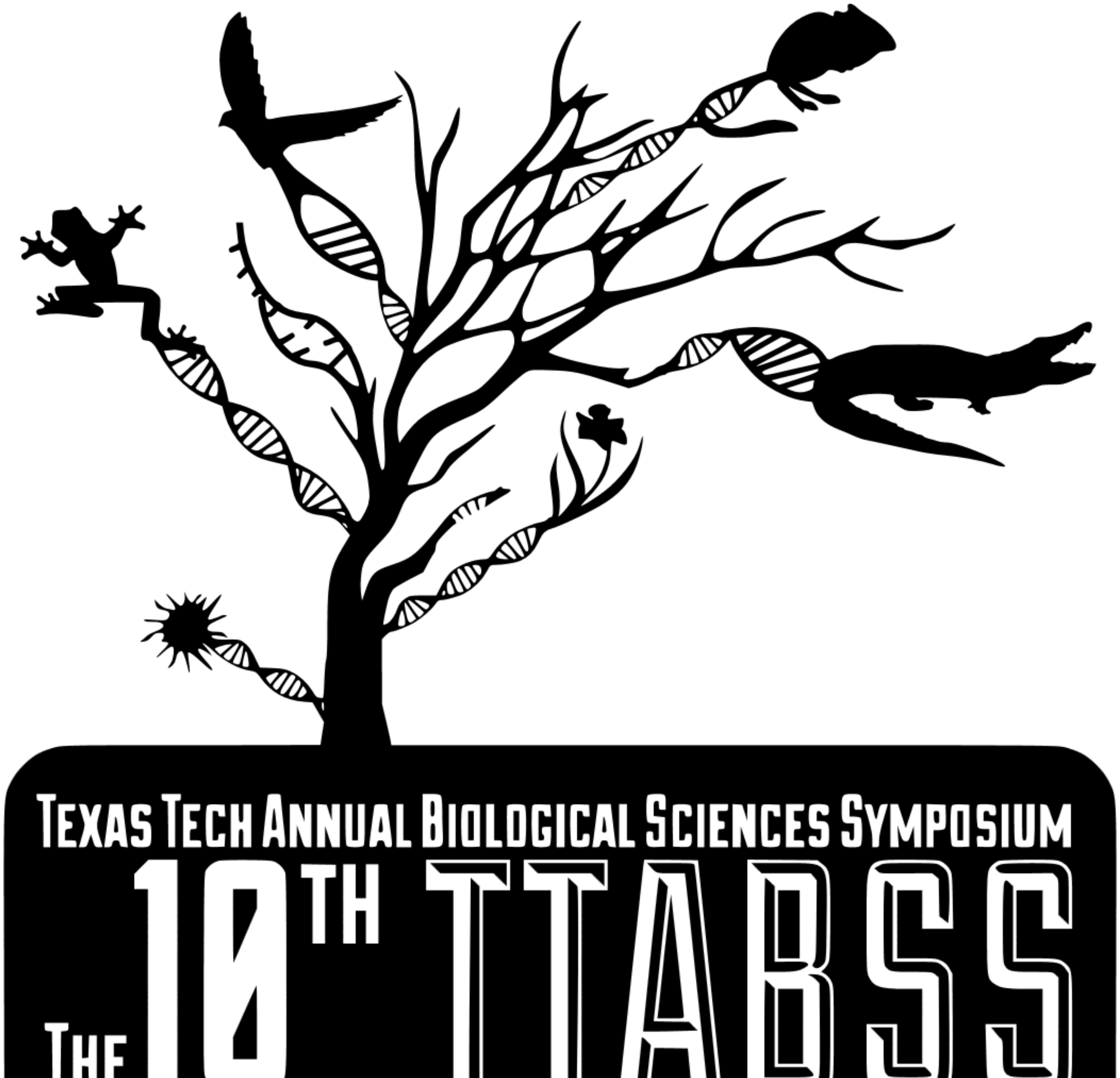
10th TEXAS TECH ANNUAL BIOLOGICAL SCIENCES SYMPOSIUM (TTABSS)



DEPARTMENT OF BIOLOGICAL SCIENCES
LUBBOCK, TEXAS
APRIL 26-27th, 2019

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Welcome Note:

It is with great pleasure we welcome everyone to the 10th Texas Tech Annual Biological Sciences Symposium (TTABSS), which is held this year of 2019, on April 26th and 27th. The Biological Sciences Symposium is hosted at the Student Union Building at 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 10 academic institutions. Our program will have 126 research presentations that include 64 poster presentations and 4 concurrent oral sessions. This year, we introduce two new categories: Computational and Mathematical Biology and Emerging Professionals. In addition, we would like to announce our two distinguished guest speakers, Dr. Ramy Karam Aziz and William Lindsay Chadderton, MSc. Each of these speakers are renowned scientists in their respective fields. Dr. Ramy Karam Aziz is from Cairo University and focuses on microbiology, immunology, and metagenomics. Mr. William Lindsay Chadderton is associated with The Nature Conservancy’s Great Lakes Project, working with invasive species. 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 2019. 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!

Macy Madden
President, TTUAB 2018 – 2019

Craig Tipton
Local Committee Chair, TTABSS 2018 – 2019

EVENT HOSTS

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

EVENT COLLABORATORS

CISER/HHMI at Texas Tech University
The Institute for Environmental and Human Health (TIEHH)
Department of Mathematics & Statistics, Texas Tech University
Department of Natural Resources Management, Texas Tech University (NRM)

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Texas Tech Health Science Center
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McLennan Community College
Wayland Baptist University
Eastern New Mexico University
West Texas A&M University
Baylor University
University of Benin

PLENARY SPEAKERS

Ramy K. Aziz is a tenured professor, at Cairo University, Egypt, faculty of Pharmacy and the chair of the department of microbiology and immunology. He is affiliated with the Argonne National Laboratory as a genome analyst in PATRIC (Pathosystems Resource Integration Center) and RAST (Rapid Annotation using Subsystem Technology) projects. He is also one of the world experts in phage genomic annotation and a co-discoverer of crAssphage, which is the most abundant virus in the human gut microbiota. Lately, he became interested in microbiome research and drug-microbiome interactions and founded the pharmacomicrobiomics database.

Ramy Aziz received his BSc. in pharmaceutical sciences from Cairo University, Egypt. Then, he received his Ph.D. in microbiology and immunology at University of Tennessee Health Science Center (UTHSC) in 2005. After graduation, he did postdoctoral work at UTHSC and became a research scientist at the Computation Institute, University of Chicago. Next, he joined University of California, San Diego as a visiting scientist at Systems Biology Research Group (Bernhard Ø. Palsson lab). Eventually, he chose to return home to Egypt to launch microbiome and genome research. Recently, he received funding to establish the Egyptian Center for Microbiome and Genome Research. He is deeply involved in education at many levels, and through many platforms (including e-learning), with his most recent endeavor being to launch a new diploma of genomics and bioinformatics at Cairo University.

Mr. W. Lindsay Chadderton is the Director for the Aquatic Invasive Species Program within The Nature Conservancy's Great Lakes Project. In this position, he is responsible for supporting policy and programmatic development limiting what is considered the most significant threat to the health of the Great Lakes—invasive species. Mr. Chadderton is part of a team in conjunction with the University of Notre Dame which developed the environmental DNA surveillance methods used to detect and track the invasion of Asian carp in the Chicago Area Waterway System and the Great Lakes. Such early detection is considered pivotal to the protection of these waterways. He previously worked for the Department of Conservation in New Zealand, managing a broad range of projects including island rat eradications, incursion responses to the marine algae *Undaria pinnatifida* and establishing spatial tools useful for freshwater systematic conservation planning systems. He was also a technical advisor to the Department of Conservation and Biosecurity New Zealand on various freshwater fish and *Didymosphenia geminata* incursion responses. Lindsay earned a BS and MS in Zoology from Canterbury University in Christchurch New Zealand, majoring in limnology.

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 2019 would not have been possible.

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Olushola Awoyemi - Department of Environmental Toxicology, TTU
Ramy Aziz - Department of Microbiology and Immunology, Cairo University
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Catherine Wakeman - Department of Biological Sciences, TTU
Mark Wallace - Department of Natural Resource Management, TTU
Lizz Waring - Department of Biological Sciences, TTU
Zhixin Xie - Department of Biological Sciences, TTU
John Zak - Department of Biological Sciences, TTU

Moderators

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Taylor Soniat – Biological Sciences, TTU
Erin Stukenholtz – Natural Resource Management, TTU
Jenny Korstian – Biological Sciences, TTU
Saba Nafees – Biological Sciences, TTU
Ryan Vazquez – Biological Sciences, TTU
Preston McDonald – Biological Sciences, TTU
Nicole Paulat – Biological Sciences, TTU
Adrienne Dale – Biological Sciences, TTU
Craig Tipton – Biological Sciences, TTU
Macy Madden – Biological Sciences, TTU

Texas Tech Annual Biological Sciences Symposium
The 10th TTABSS

The 2019 TTABSS logo was produced exclusively for the Association of Biologists at Texas Tech University by Mr. Moamen Elmassry and Miss Erin Stukenholtz.

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Dr. Lou Densmore

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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
Little Panda	1221 University Avenue	(806) 722-0888
Mesquites Sports Grill	2419 Broadway	(806) 744-9277
One Guy's Pizza	1101 University Avenue	(806) 747-1226
Raising Canes Chicken	907 University Avenue	(806) 744-8552
Rocky LaRues	2420 Broadway #B	(806) 747-6366
Ruby Tequila's	413 University Avenue	(806) 747-7829
Sazon Restaurant	1205 University Avenue	(806) 687-2572
Spanky's	811 University Avenue	(806) 744-5677
Starbucks	801 University Avenue	(806) 744-8234
Subway	1109 University Avenue	(806) 744-1535
Which Wich Sandwich	1021 University Avenue	(806) 472-9424

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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

10th Texas Tech Annual Biological Sciences Symposium
April 26-27, 2019

Venue:
Student Union Building
15th St & Akron Avenue
Lubbock, TX 79409

PROGRAM AT A GLANCE

Friday, April 26th

4:30 pm – 9:00 pm	Registration table open
4:30 pm – 5:00 pm	Poster Set-up and Registration, Student Union Building, Ballroom, Texas Tech University
5:00 pm – 5:15 pm	TTABSS 2019 kick off by Dr. John Zak, Interim Department of Biological Sciences Chair, TTU
5:30 pm – 6:30 pm	Plenary Talk – Dr. Ramy Karam Aziz, Cairo University – Ballroom, Student Union Building ***"Our Microbiome Cloud, Our Health, and Our Drugs: Common Destiny and Conflicts of Interest"***
6:30 pm – 8:30 pm	Poster Session, Judging, and Vendor Show (heavy hors d' oeuvres will be served), Ballroom, Student Union Building, Texas Tech University
8:30 pm – 9:00 pm	Poster Takedown

Saturday, April 27th

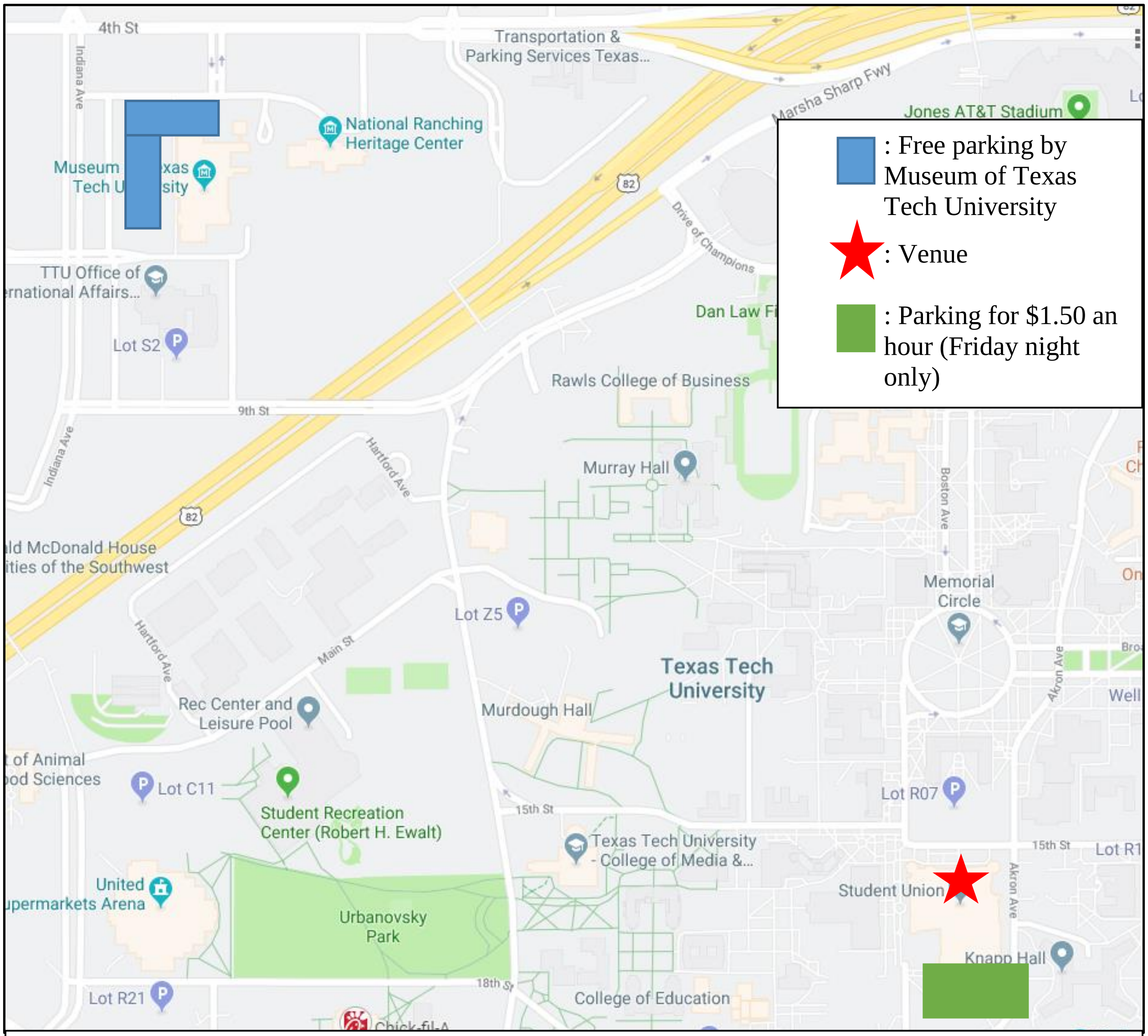
7:30 am – 9:00 pm	Registration table open

7:30 am – 8:30 am	Registration and Breakfast, Matador Room, Student Union Building, 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 – Student Union Building, Traditions Room, Canyon Room, Mesa Room, Playa Room
10:00 am – 10:15 am	Coffee Break, Matador Room
10:15 am – 12:00 pm	Oral Presentations – Student Union Building, Traditions Room, Canyon Room, Mesa Room, Playa Room
12:00 pm – 1:30 pm	Lunch Break (On Your Own)
1:30 pm – 3:00 pm	Oral Presentations – Student Union Building, Traditions Room, Canyon Room, Mesa Room, Playa Room
3:00 pm – 3:30pm	Coffee Break, Matador Room
3:30 pm – 4:30 pm	Plenary Talk, William Lindsay Chadderton MSc, Nature Conservancy– Mesa Room, Student Union Building ***“Progress towards the development of a Great Lakes surveillance program—the what, where, and how”***
6:00pm – 9:00 pm	Awards Banquet and Dinner, Matador Room, Student Union Building

EVENT LOCATION PARKING

April 26-27, 2019

Student Union Building
15th St & Akron Avenue
Lubbock, TX 79409



- On Friday night:
  - If you are a TTU student with a parking permit, regular parking rules apply to you
  - If you do not have a TTU parking permit, then you may either:
    - Park for free by the Museum of Texas Tech University and walk to the Student Union or
    - Pay $1.50 an hour in the indicated parking lot
- On Saturday, anyone can park in the green parking lot for free

DETAILED SCHEDULE OF EVENTS
POSTER SESSION
FRIDAY, APRIL 26th

Friday, April 26th

4:30 pm – 9:00 pm	Registration table open
4:30 pm – 5:00 pm	Poster Set-up and Registration, Student Union Building, Ballroom, Texas Tech University
5:00 pm – 5:15 pm	TTABSS 2019 kick off by Dr. John Zak, Interim Department of Biological Sciences Chair, TTU
5:30 pm – 6:30 pm	Plenary Talk – Dr. Ramy Karam Aziz, Cairo University – Student Union Building, Ballroom ***"Our Microbiome Cloud, Our Health, and Our Drugs: Common Destiny and Conflicts of Interest"***
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

First Floor

Student Union Building Interior Map

Poster
session
located
here

UNDERGRADUATE POSTERS

1. **AN INVESTIGATION OF PSEUDOMONAS AERUGINOSA CYAN FLUORESCENCE WITH THE MOLECULIGHT I:X BACTERIAL FLUORESCENCE IMAGING DEVICE**
   William L. Little[1*], Andrea J. Lopez[1], Andre J. Gomez[1], Klara C. Keim[1], Monique Y. Rennie[2], and Allie Clinton Smith[1]
   [1]Department of Honors Studies, Texas Tech University, Lubbock, Texas 79409, USA
   [2]MolecuLight, Toronto, Ontario M5G 1T6, Canada

2. **USE OF FLUORESCENCE AND COMPOUND LIGHT MICROSCOPE OLYMPUS BX40 WITH OLYMPUS DP74 CAMERA AS A TOOL FOR STUDING AEROALLERGENS OF THE TEXAS PANHANDLE**
   Nabarun Ghosh[1], Herlinda S. Lee[1*]
   [1]Depatment of Life, Earth and Environmental Sciences, West Texas A&M University Canyon, Texas 79016

3. **PREVALENCE AND FREQUENCY OF ENCRUSTING *MILLEPORA* ON OCTOCORALS ON THE MESOAMERICAN BARRIER REEF IN ROATAN, HONDURAS**
   S. Cole[1], S. Stewart[2], K. Singh[1*], S. Hill[2], S. Randell[2], S. Lockwood[1]
   [1]Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas
   [2]McLennan Community College, Waco, Texas

4. **EXAMINING IMMUNE-ASSOCIATED ORGAN MASSES IN TRANSGENIC AND NON-TRANSGENIC APPswe/PS1dE9 MICE, AN AMYLOID β-GENIC ALZHEIMER'S DISEASE MOUSE MODEL**
   Neel P. Roy[1*], Emily Stephens[1], Amber Loya[1], Paul L. Soto[2], Breanna N. Harris[1]
   [1]Department of Biological Sciences, Texas Tech University
   [2]Department of Psychology, Louisiana State University

5. **INITIAL RESULTS OF FORAGE SEED BANK GERMINATION RELATIVE TO LANDSCAPE LEVEL RESTORATION EFFORTS IN NORTH-CENTRAL NEW MEXICO**
   Jordan Keats[1*], Sharon E. Smythe[1], James W. Cain III[2], and Warren C. Conway[1]
   [1]Department of Natural Resources Management, Texas Tech University, Lubbock, TX 79409
   [2]Cooperative Fish and Wildlife Research Unit, Department of Fish, Wildlife, and Conservation Ecology, New Mexico State University, Las Cruces, NM 88003

6. **METFORMIN INHIBITS SLC6A14, AN AMINO ACID TRANSPORTER THAT DRIVES PANCREATIC CANCER GROWTH**

Nhu Nguyen[1]*, Devaraja Rajasekaran[2], and Yangzom D. Bhutia[2]
[1]Department of Biological Science, Texas Tech University, Lubbock, Texas 79409
[2]Department of Cell Biology and Biochemistry, Texas Tech University Health Sciences Center, Lubbock, Texas 79430

7. **TESTICULAR HISTOPATHOLOGY IN AN ALZHEIMER'S DISEASE MODEL**
   Emily R. Stephens[1]*, Breanna N. Harris[1], Christine M. Prater[1], Paul L. Soto[2], and James A. Carr[1]
   [1] Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409
   [2] Department of Psychology, Louisiana State University, Baton Rouge, LA 70803

8. **EFFECTS OF AHPCO AND BI-POLAR PLASMA NANOTECHNOLOGIES ON PARTICULATE MATTER 2.5 AND ROLE IN TREATING RESPIRATORY SYNDROMES AND ALLERGIC RHINITIS**
   Rebecca Beltran[1*], Aubrey Howard, Prabir Banerjee, Shaily Goyal and Nabarun Ghosh[2]
   [1]Department of Life, Earth and Environmental Sciences, West Texas A&M University, Canyon, Texas 79015
   [2]Department of Life, Earth and Environmental Sciences, West Texas A&M University, Canyon, Texas 79015

9. **EXERCISE PRECLUDES SALT CRAVING AND FAT CONSUMPTION IN SATISFIED FEMALE ATHLETE**
   Gracia B. Sebastiao[1]*, Aaron K. White[1], and Daniela S. Pereira, D.S.[1]
   [1]Department of Math and Science, Wayland Baptist University, Plainview, Texas 79072

10. **IMPACTS OF AMYLOID-BETA ACCUMULATION ON SHORT-TERM MEMORY IN AN APPSWE/PSEN1DE9 ALZHEIMER'S MOUSE MODEL.**
    Jordan A. Myers[1]*, Paul L. Soto[1], Breanna N. Harris[1]
    [1]Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

11. **WATER QUALITY WITHIN LUBBOCK'S CANYON LAKE SYSTEM AND ITS ASSOCIATION WITH GROWTH OF THE HARMFUL GOLDEN ALGA**
    Santos David Sotelo Jr[1*], Rakib H. Rashel[2] and Reynaldo Patiño[3]
    [1]Department of Civil, Environmental, & Construction Engineering, Texas Tech University, Lubbock, Texas 79409
    [2]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
    [3]U.S. Geological Survey, Texas Cooperative Fish & Wildlife Research Unit and Departments of Biological Sciences and Natural Resources Management, Texas Tech University, Lubbock, Texas 79409

12. AN INVESTIGATION ON THE ASSESSMENT OF THE GENOTOXICITY OF ATRAZINE BASED HERBICIDE ON *ALLIUM CEPA*

Lindsey Vande Streek[1]*, Mykala Robertson[1], Aubrey Howard[1], and Nabarun Ghosh[1]
[1]Department of Life, Earth & Environmental Sciences, West Texas A&M University, Canyon, Texas

13. BODY CONDITION AND POPULATION COMPOSITION OF RIO GRANDE COOTERS ON THE BLACK RIVER, NEW MEXICO

Laramie B. Mahan[1*], Thanchira Suriyamongkol[1], and Ivana Mali[1]
[1]Department of Biology, Eastern New Mexico University, Portales, NM 88130

