9th TEXAS TECH ANNUAL BIOLOGICAL SCIENCES SYMPOSIUM (TTABSS)

DEPARTMENT OF BIOLOGICAL SCIENCES
LUBBOCK, TEXAS
APRIL 6-7, 2018

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Welcome Note:

It is with great pleasure we welcome everyone to the 9th Texas Tech Annual Biological Sciences Symposium (TTABSS), which is held this year of 2018, on April 6th and 7th. 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 200 undergraduate, graduate and faculty participants from 19 academic institutions. Our program will have 95 research presentations that include 46 poster presentations and 4 concurrent oral sessions. In addition, we would like to announce our three distinguished guest speakers, Brian Richter, Dr. Robert W. Williams, and Clint Morgan. Each of these speakers are renowned scientists in their respective fields. Mr. Brian Richter is the chief scientist for the Water program of The Nature Conservancy, Dr. Robert W. Williams is from the University of Tennessee Health Science Center and focuses on genomics and informatics, and Mr. Clint Morgan is from the Centers of Disease Control and Prevention more specifically the Poxvirus and Rabies Branch. We are excited to have such incredible plenary speakers donate their time and support for our event.

As President 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 2018. 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!

Taylor Lenzmeier
President, TTUAB 2017-2018

Bravada Hill
Local Committee Chair, TTABSS 2018

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)

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Texas Tech University
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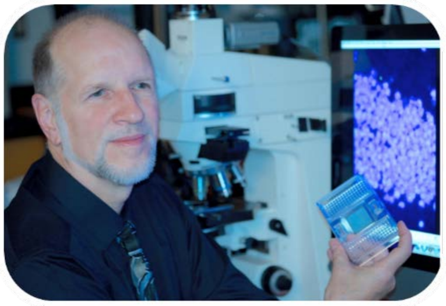
Texas Tech Health Science Center
Texas Tech University Climate Science Center
Texas Tech University at Waco
McLennan Community College
Wayland Baptist University
University of Puerto Rico
Texas Woman’s University
University of Texas of the Permian Basin
Center for Disease Control and Prevention
University of Texas Rio Grande Valley
University of Benin
West Texas A&M University
University of Texas at Arlington
Sustainable Waters
McMurry University
University of Tennessee

PLENARY SPEAKERS

Clint Morgan has led and assisted in the coordination and execution of numerous international field investigations and laboratory animal studies for the Poxvirus & Rabies Branch (PRB) within the National Center for Emerging and Zoonotic Infectious Diseases of the Center for Disease Control and Prevention (CDC) in Atlanta, GA. Working within PRB's Ecology and Evolutionary Analysis team Clint and his colleagues are tasked with understanding the ecology and reservoir species dynamics of various poxviruses and rabies, including the deadly disease Monkeypox. Initially trained in ecology and mammalogy, he received his M.S. in Biology (2015) from Angelo State University in San Angelo TX, where his thesis work was focused on mammalian natural history and conducting ecological niche modeling of *Peromyscus laceianus* (White-ankled mouse). During this time Clint was additionally responsible for conducting a baseline assessment of mammalian fauna within the 20,000-acre Devils River State Natural Area.

Brian Richter has been a global leader in water science and conservation for more than 30 years. He is the president of Sustainable Waters, a global water education organization, where he promotes sustainable water use and management with governments, corporations, universities, and local communities. He previously served as Chief Scientist for the Global Water Program of The Nature Conservancy, an international conservation organization. Brian has consulted on more than 150 water projects worldwide. He serves as a water advisor to some of the world's largest corporations, investment banks, and the United Nations.



Professor Robert (Rob) W. Williams received his Ph.D. in physiology at UC Davis in 1983. He did postdoctoral work in developmental neurobiology at Yale, then moved to the University of Tennessee in 1989. He is the chair of the Department of Genetics, Genomics and Informatics at University of Tennessee Health Science Center and holds a UT-ORNL Governor's chair in Computational Genomics. He is an affiliated professor at the Department of Pediatrics, Department of Ophthalmology, and Department of Anatomy and Neurobiology. Dr. Williams is a past president of the Society for Behavioral and Neural Genetics Society and founding director of the Complex Trait Community. Dr. Williams has 4 patents, h-index of 67 and total number of Citations over 17870.

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 2018 would not have been possible.

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Nikhail Menon – Biological Sciences, TTU
Ezinne Osuji – Biological Sciences, TTU
Kevin Sullivan – Biological Sciences, TTU
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Emma Roberts – Biological Sciences, TTU
Saba Nafees – Biological Sciences, TTU

The 2018 TTABSS logo was produced exclusively for the Association of Biologists at Texas Tech University by Mr. Mark A. Lee

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Dr. Ron Chesser

Faculty Co-Advisors
Dr. Ron Chesser
Dr. Lou Densmore
Dr. Robert Bradley

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Jumbo Joe's Burgers	3310 4th St (Right Across from Museum)	(806) 747-7900
Rosa's Cafe	4407 4th St	(806) 785-5334
Sonic	4401 4th St	(806) 771-0117
McDonald's	5201 4th 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
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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

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Name	Address	Phone
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

9th Texas Tech Annual Biological Sciences Symposium
April 6-7, 2018

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

PROGRAM AT A GLANCE

Friday, April 6th

4:30 pm – 5:00 pm	Poster Set-up and Registration, Museum of Texas Tech University
5:00 pm – 5:15 pm	TTABSS 2018 kick off by Dr. Ron Chesser, Department of Biological Sciences Chair, TTU
5:30 pm – 6:30 pm	Plenary Talk, Brian Richter, Sustainable Waters – Auditorium ***“Chasing Water in a Dynamically Changing World”***
6:30 pm – 8:30 pm	Poster Session, Judging, and Vendor Show (heavy hors d' oeuvres will be served)
8:30 pm – 9:00 pm	Poster Takedown

Saturday, April 7th

7:30 am – 8:30 am	Registration and Breakfast, Museum of Texas Tech University
8:00 am – 8:15 am	Welcoming by Dr. Lou Densmore, Graduate Advisor, Department of Biological Sciences, TTU
8:30 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 – 11:00 am	Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium
11:00am – 12:00pm	Plenary Talk – Dr. Robert Williams, University of Tennessee – Auditorium ***"Experimental Precision Medicine Using GeneNetwork"***
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, Clint Morgan, US Center for Disease Control and Prevention – Auditorium ***“Notes from the Field: Where Natural History Meets Public Health”***
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, Helen DeVitt Jones Sculpture Court, Museum of Texas Tech University

EVENT LOCATION

April 6-7, 2018

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 6th

Friday, April 6th

4:30 pm – 5:00 pm	Poster Set-up and Registration, Museum of Texas Tech University
5:00 pm – 5:15 pm	TTABSS 2018 kick off by Dr. Ron Chesser, Department of Biological Sciences Chair, TTU
5:30 pm – 6:30 pm	Plenary Talk, Brian Richter, Sustainable Waters- Auditorium
	“Chasing Water in a Dynamically Changing World”
6:30 pm – 8:30 pm	Poster Session, Judging, and Vendor Show (heavy hors d' oeuvres will be served)
8:30 pm – 9:00 pm	Poster Takedown

UNDERGRADUATE POSTERS

1. **BATS: WHO'S RELATED TO WHOM?**
   Nicole Paulat[1], Zach Nguyen[1]*, and David Ray[1]

2. **FISH ASSEMBLAGES ON THE MESOAMERICAN BARRIER REEF IN ROATAN, HONDURAS**
   Scheila R. Corujo[1,2]*, Karla J. Ramos[2], R'Shel D. Pacheco[2], Donna E. Hamilton[3], Shannon K. Hill[2], Traesha Robertson[4], Stephanie M. Randell[2], Stephanie A. Lockwood[1]

3. **CORRELATION BETWEEN BRAIN AMYLOID BETA CONCENTRATION AND SHORT-TERM MEMORY DEFICITS IN APPSWE/PS1DE9 TRANSGENIC MICE**
   Rebekah F. Salinas[1]*, Breanna N. Harris[1], Paul L. Soto[2]

4. **INVESTIGATION OF MUTATED CONE GENES AND THEIR AFFECT ON VISION**
   LaTorian C. King[1]* and Julie A. Parlos[1]

5. **EVALUATION OF THE BREAST EPITHELIAL CELL LINE EPH4-EV AS A NON-TUMORIGENIC CONTROL TO THE 4T1 TUMORIGENIC BREAST CANCER CELL LINE**
   Alana K. Quackenbush[1]*, Makayla Nicholson[1], Gary O. Gray[1], Adam J. Reinhart[1]

6. **SEA FAN ABUNDANCE AND FREQUENCY OF *MILLEPORA ALCICORNIS* ON THE MESOAMERICAN BARRIER REEF IN ROATAN, HONDURAS**
   Sarah F. Cole[1,2*], Shirley R. Stewart[2], Donna E. Hamilton[3], Traesha Robertson[4], Shannon K. Hill[2], Stephanie M. Randell[2], Stephanie A. Lockwood[1]

7. **ASSESSING THE GENETIC DIVERSIFICATION OF BATS IN THE GENUS *MONOPHYLLUS***
   Irene Vasquez[1]*, Laramie L. Lindsey[1], Julie A. Parlos[2], Robert J. Baker[1,3], Robert D. Bradley[1,3], Hugh H. Genoways[4]

8. **A GENETIC ASSESSEMENT OF POCKET GOPHERS OF THE GENUS *GEOMYS* (RODENTIA: GEOMYIDAE) IN TEXAS**
   Mariah N. Mills[1]*, Taylor J. Soniat[1], Michaela Halsey[1], Richard D. Stevens[1,2], David A. Ray[1], and Robert D. Bradley[1,2]

9. **THE STRUCTURE AND SYMMETRY OF WHISPER CALLS IN VEERIES (*CATHARUS FUSCESCENS*)**
   Brittany B. Quinones[1]*, William D. Fetzner[1], and Kenneth A. Schmidt[1]

10. **AMERICAN KESTREL BREEDING SEASON PREY USE AND DELIVERY RATES IN THE LLANO ESTACADO**

OF TEXAS
Madeleine A. Thornley[1]*, Shea D. Mullican[1], and Clint W. Boal[2]

11. SWAINSON’S HAWK RISK OF ENCOUNTERING WIND TURBINES ON MIGRATION ROUTE
Sara E. Hamilton[1]*, Katheryn A. Watson[1], Clint W. Boal[2], and James D. Ray[3]

12. BEHAVIORAL RESPONSE TO PREDATOR ODOR IN A TRANSGENIC MOUSE MODEL OF ALZHEIMER’S DISEASE
Mackenna B. Wollet[1]*, Guili M. DiMarco[1], Paul L. Soto[2], Breanna N. Harris[1]

13. CYTOTOXICITY OF *CINNAMON VERUM* (CINNAMON) AND *SALVIA OFFICINALIS* (SAGE) IN 4T1 BREAST CANCER CELLS
Makayla N. Nicholson[1]*, Alana K. Quackenbush[1], Ethan G. Nicholson[1], Robert L. Moore[1], Adam J. Reinhart[1] and Gary O. Gray[1]

14. EFFECTS OF ACUTE STRESS ON SHORT-TERM MEMORY AND ATTENTION IN A MOUSE MODEL OF AMYLOID-BETA NEUROPATHOLOGY IN ALZHEIMER’S DISEASE
Giuliana M. DiMarco[1]*, Breanna R. Roberts[1], Amber L. Loya[2], Paul L. Soto[3], Breanna N. Harris[1]

15. A COMPARISON OF ORGAN WEIGHTS IN TRANSGENIC AND NON-TRANSGENIC APPswe/PS1dE9 MICE, A MODEL OF ALZHEIMER’S DISEASE-RELATED AMYLOIDOSIS
Neel P. Roy[1]*, Emily Stevens[1], Amber Loya[1], Paul L. Soto[2], Breanna N. Harris[1]

16. SPECIES RICHNESS AND WINTER HABITAT ASSOCIATIONS OF SPARROWS (PASSERIFORMES: EMBERIZIDAE) IN AN AGRICULTURAL LANDSCAPE OF THE SOUTHERN HIGH PLAINS, TEXAS
Sharon L.A. DeMerritt[1]* and Andrew C. Kasner[1]

17. A METHODOLOGICAL COMPARISON OF THE LINE TRANSECT AND THE RANDELL-ROBERTSON MARINE SURVEY TECHNIQUE
Grace C. Gonzalez[1*], Brooke L. Allison[1], Brittlinn E. O’Quinn[1], Stephanie Randell[1,] Shannon Hill[1], Traesha Robertson[2], Stephanie Lockwood[3], Donna Hamilton[4]

18. SPECIES DISTRIBUTION MODEL OF COPPERHEADS *(AGKISTRODON CONTORTRIX)*
Pauline C. Fuentes[1]*, Joy O. Ramirez[2]*, Andres L. Rodriguez-Cordero[2], Sergio A. Balaguera-Reina[2], Mark A. Lee[2], Llewellyn D. Densmore[2]

19. **TEXAS TECH UNIVERSITY HERPETOLOGY SURVEY**
    Maggie E. Meier[1]*, Tyler Garcia[1], Mark A. Lee[1]

20. **POLYMICROBIAL INTERACTIONS AFFECT ANTIBIOTIC SUSCEPTIBILITY**
    William Little[1]* and Kelissa McCullar[1]*, Allie C. Smith[1]

21. **POLYMICROBIAL INTERACTIONS AFFECT POPULATION DYNAMICS**
    Andre Gomez[1]* and Andrea Lopez[1]*, Allie C. Smith

22. **ASSOCIATION OF BORING ORGANISMS WITH DARK SPOT SYNDROME IN ROATAN, HONDURAS**
    Erin N. Castillo[1*], Sanjuana Delgado[1], Jennifer Novak[1], Shannon Hill[1], Stephanie A. Lockwood[2], Donna E. Hamilton[3], Traesha Robertson[4], and Stephanie M. Randell[1]

<u>GRADUATE POSTERS</u>

23. **THE HISTORY OF WEST NILE VIRUS AND MOSQUITO SURVEILLANCE IN LUBBOCK COUNTY, TEXAS**
    Steven T. Peper[1]*, Alexander N. Wilson-Fallon[1], Katelyn M. Haydett[1], Hannah S. Greenberg[1], and Steven M. Presley[1]

24. **PREVALENCE OF CANINE HEARTWORM IN POTENTIAL MOSQUITO VECTOR POPULATIONS IN LUBBOCK, TEXAS, USA (2010-2016)**
    Katelyn M. Haydett[1]*, Steven T. Peper[1], Hannah S. Greenberg[1], Alexander N. Wilson-Fallon[1], and Steven M. Presley[1]

25. **OPTIMIZATION OF MECHANICAL TESTING PARAMETERS OF PVA NANOFIBROUS MEMBRANES**
    Lihua Lou[1], Jilong Wang[2], Odia Osemwegie[1], Weijie Yu[1]* and Seshadri S. Ramkumar[1]

26. **FUNCTIONAL TIO2/PVDF NANOFIBER WEBS FOR RHB PHOTOCATALYTIC**
    Lihua Lou[1]*, Jilong Wang[2], Yong Joon Lee[3] and Seshadri S. Ramkumar[1]

27. **COMPARATIVE STUDY OF POLYSTYRENE AND POLYETHYLENE DEGRADATION BY INSECT LARVAE**
    Anisha S Navlekar[1]*, Deborah L Carr[1]

28. **HUMAN *VS.* NATURE: ISLANDS AND BRIDGES WITHIN THE MICROBIOME CONTINUUM**
    Moamen Elmassry[1]*, Marwa ElRakaiby[2], Ramy K. Aziz[2]

29. **SALINITY ADAPTATION IN GOLDEN ALGA**
    Emily T. Richardson*[1], Reynaldo Patiño[2]

30. **TO COMBINE CRISPR/CAS9 GENOME EDITING, NANO-TECH AND CHEMICAL GENETICS TOWARD IN VIVO PROTEIN KINASE ANALYSIS**

Fengqian Chen[1], Degeng Wang[1]*

31. **ESTABLISHMENT OF NATIVE WOODY SPECIES IN DEGRADED TROPICAL DRY FORESTS IN THE CABO ROJO NATIONAL WILDLIFE REFUGE, BOQUERÓN, PUERTO RICO.**

Juan G. García-Cancel[1,2]*, Tatiana Velázquez-Rojas[2], Roberto Carrera-Martínez[2,3] and Oscar Díaz[4]

32. **STATUS, DISTRIBUTION, MORPHOLOGY AND GENETICS OF *SIGMODON FULVIVENTER DALQUESTI* IN THE CHIHUAHUAN DESERT ECOREGION**

Preston J. McDonald[1*], Caleb D. Phillips[1,2]

33. **PHYLOGEOGRAPHY OF ARENAVIRUSES (ARENAVIRIDAE) ASSOCIATED WITH NORTH AMERICAN WOODRAT SPECIES, *NEOTOMA***

Laramie L. Lindsey[1]*, Maria N. B. Cajimat[2], Mary Louise Milazzo[2], Charles F. Fulhorst[3], and Robert D. Bradley[1,4]

34. **EXPLORATION OF POTENTIAL PYOMELANIN MEDIATED POLYMICROBIAL COOPERATION**

Jiwasmika Baishya[1*], Obadeh Shabaneh[1], Josef Fowler[1], Catherine A. Wakeman[1]

35. **IMPACT OF TEMPERATURE DEPENDENT GLOBAL REGULATION OF BIOFILM FORMATION IN *PSEUDOMONAS AERUGINOSA***

Karishma Bisht[1] *, Jake Sellers[1], Austin G Brown[1], Jeanette Rimbey[1], Jennifer Herrera[1], Kiddist Yihunie[1] and Andrew Salazar[1]

36. **SPERM GRANULOMA ASSOCIATED PATHOLOGY IS DEPENDENT ON TESTOSTERONE ACTION IN ADULT RAT EPIDIDYMIS**

Arpita Talapatra[1*], Dibyendu Dutta[2], Nathaniel Mills[1]

37. **THE NOVEL ANTIMICROBIAL AGENT NEXT SCIENCE INFLUENCES THE WOUND HEALING PROCESS**

Kayla Bounds[1]*, Matthew Myntti[2], Jane A. Colmer-Hamood[3,4], Randall Jeter[1], and Abdul Hamood[4,5]

38. **A COMPLEMENTARY EAVESDROPPING HYPOTHESIS: ATTENTION TO HETEROSPECIFIC CUES IN SCIURID RODENTS**

Christopher A. Johnson[1]*, Kenneth A. Schmidt[1]

39. **DURING BACTEREMIA, *PSEUDOMONAS AERUGINOSA* ADAPTS BY ALTERING THE EXPRESSION OF NUMEROUS VIRULENCE GENES**

Kellsie Beasley[1]*, Nithya Mudaliar[2], Moamen Elmassry[3], Jane Colmer-Hamood[1,4], and Abdul Hamood[1,2]

40. **ENDOGENOUS STEROLS AND SPHINGOLIPIDS PROTECT *LEISHMANIA MAJOR* PLASMA MEMBRANE AGAINST MEMBRANE PERTURBING AGENTS, BACTERIAL TOXINS AND STARVATION**

Samrat Moitra[1]* and Kai Zhang[1]

41. **EFFECT OF SEASONAL SOIL TEMPERATURE ON THE BIOLOGICAL DEGRADATION OF ESTRONE AND TRICLOSAN MIXTURE BY SOIL MICROBIAL COMMUNITY.**

Ezinne Osuji[1]*, D.L. Carr[1]

42. **EVALUATING THE USE OF UAV-BASED REMOTE SENSING SYSTEM TO DETECT RANGELAND PLANT SPECIES IN THE TEXAS PANHANDLE**

Matthew R. Jackson[1]*, Carlos Portillo-Quintero[1], Robert D. Cox[1], Glen L. Ritchie[2]

43. **IS THERE SEXUAL DIMORPHISM IN THE ENDANGERED SHARPNOSE SHINER (*NOTROPIS OXYRHYNCHUS*)?**

Ryan R. Vazquez[1]*, and Gene Wilde[1]

44. **POPULATION DECLINES OF BREEDING SNOWY PLOVERS ON THE SOUTHERN GREAT PLAINS OF TEXAS, NEW MEXICO AND OKLAHOMA**

Kristen M. Heath*[1], Warren C. Conway[1], Clint W. Boal[2], Jeffrey S. Beauchamp[3], Glen Hensley[4], William P Johnson[5], Sarah T. Saalfeld[6]

45. **WEATHER PATTERNS AND VEGETATION STRUCTURE AFFECT SMALL MAMMAL ASSEMBLAGE STRUCTURE IN A LUBBOCK, TEXAS RANGELAND SITE**

Katelyn R. Vedolich[1]*, Kerry L. Griffis-Kyle[1]

46. **PHYTOREMEDIATION AND RESTORATION POTENTIAL OF RED AND BLUE BEAM LASER PHOTO STIMULATED ALFALFA (*MEDICAGO SATIVA L.*) PLANTS**

Bigyan Rimal[1], Meijun Dong[1], Deborah L. Carr[1]

DETAILED SCHEDULE OF EVENTS
ORAL SESSIONS AND AWARDS BANQUET
SATURDAY, APRIL 7th

Saturday, April 7th

7:30 am – 8:30 am	Registration and Breakfast, Helen DeVitt Jones Sculpture Court, Museum of Texas Tech University
8:00 am – 8:15 am	Welcoming by Dr. Lou Densmore, Graduate Advisor, Department of Biological Sciences, TTU
8:30 am – 10:00 am	Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium
10:00 am – 10:15 am	Coffee Break – Helen DeVitt Sculpture Court
10:15 am – 11:00 am	Oral Presentations – Kline Room, Green Room, Memorial Room, Helen DeVitt Jones Auditorium
11:00am – 12:00pm	Plenary Talk – Dr. Robert Williams, University of Tennessee – Auditorium
	"Experimental Precision Medicine Using GeneNetwork"
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, Clint Morgan, US Center for Disease Control and Prevention – Auditorium ***“Notes from the Field: Where Natural History Meets Public Health”***
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, Helen DeVitt Jones Sculpture Court, Museum of Texas Tech University

