection by overwintering waterfowl communities to develop effective conservation plans targeting multiple species of dabbling ducks. We conducted our study at the Anahuac National Wildlife Refuge (NWR) in southeastern Texas. We observed mixed-flocks of 6 *Anas*



species defined as a guild of migratory, shallow-water dabblers. We conducted aerial surveys to track monthly waterfowl habitat use from October–February, 2014–2016. We visited sites with >500 birds in an aggregated flock (used) and randomly selected locations (available) and recorded water salinity, temperature, depth, submerged aquatic vegetation (SAV), and invertebrate density. We developed a resource selection function using generalized linear models with used/available data to assess community habitat selection at multiple spatial and temporal scales. Habitat selection between years was best predicted by water depth, salinity, and temperature. Habitat selection within winter periods was best predicted by the same water characteristics and submerged aquatic vegetation. We extrapolated our data to the entire NWR using our best supported habitat metrics and produced predictive habitat use maps for large flocks of dabbling ducks. Across all years, we predicted use on ~65% of Anahuac NWR. Overlap in resource use among dabbling ducks occurs during the winter; therefore, using the guild concept in lieu of single species is likely a more efficient strategy for waterfowl habitat management.

### **79. VELOCITY FAILS TO EXPLAIN SELECTION FOR LOW WIND POTENTIAL IN MIGRATING SWAINSON'S HAWKS (*BUTEO SWAINSONI*)**

Katheryn A. Watson<sup>1\*</sup>, Clint W. Boal<sup>2</sup>, Laurie M. Groen<sup>1</sup>, and James D. Ray<sup>3</sup>

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

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

<sup>3</sup>Consolidated Nuclear Security, LLC, USDOE/NNSA Pantex Plant, Amarillo, TX 79068

Swainson's Hawks (*Buteo swainsoni*) breed in western North America and migrate over 10,000 km to Argentina. Wind energy is expanding globally, and little research has been conducted on the potential threat wind turbines pose to Swainson's Hawks. To explore this question, we attached GPS transmitters to 24 adult Swainson's Hawks near Amarillo, TX. We collected location data from May 2011 to December 2016. Using average wind speed data, we classified the migration pathway by the potential for wind energy development as high (winds > 6 m/s), moderate (4.2-6 m/s), and low (< 4.2 m/s). Previous assessments suggested Swainson's Hawks spent the majority of their migration time in low-wind-potential regions; our goal was to explore why that pattern occurred. We hypothesized that the observed pattern may not reflect Swainson's Hawks selecting for areas with low wind, but rather their movement rates may be faster when transiting high-wind regions, resulting in less time spent in those areas. A repeated-measures ANOVA revealed an interaction between wind potential and season of migration, however travel velocity was equal between areas of high and low wind. Because our hypothesis was not supported, we conclude that Swainson's Hawks may be selecting for low-wind-potential areas, and we will next explore why that occurs using landscape characteristics and further assess risk wind turbines pose to migrating hawks.

### **80. THE RATIO OF ORGANIC TO INORGANIC NITROGEN AFFECTS THE GROWTH OF ICHTHYOTOXIC GOLDEN ALGA**

Rakib H. Rashel<sup>1\*</sup>, Lindsay D. Williams<sup>2</sup>, and Reynaldo Patiño<sup>3</sup>

<sup>1</sup>Department of Biological Sciences and Texas Cooperative Fish and Wildlife Research Unit, Texas Tech University, Lubbock, TX 79409

<sup>2</sup>Department of Natural Resources Management, Texas Tech University, Lubbock, TX 79409





<sup>3</sup>U.S. Geological Survey, Texas Cooperative Fish and Wildlife Research Unit and Departments of Natural Resources Management and Biological Sciences, Texas Tech University, Lubbock, TX 79409

Golden alga (*Prymnesium parvum*) is an invasive, harmful bloom-producing microalga. In inland waters is typically found in brackish ecosystems. While nitrogen (N) is an essential general nutrient, the relative importance of the organic (N<sub>o</sub>) and inorganic (N<sub>i</sub>) fractions to golden alga growth is uncertain. N<sub>i</sub> at relatively high concentrations is toxic to golden alga and a field study of the Colorado River (TX) reported seasonal declines in golden alga abundance as levels of N<sub>i</sub> increased. Recently, a study of the Pecos River (TX and NM) reported that, in addition to a negative association with N<sub>i</sub>, golden alga abundance is also positively associated with N<sub>o</sub>. These laboratory and field observations have provided convincing evidence that N<sub>i</sub> can negatively affect golden alga growth, but data for N<sub>o</sub> are insufficient for proper evaluation. The objective of this study is to experimentally characterize the influence of N<sub>o</sub> (urea) and N<sub>i</sub> (sodium nitrate) on golden alga growth. Different molar ratios of N<sub>o</sub> to N<sub>i</sub> were tested for their effects on specific growth rate (day<sup>-1</sup>) and maximum cell density (cells/ml) while keeping total N constant (880 μM) – 0%:100%, 25%:75%, 50%:50%, 75%:25% and 100%:0% (N<sub>o</sub>:N<sub>i</sub>). Cultures were inoculated at 100 cells/ml and other conditions were standard (5 psu, 22°C, 36 μM total phosphorous). Specific growth rate was not affected by changes in initial N<sub>o</sub>:N<sub>i</sub> ratio. Maximum cell densities, reached at days 21-24 of culture, however, gradually increased with increasing relative content of N<sub>o</sub> up to 75%, followed by a precipitous decline at 100%. In conclusion, while golden alga can grow in cultures containing exclusively N<sub>o</sub> or N<sub>i</sub>, optimal growth occurs when both are present but N<sub>o</sub> is the predominant fraction. These observations are consistent with field observations and provide context for a better understanding of the association between N and golden alga growth.