14. WIND TURBINE CONCENTRATIONS AND THE THREATS THEY POSE TO SWAINSON'S HAWKS

Margaret E. Meier[1*], Katheryn A Watson[1], Clint W. Boal[2], James D. Ray[3]
[1]Department of Natural Resource Management, Texas Tech University, Lubbock, Texas, 79409, USA
[2]U.S. Geological Survey, Texas Cooperative Fish and Wildlife Research Unit, Texas Tech University, Lubbock, TX, 79409, USA
[3]Consolidated Nuclear Security, LLC, USDOE/NNSA Pantex Plant, Amarillo, TX, 79120

15. CO-OVEREXPRESSION OF *AtClCc* AND *PP2AC5* GENES TO INCREASE SALT TOLERANCE IN ARABIDOPSIS THALIANA

Lars A. Lindgren[1*], Ruvini Mathangadeera[1], Yifan Cai[1], and Hong Zhang[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

16. EXPRESSION OF THE POLYADENYLATION PROTEINS CSTF-64 AND CSTF-77 IN BACTERIA

Leola L. Eko[1]*, Petar N. Grozdanov[1], Clinton C. MacDonald[1]
[1]Department of Cell Biology and Biochemistry, Texas Tech University Health Sciences Center, Lubbock TX 79430

17. MESQUITE EFFECTS ON MICROHABITAT ALTER COMMNITY STRUCTURE BUT NOT PRODUCTIVITY IN SHORT GRASS PRAIRIE

Leah R Ortiz[1*],Nick G Smith[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

18. PRELIMINARY ASSESSMENT OF ORNATE BOX TURTLE OCCUPANCY IN ROOSEVELT COUNTY, NEW MEXICO

Alissa A. Kreikemeier[1*], Thanchira Suriyamongkol[1], Vinicius Ortega-Berno[1], and Ivana Mali[1]
[1]Department of Biology, Eastern New Mexico University, Portales, New Mexico 88130

19. PILOT STUDY: MACERATION TECHNIQUES COMPARING HYDROGEN PEROXIDE AND WATER.

Terri L. Cox[1*] and Julie A. Parlos, Ph.D.[1]
[1] Department of Biology, Texas Tech University at Waco, Waco, Tx 76708

20. PHYLOGENETIC ANALYSIS OF BATS IN THE GENUS *MONOPHYLLUS* USING MITOCHONDRIAL AND NUCLEAR GENETIC MARKERS

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
[4]University of Nebraska State Museum, Lincoln, NE

21. PHYLOGENY OF *PEROMYSCUS MANICULATUS* SPECIES GROUP USING NOVEL NUCLEAR MARKERS, *DHPS* AND *SYCE1*

Daysi Alvarez[1]*, Laramie L. Lindsey[1], and Robert D. Bradley[1,2]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX
[2]Natural Science Research Laboratory, Museum of Texas Tech University, Lubbock, TX

22. GROWTH AND RECRUITMENT OF GRAY REDHORSE IN THE LOWER COLORADO RIVER

Caroline E. Jurca*[1], Matthew R. Acre[1], Allison A. Pease[1], and Preston T. Bean[2]
[1]Department of Natural Resources Management, Texas Tech University, P.O. Box 42120, Lubbock, TX 74909
[2]Texas Parks and Wildlife Department, Heart of the Hills Fisheries Science Center, Mountain Home, TX, 78058

23. EVALUATION OF NUISANCE ALLIGATOR MANAGEMENT AND HUMAN-ALLIGATOR CONFLICT

Zachary J. Patton[1]*, Brandon A. Gross[1], J. Alex Beacher[2], Llewellyn D. Densmore III[1]
[1]Texas Tech University, 2901 Main Street, Lubbock, TX 79409, USA,
[2] Memphis Zoo, 2000 Prentiss Place, Memphis, TN 38112, USA

24. THE EFFECT OF LIFE HISTORY STRATEGIES ON STOMATAL CHARACTERSTICS USING HERBARIUM SPECIMENS FROM GUADALUPE MOUNTAINS NATIONAL PARK

Zachary W. Bailey[1]* and Dr. Matthew Johnson[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

25. TERRITORIALITY AND AGGRESSIVE BEHAVIOR OF DUSKY DAMSELFISH, *STEGASTES ADUSTUS*, IN ROATÁN, HONDURAS

Jasmine B. Reynoso[1], Maria Jose B. Lozada[1*], Hunter A. Marze[1], Elizabeth Garcia[1], Shannon Hill[1], Stephanie A. Lockwood[2], Donna E. Hamilton[3], Traesha Robertson[4], Stephanie M. Randell[1]
[1]McLennan Community College, Waco, Texas
[2] Texas Tech University at Waco, a Higher Education Site, Waco, Texas
[3] University of North Texas-Dallas, Dallas, Texas
[4]College of Coastal Georgia, Brunswick, Georgia

26. WARMING UP WITHOUT DINNER: HIBERNATING BATS WITHOUT FORAGING OPPORTUNITIES DESYNCHRONIZE FROM SUNSET DESPITE WARM-CLIMATE

Samantha N. Garcia[1*] and Liam P. McGuire[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

27. CONSERVATION GENOMICS OF PLANT POPULATIONS IN GUADALUPE MOUNTAINS NATIONAL PARK USING HERBARIUM SPECIMENS

Madeline C Slimp[1]*, Haley Hale[1,] Dr. Matthew Johnson[1]
[1]Department of Biological Sciences

28. GLUCOSE TOLERANCE IN AN APPSWE/PS1DE9 ALZHEIMER’S DISEASE MOUSE MODEL.

Madalynn J. Sealey[1]*, Breanna N. Harris[1], Paul L. Soto[2] and Vijay Hegde[3]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX
[2]Department of Psychology, Louisiana State University, Baton Rouge, LA
[3]Department of Nutritional Sciences, Texas Tech University, Lubbock, TX

29. INFLUENCE OF THERMAL PROPERTIES ON ROOST USE BY THE CAVE MYOTIS (*MYOTIS VELIFER*)

Austin L. Hargrove[1*], John D. Stuhler[1], Erin E. Stukenholtz[1], Jenna R. Grimshaw[1,2], Emma E. Guest[1], Michaela K. Halsey[1,2], and Richard D. Stevens[1,3]
[1]Department of Natural Resources Management, Texas Tech University, Lubbock, Texas 79409
[2]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
[3]Museum of Texas Tech, Lubbock, Texas 79409

30. CHRONIC STRESS ALTERS REARING BEHAVIOR AND HIPPOCAMPAL CA3 REGION STRUCTURE IN WILD-TYPE MICE

Fabiola Arzate[1]*, Jack Christian[2], Bridgette Kerr[1], Heather Blakley[1], Justin Blakley[1], Daniel Cherkowsky[1], Mohammad Jodeiri-Farshbaf[1], and Karina Alviña, PhD
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
[2]Standford University, Stanford California, 94305

31. ENSEMBLE BY ENSEMBLE: DO AFROTROPICAL BAT ENSEMBLES DIFFER IN RESPONSE TO ELEVATIONAL GRADIENTS?

Hallie Morton[1*], Iroro Tanshi[1,2], Tigga Kingston[1]
[1]Department of Biological Sciences Texas Tech University, Lubbock, USA;
[2]Department of Animal and Environmental Biology, University of Benin, Benin City, NGA

32. EFFECTS OF ACUTE STRESS AND CORTICOSTERONE ON SHORT-TERM MEMORY IN AN APPSWE/PS1DE9 MOUSE MODEL OF ALZHEIMER’S DISEASE

Sabra L. Williams[1]*, Giuliana DiMarco[1], Breanna N. Harris[1], Paul L. Soto[2]
[1]Texas Tech University, Department of Biological Sciences, Lubbock, TX
[2]Louisiana State University, Department of Psychology, Baton Rouge, LA

33. ROLE OF ERGOSTEROL AND SPHINGOLIPIDS IN NUTRIENT UPTAKE DURING STARVATION CONDITIONS ENCOUNTERED BY PROMASTIGOTE STAGE OF LEISHMANIA MAJOR.

Veronica L. Hernandez[1]*, Samrat Moitra[1], Wei Xu[2], and Kai Zhang[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
[2]Department of Molecular Microbiology, Center for Women's Infectious Disease Research, Washington University School of Medicine, Saint Louis, MO 63110

34. THE EFFECTS OF DIETARY EICOSAPENTAENOIC ACID SUPPLEMENTATION ON COGNITIVE FUNCTION IN AMYLOID BETA TRANSGENIC MICE

Kaylee Alers Maldonado[1]*, Logan Mounce[1]*, Mahsa Yavari[2], Breanna Harris[1,3], Latha Ramalingam[2,3], Naima Moustaid-Moussa[2,3]
[1]Department of Biological Sciences, [2]Department of Nutritional Sciences, and [3]Obesity Research Cluster, Texas Tech University, Lubbock, Texas 79409

35. RELATIONSHIP AMONG CORTICOSTERONE, STRESS, AND ANXIETY, AND MEMORY IN AN APPSWE/PS1DE9 MOUSE MODEL OF ALZHEIMER'S DISEASE.

Breanna R. Roberts[1]*, Paul Soto[2], Breanna N. Harris[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX
[2]Department of Psychology, Louisiana State University, Baton Rouge, LA

36. ANNUAL VARIATION IN COMMUNITY STRUCTURE AND ABUNDANCE OF SHORT GRASS PRAIRIE BIRDS IN LUBBOCK COUNTY, TX

Jonathon P. Bentley[1]*, Clint W. Boal[1]
[1]Department of Natural Resource Management, Texas Tech University, Lubbock, Texas, 79409

37. GABAERGIC DEFICITS ARE ASSOCIATED WITH SEIZURE SUSCEPTIBILITY IN A MOUSE MODEL OF SLC13A5 DEFICIENCY

Toby Anderson[1]*, Fowzia Selina[1], Rui Wang[1], Xiaobo Liu[1], Madison Hayes[1], Sabarish Ramchandran[3], Vadivel Ganapathy[2,3], and J. Josh Lawrence[1,2]
[1]Department of Pharmacology and Neuroscience, Texas Tech University Health Sciences Centre-School of Medicine, Lubbock, USA,
[2]Center of Excellence for Translational Neuroscience and Therapeutics, Texas Tech University Health Sciences Center, Lubbock, TX
[3]Cell Biology & Biochemistry, Texas Tech University Health Sciences Centre-School of Medicine, Lubbock, USA

38. DO VISUAL SYSTEM CRF RECEPTORS INFLUENCE VISUALLY GUIDED FEEDING?

Ryann N. Lockwood[1]*, Allison P. Kennedy[1], Christine M. Prater[1], James A. Carr[1], Breanna N. Harris[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX

39. INVESTIGATING THE EFFECTS OF SOCIAL INTERACTION IN MINIMIZING STRESS-INDUCED BEHAVIORAL CHANGES IN MICE

Sagufta Garasia*[1,2], Fabiola Arzate[1], Bridgette Kerr[1], Heather Blakley[1], Justin Blakley[1], Nabeela Manal [1,2], Daniel Cherkowsky[1], Mohammad Jodeiri-Farshbaf[1], and Karina Alviña, PhD[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
[2]Honors College, Texas Tech University, Lubbock, Texas 79409

GRADUATE POSTERS

40. THE DYNAMICS OF A STOICHIOMETRIC PLANT-POLLINATOR MODEL AND ITS PARAMETER SENSITIVITY

ANALYSIS.

Dilini Fonseka[1]* and Angela Peace[1]
[1]Department of Mathematics and Statistics, Texas Tech University

41. STOCHASTIC EPIDEMIC MODELS FOR ZOONOTIC SPILLOVER

Aadrita Nandi[1*] and Linda J. S. Allen[1]
[1]Department of Mathematics and Statistics, Texas Tech University

42. THE EFFECTS OF SEASONAL VARIATIONS ON DISEASE TRANSMISSION AND MOBILITY IN STOCHASTIC EPIDEMIC MODELS

Kaniz Fatema Nipa[1]* and Linda J.S. Allen[1]
[1]Department of Mathematics and Statistics, Texas Tech University, Lubbock, USA

43. NOVEL MARKERS FOR SEPSIS IN *PSEUDOMONAS AERUGINOSA*-INFECTED SEVERELY BURNED PATIENTS

Moamen Elmassry[1]*, Nithya Mudaliar[2], Jane Colmer-Hamood[2,3], Michael San Francisco[1,4], John Griswold[5], Sharmila Dissanaike[5], and Abdul Hamood[2,5]
[1]Department of Biological Sciences, TTU, Lubbock, TX
[2]Department of Immunology and Molecular Microbiology, TTUHSC, Lubbock, TX
[3]Department of Medical Education, TTUHSC, Lubbock, TX
[4]Honors College, TTU, Lubbock, TX
[5]Department of Surgery, TTUHSC, Lubbock, TX

44. GROWTH RATE ESTIMATES FOR THE RIO GRANDE COOTER (*PSEUDEMYS GORZUGI*) ON THE BLACK RIVER, NEW MEXICO

Vinicius Ortega-Berno[1]*, Thanchira Suriyamongkol[1], Andrew W. Letter[1], Korry J. Waldon[1], and Ivana Mali[1]
[1]Department of Biology, Eastern New Mexico University, Portales, New Mexico 88130

45. STUDY OF THE ROLE OF BREAST CANCER ASSOCIATED GENE 2 (BCA2) THROUGH A DOXYCYCLINE-INDUCIBLE SYSTEM

Yuhang Shi[1]*, Sergio Castro-Gonzalez[1], and Ruth Serra-Moreno[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

46. CONVERSION OF LOW-QUALITY COTTON TO BIOPLASTIC

Shaida S.Rumi[1*], Yang Hu[1], Noureddine Abidi[1]
[1]Fiber and Biopolymer Research Institute, Department of Plant and Soil Science, Texas Tech University, Lubbock, Texas 79409

47. A NOVEL TREATMENT FOR HPV-RELATED CANCERS: USING HPV16 STRUCTURAL PROTEINS TO ENCAPSULATE ANTI-CANCER DRUGS

Morgan H. Williamson[1]*, Lauren S. Gollahon[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79401

48. EFFECTIVE SURVEILLANCE OF MOSQUITOES USING NEXT-GENERATION SEQUENCING FOR METABARCODING

Robert M. Huff[1]* and Jason Pitts[1]
[1]Department of Biology, Baylor University, Waco, Texas 76706

49. ASSESSING SMALL MAMMAL RESPONSE TO MESQUITE CANOPY REMOVAL IN AN ISOLATED RANGELAND

Vedolich, K.R.[1]* and Griffis-Kyle, K.L.[1]
[1]Department of Natural Resources Management, Texas Tech University, Lubbock, TX 79409

50. CORRELATION OF METASTATIC POTENTIAL AND INCREASED ABILITY TO REPAIR MEMBRANE DAMAGE

Nicholas A. Wolpert[1*] and Lauren S. Gollahon[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

51. RECOMBINANT S5 PYOCIN: A NOVEL THERAPY FOR *PSEUDOMONAS AERUGINOSA* INFECTION

Abdulaziz Y. Alqahtani[1]*, Randal Jeter[1], Jane A. Colmer-Hamood[2],[3], and Abdul N. Hamood[3],[4]
[1]Department of Biological Sciences, TTU, Lubbock, TX
[2]Department of Medical Education, TTUHSC, Lubbock, TX
[3]Department of Immunology and Molecular Microbiology, TTUHSC, Lubbock, TX
[4]Department of surgery, TTUHSC, Lubbock, TX

52. ELUCIDATING THE GENETIC MECHANISMS INVOLVED IN THERMOREGULATION OF *PSEUDOMONAS AERUGINOSA* BIOFILM FORMATION

Karishma Bisht[1]*, Jeanette Rimbey[1], Jessica L. Moore[2], Richard M. Caprioli[2], Eric P. Skaar[3], Catherine A. Wakeman[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX
[2]Department of Chemistry, Vanderbilt University, Nashville, TN
[3]Department of Pathology, Microbiology, and Immunology, Vanderbilt University School of Medicine, Nashville, TN

53. EFFECT OF ADIPOCYTE SECRETED FACTORS UNDER LEAN MASS AND OBESE CONDITION IN BREAST CANCER CELL MIGRATION AND INVASION

Noshin Mubtasim[1*], Lauren S. Gollahon[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas-79409

54. IDENTIFICATION OF DEFENSIVE MECHANISMS IN *PSEUDOMONAS AERUGINOSA* ENABLING SURVIVAL IN POLYMICROBIAL GROWTH WITH FUNGI

J. Baishya[1]*, B. Perez[1], M. Zinah[1], A. Pillai[1], J. P. Morris[1], K. P. Nguyen[1], C.A. Wakeman[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX, U.S.

55. POLYCYCLIC AROMATIC HYDROCARBONS IN BREAST MILK OF OBESE VS NORMAL WOMEN: INFANT EXPOSURE AND RISK ASSESSMENT

Narayan Acharya[1*], Bibha Gautam[2], Seenivasan Subbiah[1], Mary Madeline Rogge[2], Todd A. Anderson[1], Weimin Gao[3]
[1]The Institute of Environmental and Human Health, Department of Environmental Toxicology, Texas Tech University, Lubbock, TX, USA
[2]School of Nursing, Texas Tech University Health Sciences Center, Lubbock, TX, USA
[3]Department of Occupational and Environmental Health Sciences, School of Public Health, West Virginia University, Morgantown, WV, USA

56. WOLBACHIA PIPIENTIS METABOLIC RESPONSE IN A CELL FREE MEDIA

Alyssa M Krafsur[1]* and Corey Brelsfoard[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

57. TOWARD UNIVERSAL FLAVIVIRIDAE SURVEILLANCE

James G. Mann[1]*, Jason R. Pitts[1]
[1]Department of Biology, Baylor University, Waco, Texas 76706

58. ANTISENSE TRANSCRIPTION AND SMALL RNA REGULATION OF ARABIDOPSIS AUXIN RESPONSE FACTOR ARF12/22 GENE CLUSTER

Pranav Dawar[1]*, Yingwen Jiang[1], Sunitha Sukumaran[1], and Chris Rock[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

59. IMPLEMENTATION OF COVER CROPPING MAY CAUSE COOLING EFFECT DUE TO INCREASE IN SURFACE REFLECTIVITY

Risa E. McNellis[1*] and Nick G. Smith[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409

60. DWARF WILLOWS SHARE THE SAME SEX DETERMINATION REGIONS

Minghao Guo[1]*, Brian Sanderson[2], Nan Hu[1], Guanqiao Feng[1], Matthew Olson[1]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
[2]Department of Botany and Plant Pathology, Purdue University, West Lafayette, Indiana 47907

61. DEVELOPMENT OF COST-EFFECTIVE METHODS TO CONTROL HARMFUL ALGAL BLOOMS USING ALLELOCHEMICALS

Mousumi A. Mary[1]* and Dr. Reynaldo Patino[2]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, Texas 79409
[2]U.S. Geological Survey, Texas Cooperative Fish and Wildlife Research Unit and Departments of Natural Resources Management and Biological Sciences, Texas Tech University, Lubbock, TX

62. BLASTX, A NOVEL ANTIMICROBIAL AGENT, INFLUENCES THE WOUND HEALING PROCESS BY ALTERING THE LEVEL OF CYTOKINES AND CHEMOKINES WITHIN THE WOUND

Kayla Bounds[1]*, Jane A. Colmer-Hamood[2,3], Matthew Myntti[4], Kandis Wright[2,5], Randall Jeter[1], and Abdul N. Hamood[3,6]
[1]Department of Biological Sciences, TTU, Lubbock, TX
[2]Department of Medical Education, TTUHSC, Lubbock, TX
[3]Department of Immunology and Molecular Microbiology, TTUHSC, Lubbock, TX
[4]Next Science, Jacksonville, FL
[5]Department of Cell Biology and Biochemistry, TTUHSC, Lubbock, TX
[6]Department of Surgery, TTUHSC, Lubbock, TX

63. ADVERSE EFFECTS OF STROBILURIN FUNGICIDES ON EARLY LIFE STAGES OF ZEBRAFISH (*DANIO*

***RERIO*)**

Naveen Kumar[1]*, Jordan Crago[1]
[1]The Institute of Environmental and Human Health (TIEHH), Texas Tech University, Lubbock, TX, USA 79416

64. IDENTIFICATION OF SECRETED METABOLITES FROM *BATRACHOCHYTRIUM DENDROBATIDIS* AND USE OF *GALLERIA MELLONELLA* AS MODEL SYSTEM TO STUDY PATHOGENICITY

Amanda M. Starr[1*] , Masoud Zabet[2], and Michael J. San Francisco[1,3]
[1]Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409
[2]Center for Biotechnology and Genomics, Texas Tech University, Lubbock, TX 79409
[3]Honors College, Texas Tech University, Lubbock, TX 79409

65. PREPARATION OF CELLULOSE-BASED MONOLITHS WITH ENHANCED SURFACE AREA AND POROSITY

Prakash Parajuli[1]*, Yang Hu[1], and Noureddine Abidi[1]
[1]Fiber and Biopolymer Research Institute, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX, USA