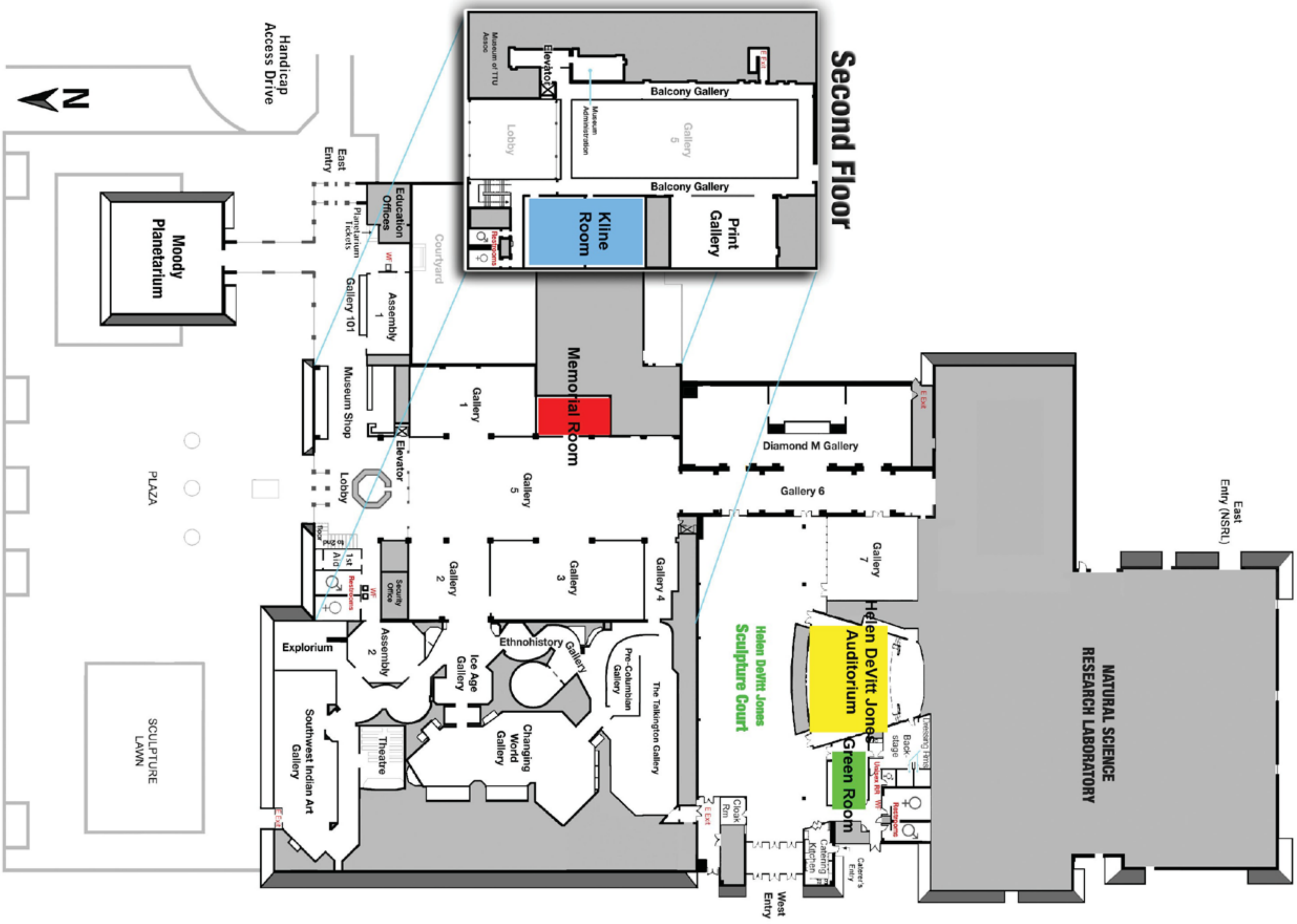
AWARDS BANQUET

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, Taylor Lenzmeier, TTUAB President
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, Dr. Mark Wallace, NRM Department Chair
- Shan L. Bilimoria Memorial Graduate Student Award, Bigyan Rimal, TechASM

8:45pm Closing Remarks

Museum of Texas Tech University Interior Map



	Wildlife & Fisheries Conservation (Auditorium)	Physiology & Evolutionary Biology (Green Room)	Undergraduate Orals (Kline Room)	Ecology & Environmental Biology (Memorial Room)
8:30 AM	**EFFECTS OF STREAMFLOW ON RECRUITMENT AND MIGRATION OF A LARGE CATOSTOMID IN CENTRAL TEXAS** Matthew R. Acre*[1], Timothy B. Grabowski[2], Dakus Geeslin[3], Allison Pease[4], Nate Smith[5], Daniel J. Leavitt[6]	**TAXONOMIC STATUS OF DIMINUTIVE FLATHEADTOADS OF THE GENUS *PELOPHRYNE* BARBOUR, 1938 (ANURA: BUFONIDAE) OF SUMATRA, INDONESIA REVEALED FROM MOLECULAR AND HABITAT NICHE MODELLING DATA** Goutam C Sarker[1]*, Amir Hamidy[2], Nia Kurniawan[3], Eric N. Smith[1]	**TESTING FOR SEXUAL DIMORPHISM WITHIN THE WHITE-LINED BROAD-NOSED BAT (*PLATYRRHINUS LINEATUS*)** Ashlyn N. Kildow[1]*, John D. Stuhler[1], and Richard D. Stevens[1,2]	**THE EFFECT OF WHISPER CALLS ON SETTLEMENT DECISIONS IN FEMALE VEERIES (*CATHARUS FUSCESCENS*)** William D. Fetzner[1]* and Kenneth A. Schmidt[1]
8:45 AM	**WINTER ACTIVITY PATTERNS OF BATS IN THE SOUTHEASTERN UNITED STATES** Brett R. Andersen[1]*, Richard D. Stevens[2], and Liam P. McGuire[1]	**INCOMPLETE LINEAGE SORTING OF THE TRANSPOSABLE ELEMENT AFROSINE IN THE FAMILY ELEPHANTIDAE** Laura Blanco-Berdugo[1]*, Neal Platt[2], and David Ray[1]	**EXPLORING THE ROLE OF SHY AND BOLD 'PERSONALITIES' IN SOCIAL DOMINANCE AND MATE CHOICE IN A PAIR BONDING FISH (AMATITLANIA SIQUIA)** Ashley M. Merkel[1]*	
9:00 AM	**EVALUATING SUITABLE HABITAT OF INVASIVE TILAPIA AND FORECASTING HOTSPOTS FOR POTENTIAL IMPACTS ON IMPERILED FISHES OF TEXAS** Elizabeth L. Roesler[1]* Monica McGarrity[2], & Matthew A. Barnes[1]	**LATE PLEISTOCENE MAMMALS AND BIRDS FROM MACY LOCALITY 100, SOUTHERN HIGH PLAINS, TEXAS** John A. Moretti[1]*	**DISTRIBUTION OF FELINE IMMUNODEFICIENCY VIRUS IN MAJOR CITIES OF TEXAS** Staci B. Nish[1]*, Julie A. Parlos[1]	**INDIRECT EFFECTS OF THE LANDSCAPE ON FRUIT PRODUCTION IN BAOBAB TREES OF KENYA** Macy A. Madden[1]*, Paul Webala[2], and Tigga Kingston[1]
9:15 AM	**ASSOCIATIONS BETWEEN THE RATIO OF ORGANIC TO INORGANIC NITROGEN AND GROWTH OF THE ICHTHYOTOXIC GOLDEN ALGA** Rakib H. Rashel[1]*, and Reynaldo Patiño[2]	**ALTERNATIVE MRNA SPLICING OF A GAMETE RECOGNITION PROTEIN, ZONADHESIN, MAY PROMOTE NEW FUNCTIONAL ADAPTATION IN MAMMALIAN REPRODUCTION** Emma K. Roberts[1]*, Emily A. Wright[1], Daniel M. Hardy[2], and Robert D. Bradley[1,3]	**HABITAT ASSOCIATIONS AND POPULATION ESTIMATES FOR THE TEXAS HORNED LIZARD (PHRYNOSOMA CORNUTUM) IN THE TEXAS PANHANDLE** Sara A. van der Leek[1]* and Andrew C. Kasner[1]	**DIVERSITY AND SPECIES RICHNESS OF FOREST INTERIOR INSECTIVOROUS BATS ALONG ELEVATIONAL GRADIENTS IN NIGERIA** Iroro Tanshi[1, 2]* and Tigga Kingston[1]
9:30 AM	**SPATIALLY EXPLICIT GENETIC ANALYSIS IS ESSENTIAL FOR GUIDING MANAGEMENT DECISIONS OF A THREATENED KANGAROO RAT** Michaela K. Halsey[1,2]*, John D. Stuhler[2], Roy N. Platt II[3], Travis C. Glenn[4], Robert D. Bradley[1,5], David A. Ray[1] and Richard D. Stevens[2,5]	**SEASONAL DYNAMICS OF CATABOLIC ENZYMES AND ENERGY STORES IN BRAZILIAN FREE-TAILED BATS** Elizabeth J. Rogers[1]*, Amie S. Sommers[1], and Liam P. McGuire[1]	**PREVALENCE AND INTENSITY OF ASPERGILLOSIS ON GORGONIA VENTALINA AND G. FLABELLUM ON THE MESOAMERICAN BARRIER REEF, ROATÁN, HONDURAS** Austin R. Biddy[1]*, Karla Resendiz[2], Traesha Robertson[3], Shannon Hill[2], Donna E. Hamilton[4], Stephanie M. Randell[2], and Stephanie A. Lockwood[1]	**CHARACTERIZING MICROBIAL COMMUNITIES IN LOWER RIO GRANDE FRESHWATER RESERVOIRS: DONNA LAKE AND IRRIGATION SYSTEM VERSUS DELTA LAKE AND EDINBURG NON-STERILE DEIONIZED WATER** A. Janiga[1]*, A. Racelis[1,2], E. Schunzel[2], C. Gabler[1], K. Lowe[2]
9:45 AM	**ASSESSING THE EFFICACY OF AND COMPARING MANUAL SEARCH AND LANDSCAPE CLASSIFICATION TO LOCATE WIND TURBINES USING SATELLITE IMAGERY** Katheryn A. Watson[1]*, and Clint W. Boal[2]	**COULD A FAILURE IN A POST-MATING ISOLATION PROTEIN ALLOW HYBRIDIZATION IN SPECIES OF DEER IN TEXAS?** Emily A. Wright[1]*, Emma K. Roberts[1], and Robert D. Bradley[1,2]		**TREE-LOVING VS TREE-HATING GRASSES: USING FIRE TO KILL ENEMIES** Xiulin Gao[1]* and Dylan W. Schwilk[1]
10:00 AM	COFFEE BREAK			

	Wildlife & Fisheries Conservation (Auditorium)	Toxicology (Green Room)	Genetics & Genomics (Kline Room)	Ecology & Environmental Biology (Memorial Room)
10:15 AM	**SEROPREVALENCE OF *NEOSPORA CANINUM* IN WILD PIGS (*SUS SCROFA*)** Katelyn M. Haydett[1]*, Steven T. Peper[1], Hannah S. Greenberg[1], Alexander N. Wilson-Fallon[1], Joshua A. Gaskamp[2], Stephen L. Webb[2], and Steven M. Presley[1]	**PREDICTING THE PROBABILITY OF CAPTURING FIVE MEDICALLY IMPORTANT MOSQUITO SPECIES IN LUBBOCK, TEXAS** Steven T. Peper[1]*, Katelyn M. Haydett[1], Hannah S. Greenberg[1], Alexander N. Wilson-Fallon[1], and Steven M. Presley[1]	**MAKING A *MYOTIS*: CONNECTING TRANSPOSONS AND MUTATIONS IN BATS** Nicole S. Paulat[1]*, Jennifer Korstian[1], Roy N. Platt[2], and David A. Ray[1]	**A TIME-SERIES STUDY OF SOIL MICROBIAL COMMUNITY COMPOSITIONAL AND FUNCTIONAL SHIFTS IN BIODIESEL VS. PETRODIESEL CONTAMINATED SOILS** Meijun Dong[1]*, Deborah L. Carr[1]
10:30 AM	**AN EVALUATION OF ABIOTIC AND BIOTIC HABITAT CHARACTERISTICS POTENTIALLY AFFECTING THE CURRENT DISTRIBUTION AND ABUNDANCE OF A RARE KANGAROO RAT** John D. Stuhler[1]*, Michaela K. Halsey[1,2], David A. Ray[2], Robert D. Bradley[2,3], R. Neal Platt[2], and Richard D. Stevens[1,3]	**METAL CONCENTRATIONS IN TISSUES FROM WILD AND CAPTIVE HAWAIIAN GREEN SEA TURTLES (*CHELONIA MYDAS*)** Katherine R. Shaw[1]*, Jennifer M. Lynch[2], Amanda D. French[1], George Balazs[3], T. Todd Jones[3], Jeff Pawloski[4], Marc Rice[5], David Klein[1]	**ASSESSING LEVELS OF DNA DEGRADATION IN FROZEN TISSUES ARCHIVED IN A NATURAL HISTORY COLLECTION** Taylor J. Soniat[1]*, Caleb D. Phillips[1,2], Kathy MacDonald[2], Jeremy Wilkinson[3], and Robert D. Bradley[1,2]	**TESTING PREDICTIONS OF OPTIMAL MIGRATION THEORY IN A SYSTEM OF MIGRATORY SILVER-HAIRED BATS** Jeff Clerc[1]*, Liam P. McGuire[1]
10:45 AM	**FLOW EFFECTS ON YOUNG-OF-YEAR GUADALUPE BASS** Heather M. Williams[1]*, Robin Verble-Pearson[2], Timothy B. Grabowski[3]	**RISK TO POLLINATORS POSED BY AGROCHEMICAL MIXTURES EMITTED FROM FEED YARDS** Eric M. Peterson* [1], Kimberly J. Wooten[1], Seenivasan Subbiah[1], Todd A. Anderson[1], Scott Longing[2], Philip N. Smith[1]	**DIGESTIVE EFFICIENCY AND GUT-MICROBIOME DYNAMICS THROUGHOUT REPRODUCTION IN THE MEXICAN FREE-TAILED BAT, *TADARIDA BRASILIENSIS*** Oscar Sandate[1]*, Matthew Fox[1], Gregory Knox[1], Marylin Mathew[1], Craig Tipton[1], Caleb Phillips[1,2]	**ANALYZING TEXAS AVIAN COMMUNITY STRUCTURE IN THE ERA OF URBANIZATION** Erin E. Bohlender[1]* and Richard D. Stevens[1,2]
11:00 AM	PLENARY TALK: ***"Experimintal Precision Medicine Using GeneNetwork"*** **by Dr. Robert Williams, The University of Tennessee, Auditorium**			
12:00pm	**Lunch (On your own)**			

	Microbiology & Medicine (Auditorium)	**Toxicology (Green Room)**	**Genetics & Genomics (Kline Room)**	**Ecology & Environmental Biology (Memorial Room)**
1:30 PM	**CHRONIC WOUND MICROBIOME COLONIZATION ON MOUSE MODEL FOLLOWING CRYOGENIC PRESERVATION** Craig D. Tipton[1]*, Nick Sanford[2], Jake Everett[3], Randall D. Wolcott[2], Kendra P. Rumbaugh[3], and Caleb D. Phillips[1,4]	**NEUROBEHAVIORAL TOXICITY STUDY OF *ENVIRONMENTALLY* RELEVANT CONCENTRATIONS OF FUNGICIDES USING AN EMBRYO- LARVAL ZEBRAFISH (*DANIO RERIO*) AS A MODEL** Naveen Kumar[1]*, Jordan Crago[1]	**TRANSPOSABLE ELEMENTS AND LINEAGE SORTING WITHIN THE GENUS *MYOTIS*** Jennifer M. Korstian[1]*, Roy N. Platt II[1], David A. Ray[1]	**SPECIES DISTRIBUTION MODELING OF POTENTIAL ZIKA VIRUS VECTORS, *AEDES AEGYPTI* AND *AEDES ALBOPICTUS*, MOSQUITOES** Hannah S. Greenberg[1]*, Alexander N. Wilson-Fallon[1], Steven T. Peper[1], Katelyn M. Haydett[1], Steven M. Presley[1], Guofeng Cao[2]
1:45 PM	**MALONATE-UTILIZATION OPERON CONTRIBUTES TO THE VIRULENCE OF *PSEUDOMONAS AERUGINOSA*** Moamen Elmassry[1]*, Jane Colmer-Hamood[2,3], Michael San Francisco[1,4], John Griswold[5], Sharmila Dissanaike[5], and Abdul Hamood[2,5]	**SEDIMENT BACTERIAL CCOMMUNITY STRUCTURES AT A NATIONAL PRIORITIES LIST SITE, THE CALLAHAN MINE SITE, AS COMPARED TO A CLEAN REFERENCE SITE** Kelsey N Thompson[1]*, Caitlin N Ryan[1], Jeremy E Wilkinson[1,2], Caleb D Phillips[3] and Gregory D Mayer[1]	**NOVEL METHOD FOR TRANSPOSABLE ELEMENT ANNOTATION ACROSS MULTIPLE TAXA** Austin B. Osmanski[1]*, Roy N. Platt II[1], Llewellyn D. Densmore III[1], Jaime Gongora[2], David A. Ray[1]	
	Microbiology & Medicine (Auditorium)	**Molecular Biology & Biochemistry (Green Room)**	**Proposal (Kline Room)**	
2:00 PM	**CHOLINE BRANCH OF KENNEDY PATHWAY PLAYS CRUCIAL ROLE DURING THE SANDFLY STAGE OF *LEISHMANIA MAJOR*** Samrat Moitra[1]*, Mattie Pawlowic[2], Fong-Fu Hsu[3], and Kai Zhang[1]	**ANALYSIS OF CUSTOM MICROARRAY DATASET FOR DISCOVERY OF DROUGHT STRESS RESPONSES AND BREEDING FOR WATER USE EFFICIENCY IN *SORGHUM BICOLOR*** Heshani De Silva Weligodage[1]*, Fangyuan Zhang[2], Manoj Samanta[3], Zhanguo Xin[4], and Chris Rock[1]	**ELUCIDATING POLYMICROBIAL INTERACTIONS THROUGH A NEW HI-C TECHNIQUE** Bravada M. Hill[1]* and Amanda M.V. Brown[1]	
2:15 PM	**ANALYSIS OF SECRETED COMPOUNDS FROM *BATRACHOCHYTRIUM DENDROBATIDIS* FOR ANTI-MICROBIAL AND ANTI-NEMATODE ACTIVITY** Amanda M. Starr[1]*and Michael J. San Francisco[1]	**CLONING OF *wi1*, *Wi2*, *Wi3* and *Wi4* MUTANTS OF MAIZE BY BULK-SEGREGANT WHOLE GENOME SEQUENCING** Anuradha Dhingra[1]* and Chris Rock[1]		
2:30 PM		**CONTINUING STUDIES ON THE INFLUENCE OF PSYCHOLOGICAL AND PHYSIOLOGICAL STRESSORS AND THE VISUAL RESPONSE TO FOOD: ANALYSIS OF SALIVARY ALPHA AMYLASE** Songhe Li[1]*, James A Carr[1]		
2:45 PM		**LOSS OF TESTOSTERONE CAUSES MALE INFERTILITY BY DISRUPTING SPERMATOGENESIS** Arpita Talapatra*[1], Dibyendu Dutta[2], Samuel Sang[3] and Nathaniel Mills[1]		
3:00 PM	PLENARY TALK: ***“Notes from the Field: Where Natural History Meets Public Health”*** **by Clint Morgan, US Center for Disease Control and Prevention, Auditorium**			

ABSTRACTS

UNDERGRADUATE POSTERS

1. BATS: WHO'S RELATED TO WHOM?

Nicole Paulat[1], Zach Nguyen[1]*, and David Ray[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

Transposable elements (TEs) are genetic components that can be used as markers for a multitude of applications. They are generally considered homoplasy-free and easy to genotype. Short interspersed elements (SINEs) TEs that are useful to study the relationships and population genetics because they are small in size, are numerous, and have a wide distribution. The Mobile Element Locator Tool (MELT) is a software package that discovers, annotates, and genotypes TE insertions. The data generated can be used quickly and accurately to infer phylogenetic trees that illustrate evolutionary relationships. However, the inferred polymorphisms are just that, inferred, and must be validated using experimental means. The experimental method to validate the insertions consists of using Polymerase Chain Reaction (PCR) to physically view the polymorphism of transposable elements on an electrophoresis gel. From the absence or presence of those elements, phylogenetic trees can be confirmed via experimental data created. I am using the output from MELT to validate ~50 inferred SINE insertions in the bat genus *Myotis*. The resulting tree will be used to map genetic traits and identify the evolutionary history of those traits and help future researchers interpret genomic data within the context of a clear set of interspecies relationships.