## **81. FEED BEHAVIORS AND PROPERTY DAMAGES OF SUS SCROFA**

Erin E. Ray<sup>1\*</sup>, Steven J. Rosscoe<sup>2</sup>, Wendi K. Wolfram<sup>3</sup>

<sup>1</sup>Department of Environmental Management, Hardin Simmons University, Abilene, Texas 79698

<sup>2</sup>Department of Geology, Hardin Simmons University, Abilene, Texas 79698

<sup>3</sup>Department of Biology, Hardin Simmons University, Abilene, Texas 79698

One of the leading concerns for agriculture and restoration conservation is the influence of invasive species and their impact on the environment. Over the years, studies have been conducted on several of these species, to include the feral hog and the damage they cause. Several studies have been conducted to find the effect of damages, and to understand the biology of feral hogs. Recognition of feeding behaviors and the connection they have with the property damages can lead to refined intuition of feral hog adaptability. By focusing on the biology and application of advances in analysis from modern technology, enhanced methods for estimating property damage by feral hogs can be identified. Within the grassland initiative program and its focus on the restoration of native grasses, this study applies plant identification through seed content in scat and looks at advancements in drone photography analysis for preference in resource availability. Knowledge from the data collected will provide improvements to the advancements in methodology for surveying feral hogs as a tool for refined management.



## **PROPOSAL**

### **82. HYPOXIA IN THE GULF OF MEXICO: LONG-TERM IMPACTS ON ATLANTIC CROAKER OTOLITHS**

Shengjian Jiang<sup>1</sup>

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

Rapidly spreading hypoxia (low dissolved oxygen concentration) is one of the major concerns for marine ecosystem. The increasing hypoxia has driven fish away from their normal habitat and shifted their behaviors. Former researchers have used otolith as an indicator, but laboratory experiments are not sufficient to determine the complete impact of hypoxia. Long term studies are needed to help understand what impacts the environmental changes have on fish and if fishes respond to them. To achieve this, we will examine Atlantic croaker otoliths from 1983, 2002 and 2016 caught in the study site around 28N 90W inside of the Gulf of Mexico. There are 2 hypotheses in this study. Hypothesis 1 is: the otolith chemistry will show a significant difference in hypoxic and normoxic environment in each year. To test this, Laser-Ablation Inductively Coupled Plasma Mass Spectrometry will be used to collect element amounts and Principle Component Analysis will be the statistical method employed. Hypothesis 2 is that the relationship between elements and dissolved oxygen will show a temporal difference and will be tested using multiple regressions. Compared to laboratory investigations, this study will better represent the natural problems and how fish respond.

### **83. SEASONAL FLEXIBILITY IN BODY COMPOSITION AND LIPID OXIDATIVE CAPACITY IN *TADARIDA BRASILIENSIS***

Elizabeth J. Rogers<sup>1\*</sup>, Amie S. Sommers<sup>1</sup>, and Liam P. McGuire<sup>1</sup>

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

As small-bodied, flying, mammalian endotherms, insectivorous bats regularly experience extreme energetic demands. During reproduction, these demands increase dramatically, particularly in late-stage pregnancy or lactation. To compensate for the high energetic costs of reproduction, we hypothesized that Brazilian free-tailed bats (*Tadarida brasiliensis*), a migratory insectivorous bat species, would exhibit flexibility in fat storage and lipid oxidative capacity throughout the summer active season. Using quantitative magnetic resonance, a non-invasive technology for rapid body composition analysis, we measured fat mass in a maternal colony of *T. brasiliensis* at multiple time points throughout the summer. The preliminary results from this analysis suggest that females exhibit greater variation in fat storage than males during the summer season, and that the energetic requirements associated with gestation and lactation lead to considerable declines in fat mass. To analyze changes in lipid oxidative capacity, we will measure the activities of carnitine palmitoyl transferase, 3-hydroxyacyl-CoA dehydrogenase, and citrate synthase in the flight muscle during each reproductive stage. These enzymes give metrics of lipid transport to the mitochondria, lipid oxidation, and overall oxidative metabolism, respectively. Additionally, we will measure the activity of fatty acid synthase in the liver to provide a metric of *de novo* fatty acid synthesis throughout the season. The results of this study will demonstrate whether insectivorous bats exhibit variation in metabolic fuel use and storage during reproduction, which will more broadly improve



understanding of how vertebrates flexibly store and expend energy to achieve energy balance during periods of intense energetic demand.