DETAILED SCHEDULE OF EVENTS
ORAL SESSIONS AND AWARDS BANQUET
SATURDAY, APRIL 27th

Saturday, April 27th

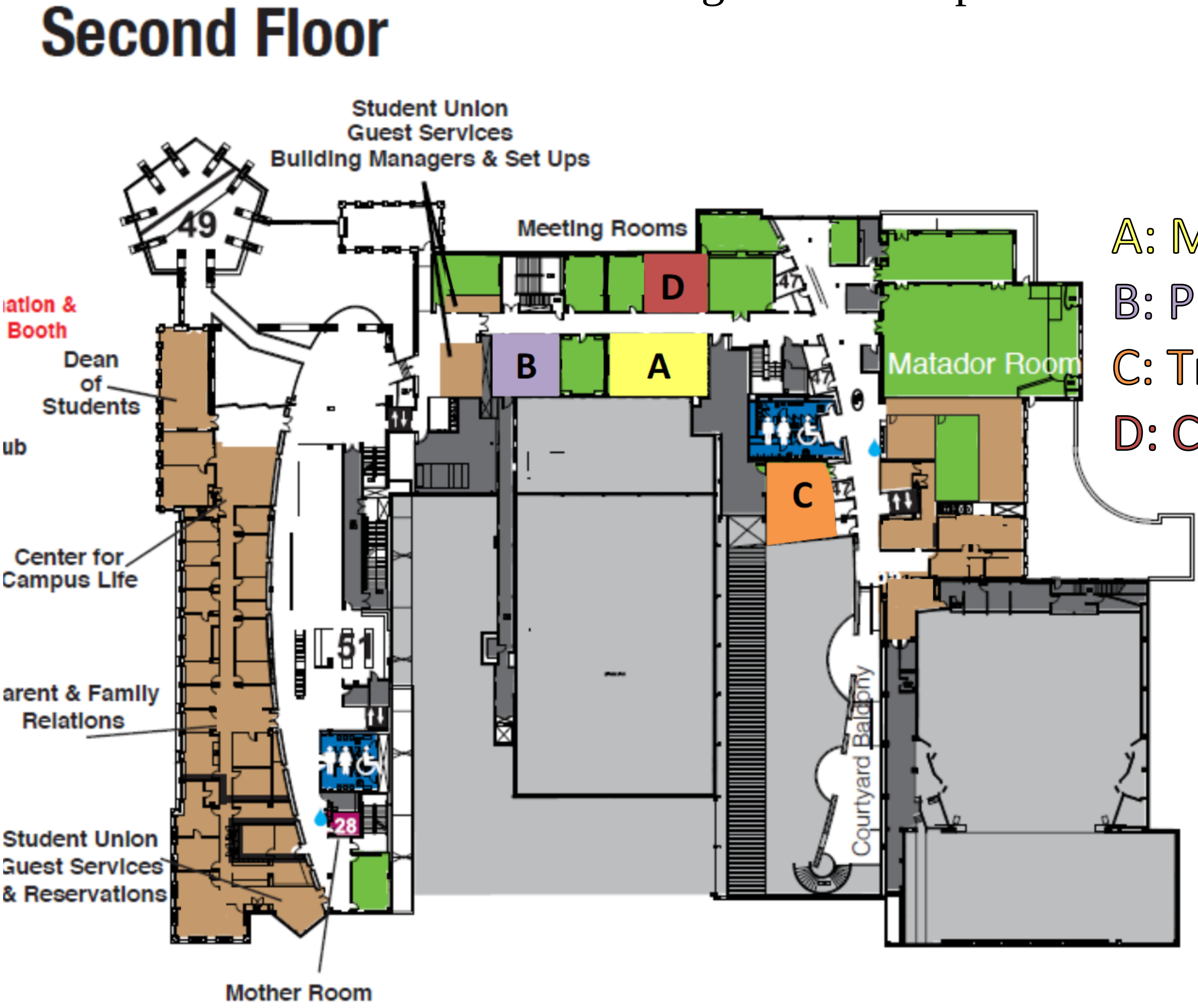
7:30 am – 9:00 pm	Registration table open
7:30 am – 8:30 am	Registration and Breakfast, Matador Room, Student Union Building, Texas Tech University
8:00 am – 8:15 am	Welcoming by Dr. Lou Densmore, Graduate Advisor, Department of Biological Sciences, TTU
8:30 am – 10:00 am	Oral Presentations – Mesa Room, Playa Room, Traditions Room, Canyon Room
10:00 am – 10:15 am	Coffee Break
10:15 am – 12:00 pm	Oral Presentations – Mesa Room, Playa Room, Traditions Room, Canyon Room
12:00 pm – 1:30 pm	Lunch Break (On Your Own)
1:30 pm – 3:00 pm	Oral Presentations – Mesa Room, Playa Room, Traditions Room, Canyon Room
3:00 pm – 3:30pm	Coffee Break
3:30 pm – 4:30 pm	Plenary Talk, William Lindsay Chadderton MSc, Nature Conservancy– Mesa Room ***"Progress towards the development of a Great Lakes surveillance program—the what, where, and how"***

6:00pm – 9:00 pm	Awards Banquet and Dinner, Matador Room, Student Union Building

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, Macy Madden, 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, Erin Stukenholtz, ANRS President Shan L. Bilimoria Memorial Graduate Student Award, Karishma Bisht, TechASM President
8:45pm	Closing Remarks

Student Union Building Interior Map



A: Mesa

B: Playa

C: Traditions

D: Canyon

	Plant & Soil Science (Mesa)	**Computational & Mathematical Biology (Playa)**	**Undergraduate Orals (Traditions)**	**Microbiology & Medicine (Canyon)**
8:30 AM	**MODELING OF ROOT WATER UPTAKE OF COTTON UNDER DEFICIT SUBSURFACE DRIP IRRIGATION** Atinderpal Singh[1]*, and Sanjit Deb1	**STUDY OF KELLER SEGEL MODEL FOR SLIME MOLD AGGREGATION** Thakshila D.Gunasingha[1]*	**DENDROCHRONOLOGICAL SUITABILITY AND CLIMATE SENSITIVITY OF *QUERCUS MOHRIANA* IN THE TEXAS PANHANDLE** William R. Watkins III[1]*, Sarah A. Macha[1], and Matthew S. Allen[1]	**HIV NEF COUNTERACTS AUTOPHAGY BY PROMOTING THE INTERACTION BETWEEN THE AUTOPHAGY INITIATOR BECN1 AND ITS INHIBITOR BCL-2** Sergio Castro-Gonzalez[1]*, Yuhang Shi[1] and Ruth Serra-Moreno[1]
8:45 AM	**GENETIC DIVERSITY ANALYSIS OF SILVERLEAF NIGHTSHADE POPULATIONS UNDER HERBICIDE STRESS** Joshua J. Singleton[1]*, Ritchel B. Gannaban[1], Puneet Kaur Mangat[1], Rosalyn B. Angeles-Shim[1]	**MODELING ELEMENTAL CONSTRAINTS ACROSS AQUATIC FOOD WEBS** Md Nazmul Hassan[1]* and Angela Peace[1]	**GRASSLAND BIRD DIVERSITY AND HABITAT ASSOCIATIONS IN THE SOUTHERN HIGH PLAINS, TEXAS** S. Leigh Ann DeMerritt[1]* and Andrew C. Kasner[1]	**PREDICTING METAGENOME-MEDICATION INTERACTIONS** Moamen M. Elmassry[1,2]*, Sunghwan Kim[2], and Ben Busby[2]
9:00 AM	**TRADE-OFF BETWEEN FORAGE QUALITY IMPROVEMENT AND CROP WATER USE FOR ALFALFA-GRASS SYSTEM** M. Dhakal[1]*, C.P. West[1], and J.O. Sarturi[2]	**SEASONAL VARIATION OF NUTRIENT LOADING IN A STOICHIOMETRIC PRODUCER-CONSUMER SYSTEM** Lale Asik[1]* , Jackson Kulik[1], Kevin R. Long[1], and Angela Peace[1]	**AN UPDATED VASCULAR FLORA OF THE RUNNINGWATER CONSERVANCY, HALE COUNTY, TX WITH COMPARISONS TO REGIONAL FLORISTIC RECORDS** Krista S. Epley[1]* and Matthew S. Allen[1]	**SYNTHESIS OF STEROLS AND SPHINGOLIPIDS PROTECTS LEISHMANIA AGAINST MEMBRANE PERTURBING AGENTS, OSMOSTRESS AND STARVATION** Samrat Moitra[1]*, Wei Xu[2] and Kai Zhang[1]
9:15 AM	**USING CROP RESIDUE AND NO-TILL TO MANAGE SOIL MICROBIAL DYNAMICS IN A DRYLAND COTTON SYSTEM IN WEST TEXAS** Diana L. Vargas-Gutierrez[1]*, Veronica Acosta-Martinez[2], Bobbie McMichael[1], and John Zak[1]	**MECHANISTICALLY DERIVED SPATIALLY HETEROGENEOUS PRODUCER-GRAZER MODEL SUBJECT TO STOICHIOMETRIC CONSTRAINTS** Md Masud Rana[1]*, Chandani Dissanayake[2], Lourdes Juan[1], Kevin R. Long[1], and Angela Peace[1]	**A LONGITUDINAL STUDY OF FISH ASSEMBLAGES ON THE MESOAMERICAN BARRIER REEF, IN ROATAN HONDURAS** Scheila R Corujo[1]*, Cassidy Dunkin[2], Stephanie Randel[2], Shannon Hill[2], Stephanie Lockwood[1]	**PATIENT GENETICS SHAPE CHRONIC WOUND MICROBIOME COMPOSITION AND IS ASSOCIATED WITH HEALING** Craig D. Tipton[1,2]*, Randall D. Wolcott[3], Nicholas E. Sanford[3], Clint Miller[3], Gita Pathak[4], Jie Sun[4], Nicole Phillips[4], Caleb D. Phillips[1,5]
9:30 AM	**MANAGING PALMER AMARANTH (*AMARANTHUS PALMERI*) WITH SEQUENTIAL APPLICATIONS OF DICAMBA AND GLUFOSINATE WITH OR WITHOUT ACETOCHLOR** Grace K. Flusche Ogden[1]* and Peter A. Dotray[1,2]	**TRAVELING WAVE PATTERN AND ITS STABILITY IN BACTERIA FOOD MODEL AND APPLICATION** Dalal K. Almutairi[1]*	**HABITAT ASSOCIATIONS AND POPULATION ESTIMATES OF THE TEXAS HORNED LIZARD (*PHRYNOSOMA CORNUTUM*) IN THE SOUTHERN HIGH PLAINS OF TEXAS** Sara A. van der Leek[1]* and Andrew C. Kasner[1]	
9:45 AM		**ANALYZING GENOMIC DATA USING TENSOR-BASED ORTHOGONAL POLYNOMIALS** Saba Nafees[1]*, Sean H. Rice[1], and Caleb D. Phillips[1]	**DOES CRUSH RESISTANCE VARY BETWEEN THE INVASIVE NEW ZEALAND MUD SNAIL (*POTAMOPYRGUS ANTIPODARUM*) AND THE NATIVE JUGA SNAIL (*JUGA ORICKENSIS*)?** Lawson Sittre[1]* and Ryan R. Vazquez[1]	
10:00 AM	COFFEE BREAK			

	Proposal (Mesa)	**Ecology & Environmental Biology (Playa)**	**Undergraduate Orals (Traditions)**	**Genetics & Genomics (Canyon)**
10:15 AM	**UNEARTHING PROXY DETERMINANTS OF THE SUBTERRANEAN NICHE FOR SPECIES DISTRIBUTION MODELS** Michaela K. Halsey[1,2*], Robert D. Bradley[1,3], Richard D. Stevens[2,3] and David A. Ray[1]	**WINTER ECOLOGY AND BIOENERGETICS OF MEXICAN FREE-TAILED BATS (*TADARIDA BRASILIENSIS MEXICANA*)** Emma L. Kunkel[1*] and Liam P. McGuire[1]	**BREEDING SEASON FOOD HABITS OF AMERICAN KESTRELS IN THE SOUTHERN GREAT PLAINS** Madeleine A. Thornley[1*], Shea D. Mullican[1], and Clint W. Boal[2]	**CRISPR – ANGEL OR DEVIL?** Fengqian Chen[1*]
10:30 AM	**WINTER MOVEMENT AND ENERGETIC DEMANDS OF THE BLACK FLYING FOX IN QUEENSLAND, AUSTRALIA** Adrienne S. Dale[1*] and Liam P. McGuire[1]	**EVALUATING THE EFFECTIVENESS OF UAV-BASED REMOTE SENSING SYSTEMS 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]	**PREVALENCE, ABUNDANCE, AND PROPORTION OF DARK SPOT SYNDROME ON STARLET CORALS ON THE MESOAMERICAN BARRIER REEF IN ROATÁN, HONDURAS** Erin N. Castillo[1*], Shannon Hill[1], Stephanie A. Lockwood[2], Traesha Robertson[3], Donna E. Hamilton[4], Stephanie M. Randell[1]	**DECIPHERING THE WHOLE GENOME STRUCTURE OF THE NIGHTSHADE SPECIES *SOLANUM LYCOPERSICOIDES*** Puneet Kaur Mangat[1*] and Rosalyn B. Angeles-Shim[1]
	Proposal (Mesa)	**Ecology & Environmental Biology (Playa)**	**Wildlife & Fisheries (Traditions)**	**Genetics & Genomics (Canyon)**
10:45 AM	**THE INFLUENCE OF MICROBIAL SYMBIOSES ON LEAF- AND WHOLE-PLANT ACCLIMATION TO ELEVATED CARBON DIOXIDE** Evan A. Perkowski[1*] and Nicholas G. Smith[1]	**COMPETITORS VERSUS FILTERS: DRIVERS OF NON-RANDOM STRUCTURE IN FOREST INTERIOR INSECTIVOROUS BAT ASSEMBLAGES ALONG ELEVATIONAL GRADIENTS** Iroro Tanshi[1,2*] and Tigga Kingston[1]	**REPRODUCTIVE BIOLOGY OF RIO GRANDE COOTER (*PSEUDEMYS GORZUGI*) ON THE BLACK RIVER, NEW MEXICO** Thanchira Suriyamongkol[1*] and Ivana Mali[1]	**MACROECOLOGY OF BUTTERFLY GENOMES** Jenna R. Grimshaw[1*], David A. Ray[1], and Richard D. Stevens[2,3]
11:00 AM	**CHARACTERIZING RETROTRANSPON ACTIVITY ACROSS RECENT HISTORY: A CASE STUDY IN THE NORTHERN FLICKER SPECIES COMPLEX** Jack P. Hruska[1*], Joseph Manthey[1]	**SPATIAL AND TEMPORAL VARIATION IN BAT ACTIVITY DURING WINTER** Brett R. Andersen[1*], Richard D. Stevens[2], and Liam P. McGuire[1]	**REVIEW OF BAT DIVERSITY, DISTRIBUTION AND CONSERVATION STATUS IN MALAYSIAN BORNEO: HOW MUCH DO WE KNOW?** Isham Azhar1*, Faisal Ali Anwarali Khan2, Mohd-Ridwan Abd Rahman3 and Roberta Chaya Tawie Tingga3	**TRANSPOSON ACTIVITY AND MUTATIONAL IMPACTS IN *MYOTIS*** Nicole S. Paulat[1*], Joseph D. Manthey[1], Roy N. Platt II[2], and David A. Ray[1]
11:15 AM	**INFLUENCE OF GRASS FUEL LOAD AND CANOPY ARCHITECTURE ON FIRE BEHAVIOR AND FIRE RESPONSE OF *JUNIPERUS VIRGINIANA* IN SOUTHEASTERN MISSOURI** Xiulin Gao[1*] and Dylan W. Schwilk[1]	**CO-OCCURRENCE PATTERNS OF BATS IN THE TRANS-PECOS REGION OF TEXAS** Holly G. Wilson[1*], Stirling J. Robertson[2], Richard D. Stevens[1,3]	**THE CROCODYLIANS OF BOLIVIA: A REPORT ON THE CURRENT STATE OF KNOWLEDGE AND REGIONAL CONSERVATION PRIORITIES** Andrés L. Rodriguez-Cordero[1], Sergio A. Balaguera-Reina[1,2], Llewellyn D. Densmore	**DIFFERENT SEX DETERMINATION SYSTEM IN NARROWLEAF WILLOW (*SALIX EXIGUA*) COMPARED WITH OTHER SHRUB WILLOW SPECIES** Nan Hu[1*], Brian J Sanderson[2], Guanqiao Feng[1], Minghao Guo[1], and Matt Olson[1]
11:30 AM	**NOSY NEIGHBORS EAVESDROP ON COMPLEMENTARY INFORMATION** Christopher A. Johnson[1*], Kenneth A. Schmidt[1]	**CHANGES IN RODENT COMMUNITY COMPOSITION DURING THE LAST HALF-CENTURY ACROSS THE RANGE OF A RARE KANGAROO RAT** John D. Stuhler[1*], Michaela K. Halsey[1,2], Robert D. Bradley[2,3], and Richard D. Stevens[1,3]	**DATA COLLECTION METHODS AND SPECIES TRAITS INFLUENCE SPECIES DISTRIBUTION MODEL PREDICTIONS** Elizabeth L. Roesler[1*], Timothy B. Grabowski[2], & Matthew A. Barnes[1]	**EXAMINING TRANSPOSABLE ELEMENT CONTRIBUTIONS TO BAT DIVERSITY AND EXTENDED AGING PHENOTYPES** Kevin A.M. Sullivan[1*], Emma Teeling[2], Sonja Vernes[3], Liliana Davalos[4], Tom Gilbert[5], Gene Myers[6], Michael Hiller[6], David A. Ray[1]
11:45 AM	**MULTI-OMICS DATA ANALYSIS OF FOUR GENOTYPES OF BANANA MICROBIOME USING A MODIFIED ENRICHMENT METHOD** Shiva Abdollahi Aghdam[1*], Kimberly Morales[1], and Amanda M. V. Brown[1]	**EFFECTS OF URBANIZATION ON TAXONOMIC AND FUNCTIONAL COMPOSITION OF AVIAN COMMUNITIES THROUGHOUT TEXAS** Erin E. Stukenholtz[1*] and Richard D. Stevens[1,2]		**A NOVEL METHOD TO CHARACTERIZE RESISTANCE EVOLUTION USING SPATIAL PROXIMITY FOR MEDICAL POLYMICROBIAL BIOFILMS** Bravada Hill[1*], Karishma Bisht[1], Catherine Wakeman[1], and Amanda M.V. Brown[1]
12:00pm	**Lunch (On your own)**			

	Molecular Biology (Mesa)	Physiology and Evolutionary Biology (Playa)	Toxicology (Traditions)	Genetics & Genomics (Canyon)
1:30 PM	**DO CATEGORICALLY DISTINCT STRESSORS AFFECT VISUAL ATTENTION TO FOOD IN HUMANS?** Songhe Li[1]*, James A Carr[1]	**PATHOGEN EVOLUTION WHEN TRANSMISSION AND VIRULENCE ARE STOCHASTIC** Pooya Aavani[1]*, Sean H. Rice[1]	**SORPTION OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS (NSAIDs) TO MICROPLASTICS UNDER FRESHWATER, SEAWATER AND ACIDIFIED WATER CONDITIONS** Armando Elizalde-Velázquez[1]*, Todd A. Anderson[1], Micah J. Green[2], Xiaofei Zhao[2], Jaclyn E. Cañas-Carrell[1]	**TRANSPOSABLE ELEMENTS AND LINEAGE SORTING WITHIN THE GENUS *HELICONIUS*** Jennifer M. Korstian[1]*, David A. Ray[1]
1:45 PM	**FUNCTIONAL PVDF/VB2/TIO2 NANOFIBER WEBS FOR DRUG DELIVERY** Lihua Lou[1]*, Seenivasan Subbiah[2], and Seshadri S. Ramkumar[1]	**MORPHOLOGY AND GENETICS OF *SIGMODON FULVIVENTER DALQUESTI* IN THE CHIHUAHUAN DESERT ECOREGION** Preston J. McDonald[1]*, Caleb D. Phillips[1]	**DIETARY NUTRIENTS (C:P) MODULATE CADMIUM TOXICITY IN AQUATIC SYSTEMS AT TWO TROPHIC LEVELS** Olushola M. Awoyemi[1]*, Kelsey N. Thompson[1], Anahi Velazquez[1], Md Nazmul Hassan[2], Angela Peace[2] and Gregory D. Mayer[1]	**ANCIENT HYBRIDIZATION DETECTION WITHIN *CROCODYLUS*** Austin B. Osmanski[1]*, Katherine Brittain[2], Elizabeth Jones[2], Jaime Gongora[2], Alexander Suh[3], David Ray[1]
	Molecular Biology (Mesa)	Physiology and Evolutionary Biology (Playa)		Emerging Professionals (Canyon)
2:00 PM	**COMPARING THE ANTI-CANCER EFFECTS ON MITOCHONDRIAL FUNCTION AND METABOLISM DISRUPTION IN BREAST CANCER CELLS BY A PLANT EXTRACT MIXTURE COMPARED TO THREE OF ITS COMPONENTS INDIVIDUALLY AND IN COMBINATION** Caroline Schuster[1] and Lauren S. Gollahon[1]	**PHYLOGENETIC INFORMATION IN SEED MORPHOLOGY AND SEED GERMINATION FOR SHORTGRASS PRAIRIE SPECIES** Yanni Chen[1]*, Robert Cox[2], Dylan Schwilk[1], Matthew Johnson[1]		***AEDES ALBOPICTUS* AND *AEDES AEGYPTI* INSECTICIDE RESISTANCE IN TEXAS** Bianca Rendon[1]*, Steve Peper[1], and Steve Presley[1]
2:20 PM				**CONNECTING PATTERNS OF MIGRATION TO FUNCTIONAL MOTIVATIONS** Jeff Clerc[1]*, Liam P. McGuire[1]
2:40 PM				**HOW MUCH DOES MICROCLIMATE MATTER? DECOUPLING THE EFFECTS OF TEMPERATURE AND HUMIDITY ON BAT HIBERNATION PHYSIOLOGY** Emily M. Johnson[1]*, Justin G. Boyles[2], Nathan W. Fuller[1], Kirk A. Silas[1], Winifred F. Frick[3,4], Liam P. McGuire[1]
3:00 PM	COFFEE BREAK			
3:30 PM	PLENARY TALK: ***"Progress towards the development of a Great Lakes surveillance program—the what, where, and how"*** **by William Lindsay Chadderton MSc, Nature Conservancy– Student Union Building, Mesa Room**			

ABSTRACTS

UNDERGRADUATE POSTERS

1. AN INVESTIGATION OF PSEUDOMONAS AERUGINOSA CYAN FLUORESCENCE WITH THE MOLECULIGHT I:X BACTERIAL FLUORESCENCE IMAGING DEVICE

William L. Little[1]*, Andrea J. Lopez[1], Andre J. Gomez[1], Klara C. Keim[1], Monique Y. Rennie[2], and Allie Clinton Smith[1]
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Chronic wounds are a current area of major clinical concern, resulting in immense morbidity and mortality of a large patient population annually. These wounds do not typically respond to normal courses of antimicrobial treatment and often require drastic therapies, including amputation of the affected limb. Many different bacterial species are known to cause infections in chronic wounds, with *Pseudomonas aeruginosa* often playing a major role in these wounds' virulence and persistence. MolecuLight has developed a bacterial fluorescence imaging device to detect the fluorescent properties of many chronic wound pathogens to aid in real-time visualization and direct specimen sampling. Bacterial species that produce the exoproduct porphyrin will fluoresce red under the MolecuLight *i:X* device. While *P. aeruginosa* is a known porphyrin producer, this organism typically fluoresces blue-green cyan under the device both *in vitro* and *in vivo*. It is thought this is due to the production of additional exoproducts with fluorescent properties, such as pyocyanin. We have partnered with MolecuLight to elucidate the mechanisms of cyan fluorescence production of *P. aeruginosa* in order to optimize the detection and utilization of the device with *P. aeruginosa*-infected chronic wounds.