2. FISH ASSEMBLAGES ON THE MESOAMERICAN BARRIER REEF IN ROATAN, HONDURAS

Scheila R. Corujo[1,2]*, Karla J. Ramos[2], R'Shel D. Pacheco[2], Donna E. Hamilton[3], Shannon K. Hill[2], Traesha Robertson[4], Stephanie M. Randell[2], Stephanie A. Lockwood[1]
[1]Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas
[2]McLennan Community College, Waco, Texas
[3]University of North Texas - Dallas, Dallas, Texas
[4]University of Coastal Georgia, Brunswick, Georgia

Composition of fish assemblages is recognized as an indicator of ecosystem health, habitat degradation, and ecosystem productivity. Fish community structure has been associated with coral coverage and diversity. Recent events, such as ocean warming, have caused extensive coral bleaching, resulting in a loss of habitat for fish and ultimately reduced fish abundance. This study was conducted to assess fish assemblages on the Mesoamerican Barrier Reef in Roatán, Honduras. The standard Roving Diver Technique was used to locate fish assemblages at two depths, 9.14 m and 15.24 m, across five dive sites. Fish communities were characterized for species presence and abundance and each dive site was sampled twice. The Kruskal-Wallis was used to determine the statistical significance between the two depths. The Shannon-Weiner index of diversity was used to measure the diversity between the two depths and the dive sites. Non-metric multidimensional scaling was used to look at how species composition varies by depth and dive site. We found no significant differences in species richness between the two depths surveyed ($p = 0.93$); there was also no significant difference between the study sites ($p = 0.06$). Bear's Den had the lowest species diversity out of all the sites, and Fish Den had the highest species diversity. Fish Den and Pillar Coral each have a unique species composition which differ in comparison, to the other sites. This study provides a baseline description of reef fish community structure. Future studies can use these results to measure changes in community structure over time.

3. CORRELATION BETWEEN BRAIN AMYLOID BETA CONCENTRATION AND SHORT-TERM MEMORY DEFICITS IN APPSWE/PS1DE9 TRANSGENIC MICE

Rebekah F. Salinas[1]*, Breanna N. Harris[1], Paul L. Soto[2]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
[2]Department of Psychology, Louisiana State University, Baton Rouge, Louisiana 70803

Alzheimer's disease (AD), the most prevalent age-related neurodegenerative disorder, is marked by amyloid beta build-up, neuronal death, and progressive memory loss. One approach to identification of therapeutic interventions for AD-associated cognitive decline is to validate a measurement of cognitive decline over time in an animal model of AD-associated neuropathology, which could be used to evaluate potential therapeutic strategies. The purpose of this study is to assess age-related memory deficits in a mouse model of AD amyloid beta neuropathology (APPswe/PS1dE9 mice) and to determine if brain levels of amyloid beta correlate with short-term memory performance. We are using an automated operant delayed-matching-to-position (DMTP) task and animals are tested from ~16 to 74 weeks of age. Following completion of the DMTP assessments, at 77 weeks of age, brain (cortex and hippocampus) amyloid beta 40 and 42 levels of all mice will be determined. We predict that transgenic mice, vs. their non-transgenic littermates, will develop memory deficits with increasing age, and that brain amyloid beta concentrations will be negatively correlated with DMTP performance. Our findings so far show that transgenic mice begin to develop memory deficits following long, but not short, delays in the DMTP task between 40-50 weeks (9-11 months) of age (n = 4-10 tg and 3-8 non-tg). Brain amyloid beta analyses will begin this summer. This study will allow us to evaluate the utility of automated methods for assessing cognitive decline that could be used for screening of experimental therapies.

4. INVESTIGATION OF MUTATED CONE GENES AND THEIR AFFECT ON VISION

LaTorian C. King[1]* and Julie A. Parlos[1]
[1]Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas 76708

Cones are photoreceptors that are involved in photopic vision. There are three well-known types of cones, commonly found among vertebrates, that detect light at different wavelengths (short, medium, and long). The phototransduction cascade is the process by which cones respond to light, and the cyclic nucleotide-gated (CNG) cation channel is a component of this cascade. Two alpha and two beta subunits comprise the CNG channel for the cones, which are coded by CNGA3 and CNGB3 respectively. There have been 82 CNGA3 mutations identified that lead to amino acid changes and, thus, altered vision. It has been suggested that CNGA3 peptides are evolutionarily conserved and have a low tolerance for amino acid variation. Previous research found mutations in CNGA3 can lead to reduced protein expression and loss of function, loss of interaction between the subunits, changes in the ion permeation pathway, or interference of the pore helix rotation during gating. The sequences for wild-type CNGA3 in *Homo sapiens* and *Mus musculus*, as well as mutated CNGA3 in *Canis lupus familiaris*, were retrieved from GenBank. These sequences will be translated, and the 3D

protein structures will be evaluated. Previous studies indicate that a CNGA3 mutation will lead to varying degrees of color blindness; therefore, we expect to observe altered 3D structures that correlate with the CNGA3 gene variations. We expect our results will aid in the comprehension of how vision can be affected by mutated protein-coding genes for cones.

5. EVALUATION OF THE BREAST EPITHELIAL CELL LINE EPH4-EV AS A NON-TUMORIGENIC CONTROL TO THE 4T1 TUMORIGENIC BREAST CANCER CELL LINE

Alana K. Quackenbush[1]*, Makayla Nicholson[1], Gary O. Gray[1], Adam J. Reinhart[1]
[1]Wayland Baptist University, Plainview TX 79072

Previous studies in our laboratory have utilized the widely used 4T1 murine breast cancer cell line to investigate cytotoxic and apoptotic effects of anti-inflammatory plant extracts and specific molecules isolated from these extracts. Although we have found numerous potential chemotherapeutic agents from plant extracts, these studies suffer from a lack specificity. The most effective chemotherapeutic agents would exhibit a higher degree of cytotoxicity or induce apoptosis in cancer cells but not their non-tumorigenic counterparts. In this study, we have used the non-tumorigenic EpH4-Ev cell line. EpH4-Ev cells are an immortalized, but non-tumorigenic murine breast epithelial cell line we tested for suitability as our “normal” control. We compared cytotoxic and apoptotic effects of various plant extracts on EpH4-Ev and 4T1 cells to determine if some plant extracts preferentially killed 4T1 cancer cells as opposed to a EpH4-Ev cell line. We found that some plant extracts were more cytotoxic to 4T1 cells than to EpH4-Ev cells, and some exhibited no difference. Additionally, we found through western blot analysis, that ginger extracts caused 4T1 cells, but not EpH4-Ev cells to activate Caspase-3 suggesting apoptosis was induced. Our conclusion is that the EpH4-Ev cell line is a valuable control cell line for comparison to 4T1 cells. In the future, we will be able to focus our research on molecular constituents of plants which are more cytotoxic to 4T1 tumor cells than the non-tumorigenic EpH4-Ev cell line.

6. SEA FAN ABUNDANCE AND FREQUENCY OF *MILLEPORA ALCICORNIS* ON THE MESOAMERICAN BARRIER REEF IN ROATAN, HONDURAS

Sarah F. Cole[1,2*], Shirley R. Stewart[2], Donna E. Hamilton[3], Traesha Robertson[4], Shannon K. Hill[2], Stephanie M. Randell[2], Stephanie A. Lockwood[1]
[1]Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas
[2]McLennan Community College, Waco, Texas
[3]University of North Texas-Dallas, Dallas, Texas
[4]University of Coastal Georgia, Brunswick, Georgia

Millepora spp. (fire coral), Sea Fans, Sea Rods, and Sea plumes make-up an abundant part of the Mesoamerican Barrier Reef system in Roatan, Honduras. Recent studies suggest that fire coral tend to parasitize octocorals and over take a vast majority of the reef. This study was conducted to assess the parasitism of *Millepora alcicornis* (fire coral) on *Gorgonia ventalina* (Caribbean Sea Fan) off the Mesoamerican Barrier Reef in comparison to other studies in the Caribbean. This study was conducted off the coast of Roatan, Honduras from May 15, 2017 through May 19, 2017. The Randell - Robertson Marine Survey Technique (RRMST) was used to observe and record sea fans, sea rods, and sea plums starting at forty feet and ending at fifteen feet. Data was recorded for healthy sea fans, or sea fans with lesions, purpling, necrosis, or parasitizing *Millepora*. If *Millepora* was present the height of the soft coral would be recorded, along with the distance to nearby fire coral. The Kruskal- Wallis Rank Sum Test was used to statistically analyze the collected data, which was followed up by Dunn's Post Hoc Test to analyze the health status of the coral forms. Through observation and data collection on the field *Millepora* spp. were more frequently associated with Caribbean Sea Fan than the sea rod or plume. Statistical analysis suggest that *Millepora* parasitized healthy sea fans compared to sea fans with lesions, purpling, or necrosis. Future studies should continue to include all three soft corals, indicate which *Millepora* spp. was present, and us a dye to determine the direction of the current.

7. ASSESSING THE GENETIC DIVERSIFICATION OF BATS IN THE GENUS *MONOPHYLLUS*

Irene Vasquez[1]*, Laramie L. Lindsey[1], Julie A. Parlos[2], Robert J. Baker[1,3], Robert D. Bradley[1,3], Hugh H. Genoways[4]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX
[2]Department of Biological Sciences, TTU Biology at Waco, Waco, TX
[3]Natural Science Research Laboratory, Museum of Texas Tech University, Lubbock, TX
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The genus *Monophyllus*, the Antillean long-tongued bats, is distributed throughout the Greater Antilles and Lesser Antilles in the Caribbean. *Monophyllus* is comprised of two species, *M. plethodon* and *M. redmani*. Based on prior knowledge (morphological data and preliminary molecular data), we hypothesize that as currently recognized, *M. redmani* can be split into more than one species based on the genetic species concept. The hypothesis was tested by evaluating molecular data generated from the mitochondrial cytochrome-*b* gene, *Cyt*b (1,140 bp). The species, *Glossophaga soricina*, was used as an outgroup. Thirty-three samples were collected from almost all subspecies of both *M. plethodon* and *M. redmani*. Tissues were obtained through the NSRL (Natural Science Research Laboratory) at Texas Tech University. Preliminary results show that *M. plethodon* and *M. redmani* are genetically divergent species with K2P values at 11.9%. The presence of genetically divergent clades within *M. redmani* suggest the possibility that multiple taxa should be recognized.

8. A GENETIC ASSESSEMENT OF POCKET GOPHERS OF THE GENUS *GEOMYS* (RODENTIA: GEOMYIDAE) IN TEXAS

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Pocket gophers (Family Geomyidae) are fossorial rodents that occur throughout the Great Plains of North America. Three genera occur in Texas (*Cratogeomys*, *Geomys*, and *Thomomys*); of these, *Geomys* occupy the largest geographic area in the state. The similar fossorial lifestyles of *Geomys* results in a similar morphological appearance, and in some cases, they are considered to be cryptic species. Consequently, the number of recognized species within the genus *Geomys* has varied (Chambers et al. 2009; Hall 1981; Jolley et al. 2000; Merriam 1895; Patton 1993; Sudman et al. 2006). Of the 12 currently recognized species of *Geomys* (Sudman et al. 2006), nine species are known to occur in Texas (*G. arenarius*, *G. attwateri*, *G. breviceps*, *G. bursarius*, *G. jugossicularis*, *G. knoxjonesi*, *G. personatus*, *G.*

streckeri, and *G. texensis).* Further, 15 subspecies are recognized in Texas, as well as two additional junior synonyms. Several of these subspecies are known only from small isolated populations and the current taxonomy, phylogenetic relationships, and genetic identities are unknown. To address these issues, it is crucial to determine a genetic haplotype that can be assigned to each nominant subspecific name. Therefore, we collected topotype samples from each of the 21 type localities. We obtained DNA sequences from the mitochondrial cytochrome-b (*cyt*b) gene of each subspecies in order to establish the magnitude the genetic divergence between subspecies and within each currently recognized species.

9. THE STRUCTURE AND SYMMETRY OF WHISPER CALLS IN VEERIES (*CATHARUS FUSCESCENS*)

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Songbirds use song to both attract mates and repel rivals, and the acoustic features within these songs can be indicative of a male's quality; however, research on how features of other acoustic signals (i.e. calls) may be indicative of male quality remains unexplored. Whisper calls are low amplitude vocalizations used by Veeries (*Catharus fuscescens*) during agonistic interactions and are attractive to females. Whisper calls are structurally unique signals, characterized by many frequency modulations and large-range frequency sweeps. These two structural components may be related to a motor constraint where only high-quality males are able to produce both high frequency and long bandwidth modulations (Podos 1997). Veeries produce two voices, one with each side of the syrinx, during a whisper call, and the ability of a male to produce symmetrical voices (frequency and temporally) may be an indicator of male quality. To determine if any patterns exist in the structural features of whisper calls, I analyzed 36 whisper calls sampled from 14 males using Raven Pro 1.5 software. For each modulation, I measured the change in frequency, the duration, the time between each crest, and compared these features between voices and across individuals. I have found that there are three types of whisper calls, and that each type varies in the symmetry between voices. This study is the first to analyze structural features of low amplitude vocalizations, and will lay the groundwork for future studies to investigate the relationship between these structural features and male quality.

10. AMERICAN KESTREL BREEDING SEASON PREY USE AND DELIVERY RATES IN THE LLANO ESTACADO OF TEXAS

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American kestrels (Falco sparverius) are a secondary cavity nesting species of falcon with a wide distribution across North America. In 2011 we initiated a program to study kestrel ecology in the region with 30 nest boxes placed in short/mixed grass prairies in Lubbock County. Due to the lack of studies on prey use by the species, one line of research is to assess how population dynamics could be influenced by regional dietary habits. We placed cameras at 4 nest boxes each year in 2016 and 2017 to study kestrel prey use and delivery rates during the breeding season. Results show the average prey delivery rates/hour for the week 1 out of 4 measured 0.84/hr and 0.96/nestling/hour, with a substantial increase by the 4th week being 2.65/hr and 0.57/nestlings/hr. The number of identified prey for the breeding season diet was dominated by reptiles (71.3%). Prairie racerunners and common spotted whiptails (Aspidoscelis sexlineata viridis and Aspidoscelis gularis) accounted for 38.3% and Texas horned lizards (Phrynosoma cornutum) accounted for 13.0% of prey deliveries. Mammalian (5.4%), avian (2.3%), and invertebrate (21.0%) prey were difficult to identify beyond genus, family, and order, respectively, but a minimum of 30 different prey species were identified. Prey as large as juvenile cottontail (Sylvilagus floridanus) and cotton rat (Sigmodon hispidus) were identified. Analysis is ongoing, and we will provide a completed analysis for breeding season prey use of kestrels in Lubbock county, with comparison to data from other regions.

11. SWAINSON'S HAWK RISK OF ENCOUNTERING WIND TURBINES ON MIGRATION ROUTE

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Swainson's hawks have the second longest migration of raptors in North America, travelling more than 10,000 km to winter in Argentina. Wind turbines are becoming prominent in North American grasslands and kill an estimated 140,000 to 328,000 birds each year. Due to their home range and migration route, Swainson's hawks are likely to encounter wind turbines while traveling to and from South America. It is unknown if migrating Swainson's hawks face mortality risk from wind turbines. Our objective is to estimate risk during migration for this species. We collected migration data by attaching GPS transmitters to 24 Swainson's hawks. We used location data to construct an estimated migration pathway with a 50 km buffer. We downloaded Sentinel-2 satellite images with a 10 m spatial resolution that occurred in the migration pathway. We visually located wind turbines using ArcMap and Google Earth. We added buffers to turbine points to estimate area of potential risk of birds encountering wind turbines at 100 m (high risk), 1.5 km (moderate risk), and 3 km (low risk). We examined bird locations to estimate the proportion of points within buffers to draw conclusions about risk during migration. Preliminary results suggest Swainson's hawks were at low risk of encountering wind turbines 16.8% of the time, at moderate risk 16.1%, and were at high risk 0.4% of the time. Swainson's hawks may be capable of avoiding wind turbines during migration, but as the wind energy industry expands in their pathway, risk is likely to increase for this species.

12. BEHAVIORAL RESPONSE TO PREDATOR ODOR IN A TRANSGENIC MOUSE MODEL OF ALZHEIMER'S DISEASE

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Alzheimer's disease (AD) is the 6th leading cause of death in the US and is primarily characterized by three physiological factors: amyloid beta (AB) plaques, neurofibrillary tangles, and overall neuronal loss in the brain. Additionally, environmental and emotional factors, like stress and anxiety, are thought to play a role in AD severity and progression. For example, in aged, non-demented humans, anxiety is associated with increased Aβ deposition before

cognitive deficits appear. Additionally, in individuals with AD, those with concurrent anxiety progress more rapidly. Thus, anxiety may be an important precursor to or exacerbator of AD. Previous research using a transgenic (tg) mouse model of AD amyloidosis (APPswe/PS1dE9) has shown elevated anxiety-like behaviors in tg mice between 4-6 months of age, but anxiety in this transgenic model has not been characterized in aged individuals. Here, we will test the hypothesis that compared to non-tg mice, aged (77 weeks) tg mice will display greater anxiety-like behavior (digging, rearing, and freezing) during exposure to predator odor, and that this response will be positively correlated to levels of two stress-responsive hormones (corticosterone and ghrelin) and with brain levels of AB. These data allow us to investigate the relationship between anxiety-like behavior and hormone levels and how those impact brain AB levels in individual mice, and we can examine the influence of environmental factors, like stress and anxiety, on behavior, hormones, and AB load in an animal model of AD.

13. CYTOTOXICITY OF *CINNAMON VERUM* (CINNAMON) AND *SALVIA OFFICINALIS* (SAGE) IN 4T1 BREAST CANCER CELLS

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Ethanolic extracts of 27 medicinal plants were tested to determine their cytotoxic effects on the 4T1 murine breast cancer cell line. The cytotoxic effects of these crude extracts were measured using CellTiter-Glo luminescent cell viability assays. Ethanolic extracts of *Cinnamomum verum* (Cinnamon) and *Salvia officinalis* (Sage) were found to be cytotoxic to the 4T1 breast cancer cells as compared to a control epithelial cell line (EpH4-Ev). Work is ongoing to purify the cytotoxic components of these plants and the mechanism(s) by which these components induce 4T1 breast cancer cell death.

14. EFFECTS OF ACUTE STRESS ON SHORT-TERM MEMORY AND ATTENTION IN A MOUSE MODEL OF AMYLOID-BETA NEUROPATHOLOGY IN ALZHEIMER'S DISEASE

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Alzheimer's disease (AD) is associated with dysregulation of the hypothalamic-pituitary-adrenal axis, which is responsible for the release and regulation of glucocorticoids such as cortisol (humans) or corticosterone (rodents). Stress and chronically increased cortisol levels are associated with changes in memory-related brain structures and increased dementia progression. In the ongoing study, short-term memory and attention of aged non-transgenic (non-Tg) and transgenic (Tg) APPswe/PS1dE9 mice, a mouse model of amyloidosis, are evaluated using a delayed match-to-position task (DMTP) or a 3-choice serial-reaction time task (3CSRTT). Correct responses produce delivery of a food pellet. Incorrect responses (responses on the non-presented lever or in the non-illuminated hole) and failures to respond (omissions) produce a 10-s timeout followed by a new trial. In the 3CSRTT, responses prior to illumination of the light (premature) and responses during the timeout period or after food pellet delivery (perseverative) are also measured. Our mice perform only one type of behavioral task (either DMTP or 3CSRTT) and are trained and tested from ~16 to 74 weeks of age. In weeks

73 and 74, mice are exposed to predator odor or a forced swim trial immediately prior to their respective behavioral task. Preliminary data (n = 15 Tg and 24 non-Tg mice) show no reliable differences among Tg vs. non-Tg mice or stress vs. non-stress sessions. We will continue to collect data as other mice reach 73-weeks of age. By understanding how stress modulates disease progression, we may be able to identify novel treatment approaches.

15. A COMPARISON OF ORGAN WEIGHTS IN TRANSGENIC AND NON-TRANSGENIC APPswe/PS1dE9 MICE, A MODEL OF ALZHEIMER'S DISEASE-RELATED AMYLOIDOSIS

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Alzheimer's disease is strongly associated with the development of amyloid beta (Aβ) aggregates and inflammation in the brain, but recent evidence indicates Aβ accumulates in other organs before neural changes are noted. Thus, organs other than those in the CNS can be altered by Alzheimer's pathology. Aβ aggregates are often considered to be one of the main culprits of neural inflammation; Aβ may also have similar effects on other organs. Specifically, recent data from humans suggests Aβ can deposit in the liver and kidneys before accumulating in the brain. Previous work in an Alzheimer's mouse model found that hemibrains of 18-month-old transgenic mice show Aβ concentrations of 90-140 nmol, which translates to ~0.005g of Aβ, suggesting Aβ deposits can contribute to measurable differences in organ mass. To date, no one has looked at organ mass differences between transgenic and non-transgenic mice from the APPswe/PS1dE9 Alzheimer's model strain. In this study, we compared adrenal, kidney, thymus, and spleen masses between 18-month-old male and female transgenic (tg) mice and their non-tg littermates. We chose three immune-associated organs, the thymus, spleen, and adrenals, and one Aβ processing and clearance organ, the kidneys. We predict that due to presence of Aβ deposition (kidneys) and associated inflammation (thymus, spleen, adrenals), transgenic mice will have higher body-mass-corrected organ masses than non-transgenic mice. If our predictions are valid, this would further corroborate the notion that organs outside of the CNS can be altered by Alzheimer's pathology and would expand our understanding of Alzheimer's disease-related pathology.