#### **84. UNDERSTANDING THE EFFECTS OF HYPERGLYCEMIA ON SUBCORTICAL PROCESSING OF FEAR AND ANXIETY IN THE AFRICAN CLAWED FROG (*XENOPUS LAEVIS*)**

Nikhil Menon<sup>1\*</sup> and James A. Carr<sup>1</sup>

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

While the metabolic effects of diabetes have been well characterized, the role this disease has on the brain is a relatively new field of study. Insulin sensitive receptors and insulin-like growth factors are crucial in regulating glucose metabolism and stimulating neuronal growth in various regions of the brain. Further studying the effects of hyperglycemia and insulin receptor dysfunction in the brain will be crucial to understanding the increased prevalence of depression and anxiety-related disorders in diabetic patients and the role of insulin receptors in the development of Alzheimer's disease. In the case of anxiety-related disorders, anxiety-inducing stimuli are processed through both a conscious, cortical pathway and a subconscious, subcortical pathway with both pathways connecting to the amygdala. Studies on the cortical pathway have already noted reduced insulin growth factor expression in the prefrontal cortex and increased dopaminergic neurotransmission in the amygdala correlating to higher levels of anxiety in rats. For my future studies, I plan to investigate the effects of hyperglycemia on the under-studied subcortical system by utilizing African clawed frogs (*Xenopus laevis*), in which visually triggered fear and the subsequent behavioral responses are driven predominately, if not entirely, through the subcortical pathway. This study will involve developing a Type I model of diabetes in *Xenopus laevis* frogs followed by behavioral studies using a novel predator apparatus. The relative transcriptional abundance of insulin receptors and concentration of relevant neuropeptides will be determined using qRT-PCR. Finally, using electrophysiological methods, the effect of hyperglycemia on neural connectivity between the subcortical regions will be determined. This study will help develop a more complete understanding of the role of hyperglycemia plays on subcortical processing of anxiety.

#### **85. STEPS TO THE PHYLOGENETIC RESOLUTION OF SPECIES-RICH GENERA**

Michaela K. Halsey<sup>1,2\*</sup>, Laura A. Blanco-Berdugo<sup>1</sup>, Nicole S. Paulat<sup>1</sup>, Roy N. Platt II<sup>1</sup>, Richard D. Stevens<sup>2</sup> and David A. Ray<sup>1</sup>

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

<sup>2</sup>Department of Natural Resources Management, Texas Tech University, Lubbock, Texas 79409

Rodents are the most successful mammals on the planet in terms of species richness. Members of the genus *Dipodomys* (the kangaroo rats; family Heteromyidae) are a curious group of rodents found only in western North America. These rats occupy a wide range of habitats, from the Sierra Nevada mountains in California to the coasts of south Texas. Furthermore, while some species are common (such as Ord's kangaroo rat, *Dipodomys ordii*) others are poorly known, rare, threatened, and even endangered (for instance, the Giant kangaroo rat, *Dipodomys ingens*). To date, a comprehensive phylogeny of all 22 members of this genus remains unresolved. Here, we attempt to improve phylogenetic understanding of *Dipodomys* using transposable elements (TEs). TEs are regions of DNA that can relocate to novel places within a genome. It is theorized that TEs influence



genomic structure and play a large role in speciation. Certain TEs, such as short interspersed elements (SINEs), are useful phylogenetic markers. Utilizing COSEG, an open source software that separates repeats into subfamilies based on small co-segregating regions, we have determined candidate SINE subfamilies for *Dipodomys*. Using these SINE subfamilies as a query, we intend to employ a mobile element scanning (ME-Scan) approach to construct the most contemporary phylogeny of the kangaroo rats. Since it is understood that there is correlation between ecology and phylogenetic position, we hypothesize that the phylogenetic trees built from this approach will follow some macroecological pattern (i.e. body size or precipitation gradient). We offer that the precision in data obtained from genomic resources can illuminate untold questions in the fields of ecology, evolution, and conservation biology.

## **86. THE INFLUENCE OF CATEGORICALLY DISTINCT STRESSORS ON ATTENTION TO VISUAL FOOD CUES**

Songhe Li<sup>1\*</sup>, James. Carr<sup>1</sup>

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

Stress can have complicated effects on food intake, and to date most studies have focused on how appetite is impacted by psychological and physiological stressors. Our hypothesis is that activation of the CeA can affect SC function through hardwired connections with the pulvinar nuclei, through activation of the HPA axis, and through activation of the SNS. We predict that exposure to stressors will lead to: a) increased detection of markers for HPA activation (salivary cortisol) and SNS (salivary alpha-amylase activity). b) Reduced time looking at food pictures relative to control pictures. All samples will be selected randomly from the student research pool in Mass Communications at Texas Tech University. Students will be asked to drink and eat as usual before testing. After signing a consent form and a brief form about pretest eating and drinking habits, students will be weighed, measured for height and calculating BMI, and hunger assessed by a visual analog test prior to testing. Students will be separated to three groups: Cold press test group, Untreated, and trier social stress test group. The entire student will take eye tracing test, at last, all of the students will be asked to take the visual function test. One way ANOVA test and paired t-test will be used to analysis the variables. Our expected result is: stress can have complicated effects on food intake, visual threats influence eye tracking in humans and lead to the firing of selective groups of nerve cells in retinorecipoent areas of the brain in primate animal models and lesioning of the primate SC eliminates visual threat detection.