2. USE OF FLUORESCENCE AND COMPOUND LIGHT MICROSCOPE OLYMPUS BX40 WITH OLYMPUS DP74 CAMERA AS A TOOL FOR STUDING AEROALLERGENS OF THE TEXAS PANHANDLE

Nabarun Ghosh[1], Herlinda S. Lee[1]*
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The study of aeroallergens in this area contributes to the identification and prevention methods used to help allergy sufferers. Pollen samples were captured by a Burkard trap placed on the roof of the Natural Sciences Building at WTAMU. Prepared slides were viewed with Olympus BX40 microscope equipped with fluorescein-isothiocyanate (FITC) filter and the tetramethylrhodamine (TRITC) fluorescent filters, a mercury lamp source, an Olympus DP-70 digital camera connected to the computer with Image Pro 6.0 software. Fluorescence Microscopy enhances the image of the allergens structure and function of the microscopic objectives. The images were taken at 40X magnification with the Olympus DP74 camera and to excite the stored molecules or proteins a high-pressure mercury lamp or UV light source was used to promote autofluorescence. To reveal the green fluorescent protiens (GFP) the FITC filter was used and the red fluorescent proteins (DsRed) the TRITC filter was used. The samples were also viewed, and images captured in a bright light field with the same microscope. A diagram was constructed to show the contrast and differences in images taken

with bright field, fluorescence with FITC and fluorescence with TRITC. Fluorescent Microscopy can be used for pollen identification and Taxonomic circumscription of the Angiosperms.

3. PREVALENCE AND FREQUENCY OF ENCRUSTING *MILLEPORA* ON OCTOCORALS ON THE MESOAMERICAN BARRIER REEF IN ROATAN, HONDURAS

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Millepora spp. (fire coral) and octocorals make-up an abundant part of the Mesoamerican Barrier Reef system in Roatán, Honduras. Recent studies suggest that fire coral parasitize octocorals and over take a vast majority of the reef. This study was conducted to assess the prevalence and frequency of encrusting *Millepora.* individuals on various octocorals (sea fans, sea whips and sea rods) found off the Mesoamerican Barrier Reef in comparison to other studies in the Caribbean. Research was conducted off the coast of Roatán, Honduras from May 15-18, 2018. *Millepora* were found more frequently associated with the common sea fan, wide-mesh sea fan, slimy sea plume and rough sea plume. Of the four, sea fans had the highest frequency of encrustation. In total, fifty-seven measurements were taken of *Millepora* encrusting various octocorals and only 17.5% of octocorals showed signs of disease. These data suggest that *Millepora* parasitized healthy octocorals compared to octocorals with lesions, purpling, or necrosis. *Millepora alcicornis* was most commonly associated with encrusted octocorals, although *Millepora cervicornis* and *Millepora squarrosa* were also found in close proximity to infected octocorals. Twenty-one percent of octocorals had no *Millepora spp.* colony present. Affected octocorals could be found touching *Millepora* or up to one hundred centimeters away from the nearest *Millepora* species; however, there was no correlation between distance and encrustation of *Millepora*.

4. EXAMINING IMMUNE-ASSOCIATED ORGAN MASSES IN TRANSGENIC AND NON-TRANSGENIC APPswe/PS1dE9 MICE, AN AMYLOID β-GENIC ALZHEIMER'S DISEASE MOUSE MODEL

Neel P. Roy[1]*, Emily Stephens[1], Amber Loya[1], Paul L. Soto[2], Breanna N. Harris[1]
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[2]Department of Psychology, Louisiana State University

Alzheimer's disease (AD) is associated with elevated levels of amyloid-beta (Aβ) in the brain, generally present in the form of Aβ plaques. These plaques are linked with pathologic inflammation of the brain and are often regarded as one of the primary drivers of AD. Interestingly, recent data from humans suggests that Aβ will accumulate in peripheral organs before it accumulates in the brain. This raises the possibility that Aβ accumulation in the body has a detrimental impact on the peripheral organs. To explore one aspect of this, we examined organ masses in aged control (non-tg) and aged transgenic (tg) mice from an Aβ-genic AD mouse model (APPswe/PS1dE9). More specifically, we examined the end-of-life masses of the thymus, spleen, and adrenals—three immune-associated organs—in 19-month-old male and female mice. We hypothesized that tg mice, with their elevated levels of Aβ in circulation, would develop Aβ aggregates in these three immune-associated organs that would, in turn, produce Aβ plaques and induce inflammation in those organs. This should yield higher average

organ masses in tg mice than those found in their non-tg littermates, allowing Aβ accumulation to be detected by organ massing. Preliminary analyses failed to support the above hypothesis. However, we have found that, regardless of genotype, females had larger body-mass-corrected organs than did males. Therefore, our current data suggest genotype does not impact peripheral organ mass, but that sex does play a role. This research was funded by the National Institutes of Health (R15AG048447).

5. INITIAL RESULTS OF FORAGE SEED BANK GERMINATION RELATIVE TO LANDSCAPE LEVEL RESTORATION EFFORTS IN NORTH-CENTRAL NEW MEXICO

Jordan Keats[1]*, Sharon E. Smythe[1], James W. Cain III[2], and Warren C. Conway[1]
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Due to historical land use and fire suppression, forests in northern New Mexico are at high risk for wildfires. In response, a coalition of agencies under a USDA Collaborative Forest Landscape Restoration Project (2010-2019) began restoring 210,000 ha in the Jemez Mountains via thinning and prescribed fire. From these restoration efforts, we are measuring changes in forage production for ungulates. From 2013-2018 we collected data from 200 vegetation plots (62 monthly; 138 annually) randomly stratified by stand and treatment type. However, because plant species diversity in the field can be affected by multiple factors, it is difficult to evaluate the effect of treatments specifically on diversity. Thus, in March of 2017 and 2018 (following seed drop, prior to germination), we collected 450 seed bank samples from our monthly plots (3-6 replicates/plot; ~100 cm^3 of soil; at 4 cm depths). From May-December 2018, we germinated 255 samples in ideal greenhouse conditions (26˚C, constant moisture), transplanted seedlings into separate cups to avoid competitive effects, and identified seedlings. In total, 1553 seedlings germinated, and preliminary results suggest mean number of germinated seedlings vary by treatment type (4.0-10.5/sample [2.2]) but do not vary by stand type (3.9-7.4/sample [1.3]). Samples treated with wildfire (MX) resulted in 505 seedlings while thinned (TRT) treatments had 398 seedlings. Samples from not treated (NT) and thinned and burned (FIN) treatments both had ~ 255 seedlings while prescribed fire (RX) had 139 seedlings. Although preliminary, these germination expression trials indicate some variation among landscape scale treatments in the Jemez Mountains.

6. METFORMIN INHIBITS SLC6A14, AN AMINO ACID TRANSPORTER THAT DRIVES PANCREATIC CANCER GROWTH

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Pancreatic cancer is the most lethal of all cancers. There is a dire need to identify better therapeutics. Our lab has identified SLC6A14, an amino acid transporter as a promoter of pancreatic cancer. Our aim here was to identify drugs to target SLC6A14. We chose metformin, an FDA-approved drug for Type 2 diabetes. Literature evidences have shown that metformin possesses anticancer property. Metformin activates AMP-activated protein kinase (AMPK), inhibits mTORC1-signaling pathway, and increases miR-23a expression. Interestingly, SLC6A14 is known to activate mTORC1. We have also found an inverse correlation between SLC6A14 and miR-23a, a computationally predicted target, which upon binding to 3'-UTR of SLC6A14, promotes its degradation. Hence, we hypothesized that metformin by increasing miR-23a expression will inhibit SLC6A14 and further inhibit mTORC1. This will result into amino acid starvation, autophagy, and ultimately attenuate pancreatic cancer growth. With that in mind we cultured pancreatic cancer cells (Capan-1 and CFPAC-1) in the presence and absence of metformin and performed Real-time PCR, Western blotting, and SLC6A14-mediated ^{3}H-glycine uptake. It was interesting to note that metformin treatment led to a reduction in both mRNA expression and function of SLC6A14 with a concomitant decrease in miR-23a. mTORC1 signaling was inhibited; asparagine synthetase (ASNS) and C/EPB-homologous protein (CHOP) were upregulated, indicating amino acid starvation. Now, whether miR-23a regulates SLC6A14 expression or whether inhibition of mTORC1 and amino acid deprivation is simply because of AMPK activation or if it is due to SLC6A14 inhibition or whether the pathways work independently or in concert needs further investigation.

7. TESTICULAR HISTOPATHOLOGY IN AN ALZHEIMER'S DISEASE MODEL

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Plaques in the brain formed through the extracellular accumulation of amyloid beta (AB) peptide are a characteristic symptom of Alzheimer's disease (AD). AB originates within the brain and peripheral tissues and contributes to pathologies in each. The blood-brain barrier (BBB) regulates the influx of AB from these peripheral sources, and membrane proteins responsible for AB clearance lose their function as AD progresses. Prompted by the recognition of AD as a whole-body problem, we examined the testes which have a blood-tissue barrier similar to the BBB and are potentially susceptible to similar AB accumulation and cell damage. Thus, we expected that the process of spermatocytogenesis in transgenic (Tg) APPswe/PS1dE9 mice would be altered relative to their non-transgenic (non-Tg) littermates and that AB would be present in testicular tissue of Tg but not non-Tg mice. Testes from adult male mice were stained with H&E, and cells from each stage of spermatogenesis were recorded. We then used immunohistochemistry to determine the cellular location of AB-immunoreactivity in testicular tissue. We found that spermatogenesis does not differ between genotypes despite the presence of immunoreactive AB in Tg testes. We will move on to more precisely determine the localization of AB in the testes of Tg mice. Because the testes are the only other organs with a blood-tissue barrier similar to the BBB, this research will elucidate details about the integrity of the body's blood-tissue barriers in AD. Furthermore, our research will add to our understanding of the cellular mechanisms underlying Alzheimer's pathology in peripheral tissues.

8. EFFECTS OF AHPCO AND BI-POLAR PLASMA NANOTECHNOLOGIES ON PARTICULATE MATTER 2.5 AND ROLE IN TREATING RESPIRATORY SYNDROMES AND ALLERGIC RHINITIS

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New terminologies were added to the Aerobiology in the recent years: PM 2.5 and particle pollution. Aerosols including Particulate Matter 2.5 are the culprits of many allergic reactions and respiratory syndromes. PM 2.5 is present in heavily polluted areas such as southern Californian cities, New Delhi, China and New York. Based on studies from clinics and hospital admissions, PM 2.5 has been positively correlated with increased cases of allergic rhinitis, asthma, bronchitis, allergic pharyngitis and many others. Due to having a diameter of only 2.5 micrometers, the particulate matter is often not visible to the human eye, will be inhaled and cause irritation to the lungs. Many cities to be discussed in this paper contain PM 2.5 concentrations much higher than the permissible limit described by the National Ambient Air Quality Standards (NAAQS). Particulate Matter 2.5 is composed of metals and products from fuel combustion. In this experiment, illite NX dust is used in order to measure particle concentration. Advanced Hydrated Photocatalytic Oxidation (AHPCO) and Bi-polar Plasma Nanotechnology are used to achieve indoor air quality improvement with reduction of particle concentration. The units are placed into a fiberglass chamber to exert their effects on the circulating dust. The rate of decay was measured at the end of this experiment to demonstrate efficacy of the AHPCO and bi-polar units.

9. EXERCISE PRECLUDES SALT CRAVING AND FAT CONSUMPTION IN SATISFIED FEMALE ATHLETE

Gracia B. Sebastiao[1]*, Aaron K. White[1], and Daniela S. Pereira, D.S.[1]
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Previous results from our laboratory showed that salt addiction is gender specific in college students from WBU: male satisfied athlete displays signs of salt addiction while female satisfied athlete avoids salty foods. We also confirmed that in athletes repeated bouts of exercise dehydrate both genders similarly. However, using the National Nutrient Database for Standard Reference Release from USDA for specific food content, macronutrients were listed for comparison to investigate if other macronutrients rather than only sodium had an effect on satisfied female food avoidance. Potassium, calcium, iron, water, total lipid, total trans fatty acids, carbohydrates, total sugars, and glucose percentages were calculated for 29 food items. Satisfied female athletes avoided bacon (1,250 mg sodium/100g food), ham (1,000 mg sodium) and peanut butter (555 mg sodium) that range from high to medium sodium content. The macronutrients were ranked by 1st, 2nd, and 3rd highest percentage within their food content. Bacon has 53.3% total lipid, 25.6% water, and 9.4% carbohydrates; ham has 75.7% water, 12.0% total lipid and 3.5% potassium; and peanut butter has 54.7% total lipid, 23.7% carbohydrates, and 9.1% total sugars. In conclusion, female satisfied athlete not only avoid salty but also fatty foods. Exercise-induced hypoestrogenism may explain the gender specificity for salty and greasy avoidance. Perhaps, low levels of the carcinogenic hormone estrogen is beneficial to avoid food addition for sodium and fat content, which in turn improves the overall cardiovascular health in 21 years old female satisfied athlete.

10. IMPACTS OF AMYLOID-BETA ACCUMULATION ON SHORT-TERM MEMORY IN AN APPSWE/PSEN1DE9 ALZHEIMER'S MOUSE MODEL.

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Alzheimer's disease (AD) is a dementia-related illness characterized by an accumulation of amyloid beta plaques, hyperphosphorylated tau tangles, and neurodegeneration, which in turn leads to decreased cognition and a loss of memory. Studies analyzing AD have shown significant correlation between the presence of amyloid beta plaques and decreased memory/ cognitive ability. We are using the amyloidgenic APPswe/PSEN1dE9 (tg) mouse model to determine how amyloid beta accumulation impacts short-term memory. Here we will determine if tg mice differ from non-tg mice in their performance in the novel object recognition test (NOR). NOR enables the analysis of short-term memory when prompted with an untrained sequence and an unfamiliar environment. Previous studies that have conducted the NOR test have found that at 6-9 months, tg mice have a decreased cognitive ability when compared to non-tg mice. For our study, mice at 18 months were used, enabling the analysis of the short-term memory in older individuals. This is important to determine age-related changes in cognitive function as amyloid beta accumulates with age in these animals. Additionally, using older mice will aid in translational research, as 18-month-old mice are roughly comparable to a 65 yr-old human. It is predicted that tg mice will spend equal time with the novel object and the familiar object, but non-tg mice will have better cognitive ability, and will be able to recall the familiar object, therefore they will spend a greater amount of time exploring the novel object. This research was funded by the National Institutes of Health (R15AG048447).

11. WATER QUALITY WITHIN LUBBOCK'S CANYON LAKE SYSTEM AND ITS ASSOCIATION WITH GROWTH OF THE HARMFUL GOLDEN ALGA

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Golden alga (*Prymnesium parvum*), a harmful bloom-producing species, is found in brackish inland habitats and typically grows during the cooler times of the year (10–15°C), mostly in spring but sometimes also in fall. Previous studies have suggested that landscape-scale variation in water quality variables such as temperature, specific conductance (proxy for salinity), and others is associated with the presence and growth of golden alga across surface waters; however, environmental drivers of bloom formation are still poorly understood. Lubbock's Canyon Lake System (CLS) has experienced golden alga blooms since 2003, but

they do not occur every year. Our laboratory began monitoring water quality and golden alga in the CLS every spring and fall since 2016 to define its spatial and temporal dynamics. Our results have shown that salinity generally decreased in a downstream direction, dissolved oxygen and pH generally increased, and turbidity showed no patterns. Golden alga was observed primarily in the upstream reach of the CLS. When sampling site was used as a random factor, regression analysis suggested that golden alga abundance is associated (negatively) only with temperature. The inverse association with temperature reflects the seasonal pattern of algal growth. Given the spatial distribution of golden alga abundance during the study period, however, its lack of association with the water quality traits examined suggests that other variables, perhaps also including abiotic variables, are responsible for its distribution in the CLS. This information will be useful to the design of future studies.

12. AN INVESTIGATION ON THE ASSESSMENT OF THE GENOTOXICITY OF ATRAZINE BASED HERBICIDE ON *ALLIUM CEPA*

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Atrazine is a wide-range tetrazine herbicide and is the most widely used herbicide in the U.S. and second in Texas (HSDB, 2002). It has been classified as a class III herbicide – slightly toxic (EPA, 1999). For over 50 years, atrazine has been used as a selective broadleaf herbicide in many capacities, from pre-plant to pre-emergence to post-emergence, depending on the crop and application. Currently, 96% of all atrazine used is for commercial applications in fields for the control of broadleaf and grassy weeds in crops such as sorghum, corn, sugarcane, pineapple and for the control of undesirable weeds in rangeland. It is known to be immunotoxic and cause endocrine disruptions and reproductive issues. Present investigation focuses on atrazine and its effect on the genomic constitution and the cell division in *Allium cepa* (green onions). *Allium cepa* is a widely used 'test organism', because it is highly sensitive to genotoxic materials due to its large chromosome size. *Allium cepa* was hydroponically grown in water as the control set and the treated sets containing variable concentrations of atrazine-based herbicide. After sufficient growth, root tips were excised and pretreated with p-DB, fixed with 1:3 Aceto-Ethanol and stained with 2% Aceto-Orcein stain. The prepared slides were viewed using a DM-750 Leica digital microscope. Mitotic Index (MI) was determined using acquired photos and graphed. MI varied among the treated and the control groups with time intervals. The control group had no significant chromosomal abnormalities. We noticed a seasonal variation in MI in which caused a gradual decrease in cell division from summer to winter. Results from the treated groups showed decreased MI with almost a cessation of division, chromosomal clumping, sticky bridges, chromosomal breakage and low tissue quality in the treated *Allium cepa* cells. Atrazine is found in groundwater in the United States 20 times more frequently than any other herbicide; further investigation is necessary for raising public awareness about the detrimental effects of atrazine and ensuring there is no current negative effects on human health.

13. BODY CONDITION AND POPULATION COMPOSITION OF RIO GRANDE COOTERS ON THE BLACK RIVER, NEW MEXICO

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The Rio Grande Cooter (*Pseudemys gorzugi*) is a relatively large freshwater turtle found in southeast New Mexico, west Texas, and northern Mexico. The species is listed as threatened in New Mexico and Species of Greatest Conservation Need in Texas. Rio Grande cooter is one of the least studied freshwater turtle species in North America, with a lack of knowledge about species' natural history and conservation status across the species range. In New Mexico, Rio Grande Cooters occur on the lower Pecos River and its tributaries. This river system is heavily utilized by oil companies and cattle ranching, which could affect the overall habitat quality for aquatic organisms, including Rio Grande Cooters. In 2018, we surveyed *P. gorzugi* using hoopnet traps along two sections of the Black River in New Mexico: 1. the upstream section managed by the Bureau of Land Management and used mainly for recreational fishing, 2. the downstream section located within private properties where the land is used for ranching and oil drilling operations. For each captured turtle, we took standard body measurements. We used plastron length as an indicator of body condition. Then, we compared the difference between turtles caught upstream and downstream using ANOVA in R software. As a preliminary result, we found that body conditions were significantly better at the downstream sites than the upstream sites. Understanding body condition data can be important when it comes to determining relativity between habitat type and success of the species.

14. WIND TURBINE CONCENTRATIONS AND THE THREATS THEY POSE TO SWAINSON'S HAWKS

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Wind energy is a hazard for flying animals, and migrating species may be at increased risk of encountering wind energy structures. Swainson's hawks (*Buteo swainsoni*) migrate annually between North America and Argentina. We equipped 24 adult Swainson's hawks with satellite transmitters to assess potential risk due to wind energy development during migration. We obtained wind farm locations from the U.S. Geological Survey for the United States, but also needed wind farm locations for 16 countries across the migration pathway. We used coarse wind energy location data from TheWindPower.net to narrow down a search area in the remaining pathway. We then downloaded and visually scanned 169 Sentinel-2 satellite images for patterns that match known wind farms in the U.S. We found 153,109 turbines, with the highest concentrations in Mexico and Uruguay. We added collision risk buffers of 100 m (high risk) and 1 km (low risk) around turbine points and assessed risk by season. Birds were at high risk of colliding with a turbine during the breeding season 0.25% of the time and at low risk 15.7% of the time. During migration, high risk was <0.0% and low risk was 0.02%. During winter, high risk was <0.0% and low risk was <0.0%. Currently,

Swainson’s hawks are at highest risk of encountering turbines while in the U.S. Wind energy is probably not an important hazard for migrating hawks outside of the U.S., though risk will increase if turbines are built in core migration pathways.

15. CO-OVEREXPRESSION OF *AtClCc* AND *PP2AC5* GENES TO INCREASE SALT TOLERANCE IN ARABIDOPSIS THALIANA

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Global environmental changes have caused an increase in salt-scarred farmlands and an increased need to fortify our agricultural practices. By manipulating the expression levels of individual genes, transgenic plants have shown much improved resistance to abiotic stresses, potentially leading to increased crop yield under stressful conditions. To test if this approach can be applied to larger-scale agriculture, we are overexpressing two genes, *AtClCc* and *PP2AC5,* in the model organism *Arabidopsis thaliana* to see if *AtClCc/PP2AC5* co-overexpressing plants perform significantly better than *AtClCc*-overexpressing, *PP2AC5*-overexpressing, and wild-type plants under single stress, multiple-stress, and normal growth conditions. The *AtClCc* gene encodes an antiporter that sequesters chloride anions into the cell’s vacuole while exporting protons, thereby increasing plant stress tolerance under salt conditions. The *PP2AC5* gene encodes a phosphatase that upregulates chloride channels such as *AtClCc*, thereby increasing *AtCLCc’s* activity. The *AtClCc/PP2AC5* co-overexpression construct was incorporated into the *Arabidopsis* genome utilizing *Agrobacterium*-mediated transformation, and homozygous transgenic plants were obtained. High-expression lines will be identified using RNA blot analysis and will be tested for physiological analysis under normal and salt conditions. The performance of *AtClCc/PP2AC5* co-overexpressing plants under high salinity conditions will be quantified by measurements of root length, shoot development, and overall yield and will be compared to both wild-type and single overexpression transgenic plants. If this project is promising, we will introduce these two genes into a more practical organism, such as cotton, to test if we can increase crop yield under high salinity conditions.

16. EXPRESSION OF THE POLYADENYLATION PROTEINS CSTF-64 AND CSTF-77 IN BACTERIA

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Polyadenylation is the process by which a poly(A) tail is added to the end of messenger RNAs. Polyadenylation is necessary to stabilize the mRNA, prevent its decay, and allow it to be translated into protein in the cytoplasm. Many proteins and multi-protein factors are involved in polyadenylation. One important factor is the cleavage stimulation factor, CstF. Two of the main CstF proteins are CstF-64 and CstF-77, which bind strongly to each other in a complex. In order to understand the function of these proteins and their role in polyadenylation, we expressed portions of CstF-64 and CstF-77 together in a bacterial expression system so that they formed a complex. We then purified the complex and characterized it biochemically. In order to express the CstF-64/CstF-77 complex in bacteria, we transformed pMalC-MT-C +RRM-Hinge plasmids into Rosetta 2 (pLys) bacterial cells, induced with isopropyl β-D-1-

thiogalactopyranoside (IPTG), and grew them at 37°C for 4 hours. The bacteria were then collected by centrifugation, re-suspended in buffer with protease inhibitors, and stored frozen at -80°C. Small aliquots were collected before the induction with IPTG and the end of the induction were subjected to electrophoresis on 12% SDS-PAGE. The proteins were then visualized using Coomassie blue dye. We were able to induce expression of the complex in bacteria to a high level. Our next step will be to purify the complex by affinity chromatography on an amylose resin column. Our ultimate goal is to make crystals from the two proteins and determine their structure using X-ray crystallography.