16. SPECIES RICHNESS AND WINTER HABITAT ASSOCIATIONS OF SPARROWS (PASSERIFORMES: EMBERIZIDAE) IN AN AGRICULTURAL LANDSCAPE OF THE SOUTHERN HIGH PLAINS, TEXAS

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We conducted winter (Dec 2017-Feb 2018) sparrow counts at forty roadside points in a row crop agriculture dominated landscape in Floyd County, Texas to determine species richness, abundance, and habitat associations. Points were evenly distributed between irrigated and dryland sites, and we recorded point-level habitat variables (composition and height of vegetation) along field edges and distance of points to playa lake bottoms using ArcGIS. A total of four sparrow species was observed, and the mean number of sparrows was not different between dryland and irrigated sites. Point-level habitat variables did not explain variability in sparrow numbers among points; however, the total number of sparrows at points was negatively correlated (r = -0.402, p=0.01) with the distance of the points to the nearest playa lake bottom (most playas were dry). Ten sparrow species were captured using mist nets and banded with USGS aluminum bands in a wooded canyon site in Floyd County from Nov 2017-Feb 2018, increasing observed sparrow richness to a total of 12 species for the study.

17. A METHODOLOGICAL COMPARISON OF THE LINE TRANSECT AND THE RANDELL-ROBERTSON MARINE SURVEY TECHNIQUE

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This comparison study was the first step in the validation of the RRMST using the LT method as the reference. Researchers predicted RRMST would be equally successful in the observation of coral species and disease coverage. This study was conducted in Roatan, Honduras from May 15-19, 2017 along the Mesoamerican Reef. Five dive sites were surveyed twice using RRMST and LT method. A higher total frequency of the coral species was observed using RRMST rather than LT. There was a significantly more diseased *Stephanocoenia intersepta* and *Orbicella annularis* observed when utilizing RRMST. Data collection showed LT exhibited a higher standard error of frequency of diseased proportion over RRMST indicating those data had a higher variability. RRMST indicated a higher average proportion of diseased coral for most species and found more diseased *Siderastrea radians* individuals than the LT method. This pilot study was the first step in the validation of RRMST. The results of this study suggested an improved likelihood of locating healthy and diseased coral when applying RRMST. In future studies, researchers should standardize the depth and distance between the two protocols to help further validate the RRMST.

18. SPECIES DISTRIBUTION MODEL OF COPPERHEADS *(AGKISTRODON CONTORTRIX)*

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Copperheads (*Agkistrodon contortrix)* are a species of North American pit viper that are found from New England to northern Mexico. Within the state of Texas, they occupy a diverse assortment of habitats including desert, forest and grassland. Species distribution models (SDMs) are useful in predicting which areas are conducive to habitation by a given species. However, previous species distribution modelling efforts for copperheads within the state of Texas have used a small number of data points (25 – 41), and failed to include the westernmost portion of their range. We estimated the distribution of copperheads within Texas using maximum entropy modelling (MaxEnt) based on 19 bioclimatic variables obtained from BioClim at ~ 1km^2 resolution and 489 geolocations obtained from iNaturalist. We have generated a more robust species distribution model for Texas copperheads, which we believe may better reflect the distribution of this species.

19. TEXAS TECH UNIVERSITY HERPETOLOGY SURVEY

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Surveys of native fauna help to determine biodiversity and the impact that human activity has on the environment. Texas Tech University owns several properties in Lubbock that vary in levels of human activity. We have surveyed the herpetofauna of several of these properties to determine the composition and richness of native reptile and amphibian species, and whether human activity has had an impact. We hypothesized that areas with high human activity and little natural land cover, such as the main campus, would have lower species richness and a different species composition than more natural areas with less human activity, such as Lubbock Lake Landmark. Presented here are the results of this ongoing survey. So far, no herpetofauna have been found on the main campus which suggests that a lack of natural land cover and high levels of human activity (e.g., foot traffic, car traffic, building maintenance) do have an effect on species richness. Likewise, Great Plains species (such as *Thamnophis marcianus*, *Plestiodon obsoletus*, and *Ambystoma mavortium)* have been found on properties with natural land cover and low levels of human activity. Moving forward we will continue to survey properties owned by TTU to determine species composition, establish presence of various herpetofauna, and defining landscape features that correlate with a higher species richness.

20. POLYMICROBIAL INTERACTIONS AFFECT ANTIBIOTIC SUSCEPTIBILITY

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Biofilm-associated infections, such as chronic wounds, are notoriously difficult to treat and cause high rates of morbidity and mortality in a large patient population in the United States annually. Biofilms harbor bacteria encased in a self-produced extracellular matrix that acts as a mechanical barrier, leading to significantly altered concentrations of antimicrobials to eradicate them compared to their planktonic (free-living) counterparts, which is extensively demonstrated in the literature. Another significant complication of biofilm-associated infections is that they exist in a polymicrobial state, caused by numerous species of bacteria, and there is evidence in the research literature that polymicrobial interactions also alter the effectiveness of antimicrobials. We have chosen four organisms commonly found in combination in chronic wound infections, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Enterococcus faecalis*, and *Acinetobacter baumanii*, and we will determine their antimicrobial susceptibility individually and in combination. Using methodologies currently employed in the clinical diagnostic setting, we hypothesize that these polymicrobial interactions significantly affect antimicrobial susceptibility.

21. POLYMICROBIAL INTERACTIONS AFFECT POPULATION DYNAMICS

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Chronic wound infections cause high rates of morbidity and mortality in a large patient population and are responsible for a huge medical cost burden in the United States annually.

Chronic wounds commonly harbor polymicrobial biofilms, and there is evidence suggesting that some combinations of microbes result in infections that are more aggressive. Our group has previously examined the interspecies interaction between two common wound pathogens, *Pseudomonas aeruginosa* (PA) and *Staphylococcus aureus* (SA), and it has been demonstrated that the wound environment significant affects how these two organisms interact compared to standard laboratory media. We seek to further this research by including additional common chronic wound pathogens *Enterococcus faecalis* (EF) and *Acinetobacter baumanii* (AB) to assess their contribution to interspecies interactions in the wound environment. In pilot studies conducted, we have demonstrated that both the wound environment and the combination of organisms used have a significant impact on population dynamics. We seek to further elucidate these factors, with the overarching goal of elucidating the mechanisms involved that allow the wound environment to promote polymicrobial infections.

22. ASSOCIATION OF BORING ORGANISMS WITH DARK SPOT SYNDROME IN ROATAN, HONDURAS

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Coral disease outbreaks have occurred since the 1970s and contribute to coral decline. Dark Spot Syndrome (DSS) was first observed in the Caribbean near Columbia during the late 1990s and causes lesions of brown, purple, or black on coral tissues. The primary coral species affected with DSS in the Caribbean are: *Siderastrea siderea*, *Siderastrea radians*, and *Stephanocoenia intersepta.* The cause and impact of DSS throughout the Caribbean has not yet been determined. Many studies have indicated that a widespread decline in overall coral health has caused a global increase in the prevalence of boring sponges. This study was conducted to assess the association of DSS with boring organisms in Roatan, Honduras. Five established dive sites were surveyed twice from May 13-21, 2017. As each of the affected corals species were observed, coral identification, DSS status, depth, presence and identification of boring organisms was recorded. In addition, an open quadrat was place over each coral and a photo taken which was later used in Image J to assess coral and DSS area, as well as boring sponge coverage. No significant difference in coral health status was observed based on the presence of sponges, the area of sponge coverage, coral area, water depth, or dive site. Proportion of all coral species with disease varied significantly across coral size, water depth, and site. Future research should investigate water chemistry, dive traffic, and proximity to features which could affect reef health and susceptibility to disease such as the island landfill and golf course.

GRADUATE POSTERS

23. THE HISTORY OF WEST NILE VIRUS AND MOSQUITO SURVEILLANCE IN LUBBOCK COUNTY, TEXAS

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West Nile virus (WNV) is a zoonotic pathogen and the causative agent of West Nile fever and the more severe West Nile neurological disease. Globally dispersed it was first detected in the United States in 1999. WNV was first reported in Texas in 2002, reaching Lubbock County in 2003. Since 2003 the Vector-Borne and Zoonoses Laboratory at Texas Tech University has conducted a WNV vector surveillance program to detect the yearly presence in local mosquito populations to aid the local vector control program with their abatement efforts. Here we report the historical human cases reported within Lubbock County and the mosquito positive results from the vector surveillance program between the years 2009 to 2017. Ideally, this poster will help bring awareness to the local community of the constant threat of West Nile virus and the need to be cautious when it comes to contact with mosquitoes, especially during the yearly peak infection seasons.

24. PREVALENCE OF CANINE HEARTWORM IN POTENTIAL MOSQUITO VECTOR POPULATIONS IN LUBBOCK, TEXAS, USA (2010-2016)

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Canine heartworm is a vector-borne disease that is globally distributed, re-emerging, and considered the most important parasite affecting dogs. The etiological agent of this zoonotic disease is *Dirofilaria immitis*, a parasitic roundworm that elicits vascular damage upon infestation of the heart. *D. immitis* third-stage larva (L3) are passed from an infected mosquito to a new host during disease transmission. *Aedes vexans*, *Culex tarsalis*, and *Culex quinquefasciatus* are some of the competent mosquito-vectors of this filarial disease, as well as West Nile virus (WNV). As part of an on-going WNV surveillance program in Lubbock, Texas, over 41,000 of these mosquito species were captured using Encephalitis Vector Survey CO_2-baited traps. Mosquitoes were then identified, pooled by species and collection site, and tested for the presence of Flavivirus spp. and WNV through use of reverse transcriptase polymerase chain reaction (RT-PCR). From this surveillance database, the RNA isolates of these pooled species are available to be tested for the L3 stage of *D. immitis* to determine the prevalence of canine heartworm in the City of Lubbock. Through this multi-surveillance approach, research will assist in creating an alternative method of canine heartworm surveillance that will allow for a more representative assessment of filarial disease in mosquito-vectors.

25. OPTIMIZATION OF MECHANICAL TESTING PARAMETERS OF PVA NANOFIBROUS MEMBRANES

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In order to discover the relationship between the mechanical properties and testing parameters of PVA electrospun nanofibrous membranes, the tensile properties of PVA nanofiber membranes were measured with 3 different parameters: gauge length, cross-head speed and membrane thickness. The tensile properties including results of extension at break (mm), Young's modulus (Mpa), maximum load (N), tensile stress at maximum load (Mpa), tenacity at break (gf/tex), and energy at break(J) were recorded and analyzed by polynomial regression, and contour plot and optimization analysis were employed to evaluate the effect of testing parameters on the tensile properties of membranes. According to the analysis of results, the optimal tensile testing parameters are: gauge length of 5 mm, cross-head speed of 5 mm/◌◌min, membrane thickness of 0.02 mm, and the parameters of significance in the effect on mechanical properties from maximum to minimum are: membrane thickness, cross-head speed and then gauge length. The R^2 of polynomial regression equations for membrane mechanical properties is about 0.7.

26. FUNCTIONAL TIO2/PVDF NANOFIBER WEBS FOR RHB PHOTOCATALYTIC

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Visible light photocatalytic electrospun PVDF/TiO_2 nanofiber webs were produced in this study and their photocatalytic properties for the degradation of rhodamine B (RhB) aqueous solution were studied. Atomic force microscope (AFM), optical micrographs, water contact angle, fourier-transform infrared spectroscopy (FTIR), and UV-vis spectrophotometer spectrum were employed to study the morphology, structure, hydrophobicity, infrared spectrum, and optical properties of PVDF/TiO_2 nanofiber webs. The mechanical properties, the mechanism of fracture and RhB degradation of nanofiber webs were also studied. PVDF/TiO_2 nanofiber webs with a TiO_2 concentration of 20% were demonstrated to have best photocatalytic activity under visible light irradiation. This study may open a new opportunity to evaluate the catalytic properties of PVDF/TiO_2 nanofiber webs under low-energy visible light circumstance (simulated sunlight).

27. COMPARATIVE STUDY OF POLYSTYRENE AND POLYETHYLENE DEGRADATION BY INSECT LARVAE

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In recent years, microbial plastic degradation has become a huge area of interest. Currently, plastic disposal occurs by recycling, conversion to a different product or chemical degradation. Until recently, polyethylene (PE) required certain chemical additives to make it degradable. To find a prudent way to deal with this challenge, researchers have concentrated their efforts on bioremediation as a solution. Yang et al. (2014) showed that polyethylene was degraded by gut microbial community of *Plodia interpunctella* (larvae of Indianmeal moths). While the gut microbiota of these larvae might possess plastic degrading capabilities, the degradation process itself is unclear. The types of microorganisms involved and any changes in their abundances during PE degradation, is still unknown. We recently completed the metagenomic study of polystyrene (PS) degradation by *Tenebrio molitor* (larvae of the Mealworm beetle).

We showed the native gut microbial community of *Tenebrio* to degrade polystyrene without much change to its community composition. However, there were certain changes seen in microbial abundances. The current study reports on metagenomic diversity and identification of major gut microbial species present in *Plodia* fed with Polyethylene only, compared to *Plodia* fed a normal diet of bran. Microbial DNA extracted from these larvae was sequenced by targeting the v3 and v4 regions of 16S rRNA. Qiime and Usearch analysis pipelines helped identify the microbial species along with statistical tests to determine any significant changes in abundances. Results from this study contribute to understanding of the functionality of this mixed community that enables it to degrade PE successfully.

28. HUMAN *VS.* NATURE: ISLANDS AND BRIDGES WITHIN THE MICROBIOME CONTINUUM

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The completion of the Human Genome Project led to the recognition that many human phenotypes, including variation in disease susceptibility and drug response, cannot be merely explained by human genetic variations. Thus, the Human Microbiome Project (HMP) was initiated to investigate the contribution of human-associated microbes to human phenotypic variations. Meanwhile, rapid advances and cost reduction of sequencing technologies led to the rapid accumulation of metagenomic and 16S rRNA data from different habitats, aiming at exploring the biodiversity of almost every samplable ecosystem. Although most of these data were published and interpreted separately, re-examining them in a holistic way may lead to new insights about microbial ecology. Here, we reanalyzed 16S microbiome sequences from 1,689 samples, representing 17 ecosystems, aiming to examine overlaps and correlations between different environments. PCoA was used for clustering different samples according to their UniFrac distances. We observed a growing microbiome continuum, in which no ecosystem (or human body site) is fully separated from others, but with samples rather spreading to overlap and span multiple clusters. Nasal microbiotas were the most diverse, ranging from a majority clustering with skin samples to a few with similarities to oral and gut samples. Overall, human-associated microbiomes were quite distinct from plant and environmental microbiomes. Interestingly, aerosol microbiomes clearly bridged both worlds. In conclusion, we observed a “microbiome continuum” with two large separate clusters (human associated and environmental) bridged by aerosol microbiomes. We expect that the accumulation of future samples may continue to fill the gaps in this continuum.

29. SALINITY ADAPTATION IN GOLDEN ALGA

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Golden alga (*Prymnesium parvum*) is a toxin-producing, euryhaline species responsible for fish-kills worldwide. Although thought to have originated in high salinity habitats, *P. parvum* abundance in US inland waters and its growth potential in the laboratory show a biphasic relationship to salinity, with peak abundance at ~10–15 psu. It is unclear, however, if *P. parvum* growth can adapt to (compensate for) long-term exposure to high salinity. This information is necessary to understand the spatial distribution of golden alga blooms and especially their absence from Texas coastal habitats. A Texas strain of *P. parvum* maintained for ~3 years at 5 psu (inland-level salinity) in modified Artificial Seawater (ASW) was subjected to the following treatments over 5 continuous batch cultures: ASW at 5 psu (ASW-5 psu), ASW-30 psu, ASW with gradually-increasing salinity to 30 psu (5-psu/batch), and Instant Ocean® (IO)-30 psu. Treatments were conducted in triplicate and each replicate served as inoculum (taken during late-exponential growth) for subsequent cultures. Cell density was measured every 3 days and exponential growth rate (*r*) and maximum density were determined. Growth rate was reduced when salinity directly increased from 5 to 30 psu in ASW but compensation occurred during the second culture. Gradual adjustment did not influence this outcome–inhibition was still observed during the fifth cycle when ASW salinity increased from 25 to 30 psu. Inhibition of maximum density was consistently observed in ASW-30 psu after direct transfer or gradual adjustment. Growth rate and maximum density in IO-30 psu were generally similar to observations in ASW-5 psu. In conclusion, adaptation to high salinity in ASW was observed for *r* but not maximum density, and relatively complex salt mixtures (e.g., IO) can compensate for the inhibitory effects of increased salinity. Findings may give insight on *P. parvum*'s ability to disperse into new environments.

30. TO COMBINE CRISPR/CAS9 GENOME EDITING, NANO-TECH AND CHEMICAL GENETICS TOWARD IN VIVO PROTEIN KINASE ANALYSIS

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The project is combining nanotechnology, CRISPR/Cas9 genome editing and the Shokat chemical genetics to develop an important but never-been-accomplished approach for studying cellular signaling – in vivo tagging, identification, and quantification of protein kinase substrates. By studying Akt1 and Akt2, we are answering a hitherto impossible question – whether the two prominent kinases have different spectrums of substrates. This will help to understand the functional differences between the two closely related kinases in development, diabetics, and cancer metastasis. Since the HCT116 colorectal cancer cells are well documented to be highly metastatic, our results will directly address the functional difference of the two kinases in metastasis, currently a puzzle in cancer biology. More importantly, the approach will be readily applied to other important protein kinases and opens up tremendous new investigative opportunities in cellular signaling in both healthy and diseased cells. In summary, a new paradigm will be established for studying protein kinases and cellular signaling.

31. ESTABLISHMENT OF NATIVE WOODY SPECIES IN DEGRADED TROPICAL DRY FORESTS IN THE CABO ROJO NATIONAL WILDLIFE REFUGE, BOQUERÓN, PUERTO RICO.

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Tropical dry forests have been experiencing shifts in their community compositions due to altered disturbance regimes, non-native species introductions and changes in global climate patterns. The affected ecosystems can then shift into novel ecosystems that have degraded community structure, species composition and species diversity. To determine if restoration of such degraded habitats into more native dominated settings is plausible we set up the following study. We focused on analyzing the effect shade might have on the establishment of native woody species transplants into the USFWS Cabo Rojo National Wildlife Refuge in Boquerón, Puerto Rico. For this, plants for which there is limited ecological knowledge were chosen to be planted in plots under 2 treatments: sunlit and shaded plots. Plants were observed for a period of 2 years. Results showed that shaded plots had higher survivorship of transplants. Species identity was also important, with individuals of *Guaiacum officiale* having the highest survivorship (90% ± 0.63). These results, expand the number of native species that can be used for passive restoration. An additional consideration can be the addition of water at critical stages, which can mitigate the effects of drought and transplant shock and provide greater success in future restoration projects.

32. STATUS, DISTRIBUTION, MORPHOLOGY AND GENETICS OF *SIGMODON FULVIVENTER DALQUESTI* IN THE CHIHUAHUAN DESERT ECOREGION

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The tawny-ellied cotton rat, *Sigmodon fulviventer dalquesti*, is a Texas endemic subspecies reported only from a single sampling near Fort Davis in 1991 (Stangl 1992a). The current population, distribution and evolutionary origin of *S. f. dalquesti* is enigmatic (Schmidly et al. 2016). The Texas Parks and Wildlife Department's Texas Conservation Action Plan designates *S. f. dalquesti* as critically imperiled within the state. Additionally, the relationship between *S. f. dalquesti* and other *S. fulviventer* subspecies in Mexico, Arizona, and New Mexico is not well understood. The current state of knowledge of *S. f. dalquesti* systematics consists of morphological distinction from *S. f. minimus* (New Mexican form) (Stangl 1992b), and a finding of mitochondrial cytochrome *b* divergence between *S. f. dalquesti* and *S. f. fulviventer* (Mexican form) roughly equivalent to 100,000 years of divergence (Peppers et al. 2002). To inform an accurate conservation assessment, a more complete understanding of *S. f. dalquesti* biology is required. We will conduct morphological and molecular phylogenetic analyses of the recognized *S. fulviventer* subspecies using existing specimens available in museum collections, as well as specimens obtained in planned field work. We will assess the population and distribution of *S. f. dalquesti* in the Chihuahuan Desert Ecoregion by Sherman Trap sampling transects in areas of the original detection in addition to other localities. Lastly, we will use niche modeling to predict *S. f. dalquesti* distribution. These efforts will improve our understanding of *S. f. dalquesti* biology, and inform future conservation management decisions.

33. PHYLOGEOGRAPHY OF ARENAVIRUSES (ARENAVIRIDAE) ASSOCIATED WITH NORTH AMERICAN WOODRAT SPECIES, *NEOTOMA*

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The genus *Arenavirus* is comprised of Old World species (lymphocytic choriomeningitis-Lassa serocomplex) and New World species (Tacaribe serocomplex). Members of the Cricetid family of rodents are the main hosts of many Tacaribe serocomplex viruses. Furthermore, many Tacaribe viruses have been described with *Neotoma* species as their principal hosts. Among the arenaviruses described in North America, 9 were isolated from members of the rodent genus *Neotoma*. For example, the Whitewater Arroyo virus (WWAV) was first isolated from *Neotoma albigula*, and Catarina virus (CTNV) was isolated from *Neotoma micropus* from southern Texas. For this study, we sequenced the cytochrome b (*Cyt*b) gene from each *Neotoma* host sample that was used in the arenavirus study, as well as samples that tested negative for arenaviruses. A phylogenetic tree was generated to depict the relationships of *Neotoma* species included in the study. ArcGIS was used to develop maps of localities of the *Neotoma* species to determine if geography and phylogenetic relationships play a role in the evolution of arenaviruses found in the genus *Neotoma*.