## **87. SOIL MICROBIAL DYNAMICS IN A LONG-TERM SUSTAINABLE COTTON FIELD FOR SEMI-ARID WEST TEXAS**

Pablo Tovar-Ballen<sup>1\*</sup>, Veronica Acosta-Martinez<sup>2</sup>, John Zak<sup>1</sup>

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

<sup>2</sup>USDA-Agricultural Research Service, Cropping Systems Research Laboratory, Lubbock, Texas 79415

Sustainable agriculture practices can improve microbial capabilities to carry out fundamental soil processes. Understanding microbial dynamics in soils within long-term sustainable practices is critical for addressing impacts of increasing climate variability within a semiarid system. This study describes microbial dynamics from a 10-year-old



sustainable cotton production system on the Southern High Plains of West Texas (no-till and stubble application). In 2016, 8 replicate plots were randomly selected from a full section center pivot irrigated cotton field. A layer of corn stubble from the previous growing season along with terminated winter wheat covered the soil. Soil samples were collected and analyzed monthly to evaluate edaphic parameters, nutrient levels, and microbial community structure. Each plot had a data logger to record hourly data on temperature and volumetric water content (VWC) through the growing season. Soil microbial biomass decreased over the growing season irrespective of soil moisture levels. Using FAME analyses, relative abundances of saprophytic fungi and arbuscular mycorrhizae were dominant (27.4% and 30.9%). Gram positive, Gram negative and Actinomycetes, relative abundance was between 26.4% and 27.6% across the growing season with little seasonal changes. Between 0.8% and 1.7% of the FAME signatures were assigned to protozoans. Lastly, 40.9% to 45.1% the total FAME relative abundances were assigned as unidentified. Nutrient analyses showed a general decrease across time. Nonmetric multidimensional scaling analysis indicated that daily temperature range (daily  $T_{max}$  – daily  $T_{min}$ ) and VWC were the two most important abiotic variables shaping microbial community structure. Across a gradient in different states, biotic and abiotic factors will be evaluated in relation to microbial dynamics and sustainability. A Safe Operating Space will be defined to assess how much variability can a cotton system experience while being productive.

## **88. NEST SITE OVERLAP OF NATIVE AND INVASIVE AVIAN SPECIES AT TEXAS TECH**

Erin E. Bohlander<sup>1\*</sup> and Richard D. Stevens<sup>1,2</sup>

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

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

The Hutchinsonian niche is a multi-dimensional hypervolume of environmental conditions and resources that enable a species to persist in particular areas. This concept allows for quantifying competitive interactions that operate through niche overlap for the same resources within a community. In urban areas, avian communities tend to be composed of introduced and native species. Invasive species often thrive in areas where they have been introduced by acting as a superior competitor or exploiting unused resources. Resources that enhance reproductive success can be highly sought after. Nest sites tend to be limited within communities generating strong interspecific competition (identified by large overlap) and possibly leading to lower rates of fecundity. Across Texas Tech's Lubbock campus, native and invasive bird species may compete for nest sites within cavities of trees or buildings, those that are close to foraging sites, etc. Analysis of community structure with a Canonical Correspondent Analysis (CCA) by using environmental and microclimatic variables, can illuminate overlap of species nest sites. Weighted averages for species nest sites from CCA scores are estimates of niche space. Niche overlap occurs when niches of two or more species overlap. With this, we can estimate levels of competition for nest sites between native and invasive species. We hypothesize that some tree nesting species (i.e. collared doves) will compete with native species for nest sites. We also hypothesize that rock pigeon nest sites will not overlap with native species due to pigeons exploiting an unused resource, buildings.



## **89. ASSESSING THE POTENTIAL CONTRIBUTIONS OF THE MICROBIAL COMMUNITIES OCCURRING WITHIN CONCRETE TO ENVIRONMENTAL CARBON FLUXES**