17. MESQUITE EFFECTS ON MICROHABITAT ALTER COMMNITY STRUCTURE BUT NOT PRODUCTIVITY IN SHORT GRASS PRAIRIE

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The *Prosopis glandulosa*, or honey mesquite tree, is an invasive tree species to the American Southwest. However, it is unclear how their microhabitat effects may impact the short-grass prairie community. The main question we address is what do these effects mean for the grassland ecosystems moving forward? To answer this question, we set up paired plots under and 1 meter outside the canopy of 40 mesquite trees in a short-grass prairie in western Texas. We then assessed the microhabitat and plant community differences between plots under the trees and plots outside the canopy of the trees. We found the plots under the trees regularly had lower soil moisture than those away from the trees. This, combined with the light interception provided by the trees reduced resource availability to the understory plants. However, we found that the biomass outside the canopy was only marginally greater than that under the tree despite the lower light and soil moisture availability. Our community measurements indicated that plant diversity was unaffected by the mesquite presence, but that the non-mesquite communities were made up primarily of the C4 grass *Bouteloua gracilis*. We found there was an 18% greater grass to forb biomass ratio in the plots outside the canopy than those under the canopy. These results suggest that with the invasion of the of the honey mesquite tree, the grassland community structure may become more productive overall without a loss in total diversity, but the species comprising the plant community will not resemble the pre-invasion community.

18. PRELIMINARY ASSESSMENT OF ORNATE BOX TURTLE OCCUPANCY IN ROOSEVELT COUNTY, NEW MEXICO

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Ornate box turtle (*Terrapene ornata*) is a terrestrial grassland species, considered near threatened by the International Union for Conservation of Nature. In New Mexico, box turtles are widespread throughout most of the state. Although widespread, little is known about the species-habitat relationships, especially in the eastern portion of the state. In 2018, we conducted visual-encounter surveys in Roosevelt County, New Mexico, to determine occupancy of *T. ornata*. From August through October, we conducted spatially replicated surveys across 34 sites, each consisting of 1x1 mile surface area. The effort at each site varied from 4 to 9 1-mi spatial replicates, with a total walk effort of 209 miles. When *T. ornata* was

encountered, we recorded standard body measurements and marked adults by shell-notching. We encountered a total of 54 *T. ornata*. Thirty-one turtles were encountered on transect lines while 23 were encountered outside of the study sites (i.e., on the road). We detected 0 to 7 turtles per survey site. *Terrapene ornata* occupied 12 of 34 sites, with naïve occupancy of 35%. Given that naïve occupancy likely does not represent the true occupancy, our next step is to develop an occupancy model which explicitly accounts for imperfect detection. Environmental data (i.e., humidity) and vegetation height will be used as detection probability covariates. Land cover, soil type, and proximity to roads will be used as ecological factors influencing box turtle occurrence. This model will provide a better understanding of species distribution and species habitat requirements.

19. PILOT STUDY: MACERATION TECHNIQUES COMPARING HYDROGEN PEROXIDE AND WATER.

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The study of gross anatomy and osteological structures is imperative to museums, curators, and researchers who utilize specimens for numerous studies and preservation in museums. Various maceration techniques are employed to remove soft tissue in a way that is both efficient and leaves the specimens in ideal condition. Although sodium hypochlorite (i.e. common bleach) was previously used as a maceration method, it has proven this to be highly caustic to osseous surfaces rendering them unsuitable for curation and research. Dermestidae colonies are widely regarded as the standard for defleshing. However, an alternative to these colonies is being explored due to meticulous upkeep of the dermestid colony, the time-consuming defleshing process, and allogenic effects on those exposed to the colonies. Alternatives to dermestid colonies can be exceptionally beneficial for museums and collections with limited space. Due to damage as a result of hypochlorite and complexities associated with Dermestidae, this study investigates optimal maceration techniques at different temperatures in comparison to different concentrations of hydrogen peroxide. Our research aims to evaluate maceration techniques in terms of dry mass lost over time. This was carried out by allowing each dry specimen to macerate at different water temperatures and hydrogen peroxide concentrations in 2.5 hr. intervals. After which, specimens were allowed to dry completely between each round of maceration. This study intends to establish parameters for techniques using water or hydrogen peroxide in a manner which would benefit small teaching collections who do not process a high volume of specimens.

20. PHYLOGENETIC ANALYSIS OF BATS IN THE GENUS *MONOPHYLLUS* USING MITOCHONDRIAL AND NUCLEAR GENETIC MARKERS

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The genus *Monophyllus*, the Antillean long-tongued bats, is distributed throughout the Greater and Lesser Antilles in the Caribbean region. *Monophyllus* is comprised of two species, *M.*

plethodon and *M*. *redmani*. *M*. *plethodon* resides in the Lesser Antilles islands and three subspecies historically have been recognized (*M*. *p*. *frater* – now extinct, *M*. *p*. *luciae*, and *M*. *p*. *plethodon*). *M*. *redmani* occurs in the Greater Antilles islands with three subspecies (*M*. *r*. *clinedaphus*, *M*. *r*. *portoricensis*, and *M*. *r*. *redmani*). Based on prior knowledge (morphological data and preliminary molecular data), we hypothesize that *Monophyllus* consists of several species and that the 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 (1,140 bp), and the nuclear beta-fibrinogen gene intron 7. The species, *Glossophaga soricina*, was used as an outgroup. Thirty-nine samples were obtained through the NSRL (Natural Science Research Laboratory) from almost all subspecies of both *M*. *plethodon* and *M*. *redmani*. Likelihood and Bayesian showed a strongly supported monophyletic arrangement of all samples identified as *M*. *plethodon*, and a monophyletic clade of *M*. *redmani*. The two clades were genetically divergent by a K2P value of 10.9%. Preliminary results suggest that *M*. *plethodon* and *M*. *redmani* are different species based on the occurrence of genetically divergent clades. Further, the preliminary analyses suggest two genetically divergent clades (9.2%) within samples representing *M*. *redmani*.

21. PHYLOGENY OF *PEROMYSCUS MANICULATUS* SPECIES GROUP USING NOVEL NUCLEAR MARKERS, *DHPS* AND *SYCE1*

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The genus *Peromyscus* (geographic distribution including much of North and Central America) is a speciose group with approximately 70+ species hypothesized to have arisen during the last 5-6 million years. Systematists have attempted to resolve species boundaries of *Peromyscus* through morphological and genetic analyses. The *maniculatus* species group is of special interest because historically it has been thought to be comprised of approximately 4 species (*P. maniculatus, P. melanotis, P. sejugis, and P. polionotus*). *P. maniculatus*, by far, has been the most morphologically and genetically diverse member of the species group, with as many as 68 subspecies being recognized. Recent efforts indicate that (based on mitochondrial, some SNP data, and chromosomes) *P. maniculatus* may be represented by 5 additional species. Through previous analyses of transcriptome data, we determined two novel nuclear markers (Dhps and Syce1) associated with reproduction that have high dN/dS ratios comparing four taxa across the Peromyscus phylogeny. Consequently, we examined these two genes in light of the proposed systematic elevations within what formally was recognized as *P. maniculatus*. For this study, liver tissues were obtained through the NSRL (Natural Science Research Laboratory). Primers were designed for a 1,058 bp region of Dhps, and a 895 bp region of Syce1 (both spanning at least one intron and one exon). Polymerase chain reaction and Sanger sequencing were conducted on individuals from the maniculatus species group. Sequences were analyzed under likelihood frameworks and preliminary results suggest that there is high sequence variability in the Dhps gene within the maniculatus species group.

22. GROWTH AND RECRUITMENT OF GRAY REDHORSE IN THE LOWER COLORADO RIVER

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Gray Redhorse *Moxostoma congestum* are typically found in upland and lowland streams and are often associated with deep, low velocity, and low turbidity habitats. Streams within the geographical range of Gray Redhorse face several threats including large reservoirs and small impoundments. Although Gray Redhorse have persisted in impounded streams, it has declined in areas with reduced discharge. Identifying recruitment in relation to abiotic variables, such as discharge and temperature, is integral for future conservation of the species. We determined age of Gray Redhorse with scales, and evaluated age structure, growth, and mortality of a Gray Redhorse population in the lower Colorado River, TX. In addition, we investigated the effects of streamflow on growth and recruitment. Scales of the Gray Redhorse indicated that growth occurs rapidly during the first three years and slowly thereafter. The maximum age of Gray Redhorse was seven years, with a mean age (± SD) of 3.70 ± 1.45 ($n = 180$). Using the weighted instantaneous annual mortality method, we estimated the annual survival (± SE) for Gray Redhorse to be 0.35 ± 0.15. We hypothesized that cohort strength is affected by variations in annual discharge and temperature, and we expected that discharge from an upstream reservoir would predict variation in cohort strength. Preliminary results suggest that Gray Redhorse cohort strength was best predicted by higher discharge, while temperature marginally explained variation in cohort strength.

23. EVALUATION OF NUISANCE ALLIGATOR MANAGEMENT AND HUMAN-ALLIGATOR CONFLICT

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The American alligator (*Alligator mississippiensis*) is an iconic North American species, a keystone predator, and an important part of many state economies. As human development encroaches into more alligator habitat, conflict between *A. mississippiensis* and humans becomes inevitable and a necessary aspect of regulation for the state wildlife departments within the alligator's range. Through communication with the state departments dealing with alligators, extensive review of incidents documented by those departments and examination of recorded human-crocodylian interactions in the United States as a whole, this investigation seeks to better understand the current nature of human-crocodylian conflict and those programs that must deal with these conflicts. One of the most important insights gleaned from this investigation is the realization that management program structures vary greatly between states. The information presented can be utilized by the departments to better implement more intentional communication of effectiveness, and push toward cooperation between the states that may lead to the development of more effective management programs.

24. THE EFFECT OF LIFE HISTORY STRATEGIES ON STOMATAL CHARACTERSTICS USING HERBARIUM SPECIMENS FROM GUADALUPE

MOUNTAINS NATIONAL PARK

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Herbarium specimens provide a window into past characteristics of plants, including a record of how they interacted with the environment. One such characteristic is stomata, openings found primarily on the underside of leaves that regulate gas exchange within a plant. Plants can respond to atmospheric conditions during leaf development; many studies show a decrease in stomatal densities related an increase in carbon dioxide. Stomatal density can be easily measured in herbarium specimens via imprints of leaves without damaging the specimen. Many studies of stomatal density do not incorporate variability within species or across life history strategies within a single ecosystem. One collection housed in the E.L. Reed Herbarium at Texas Tech, with an estimated 3,000 specimens, is from a survey of Guadalupe National Park conducted when the park opened in 1974 by Texas Tech botanists D. K. Northington and T. L. Burgess. The collection provides a botanical snapshot of floristic biodiversity just before major changes in climate and land management. For this study, stomatal density and size were sampled from 24 species representing a variety of life history strategies including grasses, trees, shrubs, and forbs. Measurements were tested for stomatal qualities within species, among species, and among plants with different life history strategies. Findings will inform future studies about the relative importance of these factors when predicting changes in stomatal density in response to elevated carbon dioxide.

25. TERRITORIALITY AND AGGRESSIVE BEHAVIOR OF DUSKY DAMSELFISH, *STEGASTES ADUSTUS*, IN ROATÁN, HONDURAS

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The dusky damselfish, *Stegastes adustus*, is a Caribbean fish that reside in shallow waters. Damselfish are well documented as aggressive and territorial towards fish that intrude on to their territories. Territories provide food and clutch space for damselfish to lay their eggs. Aggressive behaviors, depending on the intruder, can include chasing, biting, and charging. This study was conducted to assess territorial and aggressive behaviors of the dusky damselfish, *Stegastes adustus*, on the Mesoamerican Reef in Roatán, Honduras. Data was collected from May 15-18, 2018, at four dive sites in Roatán, Honduras. Each intruding fish species was recorded and the damselfish behaviors in response; feeding, cautiously watching, charging, attacking, chasing, disregard, sound, and swimming were the behaviors that were recorded in this study. “Swimming” was the behavior that was most frequently observed. “Swimming” represented the dusky damselfish moving passively in its territory. The least frequently observed behavior was “attacking”. “Attacking” was observed when the dusky damselfish had physical contact with the intruding fish. "Attacking", "chasing", and "charging" were categorized as aggressive behaviors. "Disregarding", "swimming", "feeding", and "cautiously watching" were categorized as non-aggressive behaviors. Dusky damselfish had

more aggressive interactions with herbivorous fish species and more non-aggressive interactions with omnivorous fish species. Future research should compare behavior differences between juvenile and terminal phase among damselfish species.

26. WARMING UP WITHOUT DINNER: HIBERNATING BATS WITHOUT FORAGING OPPORTUNITIES DESYNCHRONIZE FROM SUNSET DESPITE WARM-CLIMATE

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For hibernating bats, arousals from torpor are extremely energetically demanding, accounting for 80-90% of energy stores for the winter. Consequently, arousal physiology has been greatly studied. A previous study of bats from moderate climates showed that hibernating bats maintain a circadian rhythm that synchronizes arousals with sunset to allow for foraging opportunities on warmer nights. However, bats hibernating in cold-climates with little to no insect activity, seem to lose all circadian patterns and arouse randomly. We conducted an experiment to test what factors could lead to a sunset-synchronized circadian rhythm. We studied 98 tricolored bats (*Perimyotis subflavus*) collected from Mississippi and monitored their arousals from December 19, 2018 to March 5, 2019. Bats were randomly assigned to 18 cages that varied in temperature (5, 8, 11º C), and humidity (85 – 95% relative humidity). We hypothesized that (1) if maintenance of a circadian rhythm is linked to a minimal temperature necessary for winter foraging, then arousals would be synchronized with sunset in bats hibernating in warmer temperatures (11º C), (2) if external cues, such as light cycles, are what causes sunset synchronization then arousal times should randomize as time within controlled chambers increases, and (3) if endogenous factors, such as fat storage drive circadian rhythms, then as fat stores decline arousal times will synchronize with sunset. We found no evidence of circadian rhythms and arousals synchronized with sunset, regardless of experimental treatment, suggesting that maintenance of circadian rhythms in hibernation requires sensory cues indicating opportunities for foraging.

27. CONSERVATION GENOMICS OF PLANT POPULATIONS IN GUADALUPE MOUNTAINS NATIONAL PARK USING HERBARIUM SPECIMENS

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Conservation genomics is an area of study that examines the genetic viability and biodiversity of populations. The purpose of this research project is to develop a genome-wide view of the genetic health of a variety of native plant species from the Guadalupe Mountains National Park. The GUMO collection in the E.L. Reed Herbarium at Texas Tech University contains over 2000 specimens collected from the park at its establishment in 1973. These herbarium specimens possess historical value: a snapshot of the botanical community, providing physical and genetic records of the past. The two main goals of the project are to assess the utility of 353 genes for conservation genomics and to determine whether genetic variability is related to life history strategy. For this project, 24 species from the GUMO collection were selected to span a large range of life history strategies in flowering plants, including species of grasses, forbs, shrubs and trees. 95 unique plant specimens were destructively sampled for DNA extraction and sequencing. A newly developed set of 353 genes that can be amplified from any flowering plant were captured using a targeted sequencing approach. Within each species, nucleotide

diversity was assessed and associations between genetic diversity and life history strategies were made. Analysis is completed on the sequenced genes to examine the variety of the genetic pool, as well as examine nucleotide diversity. These results will serve as a point of comparison in future projects with modern samples and prove the utility of herbarium specimens in conservation genomics.

28. GLUCOSE TOLERANCE IN AN APPSWE/PS1DE9 ALZHEIMER'S DISEASE MOUSE MODEL.

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Alzheimer's disease (AD) is a progressive, age dependent neurodegenerative disorder. While the causes of AD are unclear, type 2 diabetes mellitus (T2DM) has recently been established as a risk factor for developing all cause dementia and dementia attributable to AD. In APPswePS1dE9 mouse model of AD, transgenic male mice show altered glucose tolerance, with hyperinsulinemia and insulin resistance, prior to displaying amyloid beta neuropathy by 4-6 months of age and depositions progressing with age. Here, we evaluated the glucose clearance ability of aged ~75-week-old APPswe/PS1dE9 transgenic (tg) and non-transgenic (non-tg) mice to determine if impaired glucose metabolism persists throughout life and correlates with brain amyloid beta concentration. We predict that tg mice, compared to non-tg, will display: 1). higher fasting glucose levels and 2). glucose intolerance (defined by impaired glucose clearance during a glucose tolerance test (GTT). Briefly, following 4h fasting, blood glucose was measured, and mice were injected an intra-peritoneal bolus of 1.5 g/kg glucose. Blood glucose was further determined at 15, 30, 60, 120-min post injection (GTT) to measure glucose clearance. Preliminary data show that transgenic and non-transgenic mice did not differ in baseline fasting glucose levels or in blood glucose clearance following the challenge. Additional data collection is underway. This research was funded by the National Institutes of Health (R15AG048447).

29. INFLUENCE OF THERMAL PROPERTIES ON ROOST USE BY THE CAVE MYOTIS (*MYOTIS VELIFER*)

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Bats spend a considerable portion of their life at roosting sites, such that roost characteristics may have a significant influence on bat survival and reproductive success. For example, bats rely heavily on roosts during torpor to conserve energy, particularly during periods of sub-optimal temperatures. Highway culverts could provide roosting habitat and thermal properties necessary for bats. We surveyed 88 culverts across 70 kilometers of US-84 for presence and abundance of Cave myotis (*Myotis velifer*), one of the most common bats in Texas. We measured characteristics of each culvert such as percent obstruction of entrances, culvert

height, width, and length, and internal and external temperature regimes, to identify factors influencing roost use. To characterize internal and external temperature regimes at a culvert, we deployed iButtons to record temperature every 30 minutes in order to quantify daily and monthly temperature characteristics across 5 months. We predict bat abundance to be higher in culverts with a more stable internal temperature regime (e.g., long culverts relative to short culverts). This research will contribute to existing knowledge of roosting behavior of bats by contributing to our understanding of how characteristics like temperature and culvert dimensions influence culvert use by bats as roosting sites.

30. CHRONIC STRESS ALTERS REARING BEHAVIOR AND HIPPOCAMPAL CA3 REGION STRUCTURE IN WILD-TYPE MICE

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Chronic stress due to exposure to emotional and environmental pressure can have long lasting effects on an animal's well-being. Chronic stress can manifest in different ways, although it does have an effect on the brain's chemical composition. These changes may translate into anxiety and other mental disorders. In animal models, chronic stress can alter normal behaviors such as exploration and rearing, a common behavior observed when an animal is introduced to a new environment and it stands on its hind legs to better observe its surroundings. Studies suggest that the hippocampus, a region of the brain involved in learning, memory and strongly sensitive to stress, switches to a different operational state when rearing occurs (namely, theta frequency oscillations in the hippocampus increase when rearing starts and decrease when rearing stops). Consistent with this functional data, damage to the hippocampus impairs rearing. We hypothesized that chronic stress in mice could specifically impair a hippocampal-dependent task such as rearing. To test this hypothesis, we subject the mice to a 1- or 3-week chronic stress paradigm. Once the stress paradigm was completed, we analyzed each mouse's behavior in an open field test, and specifically quantified rearing behavior. Because the hippocampus is an essential for rearing, we set out to investigate this structure in both our control and stressed mice using Timm's staining. We found a significant increase (~ 50%) in the labeled mossy fiber region (hilus and *stratum luccidum* in CA3) in male mice after the 3-week stress paradigm compared to non-stressed controls.

31. ENSEMBLE BY ENSEMBLE: DO AFROTROPICAL BAT ENSEMBLES DIFFER IN RESPONSE TO ELEVATIONAL GRADIENTS?

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Bat ensembles show different responses to elevational gradients in the Neotropics but this pattern is unclear in the Paleotropics. Bat ensembles are targeted by different trapping techniques; harp traps biased towards understory clutter-adapted species, while mist nets and acoustic surveys target forest edge and open spaces species. Employing various trapping strategies improves inventory completeness of local species composition. Our recent harp trapping along an Afrotropical elevation gradient in southeastern Nigeria, showed monotonic

decline in species richness of forest interior insectivorous bats. Here, we investigate the activity of edge and open space bats along elevational gradients and compare this to the forest interior bat species richness pattern. We employed the Anabat Walkabout ultrasound detector to conduct active acoustic recording of free flying bats for 10 minutes at five recording stations, set at 50 m intervals along 200m transects. Four transects were surveyed at five elevational strata set every 250 – 350 m in Afi Mountain Wildlife Sanctuary (AMWS), which is >1250 m a.s.l. During the 10-minute recording period, files were automatically saved every 15 seconds. Acoustic files were processed in the BatSound software and six quality bat calls identified within each file. We represent bat activity as as number of files with quality bat calls per recording time. Our results showed a decline in bat activity with elevational gradient, but the pattern is slightly different from the capture data, suggesting that Afrotropical bat ensembles may have different response to elevational gradients. This study has implications for bat surveys along elevational gradients.

32. EFFECTS OF ACUTE STRESS AND CORTICOSTERONE ON SHORT-TERM MEMORY IN AN APPSWE/PS1DE9 MOUSE MODEL OF ALZHEIMER'S DISEASE

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Alzheimer's disease (AD) is a degenerative brain disorder that causes memory loss, behavioral changes, and a decline in cognitive function. The exact etiology of AD is unknown, but accumulation of amyloid beta (AB) plaques is a defining feature. Stress and stress hormones (e.g. glucocorticoids) have been identified as risk factors as both self-reported stress and increased glucocorticoids are associated with increased progression and severity of AD. We will use APPswe/PS1dE9 transgenic (tg), a mouse model of AD-associated amyloidosis, and non-transgenic (non-tg) mice to determine if acute stress alters performance on a short-term memory task (delayed match-to-position task; DMTP). Mice are tested daily in the DMTP from 16 to 75 weeks of age. At 73 and 74 weeks, mice are exposed to a stress test (wolf urine or forced swimming) immediately before memory testing. DMTP performance data for the day prior to, the day of, and the after stress sessions are compared. At week 77, a baseline blood sample is collected, mice are exposed again to one of the two stressors, and a blood sample is collected for analysis of corticosterone. We predicted that compared to non-tg mice, tg mice would 1) perform worse on the DMTP, and 2) have higher post-stress corticosterone levels than non-tg mice. We also predicted that stressor exposure would decrease short-term memory performance, and post-stress corticosterone would be negatively associated with DMTP performance. Data analysis is still underway but preliminary data suggest that neither odor (wolf urine) stress nor genotype impact DMTP performance across trials.