34. EXPLORATION OF POTENTIAL PYOMELANIN MEDIATED POLYMICROBIAL COOPERATION

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Cystic fibrosis (CF) is a genetic disease associated with chronic lung infections, and it is mediated by a microbe-harboring mucus buildup. *Pseudomonas aeruginosa* is an opportunistic human pathogen commonly associated with CF infection. *P. aeruginosa* evolution within the CF lung often selects for the production of a secreted brown pigment known as pyomelanin, which is thought to combat the oxidative stress produced by the host immune system. Because pyomelanin is a secreted pigment, we hypothesize that this compound could represent a community resource benefitting surrounding microbes within the polymicrobial infections of the CF lung. In particular, we sought to assess the impact of pyomelanin production on the survival of *Staphylococcus aureus*, another common CF pathogen often found in chronic infections containing *P. aeruginosa*. Surprisingly, when we cultured pyomelanin-producing strains of *P. aeruginosa* with *S. aureus* we observed an induction of pyomelanin production, further suggesting the possibility of pigment-mediated cooperation. This phenomenon was quantified via a spot plate co-culture assay combined with a colorimetric analysis using ImageJ software, which revealed that the presence of *S. aureus* induces pyomelanin production in a titratable manner. Our future directions will monitor the impact of this increased pyomelanin production on the survival of both *P. aeruginosa* and *S. aureus* in the presence of oxidative stress. Finally, we seek to identify the mechanism behind *S. aureus*-induced pyomelanin production in an effort to identify drug targets disrupting microbial cooperation at the host-pathogen interface.

35. IMPACT OF TEMPERATURE DEPENDENT GLOBAL REGULATION OF BIOFILM FORMATION IN *PSEUDOMONAS AERUGINOSA*

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Biofilms are surface-associated groups of microorganisms that adhere and interact with each other using an extracellular polymeric substance matrix. Microorganisms have developed complex mechanisms to sense and react to their constantly changing environment under these conditions. One key regulatory cue for them is temperature. Studies have shown that different factors, such as temperature, can cause behavioral and morphological change in the biofilm communities. *Pseudomonas aeruginosa* is a common nosocomial gram-negative bacterium, that can cause various serious diseases in infected humans. The severity of the infections is compounded by *P.* aeruginosa's advanced antibiotic resistance mechanisms and its ability to form robust biofilms. The objective of this project is to elucidate the genes involved in the temperature regulation of biofilm formation of *P*. *aeruginosa*. For this purpose, a biofilm screen was run on a commercially-available transposon mutant library of *P. aeruginosa* at four different temperatures (room temperature, 30ºC, 37ºC, and 40ºC) to identify genes required for temperature-dependent biofilm formation. This temperature range was chosen to simulate conditions relevant to both medical and industrial settings.

36. SPERM GRANULOMA ASSOCIATED PATHOLOGY IS DEPENDENT ON TESTOSTERONE ACTION IN ADULT RAT EPIDIDYMIS

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Spermatic granuloma development in the epididymis is a concern following vasectomy or chemical insults causing abdominal and scrotal pain due to inflammation. To investigate the pathology of spermatic granulomas and their relationship with testosterone, we treated adult rats with a Leydig cell-specific toxicant ethylene dimethane sulfonate (EDS) to eliminate testosterone. At seven days post-EDS, disrupted epididymal epithelium and spermatic granulomas were observed in the caput. The spermatic granuloma and caput were collagen-filled indicating fibrosis. Numerous round apoptotic cells (TUNEL) were localized inside the caput lumen and dispersed through the spermatic granuloma. *Tnp1* (round spermatid marker) was significantly higher in the epididymis of EDS-treated groups compared to controls suggesting the apoptotic cells were round spermatids. Increases in CD68 macrophages and T cells (CD4 and CD8) support an inflammatory immune infiltration in post-EDS epididymis were found. However, testosterone replacement following EDS prevented the spermatic granuloma-associated pathology. We suggest that the immune response in the spermatic granuloma may be due to the increased numbers of apoptotic round spermatids or other testicular tissue components that may be released, in addition to regression of epididymal epithelium with testosterone loss. Thus, testosterone replacement prevents EDS-induced spermatic granuloma and ameliorates spermatic granuloma-associated pathology.

37. THE NOVEL ANTIMICROBIAL AGENT NEXT SCIENCE INFLUENCES THE WOUND

HEALING PROCESS

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Chronic wounds, which include pressure ulcers and diabetic foot ulcers, affect approximately 6.5 million persons with a high annual cost for treatment. We recently showed that Next Science (NS) wound gel, a novel antimicrobial agent, inhibits bacterial infection of chronic wounds. NS may also promote wound healing by influencing the host immune response. Using the murine model of wound infection, we examined the influence of NS on wound healing. Full-thickness wounds were generated and covered with sterile gauze (untreated wound, UTW), gauze coated with polyethylene glycol base (PEG-treated wound, PTW), or gauze coated with NS gel (NS-treated wound, NSTW). The wound bed and margins were excised at 1, 3, and 7 days post-wounding. Formalin-fixed tissues were processed and sectioned at 5.0 µm. The sections were stained with H&E for general histological observations. On day 1 post-injury, a neutrophilic infiltrate (PMNs) was present throughout the wound beds in all three treatment groups with a larger number of PMNs observed in the PTW and NSTW. By day 3, reepithelialization had begun at the margins of all three treatment groups. The UTW had a thin sanguineous crust with few PMNs visible except directly under the crust. Both the PTW and NSTW had much thicker sanguineous crusts with many more PMNs present under the crusts and at the wound margins; neovascularization was present in the wound beds. On day 7, reepithelialization had advanced in all three wounds and granulation tissue was present. Neovascularization was now present in the UTW, while healed tissue in the PTW and NSTW showed regeneration of hair follicles. A mononuclear infiltrate was move evident in the NSTW along with evidence of scar formation (fibrosis). These results suggest that keeping the wound moist (PTW and NSTW) appears to accelerate healing while the treatment with NS furthered the healing process.

38. A COMPLEMENTARY EAVESDROPPING HYPOTHESIS: ATTENTION TO HETEROSPECIFIC CUES IN SCIURID RODENTS

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Individuals incorporate information from both conspecifics and heterospecifics to reduce uncertainty of their environment1–5. Because individuals of different species perceive their world differently6,7, heterospecific vocalizations may encode additional, non-redundant information8, or instill improved certainty through greater sample size2,5. Thus, sampling this complementary information from both con- and heterospecifics would be expected to provide a greater fitness benefit than sampling either, alone. I aim to assess the influence of complimentary information on the behavior of sciurid rodents in a manipulated soundscape. Sciurid rodents have been shown to attend to heterospecific vocalizations9,10. Experimental trials will be conducted at the Cary Institute of Ecosystem Studies in Millbrook, New York. From May-August 2018, four audio playback treatments, including predator alarm vocalizations of eastern chipmunk (*Tamias striatus*), tufted titmouse (*Baeolophus bicolor*), a combination of the two, and an ovenbird (*Seiurus aurocapilla*) song control, will be broadcast to free ranging rodents across two sites (closed canopy forest and open canopy edge) to assess for

complementarity in information resulting from the informant species. Further, complementarity within spatial context will be assessed by arranging these playback combinations into two height treatments. Giving-up density and time-lapsed video will be used to passively measure foraging efficiency and vigilant behavior. Variation in food density, and changes in vigilance, reflect variation in foraging costs from perceived risk of predation11. Thus, increases in giving-up density and/or visual scanning behavior would indicate changes in perceived risk resulting from complementarity of information due to informant and/or spatial context of the information.

39. DURING BACTEREMIA, *PSEUDOMONAS AERUGINOSA* ADAPTS BY ALTERING THE EXPRESSION OF NUMEROUS VIRULENCE GENES

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Pseudomonas aeruginosa is a Gram-negative opportunistic pathogen that causes serious infections in immunocompromised hosts including severely burned patients. After multiplying within the burn wound, *P. aeruginosa* translocate into the bloodstream causing sepsis and septic shock. While previous studies analyzed the influence of infection sites on *P. aeruginosa* virulence, little is known regarding the effect of blood during systemic infection. We hypothesize that human blood significantly alters the expression of *P. aeruginosa* genes. To address this, we used RNA-seq analysis to compare the global expression of the *P. aeruginosa* strain PAO1 that was grown to an early logarithmic phase in either a laboratory medium (Luria Bertani broth, LB) or whole blood from healthy volunteers. Compared with LB broth, the growth of PAO1 in whole blood significantly ($q < 0.05$) altered the expression of 769 genes. Among the genes whose expression was significantly reduced are the quorum sensing (QS) genes, including the phenazine operons that encode the virulence factor pyocyanin. These results showed on average a 218-fold significant decrease in the expression of the phenazine biosynthesis genes in the presence of blood. We confirmed these results using qRT-PCR. To determine if the effect resides within the serum fraction, we grew PAO1 to a late stationary phase in LB broth or LB containing 10% commercially-available pooled adult human serum. Samples were collected every 2 h and the level of expression of selected genes was determined using qRT-PCR. At early log phase, serum significantly repressed the expression of different QS genes, including the phenazine operons. However, at late logarithmic and early stationary phases, serum significantly enhanced the expression of these genes. These results suggest that during sepsis, and depending on the stage of growth, serum differentially influences the expression of different *P. aeruginosa* virulence and virulence-related genes.

40. ENDOGENOUS STEROLS AND SPHINGOLIPIDS PROTECT *LEISHMANIA MAJOR* PLASMA MEMBRANE AGAINST MEMBRANE PERTURBING AGENTS, BACTERIAL TOXINS AND STARVATION

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Leishmania promastigotes reside in the sandfly midgut where they are exposed to a number of stressors including from 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. Endogenous sterols and sphingolipids are crucial in maintaining membrane integrity, forming lipid rafts and mediating vesicular trafficking. We hypothesize that ergosterol and sphingolipids protect *Leishmania* against membrane perturbation, certain bacterial toxins and help them adapt to starvation and osmolality change in sandfly midgut. To understand the role of these lipids in sandfly stage, we investigated the sensitivity of ergosterol and sphingolipid mutants against membrane perturbation agents, sandfly midgut relevant microbiota toxins and also osmotic stress. Our findings suggest that alteration of endogenous ergosterol and sphingolipids makes *Leishmania* more hypersensitive and susceptible to membrane perturbation, certain bacterial toxins, nutrient starvation along with osmotic stress encountered in sandfly midgut, thereby affecting transmission.

41. EFFECT OF SEASONAL SOIL TEMPERATURE ON THE BIOLOGICAL DEGRADATION OF ESTRONE AND TRICLOSAN MIXTURE BY SOIL MICROBIAL COMMUNITY.

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Pharmaceutical and personal care products (PPCPs) are often not completely removed by the process of waste treatment plant. PPCPs associated with land farming of municipal wastewater effluent may potentially persist as mixtures in the soil and alter soil microbial community processes. The microbial community in the soil environment is responsible for many activities relating to decontamination of the soil environment through natural attenuation or bioremediation, when it is exposed to anthropogenic contamination. The soil microbial community composition and physiology and the influence they have in decomposition and nutrient availability is affected by soil temperature. Soil with a long history of exposure to these compounds through wastewater effluent was examined at different seasons (summer and winter) to evaluate the effect of seasonality on the biological degradation of estrone and triclosan. The soil samples were spiked with estrone, triclosan, and a 1:1 mixture of estrone: triclosan and incubated for 90 days at room temperature. Control samples consisting of unspiked soil were included in the analysis to account for contaminate effects vs. seasonal effects. The community level physiological profile was examined using BIOLOG® EcoPlates™ for the ability of their microflora to utilize ecologically relevant carbon sources. Substrate activity (SA) and substrate richness (SR) was determined from this analysis. Microbial degradation rates were compared over the 90 days incubation period using high performance liquid chromatography (HPLC) and half-lives of each compound from the different soil conditions determined. Soil microbial community composition is affected by seasonal temperature changes, which thus affects the rate of degradation.

42. EVALUATING THE USE OF UAV-BASED REMOTE SENSING SYSTEM TO DETECT RANGELAND PLANT SPECIES IN THE TEXAS PANHANDLE

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Modern rangeland management in the Texas Panhandle is using new technology to help monitor plants and track wildlife. Recent technology in the fields of remote sensing, UAVs (Unmanned Aerial Vehicles), and data processing has given land managers more efficient ways of evaluating rangeland health and diversity. We are using a Phantom 3 Professional UAV paired with a Parrot Sequoia multispectral camera to capture true color and infrared imagery of the Texas Tech Native Rangeland. Flights have been flown monthly since April 2017 to test the seasonal impact of detecting plant species at the site. Each month, flights were conducted at altitudes of 30, 60, and 100 meters to test the impact of spatial resolution on detection as well. Recent innovations in supervised classification techniques in ArcGIS are being tested to determine the viability of detecting distinct plant species. Using Image Segmentation with Random Trees and Machine Learning classifiers, we expect to be able to map distinct species across the site. Our study is focusing on Honey mesquite (*Prosopis glandulosa*) and non-native Yellow Bluestem (*Bothriochloa ischaemum*). Having the ability to detect and quantify unique species on rangelands can lead to more effective management techniques that will benefit native shortgrass prairies in the Texas Panhandle.

43. IS THERE SEXUAL DIMORPHISM IN THE ENDANGERED SHARPNOSE SHINER (*NOTROPIS OXYRHYNCHUS*)?

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North American cyprinids can exhibit sexual dimorphism is different ways such as differences in size or dichromatism. Determining sexual dimorphism of Great Plains cyprinids can be quite useful for possible field identification and can be a powerful tool for their conservation. At present, there are very few studies on the determination of sexually dimorphic external traits for many Great Plains cyprinids; therefore, I propose to catalog different measurements for an endangered Great Plains cyprinid, the Sharpnose Shiner (*Notropis oxyrhynchus*), and determine if there are external features that are sexually dimorphic. To do this, mature specimens were collected from the upper basin of the Brazos River. Individuals were photographed and key external character measurements were compared to assess whether it might be possible to visually identify the two sexes in the field. Discovery of sexual dimorphism in the Sharpnose Shiner could potentially serve as an asset to conservation managers and could be useful for use in captive breeding of the species.

44. POPULATION DECLINES OF BREEDING SNOWY PLOVERS ON THE SOUTHERN GREAT PLAINS OF TEXAS, NEW MEXICO AND OKLAHOMA

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Snowy plover (*Charadriius nivosus*) population declines are generally considered to be perpetuated by habitat degradation throughout their North American range. Because of this, snowy plovers along the Pacific coast are listed as federally threatened, and state endangered in Washington and Mississippi. Although less studied, interior populations of snowy plovers have also declined due to human disturbance, high predation rates, declining groundwater, stochastic weather events and potential heavy metal contamination. According to surveys conducted in 2007 - 2009, breeding snowy plover populations at saline lakes on the Southern High Plains of Texas experienced a ~75% population decline in the preceding decade. To reassess the long-term trends of these potentially vulnerable populations, we conducted weekly surveys of the same private saline lakes (designated A, B and C) during summer 2017, following Saalfeld et al. 2013. Preliminary analyses suggest that plovers have declined significantly in the last decade at Lake B ($P >0.05$), and remained steady at Lakes A and C ($P>0.05$). Surveys at Bitter Lake National Wildlife Refuge (NWR) in New Mexico indicate long term declines across the Southern Great Plains region ($P < 0.05$). However, annual surveys at Salt Plains NWR in Oklahoma suggest that plover numbers on the refuge have remained steady over the last decade ($P > 0.05$), ranging between 3000-5200 individuals during May surveys. Long term declines of breeding snowy plovers in the Texas and New Mexico portions of the Southern High Plains indicate that regional persistence may only be maintained by plovers occurring at Salt Plains NWR.

45. WEATHER PATTERNS AND VEGETATION STRUCTURE AFFECT SMALL MAMMAL ASSEMBLAGE STRUCTURE IN A LUBBOCK, TEXAS RANGELAND SITE

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Population modeling informs us of predictors that influence the responses of small mammal assemblages to environments experiencing an increasingly variable climate. Small mammal capture-recapture data was systematically collected annually from 2010 to 2017 across 35 trapping locations throughout the isolated Texas Tech University native rangeland site. We assessed capture success with abiotic and biotic variables to better understand population dynamics seen across time. We evaluated ambient temperature, aspects of rainfall, nighttime illumination, and percent cover of vegetation functional groups. Weather, and in particular rainfall of the previous season, exhibits the strongest relationship with capture success likely because rain stimulates growth and reproduction in plants which provide food for small mammals. Using Akaike's Information Criterion, we applied information theory to evaluate biologically determined models and use model averaging to determine the relative importance of these predictors to small mammal population dynamics. The results will prompt the design of further small mammal surveys which may inform us of how changes in the environment through time affect the structure and interaction of the community as a whole.

46. PHYTOREMEDIATION AND RESTORATION POTENTIAL OF RED AND BLUE BEAM LASER PHOTO STIMULATED ALFALFA (*MEDICAGO SATIVA L.*) PLANTS

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Alfalfa possesses important characteristics for phytoremediation that includes fast growth, high biomass, and extensive tap root with a robust rhizosphere system. We conducted a greenhouse experiment to observe the phytoremediation and restoration potential of alfalfa grown in sandy loam soil contaminated by diesel (2% w/w) and weathered for 180 days. Nine replicates for both laser stimulated, and non-stimulated plants were maintained in cone-tainers. The effect of laser photo stimulation on alfalfa germination, biomass yield and diesel degradation were measured for 7 weeks. Destructive sampling of the plants and soil was done at day 0, 21, 35, 42 and 49 for quantification of remaining diesel, plant growth and biomass and microbial community diversity in rhizosphere region. No significant difference was observed in germination rate between laser stimulated and non-stimulated seeds. Dry root, shoot and overall biomass yield was significantly higher in laser stimulated cones. Lateral root development was significantly enhanced in laser stimulated plants.

ORAL (UNDERGRADUATE)

47. EXPLORING THE ROLE OF SHY AND BOLD ‘PERSONALITIES’ IN SOCIAL DOMINANCE AND MATE CHOICE IN A PAIR BONDING FISH (AMATITLANIA SIQUIA)

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The behaviors of pair-bonding fish were examined to determine how individual social status and mating preferences might be related to exploratory boldness (‘personality’) in males and females. Convict cichlids (*Amatitlania siquia*) exhibit individual differences in exploratory boldness and also establish dominance relationships in groups. The project encompassed two experiments; for the first, individuals were video recorded to determine “personality type” (bold or shy) and then placed in size-matched, same-sex groups to assess social dominance status (N=10 per sex). For the second experiment, individuals were screened for personality type and offered as potential mates; for male-choice tests, two size-matched females with opposing levels of boldness were placed with a male (N=8). The same procedure was repeated but with sexes reversed to examine female choice (N=8). Exploratory boldness may predict social status in a group setting in both males and females, with bolder individuals typically being dominant.

48. TESTING FOR SEXUAL DIMORPHISM WITHIN THE WHITE-LINED BROAD-NOSED BAT (*PLATYRRHINUS LINEATUS*)

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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 within 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 characters (i.e., eight cranial, six dental, and two mandibular) and

fourteen external characters for 94 adult bats collected from two sites in eastern Paraguay (Reserva Natural del Bosque Mbaracayú and Yaguareté Forests). Measurements were made to the nearest 0.01 mm using digital calipers. Results from a MANOVA did not indicate any significant differences in cranial characters between males and females or between the two sites. However, we found significant differences between males and females, but not between sites, for external characters. Importantly, these differences manifested in seven of the fourteen external characters, with females consistently larger. Because adult females were generally larger than males, it is possible that these differences are related to differential costs between sexes related to reproduction and rearing offspring.

49. DISTRIBUTION OF FELINE IMMUNODEFICIENCY VIRUS IN MAJOR CITIES OF TEXAS

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Feline Immunodeficiency Virus (FIV) is a common virus among domestic cats. This virus attacks and weakens the immune system, which can increase the number of diseases carried by an infected cat. Data will be collected from non-profit clinics, rescues, and shelters to map the distribution of cats that tested positive for the virus in select major cities of Texas. The data will be analyzed to evaluate whether correlations exist between sterilized (spayed or neutered) cats versus intact, and owned versus feral. We expect higher concentrations of infected cats in large cities where there are large feral cat populations. We also expect the number of infected male cats to be higher than infected female cats as the main transmission of FIV is from cats fighting and males are more aggressive and likely to engage in fights than females. Feline Immunodeficiency Virus is very similar to Human Immunodeficiency Virus (HIV) in how it weakens the host’s immune system. Because these two viruses are similar in nature, we expect that FIV research can be used to study and understand more about HIV. The objective of this research is its application to community outreach, public education, and to spread awareness. This project is intended to encourage pet owners to have their cats tested for FIV, which will contribute to controlling the spread of the virus.

50. HABITAT ASSOCIATIONS AND POPULATION ESTIMATES FOR THE TEXAS HORNED LIZARD (*PHRYNOSOMA CORNUTUM*) IN THE TEXAS PANHANDLE

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This study was conducted July-Oct 2017 using transects and area searches to locate Texas horned lizards in Hale and Floyd counties, Texas. Lizards were captured and morphological and habitat measurements were taken. PIT tags were inserted subcutaneously in lizards with SVL>40mm. A total of 33 lizards were documented on three separate research properties. Of those, 14 were PIT tagged, 16 were <40mm, 2 were encounter only (not captured), and 1 lizard was being predated by *Heterodon nasicus*. There were no recaptures of marked lizards this year, thus the high-end population estimate is 32 lizards, including hatchlings (SVL<40mm). The low-end population estimate is 26 and excludes hatchlings that could not be identified as individuals. There was no significant difference in habitat variables between male and female locations. Hatchling locations contained a higher percentage of grass (U=63.00, p<0.05) and bare ground (*U*=50.50, *p*<0.01) cover when compared to juveniles/adults. Random locations had a higher percent grass cover (*U*=239.50, *p*<0.001), lower percent bare cover (*U*=945.00, *p*<0.001), and had taller vegetation cover (*U*=140.00, *p*<0.001) than lizards' locations.