Jordan I. T. Brown<sup>1\*</sup> and Deborah L Carr<sup>1</sup>

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

Concrete made with Portland cement is the most widely used man-made material, but it has never been considered as a biologically functional part of the biosphere. My preliminary sequencing and microscopy studies show that the microscopic pores and cracks inside concrete harbor several types of bacteria. I hypothesize that diverse microbial communities are embedded inside various types of Portland cement-based concrete and that these communities, due to the vast quantities of concrete, have measurable contributions to environmental carbon fluxes. This is likely given that microbial communities consisting of bacteria, fungi, and algae have been discovered living on the surfaces of concrete, and “endolithic” microbes are known to live inside natural rock, where they alter geochemical cycles. I will continue by analyzing the structure and function of microbial communities in the interior portions of concrete samples from three environments: aboveground, belowground surrounded by soil, and submerged in freshwater. Environmental DNA from interior concrete will be extracted and subjected to PCR-amplified 16s and 18s rRNA gene sequencing to assess bacterial and fungal diversity. Scanning electron microscopy will visually confirm intact cells embedded within the samples. Microbial respiration will be quantified by periodically measuring CO<sub>2</sub> production from concrete samples in sealed containers with an infrared gas analyzer. Community-level physiological profiles regarding potential carbon metabolism will be generated for each sample via Biolog™ EcoPlate systems. These analyses will provide baseline information of the biodiversity of “endo-concrete microbiomes” and of the functional capacities of these overlooked ecosystems. These microbial communities may be as common as the concrete they inhabit, so their collective effect on carbon fluxes must be quantified and incorporated into large-scale biogeochemical models.

## **90. ADDRESSING THREATS TO LANDSCAPE SUSTAINABILITY: USING LAND-USE AND CLIMATE CHANGE SCENARIOS TO MODEL FUTURE SPATIAL AND POPULATION ECOLOGY OF THE MID-CONTINENT POPULATION OF SANDHILL CRANE ON THE SOUTHERN HIGH PLAINS**

Kathryn J. Brautigam<sup>1\*</sup>,

<sup>1</sup>Texas Tech University, Dept. Natural Resources Management, Lubbock, TX;

The southern High Plains (SHP) is one of the most agriculturally-impacted regions in the Western Hemisphere with a current landscape matrix of various crops, Conservation Reserve Program (CRP) lands, native rangelands, ephemeral playas, and pluvial-saline lakes. Approximately 82% of the Mid-Continent Population (MCP) of sandhill cranes (*Antigone canadensis*) winter on this fragmented landscape. Cranes use saline lakes and playa wetlands for roosting, loafing, and drinking, and forage in crop fields for low-cost, high-energy foods. Future changes to the current landscape may pose a threat to sandhill crane persistence on the SHP. No comprehensive assessment has been performed for the MCP that overwinter on the SHP in over 30 years. Therefore, I propose to perform an assessment of what represents a sustainable landscape for wintering sandhill cranes, to



facilitate modeling habitat and population responses to several climate and land use scenarios specific to the SHP region. I will inform models with relevant ecological and spatial data that I will collect in 2014–? and combine with 1998–2004 and 2011–2016 data (in collaboration with and collected by the USGS). I propose the following objectives are needed for informing the overall objective: 1. assess landscape cover of Southern High Plains; 2. perform resource selection analysis; 3. assess carrying capacity of cranes overwintering on SHP; 4. estimate overwinter home range (HR) size and site fidelity of MPC/SHP cranes and use HR to identify winter areas of importance; 5. describe daily winter movements; 6. assess overwinter survival and causes of mortality; and 7. describe migratory phenology and residency of cranes on the SHP. This project will fill in some of the gaps in information on arrangement, connectivity, and availability of vital habitats in the southern High Plains for the MCP. The southern High Plains region is projected to become hotter and drier, which will undoubtedly cause land use changes that could alter suitability for many wetland- and agriculture-dependent wildlife.

## **TOXICOLOGY**

### **91. ELECTROSPUN NANOFIBER MEMBRANES FOR PARTICULATE MATTER AIR POLLUTION CLEANUP**

Lihua Lou<sup>1\*</sup>, Hongnan Zhang<sup>2</sup>, Seshadri Ramkumar<sup>1</sup>, Xiaohong Qin<sup>2</sup>

<sup>1</sup>Department of Environmental Toxicology, Texas Tech University, Lubbock, TX79410

<sup>2</sup>Shanghai Key Laboratory of Advanced Micro & Nano Textile Materials, College of Textiles, Donghua University, China, 201600

Particulate matter (PM), especially PM<sub>2.5</sub>, not only leads to serious air pollution, but also have been ranked by the World Health Organization as the 13<sup>th</sup> leading cause of mortality worldwide. Nanofiber membranes have small pore size, small fiber diameter, high filtration efficiency, which has been estimated as a possible effective method to solve this problem. However, with a pressure drop of up to 1500 Pa and production rate of 0.04 g/h make it less likely to be used as commercial products. In this paper, patterned nanofiber membranes with large pore size were fabricated to adjust the pressure drop and filtration efficiency. Polyacrylonitrile was employed as the electrospinning material as it is a common and fluffy fiber. Structured receiving templates and cylinder were served as collector to prepare the patterned membranes. A needleless electrospinning method with a production rate of 20-25 g/h was used to produce nanofiber membranes. With the special structure, the pressure drop of nanofiber membranes significantly declined from 1500 Pa to about 150 Pa, with the filtration efficiency a slight decline from 99.94% to about 98% compared to traditional electrospinning nanofiber membranes. These sharp declines of the pressure drop while retaining the filtration efficiency make it an excellent filter for air pollution.