33. ROLE OF ERGOSTEROL AND SPHINGOLIPIDS IN NUTRIENT UPTAKE DURING STARVATION CONDITIONS ENCOUNTERED BY PROMASTIGOTE STAGE OF LEISHMANIA MAJOR.

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Leishmania promastigotes, in order to have successful replication and differentiation to the infective metacyclic form in the sandfly stage, 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 key components of the plasma membrane and regulate membrane stability, ligand-receptor interaction, and vesicular trafficking. Our previous research findings suggest that endogenous ergosterol and sphingolipids imbalance make *Leishmania* hypersensitive and susceptible to nutrient starvation along with osmotic stress, relevantly encountered in the sandfly midgut. Glucose uptake through membrane glucose transporters are crucial for *Leishmania major*, for it allows the cells to acquire energy and adapt to nutrient starvation when encountered in the sandfly midgut. We wanted to investigate whether altered sterols and sphingolipids impacts acquisition of small molecules and nutrients like glucose through glucose transporters by measuring its uptake over short periods of time. We hypothesized that the sterol and sphingolipid mutants will need more glucose in glucose starvation medium to compensate starvation stress. It was found that the *Leishmania* mutants with altered sterols incorporated more glucose than their wild type counterparts, possibly as a mechanism to adapt to nutrient starvation conditions.

34. THE EFFECTS OF DIETARY EICOSAPENTAENOIC ACID SUPPLEMENTATION ON COGNITIVE FUNCTION IN AMYLOID BETA TRANSGENIC MICE

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Alzheimer’s disease (AD) is a multi-factor brain disorder that results in a memory loss and cognitive decline. The exact etiology of AD is unknown, but risk factors include obesity and high-fat, high caloric diets. Obesity is associated with increased adipose tissue, brain inflammation, and cognitive impairments. Omega 3 Polyunsaturated fatty-acids from fish oil, such as eicosapentaenoic acid (EPA) are reportedly beneficial in obesity. Here, we investigate the impacts of dietary supplementation with EPA on memory. EPA supplementation can alleviate physiological aspects of diet–induced obesity, including insulin resistance and inflammation, both of which seem to worsen AD progression. In this study, we hope to address whether EPA supplementation reduces cognitive deficits associated with AD using a beta amyloidogenic mouse model of AD (APPswe/PS1dE9). Starting at 2 months of age, male and female wild type (non-Tg) and Tg mice are fed a low-fat, high-fat, or high-fat supplemented with EPA diet for 8 months. At 6 months of age, short-term memory will be assessed in the novel object recognition test; at 9 months, mice will undergo the Morris Water Maze task to assess spatial learning. We predict mice fed a high-fat diet will exhibit greater cognitive impairments than those fed low-fat diet, with Tg mice performing worse that non-Tg in both diet treatments. Additionally, we predict that EPA supplementation will protect both non-Tg and Tg mice from the negative effects of the high-fat diets. Data collection is currently underway, if successful, EPA may serve as an inexpensive, dietary, preventative approach to AD.

35. RELATIONSHIP AMONG CORTICOSTERONE, STRESS, AND ANXIETY, AND

MEMORY IN AN APPSWE/PS1DE9 MOUSE MODEL OF ALZHEIMER'S DISEASE.

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Alzheimer's disease (AD) is the sixth leading cause of death in the U.S. AD is a dementing disorder that generally affects individuals over the age of 65. AD presents with a decline in cognition, behavior, and memory. The etiology of this disease is not fully known. However, AD neuropathology has shown that amyloid beta is one of the major bio-markers for identifying AD. Additionally, stress, stress hormones (e.g. corticosterone), and anxiety are key factors in the progression and severity of AD. Elevated baseline or post-stress corticosterone can increase amyloid beta plaque production in the brain and can impair memory. Our aim is to evaluate how stress, stress-hormones, and anxiety are related to memory and amyloid beta concentrations in the APPswe/PS1dE9 mouse model of AD. To examine stress-induced changes in hormones, mice were exposed to predator odor and both baseline and post-stress blood samples were collected for corticosterone analysis. Anxiety was measured via a light/dark test. Memory was tested using novel object recognition. we predicted that transgenic mice, versus their non-transgenic littermates, would 1) have higher baseline and post-stress levels of corticosterone, 2) spend the majority of time in the dark box, and 3) have impaired memory. As expected, transgenic mice had higher corticosterone across the lifespan and this effect was driven primarily by transgenic female mice. In the light/dark test, all animals preferred the dark to the light, but genotypes did not differ in time spent in dark. We are in the process of analyzing additional light/dark and memory data.

36. ANNUAL VARIATION IN COMMUNITY STRUCTURE AND ABUNDANCE OF SHORT GRASS PRAIRIE BIRDS IN LUBBOCK COUNTY, TX

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Grassland birds are thought to be one of the fastest declining avian guilds in North America, thus it is important to understand patterns of annual variance in association with environmental factors. We used 5-minute point count surveys to measure community structure of grassland birds across 6 years. We also estimated annual density of four focal species: Cassin's sparrows (*Peucaea cassinii*), horned larks (*Eremophila alpestris*), mourning doves (*Zenaida macroura*), and western meadowlarks (*Sturnella neglecta*). Surveys were conducted in May and June from 2012 – 2017 across 50 survey points on a 635 hectare plot of land in Lubbock County, with all avian species being recorded within 75 meters. In total we made 5,488 detections of 49 different species. Using this we calculated species diversity, evenness, percent overlap among years, and we used program DISTANCE to estimate densities of focal species. Species overlap among most years was high (>80%); however, it was exceptionally low in 2013 when precipitation levels were low. This suggests a community shift during dry years to more arid adapted birds, such as the horned lark. Densities for the focal species fluctuated greatly each year; however, all species other than the horned lark, were at their peak densities immediately following the drought in 2012 and 2013. Overall, it is important to conduct further research on how these environmental factors, such as precipitation, cause changes in

the community structure of grassland birds. By understanding this, managers can optimize habitat through grazing, fire, available forage, etc. to meet conservation goals.

37. GABAERGIC DEFICITS ARE ASSOCIATED WITH SEIZURE SUSCEPTIBILITY IN A MOUSE MODEL OF SLC13A5 DEFICIENCY

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SLC13A5 is a Na^+-coupled citrate transporter (NaCT) that imports citrate into the neuronal cytoplasm from the extracellular space. Citrate is a key energy source for mitochondrial respiration and a building block in the synthesis of neurotransmitters, fatty acids, and steroids. Therefore, SLC13A5 deficiency may impact the availability of key neurotransmitters such as glutamate, GABA, and acetylcholine. These deficiencies in turn would alter synaptic function and excitation/inhibition imbalance by either weakening GABAergic function or enhancing glutamatergic function. Inhibitory neurons, especially parvalbumin-positive **(**PV) interneurons, are more active and require greater energy demands than principal neurons. In this study, we utilized SLC13A5 KO mice to test the hypothesis that SLC13A5 deficiency lowers seizure threshold to the chemoconvulsants pilocarpine **(**PILO) and pentylenetetrazole **(**PTZ) when administered intraperitonially. In an open field maze, administration of 50 mg/kg PILO impaired locomotor activity more in KO than WT mice. Seizures were scored manually using a Racine scale (index of seizure severity, from 0 to 7). In the PILO group (n=4), KO mice exhibited increased seizure severity at 0-10 min and 10-20 min. In the PTZ group (n=3), which more directly tests for impaired GABAergic signaling, KO mice exhibited shorter latency to onset and increased seizure severity. Our preliminary results from both PTZ and PILO converge on the finding that KO mice have lower seizure threshold compared to WT mice. In conclusion, these results are consistent with the hypothesis that SLC13A5 deficiency weakens GABAergic signaling. Future studies will determine whether these observations are consistent in the larger population.

38. DO VISUAL SYSTEM CRF RECEPTORS INFLUENCE VISUALLY GUIDED FEEDING?

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For an animal to survive, it must make quick judgments about when to forage and when to flee. This behavioral trade-off is crucial for survival and reproductive success. While the precise sensory cues and neuromodulators of this trade-off are not entirely understood, neuropeptides associated with stress may play a role. For example, corticotropin-releasing factor (CRF), well known for its role in the hypothalamic-pituitary-interrenal axis, is present in the optic tectum

(OT), a multisensory processing region of the brain. In the South African clawed frog (*Xenopus laevis*) CRF increases in the OT in response to a predator and elevated CRF decreases feeding. It is not yet explored if CRF inhibits food intake by acting on visual, lateral line, or multiple sensory modalities. Here, we test the prediction that injection of CRF into the OT will decrease the response to visual and multi-modal prey stimuli. Frogs were injected with one of 4 doses of CRF, saline, or left unmanipulated; 60 min later they were exposed to visual prey cues (iPad movie) and then to a live worm. Both behavioral tests were repeated 72 hrs later. All trials were videotaped for scoring of feeding-related behaviors. Data collection is currently underway, but preliminary analysis suggests that CRF decreases the response to visual stimuli and to live prey. Our data will help us better understand the neuroendocrine mechanisms behind the decisions of foraging/predator avoidance trade-offs. This work was funded by the National Science Foundation (Grant No. 1656734).

39. INVESTIGATING THE EFFECTS OF SOCIAL INTERACTION IN MINIMIZING STRESS-INDUCED BEHAVIORAL CHANGES IN MICE

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Animal and human studies have shown that stressful environments can cause maladaptive changes in the brain and may result in impaired learning and memory, detrimental effects on behavior and even neuropsychiatric disorders. The hippocampus, a region of the brain heavily involved in learning and memory, is especially vulnerable to stress. To counteract stress-induced behavioral changes, social support has been suggested as an effective coping strategy. Social support reduces stress hormone levels as well as prevents depression induced by stressful conditions.

Animal studies have validated these findings, collectively called “social buffering” of stress. Therefore, in our study we examined the behavior of wild type mice subjected to a 21-day chronic unpredictable stress (CUS) protocol in 2 conditions: stressed mice kept in the same cage with control mice (non-stressed) or kept in separate cages from non-stressed mice. At the end of the chronic stress period we examined several behaviors in all mice: exploration (open field), depression-like (forced swim test), anxiety (elevated plus maze) and working memory (novel object recognition test) and measure their corticosterone levels. Results from our project will expand our view of the positive impact that contact with non-stressed conspecifics could have in individuals undergoing chronic stress.

GRADUATE POSTERS

40. THE DYNAMICS OF A STOICHIOMETRIC PLANT-POLLINATOR MODEL AND ITS PARAMETER SENSITIVITY ANALYSIS.

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Plant-pollinator interactions play an important role in the maintenance of the balance of nature. All organisms living in the environment are composed of different ratios of chemical elements.

By considering the balance of essential chemical elements in nature, we can formulate mathematical models to study their role in the dynamics of the system as well as nature. We formulate and analyze a stoichiometric-plant-pollinator model. Our model includes a three-dimensional system of ordinary differential equations to represent the plant, pollinator populations, as well as the varying nutrient levels of the plant. We analyze the dynamics of the system such as non-negativeness and boundedness of solutions, as well as the existence and stability of boundary equilbria. We perform a bifurcation analysis of the model and also a parameter sensitivity analysis of the model using Latin hypercube sampling and partial rank correlation coefficient technique.

41. STOCHASTIC EPIDEMIC MODELS FOR ZOONOTIC SPILLOVER

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Zoonotic infectious diseases are spread from animals to humans. It is estimated that over 60% of human infectious diseases are zoonotic. Many emerging and re-emerging zoonotic diseases are of viral origin such as avian influenza, rabies, Ebola, and orthohantaviruses. Bacteria zoonotic infections are also common, such as those caused by Salmonella and anthrax. Spillover of disease from animal to humans depends primarily on the contact between animals and humans. Environmental factors, such as seasonal variations in temperature, humidity, and rainfall, also impact the spread of zoonotic diseases. In this investigation, a new Markov process model is formulated for zoonotic disease spread from animals to humans which is based on susceptible-infectious-recovered epidemic modeling for animals and humans. A branching process approximation allows estimation of the probability of the first spillover event from animal to human after the animal population is initially infected. When the animal recovery rate and the transmission rates among animals and from animals-to-humans are assumed to vary seasonally, then it is shown that the probability of spillover also varies seasonally. However, it is discovered that the highest risk of the first spillover event does not coincide with the peak value of the animal-to-human transmission. Examples to rabies and orthohantavirus outbreaks are discussed.

42. THE EFFECTS OF SEASONAL VARIATIONS ON DISEASE TRANSMISSION AND MOBILITY IN STOCHASTIC EPIDEMIC MODELS

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Seasonal changes due to temperature, humidity, and rainfall impact the spread of infectious diseases in animal populations. Pathogen transmission and population movement, such as migration, are affected by seasonal changes. Stochastic epidemic models with movement between two locations or patches are formulated to investigate the effect of periodic transmission and movement on the probability of an outbreak and on the variability in disease incidence when the disease becomes established. A nonhomogeneous Markov process accounts for the demographic and environmental variability caused by seasonal changes. A branching process approximation is used to compute the probability of an outbreak which is also shown to be periodic. However, it is shown that the peak time of outbreak does not coincide with the peak time of transmission. Applications to avian influenza and other infectious diseases are discussed.

43. NOVEL MARKERS FOR SEPSIS IN *PSEUDOMONAS AERUGINOSA*-INFECTED SEVERELY BURNED PATIENTS

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Sepsis – life-threatening organ dysfunction that may include kidney failure, cardiac abnormalities, and respiratory distress – leads to hospitalization of one million individuals in the US annually with a death rate of about 200,000. Sepsis in trauma patients is usually accompanied by bloodstream infection, often with Gram-negative bacteria such as *Pseudomonas aeruginosa*, which is frequently multidrug-resistant. We recently showed that, compared to its growth in whole blood from healthy volunteers, *P. aeruginosa* grown in whole blood from severely burned patients (SBP) significantly altered the expression of many of its genes in response to changes in levels of blood metabolites. We hypothesized that some host metabolites would be significantly reduced by bacterial consumption while bacterial metabolites would significantly increase during *P. aeruginosa* sepsis. Such alterations may serve as early markers for *P. aeruginosa* sepsis in SBP. We tested this hypothesis using the murine model of thermal injury, which mimics closely *P. aeruginosa* sepsis in SBP. Adult mice were thermally injured only or thermally injured and infected with *P. aeruginosa* and serum samples were collected after 24 hours. The levels of 531 metabolites within each sample were determined using gas chromatography time-of-flight mass spectrometry. Compared with thermal injury only, the levels of 15 metabolites were significantly increased (including thymidine, thymine, uridine, uracil, succinic acid), and those of 8 metabolites (including methionine, tyrosine, indole-3-acetate, indole-3-propionate) were significantly reduced in injured/infected mice. We suggest that some of these metabolites may serve as novel biomarkers for early diagnosis of sepsis in burn patients caused by *P. aeruginosa.*

44. GROWTH RATE ESTIMATES FOR THE RIO GRANDE COOTER (*PSEUDEMYS GORZUGI*) ON THE BLACK RIVER, NEW MEXICO

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The Rio Grande Cooter, *Pseudemys gorzugi*, is a relatively large riverine turtle native to New Mexico, Texas, and Mexico. As one of the least studied freshwater turtle species in the U.S., very little is known about this species demography. We conducted a capture-mark-recapture study of *P. gorzugi* from 2016 to 2018 on the Black River, New Mexico. We recaptured 118 individuals between the years, of which 25 were females, 36 were males and 57 were juveniles. Here, we report the somatic growth rates and length-at-age estimates for the species. We

analyzed plastron length of female and male datasets including juveniles in both groups with the assumption that juvenile females and males have similar growth rates. We estimated growth curves using the non-linear Von Bertalanffy equation and used FiSAT II to estimate the equation growth parameters *k* and *a*. As expected, there was a significant negative relationship between mean body size and growth rates. Growth constant (*k*) estimates ranged from 0.060 to 0.102 for females and 0.100 to 0.105 for males, depending on the estimation method used. Estimated age at sexual maturity is ~15 years for females while longevity was estimated at ~50 years for females and ~38 years for males. Our results demonstrate the importance of continuous multi-year studies on long-lived species in order to provide demographic data and implement sound management practices.

45. STUDY OF THE ROLE OF BREAST CANCER ASSOCIATED GENE 2 (BCA2) THROUGH A DOXYCYCLINE-INDUCIBLE SYSTEM

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Breast cancer associated gene 2 (BCA2) is an E3 ubiquitin ligase that is overexpressed in more than 50% of primary breast cancers, and its up-regulation correlates with poor prognosis. However, little is known about the role of BCA2 in breast cancer development. Whereas some studies have reported an oncogenic role for BCA2 due to its ability to promote the degradation of the tumor suppressor p21, others have found that BCA2 decreases cell proliferation by down-regulating proto-oncogene encoding proteins. Hence, there is a critical need to elucidate what the role of BCA2 is in cellular transformation. To address this, we want to assess BCA2's effects on cell cycle and proliferation at distinct BCA2 expression levels and also in different cellular environments, such as breast cancer versus normal breast cells, as well as in other cellular tissues.

In order to control BCA's expression, we have engineered inducible lentiviral vectors in which the *BCA2* coding region is under the control of the Tet operator, whose initiation is regulated by doxycycline stimulation. Using this method, we have generated stable cells lines in which we can overexpress BCA2, or different BCA2 mutants, in a dose-controlled manner. These reagents will help us investigate whether the overexpression of BCA2 affects cell proliferation, migration, and/or cell cycle progression in different cellular environments, and thus, will increase our understanding of the role of BCA2 in cancer development.

46. CONVERSION OF LOW-QUALITY COTTON TO BIOPLASTIC

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Microplastic contamination generated by petroleum-based products has become a global problem. The use of eco-friendly bioplastics can reduce the generation of microplastic wastes. In this study, low-quality cotton fiber (micronaire = 2.4) was used as a starting material to explore the conversion of cellulose-based biomass to eco-friendly bioplastics. The physical and mechanical properties of the films were significantly improved due to the plasticization and hot pressing operations. This study paves the way to use low-quality cotton fibers to prepare advanced bioproducts, such as bioplastics that could be viable alternative to petroleum-based materials.

47. A NOVEL TREATMENT FOR HPV-RELATED CANCERS: USING HPV16 STRUCTURAL PROTEINS TO ENCAPSULATE ANTI-CANCER DRUGS

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Cervical cancer accounts for 300,000 female deaths per year globally. Human Papilloma Virus (HPV), types 16 and 18, has been shown to cause 90% of cervical cancers and pre-cancerous cervical lesions. Papillomaviruses are highly epitheliotropic, establishing productive infections only within stratified epithelia of the skin, the anogenital tract and the oral cavity. The standard treatment for cervical cancer is mechanical removal of primary tumor cells and broad-spectrum chemotherapy for metastasis. Although the vaccine against HPV (Guardasil™) is nearly 100% effective, not everyone has access to it, nor are males strongly encouraged to receive it. Since the vaccine is relatively young (FDA approved in 2006), and the majority of the population has not been immunized, herd immunity has not yet developed. Thus, HPV-positive individuals are potentially infecting unvaccinated sexual partners resulting in increased incidences of associated penile cancers, as well as oropharyngeal, anal, and rectal cancers in both genders. Encapsulating anti-cancer drugs into an HPV capsid, devoid of genetic material, would facilitate selective entry into infected epithelial cells and targeted delivery of the anti-cancer drugs. In this study we will investigate the feasilibilty of encapsulating doxorubicin into HPV capsids and evaluating their efficacy in killing cancer cells *in vitro* versus doxorubicin alone. We hypothesize that if successful, this targeted delivery strategy would significantly increase treatment efficacy as well as reduce the negative side effects associated with standard chemotherapy treatments.

48. EFFECTIVE SURVEILLANCE OF MOSQUITOES USING NEXT-GENERATION SEQUENCING FOR METABARCODING.

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Mosquitoes are the most significant vectors of human diseases, causing morbidity and mortality on a massive scale across the globe. Effective surveillance of vectors depends upon accurate and sensitive species identification and is crucial for tracking mosquito populations and monitoring disease causing agents over time. Commonly used morphological methods of vector identification require extreme expertise and significant effort due to the limitation of examining individual specimens one at a time. Moreover, mosquito samples are often degraded upon retrieval from surveillance traps and are prone to either misidentification or lack of identification, thus cryptic/invasive species could be overlooked.

Recent advances in Next-Generation Sequencing can facilitate the application of genetic barcoding for vector identification to dramatically increase both the accuracy and sensitivity of species identification. Barcoding can also reduce the time and expertise required for vector surveillance by allowing for mass identification and obviating the need to handle mosquitoes individually. By incorporating unique indexing primers during PCR amplification, multiple samples can be combined, thereby reducing overall cost.

In this study, we demonstrate the utility of NGS-based surveillance via multiplexing of ten pooled samples, collected via multiple methods and distinct locations, into a single sequencing run. We use powerful bioinformatic techniques to demultiplex sequencing reads to obtain accurate and representative information about each sample at the species level. We propose that these methods can be used to complement current surveillance programs and have the potential to reduce both the time and cost constraints associated with implementing surveillance programs in new areas.

49. ASSESSING SMALL MAMMAL RESPONSE TO MESQUITE CANOPY REMOVAL IN AN ISOLATED RANGELAND

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Species composition and competitive interactions among small mammals are affected by changes in habitat structure, making small mammals useful indicators of ecological health. Studying the effects of shifts in habitat structure on small mammal population dynamics can thereby provide insight into community resilience in response to environmental changes. In the Texas Tech University, Department of Natural Resources Management Native Rangeland, highly invasive honey mesquite (*Prosopis glandulosa*) has transformed this historic short-grass prairie to shrubland. To assess the effect of restoring this rangeland back to short-grass prairie on small mammal activity, we established 24, 20 m x 20 m plots in the Rangeland and treated half by clear-cutting mesquite, removing slash, and treating stumps with herbicide. We trapped small mammals within each plot during July 2018 (pre-treatment) and October and November 2018 (post-treatment). Additionally, we recorded microclimatic and vegetation cover data for each trap location. Pre-treatment capture success did not differ significantly between control (average 10.33%) and treatment (average 11.81%) plots ($t=-1.45$, $p=0.161$, $df=22$). However, post-treatment, capture success was significantly greater in control (average 10.18%) plots than treatment (average 0%) plots ($t=-5.266$, $p<0.001$, $df=11$). This pattern suggests that the removal of canopy cover may cause short-term avoidance by small mammals, at least initially after treatment. Further work will disentangle whether this avoidance is a function of microclimate (physiological constraints) or directly related to structure (predator avoidance), and potentially how long avoidance may last.