51. PREVALENCE AND INTENSITY OF ASPERGILLOSIS ON *GORGONIA VENTALINA* AND *G. FLABELLUM* ON THE MESOAMERICAN BARRIER REEF, ROATÁN, HONDURAS

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Gorgonia ventalina, the purple sea fan, and *G. flabellum*, the venus sea fan, are two gorgonian species and common benthic organisms on Caribbean reefs. Aspergillosis is a common disease affecting *G. ventalina* and *G. flabellum,* which is caused by the fungus *Aspergillus sydowii*. This study was conducted in Roatán, Honduras to assess: 1) the prevalence of aspergillosis on *Gorgonia* spp., 2) the intensity of disease present on the sea fans, and 3) the presence and abundance of *Cyphoma gibbosum*, the flamingo tongue mollusk, on sea fans. A generalized linear regression with a post hoc ANOVA demonstrated that location was the strongest factor in determining the prevalence and intensity of disease. *Gorgonia flabellum* was more abundant than *G. ventalina* across all five dive sites. Healthy fans were more frequently observed than diseased fans. Depth and species of sea fans were not correlated with prevalence or intensity of aspergillosis. Although *C. gibbosum* was expected to be located on diseased sea fans, the species was not observed. The presence of large predatory fish in the protected and regulated Roatán Marine Park may limit the abundance of *C. gibbosum.* Future research should inquire into other vectors of *A. sydowii* and the transmission of infection to sea fans.

ORAL (GRADUATE)

ECOLOGY & ENVIRONMENTAL BIOLOGY

52. INDIRECT EFFECTS OF THE LANDSCAPE ON FRUIT PRODUCTION IN BAOBAB TREES OF KENYA

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Baobab trees (*Adansonia digitata*) span mainland Africa and observations and exclusion experiments suggest that fruit bats are the primary pollinators. Bats' nightly movements are motivated by the availability of resources in the landscape, such as water, flowers, and fruits. The distribution of water and food in the landscape is therefore predicted to indirectly influence the number pollinating visits to baobab trees, and as a consequence the number of fruit produced by baobab trees. To test the indirect effects of the landscape on fruit production, we counted the number of fruit on baobab trees in an approximately 4.0km by 3.0km plot near Nuu, Kitui County, Kenya. In addition, we recorded all possible fruiting trees (i.e., mangoes, bananas, pawpaw, and figs). We predicted that more fruit per baobab tree would occur where:

i) there is a greater density of mango trees, fig trees, and baobab trees within a 500m buffer around the focal tree; ii) the closer the focal baobab is to its nearest neighbor (e.g., baobab, mango, or fig tree); and iii) the closer the focal baobab is to a water source. Initial findings suggest that the number of baobab fruit per tree is influenced by the density and proximity of other baobab trees, not other possible food resources such as mangoes and figs or distance to a water source. This suggests that landscape characteristics among the baobab population itself, such as spatial distribution of baobabs, could influence pollination by bats.

53. CHARACTERIZING MICROBIAL COMMUNITIES IN LOWER RIO GRANDE FRESHWATER RESERVOIRS: DONNA LAKE AND IRRIGATION SYSTEM VERSUS DELTA LAKE AND EDINBURG NON-STERILE DEIONIZED WATER

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The Donna Reservoir and Irrigation System in Donna, Texas plays an important role in providing farmers and municipalities with freshwater as well as serving as a diverse ecosystem. However, there is critical polychlorinated biphenyl (PCB) pollution problem. EA Engineering, Science, and Technology, Inc., PBC prepared a review of the ecological impacts of the pollution on local avia, reptiles, fish, and mammals, but did not include an analysis of any impact of PCB on microbial communities. This investigation compares the growth rate and carbon metabolism capability among microbial communities from the DRIS and from non-PCB polluted waters. BIOLOG Ecoplates were used to compare carbon metabolism potential among the samples. Community level physiological profiles suggest that symbiosis with plants contributes to function similarities more than the location of the sample. When exposed to 0.0004 g/L of biphenyl in a methanol solution, there was no difference in growth within the samples compare to the control of just methanol. However, there was a significant difference in the growth rates samples that potentially interacted with plants and those that didn't. The results from both test suggest that interaction with plant life has more impact than exposure to PCB pollution on growth and metabolism in microbial communities. Further research on this project include community catalogue with next generation sequencing and quantifying the presence of a gene that promotes PCB degradation in bacteria.

54. TESTING PREDICTIONS OF OPTIMAL MIGRATION THEORY IN A SYSTEM OF MIGRATORY SILVER-HAIRED BATS

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Optimal migration theory has been used for over 25 years as a theoretical framework to evaluate tradeoffs in migratory strategies. The most frequently considered strategies by migration theory are time minimizing, whereby migration is completed as quickly as possible, and energy minimizing, whereby migration is completed as energetically inexpensive as possible. Despite an extensive amount of literature dedicated to analytically generating predictions about differences in migratory strategies, identifying appropriate study systems to empirically test predictions is difficult. Due to the qualitative nature of migration theory predictions that compare migratory strategies, empirical tests require that both time-minimizers and energy-minimizers are present in the same population. We investigated a system of spring migratory silver-haired bats where males and females exhibit different migratory strategies as a function of their life history traits. We tested migration theory predictions related to fuel loads in time-minimizers and energy-minimizers. We show that, as predicted, time-minimizers have an increased fuel load relative to energy-minimizers. We then use two methodologically novel approaches to investigate if increased fuel loads were achieved by a decrease in energy expenditure, an increase in digestive efficiency, or an increase in foraging effort. Preliminary results suggest that in silver-haired bats, time-minimizers increase their fuel load relative to energy-minimizers by increasing foraging effort. This research is the first of its kind to validate a migration theory prediction in a system of both time and energy minimizers. Further, this research exemplifies how to use novel methodological approaches to uncover underlying mechanisms of migratory stopover use.

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

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Emerging research has shown that many species of birds utilize low-amplitude vocalizations (LAVs) in a variety of social interactions, including male-male aggressive interactions. However, the function of these aggressive vocalizations in shaping the spatial dynamics of individuals within breeding populations remains unexplored. Since females may be attracted to settle near highly-aggressive males, LAVs may function to attract females to settle closer to males that use LAVs. Thus, to determine a putative role of LAVs in the context of territory establishment, I experimentally tested the function of LAVs in the settlement decisions of a migratory songbird (the Veery; *Catharus fuscescens*) in a forest soundscape. Twenty sites were manipulated using playbacks of previously recorded male songs. Half of these sites had a 6-minute track that played back LAVs (i.e., whisper calls) after approximately every five songs while the other half broadcasted only the male song as the control treatment. Thirty nests were found during the 4-week experiment (20 near whisper call sites, 10 near control). Although nesting in proximity (within ~150m) to whisper call sites was marginally non-significant ($p = 0.055$), females nested at whisper call sites more often and earlier in the breeding season, and whisper call sites had higher numbers of breeding females in near proximity. These findings support the increasing number of studies that have shown LAVs to be aggressive signals in songbirds. However, this is the first study to experimentally show how a low-amplitude, aggressive signal can affect female settlement decisions.

56. DIVERSITY AND SPECIES RICHNESS OF FOREST INTERIOR INSECTIVOROUS BATS ALONG ELEVATIONAL GRADIENTS IN NIGERIA

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Bat species richness patterns along elevational gradients vary across mountains and may decrease monotonically, peak at mid-elevation or plateau before decreasing sharply. The bat fauna of the Cameroon/Nigerian mountain range are hitherto unstudied. As temperature and water are highest at mountain bases, we hypothesize a monotonic decline in species richness with increasing elevation. We conducted bat surveys at five and six elevation strata (at 250 – 400 m intervals) respectively in Afi Mountain Wildlife Sanctuary (AMWS) and Cross River National Park (CRNP) in southeastern Nigeria. Using four-bank harp traps (HT) set for two consecutive nights along 200 m transects and mistnets (MN) set over streams, we captured insectivorous bats during 224 and 264 HT nights and 28 and 68 MN hours from AMWS and CRNP respectively. A total of 399 and 248 individuals belonging to 19 and 21 species were captured from AMWS and CRNP respectively. We computed diversity statistics, nestedness analysis and dissimilarity indices on forest interior insectivorous bat ensemble. We report new country and species elevational range records. Species richness declined monotonically with elevation and sample-based rarefaction curves did not reach an asymptote on both gradients. High ensemble similarity was observed between gradients, while stratum-level pairwise analysis suggest ensemble similarity from low to mid elevations on both mountains. Nestedness temperature (T) metric for both ensembles show that higher ensembles are significantly nested in low level ensembles. The mechanistic drivers of these diversity, richness and ensemble patterns will be investigated in further analysis.

57. POPULATION GENETICS OF THE NORTH AMERICAN PORCUPINE (*ERETHIZON DORSATUM*) ACROSS WESTERN TEXAS

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The North American porcupine (*Erethizon dorsatum*) is a highly mobile, generalist species with an extensive geographical distribution in North America. The porcupine was first documented in southwestern Texas in the early 20th century, but today occurs in most of the western two-thirds of the state. The objective of this study was to describe population genetic metrics of porcupines across western Texas by examining variation in 17 polymorphic microsatellites. Tissue samples from 100 porcupines were collected from the High Plains, Rolling Plains, and Edwards Plateau ecoregions, and genotyped for 17 polymorphic loci to estimate genetic variation and population structure. Resulting genotypes support moderate genetic variation and minimal population structure throughout the study area. Overall expected heterozygosity ($H_E = 0.8327$) exceeded observed heterozygosity ($H_O = 0.7748$). STRUCTURE and Detrended Correspondence Analysis illustrated a primary genetic cluster (K = 1) with minimal grouping by ecoregion. An overall $F_{ST} = 0.0022$ detected little to no divergence. An overall G_{ST} value of 0.0019 was obtained for porcupines across all ecoregions, suggesting that panmixia may be widespread throughout western Texas due to low variation of allele frequencies. This research reveals that porcupines throughout western Texas are indeed vagile. The lack of population structure detected is likely the result of a relatively short life history and recent arrival of porcupines into the state. Moderate genetic diversity reflects porcupine's wide use of habitat throughout the western portion of the state. This knowledge is beneficial in the management of this species and to the overall understanding of the porcupine.

58. TREE-LOVING VS TREE-HATING GRASSES: USING FIRE TO KILL ENEMIES

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Savannas, where grasses dominate with scattered trees, are fire-dependent systems: recurrent grass fires limit tree cover and maintain high light habitats that are favorable to grasses. Thus, grass-fueled fire is positive feedback that can lead to alternative stable states: either prairie or closed-canopy woodland. Although it is well established that fine grass fuels play a role in suppressing woody savannas plants, studies tend to treat grasses as homogeneous fuels and pay less attention has to fire-mediated interactions among different grass species and their woody competitors. Although fires can favor grasses by decreasing competition for light, in many woodlands and savannas grass species, show local habitat differentiation with some species being restricted to open habitats and others persisting under tree canopies. If increased flammability is beneficial to grasses because it leads to reduced tree cover, we would expect the greatest benefit to shade-intolerant species. Thus, it is possible that shade tolerance and enhanced flammability are evolutionary correlated. This proposed project aims to determine if there is an association between interspecies flammability variation and plant microhabitat preference; and if canopy architecture causes such variation. We will survey grass distribution pattern relative to tree canopy in western Texas mountain ranges; collect samples for tree-loving and tree-hating grasses given survey result and measure plant flammability and functional traits. Differentiation in savanna grass flammability helps explain long-term species composition stability in savannas because variation in flammability dampens or strengthens positive vegetation-fire feedbacks which would lead to extreme case.

59. SPECIES DISTRIBUTION MODELING OF POTENTIAL ZIKA VIRUS VECTORS, *AEDES AEGYPTI* AND *AEDES ALBOPICTUS,* MOSQUITOES

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Aedes (*Stegomyia*) *aegypti* and *Aedes* (*Stegomyia*) *albopictus* mosquitoes vector several pathogens of human health importance, namely chikungunya, dengue, yellow fever, and Zika viruses. Though both mosquito species originally had tropical and subtropical ranges, they have been progressively reported from further poleward locations. Their augmented range increases the number of people at risk of being infected through these mosquito vectors. Local mosquito-borne transmission of Zika virus was reported from Texas during November 2016, and is believed to be vectored only by *Stegomyia* spp. This study focused on two objectives, conducting surveillance for these mosquitoes throughout Texas, and to create and evaluate geospatial predictive models utilizing this data. Surveillance for gravid females of both species was conducted using ovitraps from August – November 2016 in 28 counties of the Texas Panhandle Region, and from June – October 2017 in 33 counties throughout Texas. Surveillance findings resulted in *Ae. aegypti* being newly identified in nine counties, while *Ae. albopictus* was newly identified in nine counties, and the occurrence of both species was newly identified in six counties. Maximum entropy modeling (MaxEnt) was used in R Statistical Software to estimate distributions for both species in the United States, and compared with the currently known ranges of these species in Texas specifically. Determining *Ae. aegypti* and *Ae. albopictus* species' distributions in Texas and predicting their future species' distributions in the United States using MaxEnt modeling could influence public health decision-making and guide future practices.

60. A TIME-SERIES STUDY OF SOIL MICROBIAL COMMUNITY COMPOSITIONAL AND FUNCTIONAL SHIFTS IN BIODIESEL VS. PETRODIESEL CONTAMINATED SOILS

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The spill of petrodiesel on land can irreversibly damage the soil ecosystem, and there are limited studies comparing petrodiesel and biodiesel impacts on soil microbial communities. Biodiesel has been considered as a viable substitute for petrodiesel, however the degree to which biodiesel is more microbial friendly than petrodiesel is inconclusive. Previous studies of soil microbial community on contaminated sites failed to reveal the dynamic changes of soil microbial communities. This laboratory study compared the effects of petrodiesel and three types of biodiesel on soil microbial communities in sandy loam soils. Contaminated soil samples were investigated at day 0, day 7 and day 180 to evaluate their effects on the composition and function of soil microbial communities. Soil microbial composition were addressed by 16s rRNA gene sequencing of V3-V4 regions. Results suggested that biodiesels were not statistically different from petrodiesel in terms of their adverse impacts on soil microbial communities. In conclusion, our results suggested that biodiesels should not be automatically considered as harmless substitutes for petrodiesel.

61. ANALYZING TEXAS AVIAN COMMUNITY STRUCTURE IN THE ERA OF URBANIZATION

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Today, over half of the human population lives in or near developed areas. Urbanization has a profound impact on biodiversity by decreasing the amount of natural habitat and resources for wildlife and increasing fragmentation and quantity/intensity of interactions between native and exotic species. Due to rapid land transformation, urbanization has been considered one of the main contributors to contemporary rates of extinction. To study impacts of urbanization on biodiversity, birds make an ideal taxonomic group. At least 2,000 avian species are found in urban environments worldwide, and they are easily observed and studied. Birds are also ecologically diverse and provide a variety of ecosystem functions to humans. Avian richness decreases with increased urbanization, and this is associated with homogenization of species composition of bird communities. However, very few studies have examined relative contributions of local environmental and regional processes to community composition. This is especially so when it comes to migratory vs. non-migratory and native vs. invasive species that are distributed along urban gradients at larger spatial scales. This study examined multiple avian communities throughout Texas, which has experienced much urbanization. Percentages of vegetation, land use, and levels of urbanization (e.g. neighborhoods to industrial), and average and variability of precipitation and temperature were measured for each community. We predict that urban areas will be composed mostly of generalist and invasive species, while migratory and specialist species will avoid urban areas and be found in more natural areas.

GENETICS & GENOMICS

62. TRANSPOSABLE ELEMENTS AND LINEAGE SORTING WITHIN THE GENUS *MYOTIS*

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The genus *Myotis* includes more than 100 species and is one of the most expansive mammalian species radiations. The exact evolutionary relationships within the genus *Myotis* remain unclear because of conflict between mitochondrial and nuclear phylogenies, which show different relationships between species. A number of factors can drive conflict between markers, such as hybridization, phylogenetic error, and incomplete lineage sorting. Transposable elements (TEs) are DNA sequences that can move around in the genome and are powerful genomic markers. Retrotransposon TEs, such as SINEs, make excellent phylogenetic markers for several reasons: they are vertically inherited, rarely excised, easily scored for presence/absence, the ancestral state can be safely assumed, and are virtually homoplasy free because of their copy-and-paste mechanism of transposition. We examined the genomes of 11 North American bats from the genus *Myotis* and used the Mobile Element Locator Tool (MELT) to identify differential insertion patterns an abundant SINE (Ves) in each species. We have mapped those insertions onto the most recent nuclear phylogeny of the clade. Preliminary results suggest that the early, rapid diversification was associated with significant lineage sorting.

63. MAKING A *MYOTIS*: CONNECTING TRANSPOSONS AND MUTATIONS IN BATS

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Transposable elements (TEs) are DNA sequences that mobilize through copy-and-paste or cut-and-paste mechanisms, expanding within a host genome. Typical mammal genomes are dominated by the copy-and-paste variety, also known as retrotransposons. An exception to this rule is the vesper bat family Vespertilionidae, which have experienced an unorthodox TE history and are the most species rich of bat clades. Genomes of these bats 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 recruitment of low-fidelity 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. Retrotransposons likely have a similar, but lesser mutational impact, as the elements insert via single-stranded nicks, and do not excise themselves. An analysis of transposon polymorphisms in eleven *Myotis* species will reveal the influence of TEs on local mutation rates across the genome and on nearby genes. 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.

64. DIGESTIVE EFFICIENCY AND GUT-MICROBIOME DYNAMICS THROUGHOUT REPRODUCTION IN THE MEXICAN FREE-TAILED BAT, *TADARIDA BRASILIENSIS*

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The gut-microbiome contains almost three-quarters of all microorganisms in the body and is an essential contributor to many bodily processes such as metabolism, nutrient extraction and acquisition, nutrient storage and even immunological modulation. Given the nature of its function, the effective contributions of the gut-microbiome would be assumed to be greater during periods when host energetic demands are increased such as throughout pregnancy and lactation. The mammalian reproductive period is an energetically expensive time in a female's life with lactation usually considered the most energetically costly. In relation to other mammals, bats already have unusually energy energetic demands. They are volant, have shortened digestive tracts, and support large fetuses relative to their body size. The reproductive period for bats further increases their already maximized energy expenditure. Because of these exceptional metabolic attributes throughout reproduction, the digestive efficiency of bats should be crucial to the reproductive and overall survival success of bats. In this study we are investigating the relationship and response of digestive efficiency to potential predictors such as dietary composition, microbiome composition and function, bacterial microbiome load and pregnancy stage. High throughput 16s rDNA gene sequencing will be used to understand microbiome community composition and function throughout the different reproductive stages. In addition, COI sequencing will allow us to characterize the dietary composition of bats temporally. Finally, we will integrate bomb calorimetry to quantify and assess digestive efficiency throughout the reproductive period and its relation to the numerous predictor variables. Our results will provide insight into the relationship between metabolizable energy, the factors that affect it and its significance for reproductive success.

65. ASSESSING LEVELS OF DNA DEGRADATION IN FROZEN TISSUES ARCHIVED IN A NATURAL HISTORY COLLECTION

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Frozen tissue samples housed in natural history collections have many uses in the field of biology; including ecology, virology, taxonomy, and evolution. The recent increase in genomic level sequencing has generated an ever-increasing interest in using properly archived tissue samples. Therefore, it is imperative that frozen tissue collections are preserved and maintained in perpetuity. In order to accomplish this, tissue samples should be maintained in an environment that is sufficiently cold as to prevent damage to the tissue and DNA. Historically, -20°C and -80°C was used for most frozen tissue collections. However, many institutions are starting to implement a liquid nitrogen freezing system, which is able to maintain samples at -196°C. To assess whether tissues are being properly stored, tissues covering a range of 30 years, as well as multiple storage mediums were examined. Tissues will be transported to a private robotics research laboratory where DNA was extracted, and analyzed on a Fragment Analyzer. Data were returned in the form of excel files. Each tissue sample had a listing of the density of respective base pair lengths. An Analysis of Variance (ANOVA) was performed on the data, as well as a Principal Components Analysis (PCA), to see if there is a significant difference in DNA quality throughout the time frame, as well as between storage temperatures, and tissue types.

66. NOVEL METHOD FOR TRANSPOSABLE ELEMENT ANNOTATION ACROSS MULTIPLE TAXA

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In contrast to other major vertebrate clades, which have undergone vast diversifications, crocodilians exhibit remarkable conservation at the ecological, morphological and genomic levels. The recent publication of three crocodilian genomes established these taxa as an emerging model given their robust immune systems, low cancer incidence and their unusually slow rate of genomic evolution. Despite these unique adaptations and the conservation status of many of the component taxa the molecular basis of these adaptations remain poorly understood. To address this a collaborative sequencing effort between the University of Sydney and Texas Tech University generated ~15X-coverage whole-genome paired-end Illumina Hi-seq data for 9 crocodilian species: *Crocodylus moreletii, C. acutus, C. rhombifer, C. niloticus, C. palustris, C. siamensis, C. johnstoni, C. mindorensis,* and *C. novaeguineae*. Additionally, we also sequenced an individual from the unique dwarf population of *C. johnstoni*. Reference-based genome assemblies were constructed using the newly sequenced dove-tail *C. porosus* genome as the reference. Reads were mapped to the *C. porosus* genome using BWA and differential SNPs were called using the Genome Analysis Toolkit. Final reference-based assemblies were generated using a modified version of Pseudo-it, which decreases mapping biases by iteratively building pseudo-references while incorporating species-specific SNP variation. Genomic analyses of selection detection and ancient hybridization events are ongoing, but initial genome-based phylogenies corroborate previously published crocodilian species trees. Together, these genomes represent the molecular toolkit required to increase our understanding of the unique evolutionary history of this enigmatic clade of ancient organisms.