### **92. MODELING THE MOST ABUNDANT MOSQUITO SPECIES (*Aedes vexans* AND *Culex tarsalis*) IN LUBBOCK, TEXAS, UNITED STATES**

Steven T. Peper<sup>1\*</sup>, Daniel E. Dawson<sup>1</sup>, Grant E. Sorensen<sup>1</sup>, Jordan Hunter<sup>1</sup>, Francis Loko<sup>1</sup>, Sadia Almas<sup>1</sup>, Kevan Athanasiou<sup>1</sup>, Anna G. Gibson<sup>1</sup>, Steven M. Presley<sup>1</sup>

<sup>1</sup>Vector-Borne Zoonoses Laboratory, Department of Environmental Toxicology, Texas Tech University, Lubbock, TX, 79416



Vector control programs (VCPs), commonly associated with local governments, are regularly tasked with monitoring and controlling mosquito species throughout their jurisdictions. Mosquitoes are often considered as a nuisance or a public health concern as they are capable of transmitting diseases to humans. Unfortunately, VCPs often do not have the necessary information to aid in effective control efforts. Currently, the Lubbock VCP treats for mosquitos based on complaints called in by citizens or by blanket spraying the city during peak periods throughout the year. This method often leads to wasted resources as well as over spraying of insecticides within the city. Over spraying can lead to development of insecticide resistance among mosquito populations as well as environmental complications. As part of an ongoing West Nile virus surveillance program, we collected mosquitoes between 2009-2015 and developed a statistical model based on weather factors to predict the abundance of the two most abundant mosquito species in Lubbock, Texas. The model developed in this study, in conjunction with a model we developed to predict the probability of mosquitoes having West Nile virus, will aid the Lubbock VPC in utilizing their time and resources more effectively and ideally reducing the amount of insecticide being sprayed within the city.

### **93. THE UPTAKE OF SEVERAL SHORT AND LONG-CHAIN PERFLUORINATED COMPOUNDS (PFCS) BY CARROTS (*DAUCUS CAROTA*), RADISHES (*RAPHANUS SATIVUS*), ALFALFA (*MEDICAGO SATIVA*), AND TOMATO (*SOLANUM LYCOPERSICUM*) GROWN IN SOILS CONTAINING DIFFERENT ORGANIC CARBON CONTENTS**

\*Steven Lasee<sup>1</sup>, Seenivasan Subbiah<sup>1</sup>, William Thompson<sup>1</sup>, Paxton Payton<sup>2</sup>, & Todd A. Anderson<sup>1</sup>

<sup>1</sup>The Institute of Environmental and Human Health, Texas Tech University, Lubbock, Texas 79409

<sup>2</sup>United States Department of Agriculture, Lubbock, Texas 79416

Perfluorinated compounds (PFCs) are incredibly stable environmental contaminants. In 2014, the United States Environmental Protection Agency labeled perfluorooctanoic acid and perfluorooctanesulfonic acid, the most persistent and toxic PFCs, as emerging contaminants due to their persistence in the environment. Data from animal studies on perfluorinated compounds indicate that they can cause several types of tumors, neonatal death, and may have toxic effects on the immune, liver, and endocrine systems. While many studies have evaluated the fate of PFCs in aquatic environments, the objective of this study was to determine PFC levels taken up by vegetation under a maximum availability scenario for a terrestrial environment. We grew carrots (*Daucus carota*), radishes (*Raphanus sativus*), alfalfa (*Medicago sativa*), and Tomato (*Solanum lycopersicum*) in laboratory grade sand, potting soil, and a 1:4 potting soil:sand mix. Sand was chosen due to its low organic carbon content making PFC bioavailability highest. The soils were spiked with 100 ng/g (100 ppb) of perfluorooctanoic acid, perfluorooctanesulfonic acid, perfluorohexanesulfonic acid, perfluorobutanesulfonic acid, perfluorononanoic acid, or perfluoroheptanoic acid; six PFCs that are currently or previously used in manufacturing and vary in chemical chain length. The plants were watered as needed with nutrient solution and allowed to mature (roughly 60 d). PFC concentrations in mature plant tissue were determined by LC-MS in an effort to calculate root, stem, leaf, and seed/fruit bioconcentration factors under this scenario.





## **94. ANALYSIS OF ANIMAS WATERSHED SEDIMENT BACTERIAL COMMUNITIES AFTER THE GOLD KING MINE BREACH**

Kelsey N. Thompson<sup>1,2\*</sup>, Jeremy E. Wilkinson<sup>1,2</sup>, Philip N. Smith<sup>1</sup>, and Gregory D. Mayer<sup>1,2</sup>

<sup>1</sup>The Institute of Environmental and Human Health, Department of Environmental Toxicology, Texas Tech University

<sup>2</sup>RTLGenomics, Lubbock, Texas 79407

On August 5, 2015 a tailing pond at the Gold King Mine near Silverton, CO was breached when workers attempted to add a tap to aid in restoration efforts. As a result, approximately three million gallons of water containing elevated concentrations of cadmium, lead, arsenic, zinc, copper, iron, beryllium and other toxicants were released into the Animas watershed. Presumably, deposition of metals in sediments along the watershed could present a selective pressure for sediment-borne bacteria inhabiting these niches. Here we report on the structure of sediment bacterial communities along the path of the waste outflow from the mine through Cement Creek, the Animas River, and proximal regions of the San Juan River. In the absence of baseline data collected before occurrence of the breach, samples from the Animas river upstream of its confluence with Cement Creek and the San Juan River upstream of its confluence of the Animas were collected to serve as unaffected controls. Analysis of 16S rDNA sequence was used to determine diversity metrics and population structure within the sediment-borne communities and these were compared with communities from unaffected sites. Additionally, abundance of metal resistance determinants was analyzed to garner information regarding how native bacterial communities adapt to mixed metal stressors.