50. CORRELATION OF METASTATIC POTENTIAL AND INCREASED ABILITY TO REPAIR MEMBRANE DAMAGE

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Previous studies have demonstrated that the more metastatic the cancer cell, the greater the cell’s deformability properties. (1) Currently, no studies have investigated whether this characteristic is correlated with an increased rate of cellular membrane repair. Thus, we hypothesize that cancer cells have an enhanced ability to repair mechanical membrane damage and this facilitates metastatic success and that the more metastatic the cancer cell, the greater the repair capability. This hypothesis is based on the data showing that metastatic cancer cells are better able to withstand physiological shear stress, abrasion and pressures en route to their secondary site. In order to test this hypothesis, three breast cell lines with differing

levels of metastatic potential will be exposed to varying doses of Streptolysin O (SLO) from *Streptococcus pyogenes*. SLO is a pore forming toxin (PFT) that perforates the cellular membrane causing the cells to lyse. (2) We predict that the metastatic cancer cells will be more resilient to this treatment and that their membranes will be repaired at a faster rate than either cancer cells with lower metastatic potential or normal cells. The cells lines to be tested include the highly metastatic, triple negative MDA-MB-231 breast cancer cells, the non/low metastatic, triple positive MCF7 breast cancer cells, and the noncancerous MCF7-10A breast cells. The dosage of SLO to be administered will be 18 ug/mL (the reported concentration for lysing ~50% of HeLa cells). (3) One-way ANOVA ($p<0.05$) will be used to determine statistical significance of cell membrane repair, evaluated by time to cell lysis in the different cell types.

51. RECOMBINANT S5 PYOCIN: A NOVEL THERAPY FOR *PSEUDOMONAS AERUGINOSA* INFECTION

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Complex wounds occur in the setting of chronic diseases such as venous insufficiency and diabetes. Within chronic wounds, infecting bacterial pathogens often exist in protective structures termed biofilms in which the microbes are encased in a self-synthesized extracellular polymeric substance. *Pseudomonas aeruginosa* is one of the most common bacteria isolated from chronic wounds. One such therapy is the utilization of pyocins, which are narrow-spectrum antimicrobials produced by *P. aeruginosa* to eliminate other competing bacteria. The S-type pyocins are simple proteins that have different killing domains. Pyocin S5 is a 56-kDa pore forming enzyme that kills its target bacterium through membrane damage leading to leakage of intracellular compounds. In this study, we produced and purified recombinant pyocin S5 (rS5) and examined its inhibitory effect on biofilms produced by *P. aeruginosa* S5 sensitive strains. Using suitable primers, we synthesized a 1497-bp fragment carrying the S5 open reading frame. The fragment was cloned in-frame in the *E. coli* expression vector pBAD-TOPO. We then overproduced rS5, purified it by nickel-nitrilotriacetic acid affinity column chromatography, and confirmed the purification with SDS-PAGE. Using the zone of inhibition assay and rS5, we screened 51 *P. aeruginosa* clinical isolates: 7 were completely sensitive, 23 were partially sensitive, and 21 were resistant. The minimum bactericidal concentration for the rS5 sensitive strain CF2351 was 12.5 µg/mL. At a concertation of 300 µg/mL, rS5 reduced mature biofilm formed by CF2351 by 99.99997%. These results suggest that rS5 could be effective in eliminating *P. aeruginosa* rS5 sensitive strains from an infected wound.

52. ELUCIDATING THE GENETIC MECHANISMS INVOLVED IN THERMOREGULATION OF *PSEUDOMONAS AERUGINOSA* BIOFILM FORMATION

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Biofilms are groups of microorganisms that adhere to surfaces and interact with each other using an extracellular polymeric substance (EPS). Biofilm growth can aid in microbial survival in a constantly changing environment. *Pseudomonas aeruginosa* is a common environmental isolate and nosocomial pathogen that is known to form biofilms in all the various niches it occupies. The ability to form robust biofilms contributes to the antibiotic resistance and immune evasion mechanisms of *P. aeruginosa*. We hypothesize that the fluctuations in temperature in the different niches that *P. aeruginosa* occupies drive the formation of biofilms specifically adapted to survival within that environment. Using MALDI IMS, we have demonstrated that biofilms grown under these different temperature conditions exhibit dramatically different protein expression profiles, which supports the possible presence of unique temperature-specific biofilm adaptations. 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 using a commercially-available transposon mutant library containing over 5,000 unique mutants of *P. aeruginosa* at four different temperatures (~25ºC, 30ºC, 37ºC, and 40ºC) to identify genes required for temperature-specific biofilm formation. The potential hits were then carried forward towards the secondary screen followed by the analysis of EPS composition of the mutant hits and wildtype at different temperatures using Scanning Electron Microscopy (SEM) and biochemical assays. Effectively this project will reveal the genetic mechanisms utilized by *P. aeruginosa* to establish biofilm growth at temperatures relevant to medical, industrial, and natural environments.

53. EFFECT OF ADIPOCYTE SECRETED FACTORS UNDER LEAN MASS AND OBESE CONDITION IN BREAST CANCER CELL MIGRATION AND INVASION

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One of the hallmarks of metastasis is the epithelial to mesenchymal transition where cancer cells lose their adhesive properties and become more deformable. Besides acquiring greater membrane plasticity, the contractile force generation through the dynamic formation and disassembly of actin filament imbues cancer cells with the ability to migrate and invade the surrounding extracellular matrix (ECM). In general, the Rho family GTPases regulate such reorganization of the actin cytoskeleton in response to extracellular cues. Emerging evidence have noted adipose tissue (mostly consists of adipocyte) present in the tumor microenvironment (TME) as one of the most critical players behind this aggressive transformation of cancer cells. Numerous *in vitro* and *in vivo* molecular studies have investigated the association of adipocyte secreted factors under lean mass and obese conditions with breast cancer metastasis, specifically their influence in altering genomic and proteomic expression relating to cell growth, proliferation, migration and invasion. However, the influence of those secretions on cytoskeletal remodeling and their subsequent impact on cell migration and invasion remain unexplored. Hence, the aim of this study is to investigate the influence of preadipocyte and mature adipocyte secreted factors from murine 3T3-L1 cells to mimic lean mass and obese conditions *in vitro* respectively, in the expression of Rho family GTPase and their downstream effector proteins in regulating breast cancer cell migration and

invasion. The observations will give us a better understanding of the underlying biology of adipose tissue in TME in empowering breast cancer cells with aggressive behavior.

54. IDENTIFICATION OF DEFENSIVE MECHANISMS IN *PSEUDOMONAS AERUGINOSA* ENABLING SURVIVAL IN POLYMICROBIAL GROWTH WITH FUNGI

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Microbial communities are an amalgam of different species of microorganisms where some members of the community occupy overlapping niches. These microorganisms attempt to outcompete each other to reduce competition in terms of limited nutrients and space via secretion of a range of molecules. The functions of these molecules can range from being toxic to being protective to enabling more efficient resource scavenging. In that direction, our lab is interested in identifying the genes encoding defensive molecules in Gram-negative bacterium *Pseudomonas aeruginosa* in response to fungal species it may encounter within the various environmental or infectious niches it occupies. Not much is known about the defensive molecules *P. aeruginosa* produces to protect itself from toxic molecules secreted by neighboring competitors. In our experiments, we have used GFP-labelled *Cryptococcus neoformans* as our model for discovering *P. aeruginosa*'s defensive molecules via its interaction with the fungi. The soil fungus *C. neoformans*, known as the causative microbe for meningitis in immunocompromised human hosts, produces toxic molecules against human hosts and as well as microbial species. For our studies, we have co-cultured *C. neoformans* with a commercially available transposon-mutant library of *P. aeruginosa* to identify genes necessary for competitive growth. Mutants of *P. aeruginosa* depicting reduced growth in the primary screening have been subjected to secondary screening to further confirm the requirement of the deficient gene in *P. aeruginosa*'s defensive mechanisms. Once identified, we seek to unravel the metabolic pathways involving these genes to understand interspecies interactions between *P. aeruginosa* and fungal species.

55. POLYCYCLIC AROMATIC HYDROCARBONS IN BREAST MILK OF OBESE VS NORMAL WOMEN: INFANT EXPOSURE AND RISK ASSESSMENT

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Biomonitoring of human breast milk is one of the best ways to identify body burdens of contaminants and associated risk estimation. The objectives of the current study were to evaluate milk concentrations of persistent organic pollutants (POPs), mainly polycyclic aromatic hydrocarbons (PAHs), associated exposure estimation, and the role of body mass index (BMI) in their bioaccumulation. A total of 45 breast milk samples were collected from 24 women with BMI>30 (obese) and 21 women with BMI<25 (18.5-24.9, normal) from 14 different counties surrounding Lubbock in west Texas/New Mexico; age ranged from 18-34 years.

Samples were analyzed using high resolution gas chromatography coupled with mass spectrometry (GC-MS). A total of 31/45 (69%) of samples tested positive for PAHs. Phenanthrene was the most frequently detected PAH followed by pyrene and fluoranthene. The mean of individual PAH concentration for all samples ranged from 0 to 25.1 ng/g milk fat; the sum of all means of individual PAHs was 146.9 ng/g milk fat. The mean concentration of total PAHs in the BMI>30 group was 224.8 ng/g milk fat, which was approximately 4 times the mean concentration of total PAHs in the BMI<25 group (57.9 ng/g milk fat). None of the samples from the BMI<25 group contained higher molecular weight (5-6 rings) PAHs, while in the BMI >30 group, a total of 11 PAHs including listed EPA priority pollutants were observed. In this study, benzo(b)fluoranthene was found to contribute the highest percentage of carcinogenic PAHs (32.08%), yet it was not detected in any samples from the BMI<25 group. The estimated total PAHs intakes by infants via obese and normal mothers' milk were 1.26 (µg/kg/day), which is 0.049 (µg/kg/day) B[a]P equivalent, and 0.32 (µg/kg/day), which is 0.003 (µg/kg/day) B[a]P equivalent, respectively. These findings suggest that breastfed babies from obese mothers are potentially at higher risk of exposure to carcinogenic PAHs.

56. WOLBACHIA PIPIENTIS METABOLIC RESPONSE IN A CELL FREE MEDIA

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Wolbachia pipientis is an intracellular maternally inherited symbiotic bacteria that has been estimated to infect 55% of insect species. *Wolbachia* causes reproductive modifications in its host and has been used to drive desirable phenotypes into natural populations of mosquitoes. For example, *Wolbachia* infected *Aedes aegypti* mosquitoes that have a reduced ability to transmit mosquito borne viruses to humans have been released into natural populations with the ultimate goal of reducing virus transmission. An alternative disease control approach would be to genetically modify *Wolbachia* to produce specific anti-parasitic molecules and use a *Wolbachia* induced reproductive advantage to drive this desired trait into natural populations. However, *Wolbachia* has yet to be genetically modified due to the inability to culture the bacteria outside of its host cell. Here, we use phenotypic microarrays to gain insight on the survival and metabolism of *Wolbachia* outside of its host cell. We investigated the metabolic response and survivorship of *Wolbachia* isolated from *Aedes albopictus* Aa23 mosquito cells in an axenic media with different pH and amino acid concentrations and in ambient oxygen concentrations to mimic similar conditions inside of insect cells. An increase in metabolic response was observed in media with a pH of 6.5 and a 1 mg/ml concentration of casamino acids. Results suggest that pH and amino acids may be key components for the development of *Wolbachia* axenic culture media, and that further investigation is needed to isolate additional media components to increase the survivorship and longevity of a *Wolbachia* in a cell free media.

57. TOWARD UNIVERSAL FLAVIVIRIDAE SURVEILLANCE

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Mosquitos act as vectors for a variety of arboviruses that cause disease in humans. Two virus families, Flaviviridae and Togaviridae, account for the majority of mosquito-borne illnesses worldwide, which includes such maladies as Dengue and Yellow Fevers, Chikungunya, and Eastern Equine Encephalitis. Current mosquito surveillance programs typically seek to identify specific arboviruses and are thus oblivious to the potential circulation of others, as demonstrated by the Zika outbreak in the Western hemisphere in 2015. The ability to detect a broader range of arboviruses with high sensitivity and in the absence of prior knowledge is paramount to public health globally. Utilizing isolated RNA reverse transcribed as a template for PCR amplification of conserved regions of Flavivirus and Togavirus genomes and degenerate “universal” primers that we have designed based upon multiple genome alignments. Along with amplicon detection carried out via gel electrophoresis and sequencing plasmids with amplicon insert, we have successfully demonstrated the feasibility of this strategy using two distinct primer pairs and purified RNA from multiple arboviruses including DENV-1, DENV-2, DENV-3, DENV-4, Zika, and West Nile (Flaviviridae); and Chikungunya, Mayaro, and Sindbis (Togaviridae). Additionally, we have successfully demonstrated the utility of our universal Flaviviridae primer set to amplify West Nile Virus (WNV) from a pool of field-collected Culex quinquefasciatus females. With this approach or similar derivations, we anticipate being able to enhance existing surveillance programs, both domestically and abroad, that will promote increased detection sensitivity of emerging arboviruses.

58. ANTISENSE TRANSCRIPTION AND SMALL RNA REGULATION OF ARABIDOPSIS AUXIN RESPONSE FACTOR ARF12/22 GENE CLUSTER

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Auxin, being a master switch among all the phytohormones, regulates many plant growth and developmental processes. Auxin mediates its effect through various signaling pathways, specific to plant tissues/organs, which involves the participation of various plant-specific gene families like Auxin Response Factors (ARF), Aux-IAAs, etc. In Arabidopsis, ARF gene families comprise of 23 members in four clades differentiated, in evolutionary terms, based on being targeted by different microRNAs or small interfering RNAs (siRNAs). The ARF12/22 clade consists of seven highly homologous and tightly linked genes on chromosome 1 expressed only in the female gametophyte and during embryogenesis. So far, the functions of ARF12/22 genes are not known and the prospects for genetic dissection are limited by a lack of recombination between individual knockout alleles. We are using genome editing (CRISPR-Cas9) approach to target ARF12/22 cluster and elucidate the roles of these genes in plant growth and development. Analogous to ARF10/16/17 clade of genes, there exists a weak candidate miR160 binding site in the exon 8 of all the genes in the ARF12/22 cluster. Lending credence to the hypothesis that RNA interference is involved in ARF12/22 post-transcriptional regulation is the existence of a natural-*cis*-antisense transcript for ARF14 and sense and antisense siRNAs unique within, and conserved between, ARF12/22 paralogs clustered around the cryptic miR160 site. We have recent evidence from tobacco consistent with the hypothesis. We propose that ARF12/22 gene cluster could function as a 'target mimic' for miR160; preventing post-transcriptional gene silencing of other bona fide miR160 targets like *ARF10, ARF16, and ARF17*, thus regulating the developmental processes in plants. The significance of this work is a better mechanistic understanding of gene silencing associated with smRNAs and potential functions of ARF12/22 gene cluster in embryogenesis.

59. IMPLEMENTATION OF COVER CROPPING MAY CAUSE COOLING EFFECT DUE TO INCREASE IN SURFACE REFLECTIVITY

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The reflectivity of the Earth's surface has substantial effects on climate due to the near invisibility of the atmosphere to short-wave solar radiation. Cover crops alter winter albedo by changing the surface from bare soil to plant cover, and thus may increase winter temperatures up to 3°C. We used a simple model to explore the variability in albedo due to solar angle, leaf area index, and leaf reflectivity. We also accumulated literature data to determine the range in albedo of wet and dry soil as well as a variety of crop species. In the model, plant albedo is primarily determined by leaf reflectivity and transmittance in the photosynthetically active and near-infrared spectrum, with a nearly linear relationship between leaf reflectivity and albedo. Literature values of albedo show an average of 0.13 (± 0.04) in wet soil and 0.24 (± 0.06) in dry soil. Crops have an average albedo of 0.19 (± 0.06) in the growing season and 0.29 (± 0.17) in the winter. While the crop species included in this analysis are limited, the data shows that winter crop albedos can potentially be three times higher than summer albedo, and similar to dry soil albedo. Considering the relationship between albedo and leaf reflectivity in the model, leaf reflectivity likely increases in the winter and is not accounted for in previous analyses of effects of cover crop albedo on temperature. Winter cover crops having an equal or higher albedo than soil signifies a cooling effect solely through change in reflectivity.

60. DWARF WILLOWS SHARE THE SAME SEX DETERMINATION REGIONS

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Trees and shrubs in the *Salicaceae* family are predominately dioecious, which provides an opportunity to study changes in sex determination after the evolution of dioecy in plants. The location and type of homomorphic sex chromosomes is evolutionarily labile in the Salicaceae. For instance, in *Populus trichocarpa* the sex determination region (SDR) is on chromosome 19 and exhibits male heterogamety (X-Y), whereas the SDR in *Salix purpurea* is on chromosome 15 and exhibits female heterogamety (Z-W). For this project, we mapped the SDR in two new sister species of dwarf willow, *Salix nivalis* and *S. reticulata* using a custom sequence capture array and comparing differentiation (Fst) among 24 males and 24 females for each species. The SDR was identified as a region of elevated Fst between males and females. The results showed that the sex chromosomes of *S. nivalis* and *S. reticulata* are both located at chromosome 15 and are ZW systems, which is same as in *S. purpurea*. Data will be presented regarding comparisons of gene content and genetic diversity in the SDRs in *S. nivalis*, *S. reticulata*, and *S. purpurea*. The results provide a window into the evolution of sex chromosomes in plants.

61. DEVELOPMENT OF COST-EFFECTIVE METHODS TO CONTROL HARMFUL ALGAL BLOOMS USING ALLELOCHEMICALS

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Prymnesium parvum is a euryhaline haptophyte known in North America as golden alga. This species can produce compounds that are highly toxic to fishes and other gill-breathing aquatic organisms. Harmful blooms of golden alga have occurred in all continents except Antarctica. Effective methods to control its toxic blooms in the field, however, are not available. Previous studies by our laboratory showed that methanolic and water extracts of giant reed (*Arundo donax*), itself a harmful invasive plant, strongly inhibit growth of golden alga thus suggesting this plant could be a source of natural, environmentally friendly products for bloom control. The objective of this study is to screen major known constituents of giant reed extracts for their ability to influence golden alga growth. Several of the chemicals examined to date have demonstrated allelopathic activity. In addition, a synthetic derivative of the natural allelochemical gramine, dichlorogramine, showed relatively strong algicidal activity. Not all of the compounds tested inhibited growth, however. Oleamide, a major constituent of water extracts, showed a surprising level of growth-stimulating activity. These observations indicate that individual compounds found in giant reed extracts can inhibit or stimulate growth of golden alga. This study is still ongoing.

62. BLASTX, A NOVEL ANTIMICROBIAL AGENT, INFLUENCES THE WOUND HEALING PROCESS BY ALTERING THE LEVEL OF CYTOKINES AND CHEMOKINES WITHIN THE WOUND

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Wound healing occurs through overlapping steps involving different host cell types and mediated by cytokines and chemokines (C/C). We examined the influence of BlastX on the level of C/C affecting the stages of healing. We generated full-thickness skin wounds in mice and covered them with sterile gauze (NT), polyethylene glycol base (PT), or BlastX (BT). At D1, D3, and D7, the wound bed and margins were excised. Proteins were extracted from portions of the tissues for analysis of C/C levels. Remaining tissues were formalin-fixed, sectioned, and stained specifically for M2 macrophages. On D1, levels of pro-inflammatory C/C CCL3, IL-1β, IL-6, IL-12p70, IL-17F, and CXCL1 were elevated with BT but lower than NT and PT; in contrast, the level of CXCL10 was increased. On D3, levels of the same C/C, now related to reepithelialization and angiogenesis, remained reduced in BT mice, while CXCL10 was elevated. On D7, levels of C/C responsible for keratinocyte hyperplasia were elevated by BT: GM-CSF, IL-17F, IL-6, and CXCL1. At D1, no M2 macrophages were observed; on D3, M2

macrophages were present in tissues of BT mice; while by D7, M2 macrophages were present in tissues from all treatments. These results suggest that BT prevents over-exuberant inflammation in a clean wound by reducing the level of pro-inflammatory cytokines while promoting the appropriate formation of blood vessels by increasing CXCL10 on D1; accelerates wound healing by enhancing the numbers of M2 macrophages on D3; and advances reepithelialization on D7 by increasing levels of C/C involved in keratinocyte hyperplasia.

63. ADVERSE EFFECTS OF STROBILURIN FUNGICIDES ON EARLY LIFE STAGES OF ZEBRAFISH (*DANIO RERIO*)

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Strobilurins (azoxystrobin and pyraclostrobin) are broad spectrum fungicides that have been measured in the aquatic environment. Their mode of action is by inhibiting mitochondrial respiration by binding to the mitochondrial respiratory complex III, and because of this non-specific, there is a chance for off- target toxicity in aquatic organisms. The goal of this study was to investigate the toxicity of azoxystrobin and pyraclostrobin, using multiple level endpoints, such as behavioral, growth, enzymatic and molecular biomarkers associated with mitochondrial function, and oxidative stress in the developing zebrafish (*Danio rerio*). Results from the molecular biomarkers indicates that there was an increase in oxidative stress and apoptotic mRNA transcripts as GST, Bax, p53, Casp9, were all significantly induced as compared to the control. Furthermore, strobilurin fungicides reduced the swimming behavior, body length, and dissolved oxygen consumption in larval zebrafish. In conclusion, both azoxystrobin and pyraclostrobin caused mitochondrial dysfunction, decreased body length and distance travelled, and induced oxidative stress and apoptotic mRNA transcripts. Results from this study will benefit risk assessors by comparing developmental toxicity of two common strobilurin fungicides, azoxystrobin and pyraclostrobin, help them make informed decisions to protect environmental and human health.

64. IDENTIFICATION OF SECRETED METABOLITES FROM *BATRACHOCHYTRIUM DENDROBATIDIS* AND USE OF *GALLERIA MELLONELLA* AS MODEL SYSTEM TO STUDY PATHOGENICITY

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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. Published work indicates *Bd* can produce immunomodulatory compounds and compounds that regulate the growth of the fungus. Filtrates of *Bd* grown in media and water were analyzed by high performance liquid chromatography-mass spectrometry with post analysis using Compound Discoverer 3.0. A total of 71 compounds were identified as being secreted from *Bd* as compared to the control ($n=3$, $p \leq 0.01$, log fold change ≥ 2, and matched to MS/MS data). Identification of specific compounds whose functions were of interest were verified by their retention time and fragmentation patterns. Previous studies have analyzed the effects of *Bd* on amphibian models, *in vitro,* or in cell culture. We studied the effects of filtrates and living *Bd* cells on wax moth larvae (*Galleria mellonella)* and observed for a reduction in the health of the organism. Concentrated filtrates caused melanization to occur within 24 hours, while living *Bd* cells caused melanization within 48 hours. Our results show that *Bd* is capable of producing a suite of secreted metabolites previously unrecognized in this fungus, and establishes the use of a non-amphibian model system to study pathogenicity traits from the fungus.