MICROBIOLOGY & MEDICINE

67. CHOLINE BRANCH OF KENNEDY PATHWAY PLAYS CRUCIAL ROLE DURING THE SANDFLY STAGE OF *LEISHMANIA MAJOR*

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Leishmania contain a diverse pool of phosphatidylcholine (PtC), the most abundant lipid in these parasites, like many eukaryotes. Synthesis of PtC occurs via the choline branch of the Kennedy pathway (choline ⇒ choline-phosphate ⇒ CDP-choline ⇒ PtC) and the N-methylation of phosphatidylethanolamine (PtE). To understand the role of choline branch *de novo* PtC synthesis in *L. major*, we investigated its key enzyme, choline-phosphate

cytidylyltransferase (CPCT) which forms CDP-choline, an intermediate to generate PtC. CPCT-null mutants could not incorporate choline into PtC, but possessed a similar phospholipid composition, were fully viable and replicative in regular medium, and showed a near-normal level of virulence in mice as wild type parasites. These findings suggest that the ethanolamine branch of the Kennedy pathway alone is sufficient to compensate the loss of CPCT in culture. However, otherwise dispensable, 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. This indicates *Leishmania major* parasites need the choline branch during ethanolamine depletion, and to survive the competitive environment in sandfly midgut. We are in the process of characterizing other Kennedy pathway enzymes to determine their roles in in *Leishmania* life cycle and evaluate their potential as drug targets.

68. CHRONIC WOUND MICROBIOME COLONIZATION ON MOUSE MODEL FOLLOWING CRYOGENIC PRESERVATION

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Slough isolated from chronic wounds was recently shown to re-establish polymicrobial biofilm infections in the mouse model, providing an *in vivo* experimental design to study wound microbiota. Cryogenic biobanking of wound-isolate has clear application for genome and microbiome related research questions, but polymicrobial viability through freezing and utility for *in vivo* modeling is unknown. Thus, the purpose of the study was to investigate the effects of cryogenic preservation on microbiome colonization by slough transfer. Slough from five patients was homogenized and sub-divided into three preservation strategies which included refrigeration until infection as previously reported, and being frozen in liquid nitrogen with or without glycerol. Individual mice were subsequently infected with slough treatments and matched with controls. Four days following inoculation, wound microbiota were characterized by 16s rDNA community profiling and quantitative PCR. Analyses were conducted to understand the effect of patient origin and preservation strategy on microbiome composition. Patient origin explained a significantly greater amount of variation than treatment, which indicated patient wound microbiome could be partially re-established following preservation. The prior relative abundances of individual species and overall bioburden in slough from patients had significant effects on colonization success into mice. Cell viability comparisons among preservation treatments were also made with samples from an additional 11 patients where it was found that neither freezing strategy presented a significant reduction in viability. Overall results indicate that cryogenic archives of wound material are a useful tool for *in vivo* approaches to studying biofilms and infection.

69. MALONATE-UTILIZATION OPERON CONTRIBUTES TO THE VIRULENCE OF *PSEUDOMONAS AERUGINOSA*

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In the United States, more than 1 million individuals with severe sepsis are hospitalized annually. Trauma patients are susceptible to sepsis. The opportunistic pathogen *Pseudomonas aeruginosa* is a leading cause of trauma-related sepsis. *P. aeruginosa* produces numerous virulence factors. Despite numerous studies, the pathogenesis of *P. aeruginosa* infection during trauma-induced sepsis is not defined. We recently showed that the growth of the *P. aeruginosa* strain UCBPP-PA14 (PA14) in blood from trauma patients significantly enhanced the expression of the malonate-utilization operon (MUO). We hypothesized that the MUO contributes to *P. aeruginosa* virulence since malonate is important in the fatty acid metabolism and energy production. We compared the effect of growth of PA14 in M9, a minimal medium, containing either glycerol (GM9) or malonate (MM9), as a sole carbon source, on the expression/production of virulence factors. The growth of PA14 in MM9 significantly enhanced pyocyanin production and the expression of the phenazine operon. In contrast, the growth in MM9 significantly reduced the production of the QS autoinducers. Upon the growth of PA14 in MM9 aggregates of variable sizes were formed. Scanning electron microscopy analysis of these aggregates revealed the formation of structures that resemble the biofilm-related extracellular polymeric substance (EPS). Since the main component of EPS is DNA, and to confirm the nature of this EPS-like material, we treated the aggregates with DNase, which promptly dissolved the aggregates. From these results we suggest that the utilization of malonate through the MUO uniquely contributes to *P. aeruginosa* virulence.

70. ANALYSIS OF SECRETED COMPOUNDS FROM *BATRACHOCHYTRIUM DENDROBATIDIS* FOR ANTI-MICROBIAL AND ANTI-NEMATODE ACTIVITY

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The decline of amphibians worldwide has been partially accredited to the fungus *Batrachochytrium dendrobatidis (Bd).* This fungus causes inflammation and thickening of the keratinized layer of amphibian skin disrupting the osmotic balance leading to cardiac arrest. We have shown the fungus can kill nematodes with attachment, but secreted supernatants have not been tested. The fungus may secrete compounds capable of killing the host or similar organisms. Published work indicates *Bd* can produce immunomodulatory compounds. While some compounds have been identified, we show evidence that *Bd* may produce additional toxic molecules. Previously, *Bd* has been linked to possess the biosynthetic pathway to produce an epipolythiodioxopiperazine (ETP) class of toxin. Three different methods of extraction of 4- and 8-day culture supernatants were analyzed by UPLC. The extracts were analyzed for the presence of anti-nematode and anti-bacterial activity. The best method of extraction was a chloroform-based approach on day 8 of fungal growth with additives. Unique compounds secreted from *Bd* were present in those supernatants. Bioassays using bacteria and nematodes showed variable results. Toxin production is important in the virulence of *Bd.*

These studies will contribute to our understanding of the mechanisms by which *Bd* infects and kills amphibians.

MOLECULAR BIOLOGY & BIOCHEMISTRY

71. CLONING OF *wi1*, *Wi2*, *Wi3* and *Wi4* MUTANTS OF MAIZE BY BULK-SEGREGANT WHOLE GENOME SEQUENCING

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A single gene mutation in plants can have pleiotropic effects on the physiology and fitness of the plant. *Wilty2* (*Wi2*), *Wilty3* (*Wi3*) and *Wilty4* (*Wi4*) are a class of non-allelic EMS-induced dominant mutants of maize which manifest severe wilting phenotype under well-watered conditions. *Wilty1* is a recessive mutant described by Oliver Nelson in the 1950s. These mutants show a varying degrees of pleiotropy with *Wi4* showing a highly reduced growth and biomass followed by *wi1*, *Wi2,* and *Wi3* showing less stunted phenotypes. The wilting phenotype manifests at the three to five-leaf stage and the mutants have smaller, yet more abundant vascular bundles per unit stem and leaf area as compared to their wild type siblings. Histochemical staining of the fresh internodes and biophysical analysis of extracted vascular bundles (VBs) suggests difference in cellulose and lignin content in the vascular bundles. We analyzed the differentially expressed genes of the *Wi4* and wild type leaf tissue by mRNA-Seq under unstressed and drought-stressed condition. We propose to identify the candidate genes for these mutants by bulk-segregant whole genome sequencing with a potential map resolution of 0.65 centiMorgans. This method will reveal new insights into the molecular mechanisms of cell wall formation and drought adaptation via feedback and/or feedforward loops from vascular development programs, elucidated by systems biology approaches and transgene complementation experiments going forward. The knowledge gained from cloning these genes may provide engineering strategies for translational improvements to production of biomass and biofuels.

72. LOSS OF TESTOSTERONE CAUSES MALE INFERTILITY BY DISRUPTING SPERMATOGENESIS

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Declining birth rate in developing countries is a significant social complication. Forty to fifty percent of infertility accounts for male infertility, effecting fifteen percent of all males. Due to lifestyle changes, humans are exposed to hazardous chemicals resulting prenatal Leydig cell and Sertoli cell dysfunction due to low level of androgen and disabled germ cell development during spermatogenesis. Testosterone is the known major player of spermatogenesis but hardly anything is known about its mode of action. We injected Ethylene dimethane sulfonate (EDS) in male rats which ablates mature Leydig cells, thus, eliminating endogenous testosterone. Testosterone loss compromised blood-testis-barrier (BTB) integrity and decreased anchoring junction proteins. Nuclear androgen receptors (nARs) were identified in Sertoli & myoid cell nuclei and stripped cytoplasm from spermatids but not on germ cells. Testosterone present in high concentration in testis can act either through canonical or non-canonical manner. Non-canonical pathways of testosterone actions include interaction with membrane receptors and influencing other cellular functions instead of the canonical pathway inducing nuclear receptors and influencing gene regulation. Progesterone, a steroid hormone regulating mainly female reproduction, mainly focuses on nuclear receptors but can also change ion influx and intracellular Ca2+ along with other second messengers of the non-genomic pathway mediated by Membrane Progesterone Receptors (mPRs). We have initiated studies to find and characterize mRNAs for mPRs & membrane progesterone/ adiponectin receptors (mPAQRs) by RT–qPCR. We found at least 5 mPRs mRNAs expressed in testes but do not know the cells of origin using total RNA from whole testes.

73. ANALYSIS OF CUSTOM MICROARRAY DATASET FOR DISCOVERY OF DROUGHT STRESS RESPONSES AND BREEDING FOR WATER USE EFFICIENCY IN *SORGHUM BICOLOR*

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Since the initial discovery of structure of DNA, there has been a rapid advance of genomic-scale sequencing that has permitted ad hoc means to progress the breadth and depth of our understanding of biological complexity. Custom microarray as a robust parallel assay to sample all RNA species in a reference genome has certainly sparked the field of genomics and still been adopted by small labs to impact the ‘genome to phenome challenge’. Our working hypothesis is to test whether the quantitative agronomic trait of water use efficiency can be modeled as a parameter of well-studied drought responses. We have conducted a microarray experiment with HD2 Roche/Nimblegen chip design to characterize the drought stress response of BTx623 compared to unstressed gene expression of two different genotypes bred for high (Liang Tang Ai, PI584085) or low (Tx7078, BTx399) water use efficiency. We utilized limma (linear models of microarray data), an R software package for the background correction and normalization of microarray data within and between arrays to make comparisons between control and drought stressed sorghum plants on the same measurement scale. We have validated our drought stress results relative to claims for drought stress responses from a low-tech cDNA spotted microarray and high-tech RNA-Seq experiment reported in the literature that showed 70% concordance with the gene expression profiles from our drought experiment. Moreover, we have been able to identify several drought inducible genes in the comparison of low WUE to high WUE genotypes revealing a considerable correlation between high WUE and drought.

74. CONTINUING STUDIES ON THE INFLUENCE OF PSYCHOLOGICAL AND PHYSIOLOGICAL STRESSORS AND THE VISUAL RESPONSE TO FOOD: ANALYSIS OF SALIVARY ALPHA AMYLASE

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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. In order to deal with the fears in visual, we also need to concentrate on the sympathetic nervous system and HPA axis. All subjects will be recruited from the Sona System in the college of Media and Communications at Texas Tech University. Students will be asked to drink and eat as usual before testing. After signing a consent questionnaire and a brief form about pretest eating and drinking habits, students will be weighed, measured for height and calculated BMI, Hunger will be assessed by a satiety scorecard prior to testing. Students will be separated to three groups: Cold press test group, control group, and trier social stress test group. All subjects will perform eye tracking test. Lastly, all of the students will be asked to take the visual function test. 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. The long term goal of this work is to understand hormonal regulation of food intake in the context of optimal foraging strategies. The proximal goal of this study is to determine if psychological and physical stressors, known to increase stress hormone release, influence the attention to visual food cues in humans.

PHYSIOLOGY & EVOLUTIONARY BIOLOGY

75. INCOMPLETE LINEAGE SORTING OF THE TRANSPOSABLE ELEMENT AFROSINE IN THE FAMILY ELEPHANTIDAE

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Transposable elements (TEs) are DNA sequences that can move and replicate within a genome. In some mammalian genomes more than half of the genome is composed of TEs, and they also play a crucial role in many processes including genome evolution, gene expression regulation and genomic instability. The genetic variation introduced by TEs can also be advantageous during speciation. Afrotheria is a superorder comprised of several African mammals such as elephants, hyraxes, sea cows and aardvarks. In this study we focus on the Afrotheria family Elephantidae, which are large herbivorous animals collectively called elephants and mammoths. Our analyses focus on the afroSINEs a subfamily of SINEs (Short INterspersed Elements) that mobilize themselves utilizing an RNA intermediate, allowing them to make copies of themselves and insert them in different genomic locations. SINE insertions are believed to be irreversible events that have low probability of inserting themselves into the same genomic location independently in different lineages during evolution, making them a virtually homoplasy-free marker. In this study we utilized whole genome sequences for all three species of modern elephants (*Loxodonta africana, Loxodonta cyclotis and Elephas maximus)* to analyze 2281 polymorphic SINEs presence/absence markers and possible incomplete lineage sorting (ILS). We found 72 potential ILS events in the family Elephantidae that occurred in the distant past during the divergence of the extant elephant species. We provide evidence of high support of ILS between the African and Asian elephants.

76. LATE PLEISTOCENE MAMMALS AND BIRDS FROM MACY LOCALITY 100, SOUTHERN HIGH PLAINS, TEXAS

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Investigations of stream deposits at Macy Locality 100 on the eastern edge of the Southern High Plains, Texas, have produced a rich sample of the regional late Pleistocene fauna. Recovered skeletal remains, representing all vertebrate classes, have been identified taxonomically based on morphological characters. The sampled deposits at Macy Locality 100 are oriented in time by a series of radiocarbon ages spanning from approximately 11,500-11,000 ^{14}C yrs BP. Avian and mammalian taxa represent major components of the vertebrate assemblage. A diverse suite of extinct mammalian megafauna occur alongside extant and extralimital species. Extralimital mammals in the assemblage are generally associated with mesic habitats. Similarly, aquatic forms predominate within the avian sample. The total vertebrate assemblage is significant in documenting regional biodiversity prior to the extinctions and extirpations that characterize the Pleistocene-Holocene transition across North America. These biotic changes are associated with contemporaneous environmental change. Alluvial sediments at the locality record portions of the paleo-valley axis and margin within the Spring Creek drainage, a tributary of the upper Brazos River basin. These deposits document shifts in the fluvial regime within the paleo-valley that were manifestations of late Pleistocene local landscape evolution and regional climatic change. In general, these deposits record a reduction in the energy and capacity of the local fluvial regime. The comprehensive view of a late Wisconsinan vertebrate community provided by Macy Locality 100 offers context for understanding extant regional faunal composition and biogeography.

77. SEASONAL DYNAMICS OF CATABOLIC ENZYMES AND ENERGY STORES IN BRAZILIAN FREE-TAILED BATS

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According to life-history theory, animals should trade-off aspects of their physiology and behavior to compensate for changes in energy demand. As small, flying, mammalian endotherms, bats are adapted to operate at extreme levels of energy expenditure. During the active season, bats experience substantial, albeit variable, energy demands that may push the limits of their maximal metabolic capacity. To test whether bats use physiological compensations to cope with elevated demands, we examined variation in energy storage and biochemical pathways for oxidative metabolism in Brazilian free-tailed bats (*Tadarida brasiliensis*) in relation to costs associated with reproduction and migration. We collected pectoral muscle from female *T. brasiliensis* at six time points during the active season and measured changes in the activity of three catabolic enzymes involved in lipid transport and oxidation. We observed a 13% decrease in body mass during lactation, when reproductive costs peak, and a 45% increase prior to migration, suggesting rapid use and accumulation of fat stores in response to current or anticipated energy demand. For all three catabolic enzymes measured, we found that activity increased by 24-81% in lactating bats relative to bats in early pregnancy. The observed variation in fat mass and catabolic enzyme activity in *T. brasiliensis* demonstrates that pathways for lipid transport and oxidation are flexible and respond to changes in energy use. These results suggest that highly aerobic mammals, such as insectivorous bats, have evolved physiological mechanisms to optimize metabolic capacity based on energetic need and maintain energy balance despite extreme levels of expenditure.

78. TAXONOMIC STATUS OF DIMINUTIVE FLATHEADTOADS OF THE GENUS *PELOPHRYNE* BARBOUR, 1938 (ANURA: BUFONIDAE) OF SUMATRA, INDONESIA REVEALED FROM MOLECULAR AND HABITAT NICHE MODELLING DATA

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Frogs of the genus *Pelophryne* are easily recognizable with their distinctive diminutive size and almost fully-webbed hands. However, morphologically they are difficult to differentiate to each other at the species level. Also, the taxonomic relationship of the genus *Pelophryne* has long been unresolved and debated. Particularly, two species, *P. signata* and *P. brevipes,* which keeps scientist in dilemma regarding their recognition and phylogenetic relationship to each other for years. In past, these two species have been synonymized and resurrected more than once based on their morphology. Out of 12 extant described species of the genus, *P. brevipes* is considered to have the widest distribution which ranges across Sumatra to the Mindanao Island of the Philippines and believed to be co-occurred in Sumatra, Peninsular Malaysia, and Borneo along with *P. signata*. Whereas the other 10 species show point endemism in different mountains of Borneo and Philippines and do not show sympatry to each other except with *P. signata* and *P. brevipes*. To address all the uncertainties towards the taxonomic relationships we used molecular phylogenetic and environmental niche modeling tools. We sequenced 45 *Pelophryne* specimens from Sumatra and 1 specimen from Borneo along with all 14 available Genbank *Pelophryne* sequences. Our analysis recovers a monophyletic relationship among all the *Pelophryne* of Sumatra. The Sumatran clade is genetically divergent and very distinct from the Bornean and Philippine toads denoting Sumatran toads are neither *P. signata* nor *P. brevipes* rather a potential cryptic species complex. Our niche modeling data shows that *P. brevipes* is an endemic species restricted to Mindanao islands of Philippines and *P. signata* is another Bornean endemic species.

79. ALTERNATIVE MRNA SPLICING OF A GAMETE RECOGNITION PROTEIN, ZONADHESIN, MAY PROMOTE NEW FUNCTIONAL ADAPTATION IN MAMMALIAN REPRODUCTION

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The birth of new genes with novel functions serves as a major contributor to adaptive evolutionary innovation. It has been shown that novel genes commonly arise from messenger RNAs of ancestral genes, protein-coding genes metamorphosing into new RNA genes, and RNA genes composed from scratch. Alternative splicing during mRNA processing may lead to neogenesis, the process of gene birth, and promote potentially functional adaptations, especially if expressed in the gametes. We characterized the molecular evolution of zonadhesin (ZAN), a large, mosaic protein in the sperm acrosome that mediates species-specific adhesion to the egg's zona pellucida. Intra-species differences in the gene are under strong selective pressures and may be undergoing alternative RNA splicing which contribute to speciation. In marine invertebrates, rapid molecular evolution of egg recognition proteins confers species specificity to fertilization and promotes pre-zygotic reproductive isolation. Herein, we examine the same molecular process in mammals and evaluate alternative mRNA transcripts present in 21 species and 9 suborders of mammals. Further, ZAN protein sequence divergence, with domain duplications unique to some species of rodents, produced dramatic species differences in mature ZAN polypeptide sizes. Phylogenetic analyses indicate alternative transcripts are present in all mammal species examined. However, domain duplications appear to be restricted to the suborder Myomorpha in Rodentia, possibly indicating molecular mechanisms involved in duplication events were initiated following the divergence of the Myomorpha from the other rodent suborders. Alternative splicing during ZAN mRNA processing and extensive domain expansions in some taxa may contribute to potentially functional adaptations for reproductive isolation.

80. COULD A FAILURE IN A POST-MATING ISOLATION PROTEIN ALLOW HYBRIDIZATION IN SPECIES OF DEER IN TEXAS?

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White-tailed deer (*Odocoileus virginianus*) and mule deer (*Odocoileus hemionus*) occur naturally in Texas. Hybridization is thought to commonly occur between these two species in the Trans-Pecos region and along the edges of the Llano Estacado. Given that hybridization occurs and it is known that viable F_1 offspring may be produced, perhaps the molecular mechanism that serves as a post-mating isolation barrier fails, allowing the two species to mate. One of these genes is zonadhesin (ZAN), a sperm protein that is crucial in species-specific binding of the spermatozoa with the zona pellucida of the egg during fertilization. ZAN is the only mammalian protein which shows species specificity across multiple taxa and may act as a potential post-mating isolation mechanism that prevents two species from interbreeding. If the ZAN pathway fails and no longer serves as a barrier for reproductive isolation, then the sperm cell of one species is able to recognize the egg cell of the other species, allowing fertilization to occur; thus, producing hybrids naturally. The focus of this study is to understand the mechanism that allows hybridization between white-tailed and mule deer. ZAN sequences will be analyzed for differences (nucleotide and amino acids) between hybridizing taxa. Furthermore, ZAN sequences of parental and hybrid individuals will be generated to study the level of divergence to determine if the presumptive failure of ZAN allows introgression to occur. Additional molecular markers will be utilized to develop a multi-locus genotype, which will determine the directionality of introgression between the two deer species.