## **95. EXTRACTION METHOD VALIDATION AND STABILITY OF NEONICOTINOIDS IN WATER**

Michelle M. McManus<sup>1\*</sup>, Subbiah Seenivasan<sup>1</sup>, and Jaclyn E. Cañas-Carrell<sup>1</sup>

<sup>1</sup>Department of Environmental Toxicology, Texas Tech University, Lubbock, 79409

Neonicotinoids are systemic, broad spectrum insecticides commonly used in agriculture. Exposure of non-target aquatic species to neonicotinoids has become an increasing concern given the high solubility of this pesticide class. Researchers are concerned about the potential underestimation of contamination of surface waters. Given the potential underestimation and risk to aquatic organisms, it is important to understand the impact of water components on the extraction efficiency and stability of three common neonicotinoids, clothianidin (CLO), imidacloprid (IMI), and thiamethoxam (TMX). To investigate this, three studies were conducted: 1) Solid phase extraction (SPE) efficiency of commonly used cartridges 2) stability of neonicotinoid samples both prior to and after extraction, and 3) analysis of field samples using the results of the first two studies. Two SPE cartridges were tested, C18 and Oasis HLB. Two-way ANOVA was used to assess the impact of dissolved organic carbon (DOC) and pH on percent recovery using C18 cartridges. The recovery of CLO, IMI, and TMX was significantly impacted by DOC but not pH ( $p < 0.05$ ). No effect on extraction efficiency was observed when using HLB cartridges. Neonicotinoids were stable in simulated field water for nine days stored at 4°C ( $p > 0.05$ ). Ongoing studies will confirm the effect of DOC on extraction using C18 cartridges and storage stability of neonicotinoids using spiked field water.

<b>A.</b>	<b>D.</b>	<b>H.</b>
Acosta-Martinez, V: 30, 87	Dang, T: 39	Harris, B: 13, 14, 64
Aguirre, Kelsey: 14	Dawson, D: 92	Harvey, C: 8
Ahmed, A: 38	Densmore, L: 67	Harvey, M: 67
Almas, S: 92	Derderian, D: 2, 42	Haukos, D: 78
Alqahtani, A: 31	Dhingra, A: 45	Head, D: 78
Anderson, S: 29	Dissanaike, S: 31, 69	Hendrix, S: 36
Anderson, T: 93	Dissanayaka, P: 17	Hensley, L: 70
Arida, E: 20	Dobrowolski, J: 24	Herrera-Gonzalez, M: 2
Arimbi, A: 20	Dong, M: 57	Howard, A: 23
Athanasίου, K: 92	Dunbar, T: 36	Hsu, F: 32
Athearn, N: 34	Dutta, D: 33	Huang, S: 15
Atkins, L: 71	<b>E.</b>	Hunter, J: 92
<b>B.</b>	Edie, A: 10	<b>I.</b>
Barnes, M: 37	Ellingson, L: 47	Islam, R: 46
Beck, B: 48	Elmassry, M: 69	<b>J.</b>
Bennert, Jeff: 23	Ernst, T: 74	Jeter, R: 25, 31
Bennert, Jon: 23	Esmaeili, N: 44	Jiang, S: 82
Bittner, R: 37	<b>F.</b>	Johnson, B: 12
Blanco-Berdugo, L: 85	Faircloth, K: 21	Johnson, E: 22, 27
Boal, C: 79	Feria, P: 3	Johnson, W: 34
Bohlender, E: 88	Fetzner, W: 55	Jones, L: 27
Bounds, K: 25	Fox, M: 35	<b>K.</b>
Bradley, R: 43, 52, 62, 63, 68, 77	Francis, J: 63	Kannan, R: 15
Brautigam, K: 34, 90	Fumagalli, S: 65	Kasner, A: 7, 41
Brooks, T: 29	<b>G.</b>	Kelly, S: 40
Brown, J: 89	Gao, X: 61	Kildow, A: 11
Brozek, J: 40	Gentles, A: 29	Kingston, T: 53, 54
Burrow, T: 40	Ghosh, B: 17	Knox, G: 35
<b>C.</b>	Ghosh, N: 23	Kottapalli, K: 49, 50
Cañas-Carrell, J: 95	Gibson, A: 92	Kottapalli, P: 49, 50
Cai, Y: 44	Gollahon, L: 51	Kroll, M: 10
Carr, D: 16, 24, 57, 60, 89	Gonzales, M: 42	Kumar, P: 49, 50
Carr, J: 14, 46, 64, 84, 86	Gonzalez-Herrera, M: 32	Kurniawan, N: 28, 66
Challa, A: 49	Grabowski, T: 37	<b>L.</b>
Chen, F: 18	Gray, G: 40	Lane, T: 78
Clerc, J: 58	Grisham, B: 34, 78	Lasee, S: 93
Cole, S: 1	Griswold, J: 69	Leasure, D: 15
Coleman, B: 14	Groen, L: 79	Letbetter, T: 6
Collins, D: 34	<b>H.</b>	Li, S: 86
Colmer-Hamood, J: 25, 31, 69	Halsey, M: 52, 85	Limboy, C: 13
Conway, W: 34, 78	Hamidy, A: 20, 28, 66	Lindsey, L: 62
Coots, A: 23	Hamilton, D: 1, 8, 10	Locke, A: 4
Crasto, C: 38, 39	Hamilton, S: 5	Lockwood, S: 1, 8, 10
<b>D.</b>	Hamood, A: 6, 25, 31, 69	Logan, K: 36
Dasgupta, S: 33	Hardy, D: 43, 68	Loko, F: 92

<b>L.</b>	<b>Q.</b>	<b>S.</b>
Lou, L: 91	Qaiser, U: 71	Spiegel, H: 14
<b>M.</b>	Qin, X: 91	Sprinkles, K: 6
MacDonald, K: 77	Quintana, A: 39	Starr, A: 73
Madden, M: 53	<b>R.</b>	Steep, J: 21
Martinez-Andrade, F: 37	Raleigh, D: 34	Stevens, R: 5, 11, 52, 56, 85, 88
Masoud, Z: 51	Ramkumar, S: 91	Stonum, P: 29
Mathew, M: 35	Randell, S: 1, 8, 10	Stuhler, J: 11, 52
Mayer, G: 70, 94	Rashel, R: 80	Stukenholtz-Bohlender, E: 4, 88
McGuire, L: 58, 59, 83	Ray, E: 81	Su, J: 17
McManus, M: 95	Ray, D: 26, 52, 62, 85	Subbiah, S: 93
McMichael, B: 30	Ray, J: 79	<b>T.</b>
Menon, N: 84	Reed, H: 76	Talapatra, A: 33, 48
Mills, N: 33, 48	Reinhart, A: 40	Thammachoti, P: 28
Mirza, S: 6	Revanna, C: 23	Thompson, K: 70, 94
Mitu, B: 51	Rice, S: 65	Thompson, W: 93
Moitra, S: 12, 32, 72	Rimal, B: 24	Tipton, C: 35
Moon, J: 78	Ríos-Blanco, C: 5, 56	Tovar-Ballen, P: 87
Moretti, J: 22	Roberts, E: 43, 68	Trujillo, V: 40
Morales, J: 2, 42	Robertson, T: 1, 8, 10	<b>U.</b>
Mudaliar, N: 6, 31, 69	Roche, B: 75	<b>V.</b>
Myntti, M: 25	Rock, C: 45	van der Leek, S: 7
<b>N.</b>	Rodriguez, B: 10	Vargas-Gutierrez, D: 30
Navlekar, A: 16	Roesler, E: 37	Vazquez, R: 67
Nguyen, V: 39	Rogers, E: 59, 83	<b>W.</b>
<b>O.</b>	Rollins-Smith, L: 51	Walsh, M: 20
Obitte, B: 54	Roscoe, S: 81	Wang, D: 18
Oldenburger, S: 34	<b>S.</b>	Watson, K: 79
Osborne, S: 15	San Francisco, M: 69, 71, 73	White, A: 2
Osuji, E: 60	San Francisco, S: 51, 73	White, J: 36
<b>P.</b>	Seenivasan, S: 95	Wilde, G: 67
Patiño, R: 9, 80	Smart, U: 28, 66	Williams, J: 5
Paulat, N: 26, 85	Smith, Eric: 20, 28, 66	Williams, L: 9, 80
Pawlowic, P: 32	Smith, Ernest: 29	Wolfram, W: 81
Payton, P: 44, 49, 50, 93	Smith, J: 34	Wooten, K: 70
Pecos, C: 14	Smith, P: 70, 94	<b>X.</b>
Peper, S: 92	Smythe, S: 18	<b>Y.</b>
Phillips, C: 35, 62, 63, 77	Solis, V: 41	<b>Z.</b>
Pintos, M: 3	Sommers, A: 59, 83	Zabet-Moghaddam, M: 38
Platt, R: 52, 62, 63, 85	Soniat, T: 23, 77	Zak, J: 30, 87
Prater, C: 64	Sorensen, G: 92	Zhang, H: 44, 91
Premarathna, G: 47	Sorg, A: 36	Zhang, K: 12, 32, 72
Presley, S: 92	Soto, P: 13	

We thank you for being a part of TTABSS 2017!  
We will see you next year for the  
9<sup>th</sup> Texas Tech Annual Biological Sciences Symposium!  
For updates, please visit our website below in January.



*Association of Biologists at*  
**TEXAS TECH UNIVERSITY**

<http://www.biol.ttu.edu/ttuab/home.aspx>