PROPOSAL

81. ELUCIDATING POLYMICROBIAL INTERACTIONS THROUGH A NEW HI-C TECHNIQUE

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Polymicrobial biofilms associated with cystic fibrosis (CF), diabetic ulcers, and chronic wounds are a significant challenge to patient healing, and a large healthcare burden. In these polymicrobial infections microbes are known to interact metabolically and coevolve, but our understanding of these processes is hindered by a lack of techniques to characterize mutations in a spatial context. To address this problem, we have developed a new technique that we name Lysis-Hi-C. With this modified high-throughput chromosome conformation capture (Hi-C) method (5, 6), we hope to simultaneously elucidate both spatial and genomic information in neighboring cells in coevolving, spatially-structured microbial communities. Both CF lungs and chronic wounds are dominated by *Pseudomonas aeruginosa* and *Staphylococcus aureus,* which are known to evolve to form a cooperative association during chronic infections (2,3,4) in which gene expression and metabolism changes and gene loss accumulates due to long, stable associations within hosts (7). Through application of this new method, we will investigate genome-wide evolutionary evidence of complementary mutations among neighboring populations in infections, comparing the pattern with *S. aureus* and *P. aeruginosa* mutations in monoculture and coculture in vitro. Using Lysis-Hi-C, we will test theory predicting rapid loss of processes that can be complemented by neighboring microbes. We predict strong correlation between distance of microbial genotypes with complementary losses within biofilms. Experiments to date have focused on first testing and optimizing our Lysis-Hi-C protocols on artificial biofilms and providing a baseline for distance-detectability prior to our phase-2 experiments on human CF and wound samples.

TOXICOLOGY

82. PREDICTING THE PROBABILITY OF CAPTURING FIVE MEDICALLY IMPORTANT MOSQUITO SPECIES IN LUBBOCK, TEXAS

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Canine heartworm (*Dirofilaria immitis*) is one of the most serious parasitic diseases for dogs in North America, and although rare, has been reported to infect humans. Though typically not fatal in humans, human infections are often misdiagnosed as cancer. These misdiagnosed cases are often known to cost upwards of $80,000 per patient. Canine heartworm is found in every state in the US, however, Texas has one of the highest risks of infections and incidences. Unfortunately, canine heartworm is often beyond the scope of vector control programs as resources are commonly reserved for pathogens considered of greater concern such as West Nile virus. Canine heartworm is transmitted through mosquitoes, several species of which are found in Lubbock. As part of an ongoing West Nile virus vector surveillance program we collected mosquitoes from around the city of Lubbock, Texas. We selected five of the more common species found in Lubbock and developed statistical models to predict the probability of capturing these species in Lubbock County. These models can aid the Lubbock County Vector Control programs in guiding their abatement effort. Ideally, these models will help prevent the overuse of insecticides in the environment within Lubbock County.

83. RISK TO POLLINATORS POSED BY AGROCHEMICAL MIXTURES EMITTED FROM FEED YARDS

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Insect pollinator populations are declining across the United States. Potential causes of observed declines in insect pollinators include, but are not limited to, reduced wildflower availability, monoculture agriculture, parasites, diseases, malnutrition, and pesticides. Livestock production facilities in general, and specifically beef cattle feed yards, use a variety of veterinary pharmaceuticals and pesticides to enhance growth and health of animals, and to control unwanted pests and parasites. Since growth promoters and antibiotics have recently been detected on particulate matter emanating from feed yards, we examined wildflowers and insect pollinators near feed yards in the Southern High Plains for occurrence of antibiotics, beta-agonists, other feed yard-related agrochemicals (macrocyclic lactones), and neonicotinoids. All wildflower samples contained at least one target analyte, while the majority (82%) contained multiple pharmaceuticals/pesticides including 12% of wildflowers containing antibiotics, ractopamine, moxidectin, and a neonicotinoid. To further understand potential risk, Painted Lady butterflies were used as a surrogate species for toxicity testing. Moxidectin was determined to be relatively non-toxic in adult butterflies, but significantly more toxic in larvae. While other chemicals are not overtly lethal, mixtures of moxidectin with other agrochemicals may pose greater risk. These results demonstrate the potential for insect pollinators occurring near feed yards to become exposed to toxic mixtures of feed yard-derived agrochemicals as well as pesticides used on nearby row crops.

84. METAL CONCENTRATIONS IN TISSUES FROM WILD AND CAPTIVE HAWAIIAN GREEN SEA TURTLES (*CHELONIA MYDAS*)

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The Hawaiian subpopulation of green sea turtles is listed as threatened under the U.S. Endangered Species Act. Toxic heavy metals have been shown to decrease immune function, impair growth and decrease reproduction in wildlife. This study compares metal concentrations in green sea turtles living in captivity at Sea Life Park on Oahu, Hawaii, to wild green sea turtles around the Main Hawaiian Islands. Blood and scute samples from six green turtles at Sea Life Park and nine similarly sized wild green turtles were selected from the NIST Biological and Environmental Monitoring and Archival of Sea Turtle Tissues (BEMAST) specimen

bank. Samples were analyzed for metals by Inductively Coupled Plasma - Mass Spectrometry (ICP-MS). Blood provides a good representation of recent exposure to metal contaminants, while scutes sequester elements and indicate long term exposure. The essential elements Cu, Se, V, and Cr were determined to be higher in the scutes of captive turtles whereas concentrations of a non-essential element, As, was significantly higher in wild turtles. Lead concentrations were below the detection limit in the scutes of both captive and wild green turtles but was significantly higher in the blood of wild green turtles than captive green turtles. This is the first study to compare metal concentrations between captive and wild green sea turtles. The captive turtles may provide a baseline of contaminant levels of heavy metals including As and Pb. Establishing a baseline of blood and scute elemental concentrations will allow future studies to quantify changes in sea turtles.

85. SEDIMENT BACTERIAL CCOMMUNITY STRUCTURES AT A NATIONAL PRIORITIES LIST SITE, THE CALLAHAN MINE SITE, AS COMPARED TO A CLEAN REFERENCE SITE

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The Callahan mine was a copper and zinc mine that operated from the 1880s-1972, in Brooksville, Maine. After the closure of the Mine the area was highly polluted by waste mine tailings. In 2001, the site was added to the National Priorities List under the auspices of the CERCLA, and in 2011 remediation of the site began. Studies from before the EPA's remediation of the area found elevated levels of several toxic metals in the sediment and fauna of the Goose Pound Estuary. We collected samples of sediment from a salt marsh in the Esturary in 2012, 2014 and 2015, during the remediation of the site. During this phase, soil from the mine was either removed to an offsite location or placed in the Tailings Impoundment. The focus of remediation was the removal of PCB contaminated soil from the site. We found that sediment samples collected closest to the tailing impoundment had a significantly different bacterial composition than the sediment samples collected further down the tailings gradient (unweighted ADONIS, $p = 0.001$). These samples had an increasingly high relative abundance of the genera *Dehalococcide,* a genus that obtains energy by oxidation of hydrogen, which leads to reductive dehalogenation of halogenated organic compounds. Thus, this genus of bacteria is known to remediate many anthropogenic compounds such as, PCE, TCE and PCBs. The presence of *Dehalococcide* serves as an indicator of PCBs in the marsh, which were presumably disturbed and redistributed during remediation. However, its presence could also indicate natural remediation.

86. NEUROBEHAVIORAL TOXICITY STUDY OF *ENVIRONMENTALLY* RELEVANT CONCENTRATIONS OF FUNGICIDES USING AN EMBRYO- LARVAL ZEBRAFISH (*DANIO RERIO*) AS A MODEL

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Current application of fungicides in cereals, fruits, and vegetables has led to adverse effects on aquatic ecosystem. Recent studies have shown a significant amount fungicide in streams, groundwater, and sediments. In the current study, we compared the neurobehavioral toxicity of two classes of fungicides (azole and strobilurin) on larval zebrafish (*Danio rerio*). The goal of this project was to relative fungicide toxicity using several behavioral endpoints and molecular biomarkers associated with neurodevelopment. Zebrafish embryos were exposed to fungicides (tebuconazole, propiconazole, myclobutanil, azoxystrobin, and pyraclostrobin) at different environmentally relevant concentrations, 10 ng/L, 100 ng/L, 10 ug/L, 100 ug/L and 1 mg/L, starting at 4 h post- fertilization (hpf) to 5 days post fertilization (dpf). All experiments were conducted according to an approved protocol from the Institutional Animal Care and Use Committee (IACUC), Texas Tech University. The behavior assays were conducted to examine swimming behavior (total distance and velocity) at 5 dpf using Danio Vision®. The stability of fungicides under experimental conditions were conducted and analyzed using LC-MS/MS. Gene expression and enzymatic assays were measured to assess relative toxicity amongst fungicides. The velocity and distance travelled by zebra fish larvae when exposed to triazole fungicides (tebuconazole, propiconazole, and myclobutanil) were not significantly different from the controls. However, in case of strobilurin chemical class, there was a significant change in the swimming behavior of the fish larvae and causing oxidative stress and apoptosis.

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87. ASSOCIATIONS BETWEEN THE RATIO OF ORGANIC TO INORGANIC NITROGEN AND GROWTH OF THE ICHTHYOTOXIC GOLDEN ALGA

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Golden alga (GA, *Prymnesium parvum*) is a harmful bloom-producing microalga which in inland ecosystems is typically found in brackish waters. Nitrogen (N) is an essential general nutrient for GA growth but the relative importance of its organic (N_O) and inorganic (N_I) fractions is uncertain. Field studies reported, a negative association of GA abundance with N_I and a positive association with N_O. Thus, while field observations point to the suggestion that GA growth is negatively associated with N_I, the positive association with N_O requires further evaluation. The objective of this study is to determine the influence of N_O (urea or glycine) and N_I (sodium nitrate) on GA growth performance under laboratory conditions. Different molar ratios of N_O to N_I were tested for their effects on exponential growth rate (r, day^{-1}) and maximum cell density (cells ml^{-1}) while keeping total N constant (880 µM) – 0%:100%, 25%:75%, 50%:50%, 75%:25% and 100%:0% (N_O%:N_I%). Cultures were conducted under standard conditions (initial density, 100 cells ml^{-1}; 5 psu; 22°C). Growth rate was not affected by changes in initial N_O:N_I ratio. Maximum cell density, however, gradually increased with increasing relative content of N_O up to 75%, followed by a decline at 100%. In conclusion, while GA can grow in cultures containing exclusively N_O or N_I, optimal growth occurs when both are present and N_O is the predominant fraction. These observations are consistent with field observations and provide context for a better understanding of the association between nutrient stoichiometry and GA growth.

88. EFFECTS OF STREAMFLOW ON RECRUITMENT AND MIGRATION OF A LARGE CATOSTOMID IN CENTRAL TEXAS

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Alteration of flow regime, e.g., timing, duration, flashiness, and magnitude of discharge, has serious implications to fluvial specialists inhabiting large rivers that have evolved flow-dependent life histories. Blue Sucker *Cycleptus elongatus*, is a fluvial-specialist considered vulnerable throughout its range due to habitat requirements and life-history traits. However, relationships between river discharge, migratory behavior, and Blue Sucker recruitment have not been thoroughly examined, particularly in southern portions of its range. The primary objectives of this research were to assess effects of varied streamflow, regulated by water releases from upstream reservoirs, on Blue Sucker movement, habitat use, and recruitment in the lower Colorado River downstream of Austin, Texas. Radio telemetry was used to characterize movement in response to river discharge changes. Quantile regression suggests that large-scale movements are related to seasonal changes in temperature and river discharge prior to relocation. Directional movement models incorporating temperature and streamflow predicted migrations with high accuracy and precision. Furthermore, home range and minimum displacement were correlated with riffle density and habitat complexity. Fin-ray sections (n = 200) taken from specimens during mark-recapture efforts were used to estimate age and associate relative year-class strength with historical discharge. Preliminary results suggest the population in the lower Colorado River has had limited recruitment, and stronger cohorts appear to be associated with years with higher discharge. This work will provide critical information for replicating natural flow regimes vital to fluvial specialist's life history cycles, including Blue Sucker, and inform water management policy decisions in the lower Colorado River, Texas.

89. EVALUATING SUITABLE HABITAT OF INVASIVE TILAPIA AND FORECASTING HOTSPOTS FOR POTENTIAL IMPACTS ON IMPERILED FISHES OF TEXAS

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Tilapia represent popular aquaculture fishes which have had considerable invasive success worldwide, facilitated by commercial escapes and bait-bucket introductions. We conducted a comprehensive literature review to evaluate tilapia research and research gaps, specifically related to invasive tilapia and potential impacts on fish Species of Greatest Conservation Need in Texas. Furthermore, we developed species distribution models in Maxent to predict the extent of suitable habitat of four focal invasive tilapia species: Blue Tilapia *Oreochromis aureus*, Mozambique Tilapia *O. mossambicus*, Nile Tilapia *O. niloticus*, and Wami Tilapia *O. urolepis*. These focal species are already present or have been previously documented in the wild in Texas, and are currently permitted for aquaculture and/or pond stocking, with the exception of *O. urolepis*. *O. urolepis* is commonly used in aquaculture in other states and sold online; therefore, introductions could potentially occur in Texas. Predictions of suitable habitat in Texas differed between species. Invasion success, in terms of area occupied, was predicted to be greatest for Blue Tilapia, with a modeled distribution potential of almost the entirety of the state. Our combination of literature review and distribution modeling provides insights that may help to target future research and management of invasive tilapia in areas where most effective for evaluating and minimizing potential impacts to imperiled fishes.

90. ASSESSING THE EFFICACY OF AND COMPARING MANUAL SEARCH AND LANDSCAPE CLASSIFICATION TO LOCATE WIND TURBINES USING SATELLITE IMAGERY

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Prior to investing large amounts of time on any project, it helps to assess the efficacy of the methodology and to compare different potential methods. We are conducting research on Swainson's hawks (*Buteo swainsoni*), a large migratory raptor, to see if the wind energy industry might pose a risk to this species. We attached GPS platform transmitter terminals (PTT's) to 24 adult Swainson's hawks breeding near the Amarillo area of Texas in 2012 and 2013 to assess risk that the wind energy industry might pose. Swainson's hawks breed across western North America and winter in Argentina, with a fairly narrow migration pathway that crosses national borders of 17 countries. Because wind turbine locations are unknown internationally, we are starting a project to locate wind turbines across the entire global region relevant to Swainson's hawks in our study. We have identified four methods to do so, and have assessed the efficacy of each method. The first two, using Google Earth and ArcMap basemaps, had imagery that was too old to be relevant to this study. We used a 2013 USGS known-turbine-location dataset to assess detection rate of manual search using imagery from the Sentinel-2 satellite as a single-blind experiment, where the searcher was unaware of the assessment. We also ran landscape classification models in ERDAS imagine with known turbines as training data, using the same satellite imagery, to assess efficacy of that method and to compare the two methods. Projects are ongoing, and results will be presented at the meeting.

91. SPATIALLY EXPLICIT GENETIC ANALYSIS IS ESSENTIAL FOR GUIDING MANAGEMENT DECISIONS OF A THREATENED KANGAROO RAT

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Comprehensive studies that document the abundance, distribution and evolutionary potential of imperiled species are vital for conservation management strategies. The Texas kangaroo rat (*Dipodomys elator*) is a threatened rodent currently found in five counties in north-central Texas. Its distribution spans two Texas ecoregions: the cross timbers and prairies to the east and the rolling plains to the west. Since 2015, we conducted surveys across the historical range of *D. elator*. Here, we report typical population genetic measures obtained via 3RAD, a variant of a reduced representation, next-generation sequencing approach. We analyzed sequence data from 36 individuals using STACKS. To account for computational stochasticity, we varied the minimum locus stack depth to provide both liberal and conservative population genetic estimates. Both sets reveal some population genetic structure within *D. elator* and show little evidence that the population conforms exclusively to the isolation-by-distance model. This suggests other factors, such as geographic or anthropogenic barriers, isolation-by-resistance or isolation by some other source playing a role in the genetic substructure of the population. Moreover, there is a large sampling hole or area where no samples were available in the center of the *D. elator* distribution, making population genetic inferences challenging. We posit that though traditional population genetic estimates such as heterozygosity and *F*-statistics offer some immediate insight to the management of the species, we stand to gain more from a spatially explicit perspective. Thus, incorporating models that focus on aspects of the physical landscape is critical for evaluating the evolutionary potential of this threatened species.

92. AN EVALUATION OF ABIOTIC AND BIOTIC HABITAT CHARACTERISTICS POTENTIALLY AFFECTING THE CURRENT DISTRIBUTION AND ABUNDANCE OF A RARE KANGAROO RAT

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Understanding species distributions is essential to ecology, evolution, and conservation biology. For example, rare species often have sparse or restricted spatial distributions. Identifying factors influencing the presence of these taxa across their geographic range may be important to better understand factors influencing their rarity. We surveyed the rodent community and sampled vegetation and soil at 35 sites across the historical range of the Texas kangaroo rat (*Dipodomys elator*), a rare and threatened species in north-central Texas, to evaluate abiotic and biotic characteristics that we hypothesized potentially limit its present-day distribution. Of the 13 rodent species that we encountered, *D. elator* was the fifth most widely-distributed species (i.e., present at six of our sites). We found no evidence that interspecific interactions influence the distribution of *D. elator*. Soil and vegetation characteristics appear to be more influential in determining the present-day distribution of this species, although there was overlap in habitat characteristics between sites of presence versus sites of absence of *D. elator*. These findings suggest that the Texas kangaroo rat may not be saturating all available suitable habitat. If so, future research should focus on patterns of dispersal and inter-patch movement for this species. Results from our work should improve understanding of factors contributing to the rarity of this kangaroo rat species and its vulnerability to habitat change and help inform conservation and management strategies for rare species.

93. WINTER ACTIVITY PATTERNS OF BATS IN THE SOUTHEASTERN UNITED STATES

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Throughout the eastern United States, white nose syndrome (WNS; *Pseudogymnoascus destructans*) has negatively affected populations of cave-roosting bats. However, in the southeastern United States where caves are noticeably absent, several of these cave roosting species such as the big brown bat (*Eptesicus fuscus*), the tricolored bat (*Perimyotis subflavus*), the southeastern myotis (*Myotis austroriparius*), and the federally threatened northern long-eared myotis (*M. septentrionalis*) are active year-round. The presence of these species in winter and the absence of WNS in the region provides a unique opportunity to study the natural activity patterns of bats. In this study, we are investigating spatial and temporal activity patterns of bats in managed forests of central Louisiana and eastern Texas using acoustic detectors from late-December through late-March. Data collected in this study will provide insight into habitat selection of different species and those weather conditions that facilitate winter activity. We can use this information to provide management recommendations for forestry practices in the southeastern United States.

94. SEROPREVALENCE OF *NEOSPORA CANINUM* IN WILD PIGS (*SUS SCROFA*)

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Neospora caninum is a protozoan parasite reported as a leading cause of cattle abortions and reproductive failure worldwide. After ingestion of infected tissues, definitive hosts such as coyotes and dogs excrete oocysts into the environment and can contaminate food and water sources available to livestock. Ingestion of *N. caninum* oocysts results in infection of cattle and other intermediate hosts. The parasite can then be vertically transmitted, resulting in spontaneous abortions, fetal reabsorption, and decreased milk production; costing the cattle industry approximately $1.3 billion dollars annually. With wild pig populations nearing 6 million in the United States, contact between wild pigs and livestock is inevitable. This is a result of an already widespread geographic distribution combined with continuous, rapid range expansion. As a known reservoir for numerous bacterial, viral, and parasitic diseases, wild pigs are of particular importance for public and veterinary health relative to the prevention of infectious diseases. In collaboration with the Noble Research Institute, 388 wild pigs were captured in southern Oklahoma over approximately 11,000 acres during a three-year study. From this collection, 84 pigs were screened for *N. caninum* antibody presence using a qualitative sandwich porcine *Neospora caninum* antibody ELISA Kit and a competitive inhibition ELISA. This data signifies the importance of disease surveillance in wild pigs to better understand the threat of environmental exposure and the role wild pigs play in disease transmission to livestock.

95. FLOW EFFECTS ON YOUNG-OF-YEAR GUADALUPE BASS

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Guadalupe Bass *Micropterus treculii* is a species of greatest conservation need in Texas due to habitat loss and introgressive hybridization. In addition to these threats, habitat alteration due to altered flow regimes is thought to be a major contributing factor to declines in Guadalupe Bass abundance. The purpose of this project is to evaluate the mechanisms by which streamflow impacts young-of-year (YOY) Guadalupe Bass. Guadalupe Bass were collected from the North Llano (NLR) and South Llano (SLR) Rivers in Kimble County, Texas every ten days from June – August in 2016 and 2017. While the SLR is a relatively undistributed stream system, maintaining a constant flow throughout the summer months, the NLR is subject to annual dewatering and has a more variable flow regime. Stomach contents were examined (n=1270) to evaluate the relative contribution of drift to YOY Guadalupe Bass diet under different flow conditions. Percent contribution by count and volume of prey categories were compared using ANCOVA, with stream discharge and total length as covariates. Catch-curve based methods will be used to estimate mortality rates on a weekly basis throughout the summer months. Preliminary results suggest a negative correlation between low discharge and YOY Guadalupe Bass recruitment and drift prey availability. This work provides important information for the development of instream flow recommendations to benefit fluvial species of conservation concern, such as Guadalupe Bass.

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