65. PREPARATION OF CELLULOSE-BASED MONOLITHS WITH ENHANCED SURFACE AREA AND POROSITY

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Aerocellulose are light weight, coherent, open porous network of loosely packed particles prepared from cellulose. The intriguing characteristics of aerocellulose such as high specific surface area, high porosity, low density, high pore volume etc. have made them an attractive solid material for important applications such as dye adsorption, nanoparticles carrier, biomedical scaffolds etc. This study reports on the effects of the addition of surfactant and salt particles on the surface area, the pore size, and the pore size distribution of low-density aerocellulose monoliths. Aerocellulose monoliths were prepared by dissolving microcrystalline cellulose in NaOH/water solvent system using a dissolution-solvent exchange-drying “sol-gel” route. Triton X-100 (surfactant) and sodium chloride particles (salt) were added to the cellulose solution before gel formation. The effect of salt and surfactant on the surface area, pore characteristics and microstructure was analyzed using N_2-adsorption isotherm and scanning electron microscopy. The physicochemical properties of aerocellulose monoliths were characterized using Fourier Transform Infrared spectroscopy, X-rays diffraction, and Thermogravimetric analysis. The results showed that the addition of sodium chloride particles and surfactant leads to an increase in the specific surface area of aerocellulose monoliths from about 122 m^2/g to about 214 m^2/g. Moreover, the cumulative pore volume, the porosity, and the thermal stability were also enhanced. This study demonstrated the effectiveness of sodium chloride particles and surfactants to tune the pore characteristics of the aerocellulose materials without compromising other properties. Furthermore, this study offers a facile route to achieve enhanced surface area and improved pore characteristics of aerocellulose monoliths.

ORAL (UNDERGRADUATE)

66. DENDROCHRONOLOGICAL SUITABILITY AND CLIMATE SENSITIVITY OF *QUERCUS MOHRIANA* IN THE TEXAS PANHANDLE

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Variability in tree-ring growth is used as an indicator of historic environmental conditions, but few dendrochronological studies have been conducted in the Texas Panhandle region. In this study, we obtained cores from Mohr oak (*Quercus mohriana*) at Caprock Canyon State Park in Briscoe County, TX in order to determine their suitability for dendrochronological analysis. The objective of our study was to determine if tree-ring growth patterns were consistent among individual trees and then assess their sensitivity to climate conditions. Trees ranged from 31 to 81 years of age. Growth patterns were consistent across trees with an average interseries correlation of 0.598 which facilitated the assignment of calendar years to each tree-ring. Additionally, most sampled trees exhibited periodic cambial damage from early spring freeze events (frost rings) from the 1940s to the 1990s but no frost rings have been recorded since 1993. Preliminary analysis suggests the tree growth is significantly correlated with annual precipitation (p = 0.0004), but further analysis is needed to help better understand the contribution of streamflow/hydrological variability from groundwater in this canyon environment. Ongoing research will examine these issues and will focus on sampling more trees in order to build a robust chronology of tree-ring recorded environmental variability in the region.

67. GRASSLAND BIRD DIVERSITY AND HABITAT ASSOCIATIONS IN THE SOUTHERN HIGH PLAINS, TEXAS

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Birds were surveyed in winter (Dec 2017-Feb 2018; Floyd County, Texas) and summer (May-June 2018; Cochran, Terry, Yoakum counties, Texas) to determine diversity, abundance and habitat associations in the Southern High Plains agricultural landscape. Winter surveys utilized road-side point-counts in farmland and grassland and mist-net capture in brushy canyonlands. Summer surveys utilized 100-m transects established in 4 habitats (mesquite, sand-sage, treated shin-oak, and untreated shin-oak) in Yoakum Dunes Wildlife Management Area (YDWMA). Three species totaling 124 birds were detected during winter point-counts in Floyd Co., and number of sparrows at points was negatively correlated (P=0.01) with distance from points to the nearest playa bottom (most were dry). Ten species were captured in the canyonland site, increasing observed winter sparrow richness to 11 species. At YDWMA, 19 species totaling 119 birds were detected. Average number of birds was similar between mesquite and sand-sage and between untreated and treated shin-oak; however, average number of birds was higher in mesquite and sand-sage than in either of the shin-oak habitats (P<0.001). Species richness varied among habitats (mesquite=14, sand-sage=9, untreated shin-oak=8, treated shin-oak=3). Shannon's Index of Diversity was highest in mesquite (2.47) and lowest in treated shin-oak (0.9). Mesquite bird community was least similar to the other three habitats (Jaccard's Coefficient of Similarity CC_J: sand-sage= 0.35, untreated shin-oak=0.29, treated shin-oak=0.13), while the untreated shin-oak and sand-sage habitats were most similar (CC_J= 0.42). Although treated shin-oak had low species richness, Lesser Prairie-Chicken was present in this habitat, which is the management objective for shin-oak reduction.

68. AN UPDATED VASCULAR FLORA OF THE RUNNINGWATER CONSERVANCY, HALE COUNTY, TX WITH COMPARISONS TO REGIONAL FLORISTIC RECORDS

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Located within the high plains of West Texas, the Runningwater Conservancy in Hale County is a grassland remnant with native, unplowed upland prairie and a playa lake. It is a 29 ha site approximately 25 kilometers west-northwest of Plainview, TX. It is currently enrolled in the Wetland Reserve Program. Inventories of the vascular plant flora in the southern high plains region are limited with few surveys completed recently. The goal of this project is to catalog all vascular plants occurring in the study area. This project was initiated in the fall of 2017 with walking surveys. Surveys will continue during the growing seasons at least through the fall of 2020. Voucher specimens for all identified taxa will be deposited in the E. L. Reed Herbarium at Texas Tech University. To date, we have identified over 50 plant species in more than 45 genera in 19 families. Additionally, we seek to compare the floristic diversity of this location with other floristic records of the region. This study will improve our floristic knowledge in an understudied region.

69. A LONGITUDINAL STUDY OF FISH ASSEMBLAGES ON THE MESOAMERICAN BARRIER REEF, IN ROATAN HONDURAS

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Composition of fish assemblages is recognized as an indicator of ecosystem health and 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 fish abundance. This study was conducted to assess changes in fish assemblage structure across depths between 2017 and 2018 on the Mesoamerican Barrier Reef in Roatán, Honduras. Fish communities were characterized for species presence and abundance and each dive site was sampled twice. No significant difference in species richness was identified between the two depths or study sites surveyed. Four Sponges data collection site had the greatest diversity, and Bear’s Den had the least diversity in 2018. In 2017, Pillar Coral had the greatest diversity and Mandy’s Eel Garden had the least diversity. Fish Den and Bear’s Den had less similar species composition in 2017, whereas the two sites had a more similar composition in 2018. In 2017, the dive sites visited had a larger difference in species composition than the dive sites visited in 2018, which had a more similar composition. Fish community assemblages did not statistically differ between 2017 and 2018 for either depth. This study continues to provide a baseline of the reef-fish community structure on the Mesoamerican Barrier Reef in Roatán, Honduras and future studies can use these results to measure changes in community structure over time.

70. HABITAT ASSOCIATIONS AND POPULATION ESTIMATES OF THE TEXAS HORNED LIZARD (*PHRYNOSOMA CORNUTUM*) IN THE SOUTHERN HIGH PLAINS OF TEXAS

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The Texas horned lizard (*Phrynosoma cornutum*) is a threatened species within Texas. Population abundances and habitat use analyses are vital to conservation efforts. This study was conducted from May-Sept. 2016, July-Oct. 2017, and April-Sept. 2018 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. In 2017 and 2018, PIT tags were inserted subcutaneously in lizards with SVL>40mm. The Schnabel Index indicated that the population estimate for adult and juvenile lizards at the Hale County site in 2018 was 169 markable (SVL>40mm) individuals. Including hatchlings (that could be identified as individuals), the population estimate is 212. Using the Schnabel Index result there is a density of 46 lizards/ha at the Hale County site. Habitat at male and female lizard locations was not different. Habitat at hatchling, juvenile, and adult locations was not different. Lizard locations had a lower percent grass ($P=0.0472$), lower percent forb ($P=0.0004$), higher percent bare ground ($P<0.0001$), and a lower vegetation height ($P<0.0001$) than did transect sample points without lizards. At the Floyd County site, disturbance from heavy, short-term grazing had an impact on horned lizard numbers (2016, pre-grazing=21; 2017, during grazing=6; 2018, post-grazing=5). However, there were no significant differences in horned lizard location habitat between years at this site. Horned lizards select for specific habitat in the Southern High Plains. Intense, short-term grazing has a negative impact on horned lizard abundance.

71. PREVALENCE, ABUNDANCE, AND PROPORTION OF DARK SPOT SYNDROME ON STARLET CORALS ON THE MESOAMERICAN BARRIER REEF IN ROATÁN, HONDURAS

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Coral disease outbursts have occurred since the 1970s and have added to coral decline in the Caribbean. Dark spot syndrome (DSS) was first observed in the Caribbean near Columbia during the late 1990s and causes lesions of brown, black, or purple on coral tissue. The primary coral species affected with DSS in the Caribbean are the starlet corals; *Siderastrea siderea*, *Stephanocoenia intersepta* and *Siderastrea radians*. The cause and impact of DSS throughout the Caribbean has not yet been determined. Some researchers have suggested that DSS is a general stress response exhibited by the coral and an indicator of coral reef health. This study was conducted to assess the prevalence, abundance, and proportion of DSS on starlet coral in Roatan, Honduras. Four established dive sites were surveyed twice from May 15-19, 2018. As each of the affected corals species were observed, coral identification, DSS status, and depth was recorded. In addition, an open quadrat was place over each coral and a photo taken which was later used in ImageJ to assess area of coral and DSS. Only four DSS affected coral were recorded, three were at Bears Den dive site. The dive site located closest to the municipal dump, Tuk’s Treasure, had no DSS recorded, though this is where the most samples of coral were recorded. Future research should investigate water chemistry, dive traffic, water currents, and proximity to features, such as the island landfill and golf course, which could affect reef health and susceptibility to disease.

72. BREEDING SEASON FOOD HABITS OF AMERICAN KESTRELS IN THE SOUTHERN GREAT PLAINS

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American kestrel (*Falco sparverius*) populations are generally declining across their North American distribution. However, the species appears to be stable or increasing in the southern Great Plains region, an area that likely had very low natural presence of the species pre-European settlement. In 2011 we initiated a nest box program to study kestrel ecology in short/mixed grass prairies of Texas. One line of inquiry was assessing how population dynamics may be influenced by regional dietary habits. We recorded over 3,100 prey deliveries during four-week brood-rearing periods at nest boxes in 2017. Average prey delivery rates/hour increased from 0.84/hr and 0.96/nestling/hr during the first week to 2.65/hr and 0.57/nestlings/hr during the fourth week of brood rearing. The breeding season diet was dominated by reptiles (71.3%). Prairie racerunners and common spotted whiptails (*Aspidoscelis sexlineata viridis* and *A. 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 where difficult to identify beyond genus, family, and order, respectively, but a minimum of 30 different prey species were identified. Prey as large as juvenile cottontails (*Sylvilagus floridanus*) and cotton rats (*Sigmodon hispidus*) were delivered to nest boxes. Biomass assessments are underway for complete presentation of breeding season prey use of kestrels in our study, with comparison to data from other regions.

73. DOES CRUSH RESISTANCE VARY BETWEEN THE INVASIVE NEW ZEALAND MUDSNAIL (*POTAMOPYGRUS ANTIPODARUM*) AND THE NATIVE JUGA SNAIL (*JUGA ORICKENSIS*)?

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New Zealand mud snails (mud snails) have recently invaded Redwood Creek Estuary in Redwood National Park. These mud snails outcompete many native aquatic macroinvertebrates and have a proclivity to spread in invaded watersheds. The Redwood Creek watershed has a native snail, the Juga snail, which is an integral prey item for different aquatic predators. One strategy used by predators to eat snails is to crush their shells, however, shell crush resistance can vary among snail species. If native snail crushing predators were to encounter a mud snail, would they be able to crush its shell to ingest it. We tested the crush resistance of the shells of both Juga snails and mud snails using a crushing apparatus by selecting 50 similar sized snails of both species and recording their crush resistance in grams. We also measured shell length, first whorl width, and the presence of spines in mud snails. We found that Juga snails had a higher average crush resistance than mud snails. However, after accounting for shell length and first whorl width, the crush resistance of both species was not significantly different. When considering how the presence of spines in mud snails could affect crush resistance, they were statistically similar. Therefore,

we conclude that native predators in the Redwood Creek watershed could crush the shells of the invading snails.

ORAL (GRADUATE)

COMPUTATIONAL & MATHEMATICAL BIOLOGY

74. STUDY OF KELLER SEGEL MODEL FOR SLIME MOLD AGGREGATION

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In pioneering work by Keller Segel “PDE modeling of chemotaxis and application in environmental problem” biological process of slime (amoebae) mold aggregation was modeled using dynamical PDE equation with four unknown variables, Concentration of amoebae, Concentration of acrasin, Concentration of acrasinase and the complex formed by reaction of acrasin and acrasinase.

This system then reduced to only two unknowns: concentration of amoebae and chemotractor generated by amoebae themselves. There are two major possibility in dynamics of this biological process: uniform space and time independent distribution of slime mold and development of new “body” development as a new phase in evolution of the of primitive amoebae. In Keller Segel study development of new phase in slime mold evolution is interpreted as the mathematical instability of original initial boundary value problem for cross-diffusion non-linear parabolic system of equation. Namely Keller Segel introduced a homogeneous non-trivial equilibrium as a solution of system of algebraic equations and using classical Turing approached proved existence of the time dependent solution of linearized around equilibrium system of PDE.

Aim of our research is, generalize the Keller Segel approach in two directions from biological and mathematical point of view. Namely we are Introducing:

1. Additional variable for food for amoebae, and corresponding equation which coupled with equation for amoebae itself;
2. Non-homogeneous and oscillating in time equilibrium state studying its stability. All obtained results illustrated via COMSOL Multiphysics computation.

75. MODELING ELEMENTAL CONSTRAINTS ACROSS AQUATIC FOOD WEBS

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Accurately assessing the risks of contaminants require more than an understanding of the effects of contaminants on individual organism, but requires further understanding of complex ecological interactions, elemental cycling, and the interactive effects of natural stressors, such as resource limitations, and contaminant stressors. There is an increasing evidence that organisms experience interactive effects of contaminant stressors and food conditions, such as resource stoichiometry and nutrient availability. We are developing and analyzing a series of empirically testable and robust mathematical models of populations dynamics subject to stoichiometric and contaminant stressors. In parallel to developing the models, we will integrate sufficient data from existing and new experiments to parameterize, test, and improve them. The synthesis of the models and experiments will result in the development of a robust theoretical framework appropriate for improved risk assessment applications in ecotoxicology that incorporate the effects of stoichiometric constraints on concurrent ecological and toxicological processes. In particularly, we are presenting how the toxicant bio-accumulates to the upper food webs under concurrent stoichiometric and toxicological constraints.

76. SEASONAL VARIATION OF NUTRIENT LOADING IN A STOICHIOMETRIC PRODUCER-CONSUMER SYSTEM

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Recent discoveries in ecological stoichiometry have indicated that food quality in terms of the phosphorus: carbon (P: C) ratio affects consumers whether the imbalance involves insufficient or excess nutrients. This phenomenon is called stoichiometric P: C knife-edge." In this study, we develop and analyze a producer-consumer model which captures this phenomenon. It assesses the effects of (external) nutrient (P) loading on consumer dynamics in an aquatic environment by mechanistically deriving and accounting for seasonal variation in nutrient loading. In the absence of seasonal effects, previous models suggest that the dynamics are Hopf bifurcation, saddle-node bifurcations, and limit cycles. However, seasonal effects can have major implications on the predicted solutions and enrich population dynamics. Bifurcation analysis demonstrates that seasonal forcing can cause both periodic and quasi-periodic solutions.

77. MECHANISTICALLY DERIVED SPATIALLY HETEROGENEOUS PRODUCER-GRAZER MODEL SUBJECT TO STOICHIOMETRIC CONSTRAINTS

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Known stoichiometric models of a two species producer-grazer ecosystem have either neglected spatial dynamics or failed to track free phosphorus in the media. Here we present a spatially heterogeneous model that tracks phosphorus content in the producer and free phosphorus in the media. We simulate our model numerically under various environmental conditions. Multiple equilibria, with bistability and deterministic extinction of the grazer, are possible here. In conditions that had been previously studied without tracking free phosphorus we find cases where qualitatively different behavior is observed. In particular under certain environmental conditions previous models predict stable equilibria where our model predicts stable limit cycles near the surface. Oscillatory dynamics can have consequences on the population densities, which may spend some time at low values throughout the cycles where they are in danger of stochastic extinction.

78. TRAVELING WAVE PATTERN AND ITS STABILITY IN BACTERIA FOOD MODEL AND APPLICATION

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We propose a model of cell formation accounting for cell food interaction. This model is presented as a system of non-linear partial differential equation of chemotactic type. Motivated by experimental observations regarding Escherichia coli movement in the present (towards) of the food (sugar) we generalize Keller-Segel model assuming diffusion of the food.
We impose a quasi-steady state assumption and analyze the resulting systems of equations. We focus on the existence and stability of equilibrium solutions of traveling wave type and its stability with respect to perturbation defined by diffusion of the food. We proved that under some physically justified parameters on the model traveling wave solution is stable. Obtained result can be used to determine by the governing parameters with the results interpreted in terms of their potential bio-medical implications.

79. ANALYZING GENOMIC DATA USING TENSOR-BASED ORTHOGONAL POLYNOMIALS

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Rapid increases in the availability of genomic data for diverse organisms has spurred the search for better mathematical and computational methods to investigate the underlying patterns that connect genotypic and phenotypic data. Large genomic datasets make it possible to search for higher order epistatic interactions, but also highlight the need for new mathematical tools that can simultaneously represent sequences and phenotypes. We propose a multivariate tensor-based orthogonal polynomial approach to characterize nucleotides or amino acids in a DNA/RNA or protein sequence. Given phenotype data and corresponding sequences, we can construct orthogonal polynomials using sequence information and subsequently map phenotypes on to the space of the polynomials. This approach provides information about higher order associations between different parts of a sequence, and allows us to identify both linear and nonlinear relationships between phenotype and genomic or proteomic sequence data. We use this method to assess the relationship between sequences and transcription activity levels in a large raw mammalian enhancer dataset downloaded from NCBI. We provide insights into the bioinformatics and computational pipeline necessary to curate and translate large-scale genomic data to extract and quantify complex genome-phenotype interactions.

ECOLOGY & ENVIRONMENTAL BIOLOGY

80. WINTER ECOLOGY AND BIOENERGETICS OF MEXICAN FREE-TAILED BATS (*TADARIDA BRASILIENSIS MEXICANA*)

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During periods of harsh weather and resource scarcity, animals may balance their energy budget by acclimating to changing conditions or migrating to environmentally favorable habitat. Many migratory species are partially migratory, with populations made up of migratory and non-migratory individuals. Mexican free-tailed bats (*Tadarida brasiliensis mexicana*) are considered a migratory species but remnant populations have been reported overwintering in the Southern United States for nearly 50 years. It is unknown why some individuals choose to remain north and how these small mammals maintain energy balance during winter. We hypothesized *T. b. mexicana* regularly reduce their body temperature (T_b) during periods of inactivity (i.e. enter torpor) to minimize energetic costs and can time activity with weather conditions favorable for foraging. We predicted nights with higher ambient temperature (T_a) would have increased bat activity and bats would use torpor more frequently on nights with lower T_a and when inactive during the day. We predicted torpor bout length would vary with weather, extending over multiple days during longer periods of low T_a. We deployed an acoustic recorder at a roost from September 2018–April 2019 to quantify activity and attached temperature-sensitive radiotransmitters to 30 bats in February 2019 to continuously measure T_b. We captured >700 bats at a winter roost site from September 2018-April 2019 to assess which characteristics are favored for winter residency. Preliminary results indicate there was a strong male sex bias in winter residents, resident bats regularly used torpor to save energy, and activity levels increased with favorable weather conditions.

81. CHANGES IN RODENT COMMUNITY COMPOSITION DURING THE LAST HALF-CENTURY ACROSS THE RANGE OF A RARE KANGAROO RAT

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Given the growing biodiversity crisis related to accelerated extinction rates, understanding effects of environmental change on species represents a significant challenge for conservation. For example, both land use and climate change have had well-documented, profound impacts on species distributions and biodiversity patterns. Although it is becoming increasingly clear that climate change will continue alongside human modification of the landscape, few studies have jointly examined both land use and climate change as potential drivers of faunal change in terrestrial systems despite their potentially synergistic effects. We used historical museum specimen records coupled with recent field surveys to identify trends in rodent community composition across the historical range of a rare kangaroo rat (*Dipodomys elator*) in north-central Texas. Specifically, we examined changes in species composition and traits, including habitat association (i.e., mesic versus xeric), body size, locomotion (i.e., bipedal versus quadrupedal), and diet (e.g., omnivore, granivore, folivore). We predict spatial variability in the impacts of climate change on rodent community composition based on differential species responses to underlying differences in land use practices, particularly in the eastern versus western portions of the region. Importantly, this work demonstrates the value of museum records for characterizing and understanding faunal changes in response to shifts in climate and land-use practices. Moreover, results from our work should improve understanding of drivers of faunal change within this region, with implications for managing rare species in the face of future environmental change.

82. EFFECTS OF URBANIZATION ON TAXONOMIC AND FUNCTIONAL COMPOSITION OF AVIAN COMMUNITIES THROUGHOUT TEXAS

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Global growth of urbanization has increased fragmentation, habitat loss and quality, pollution, and opportunities for negative interactions between native and invasive species. Adverse effects of urbanization increase threats to biodiversity and contribute to extinction risk. To study effects of urbanization on biodiversity, we estimated avian metacommunities distributed throughout Texas. In particular, we wanted to better understand how local environmental and regional spatial factors influence communities. Community structure was measured using taxonomic and functional characteristics. Stochastic and spatial processes may be more influential to taxonomic composition, while functional characteristics of a community may have a more significant association with deterministic process (i.e., environmental filtering). Taxonomic characteristics included species identity and abundance, while functional traits were morphological and niche characteristics (i.e., diet, body mass, dispersal ability, etc.) that influence a species ability to persist in an environment. We examined taxonomic and functional trait responses to environmental classifications (i.e., developed, forested, grasslands, etc.) and spatial variables within a multivariate framework. We predicted that birds that are granivorous, invasive, or non-migratory will be highly associated with urban environments. Furthermore, we predicted birds that are insectivorous, nest on the ground, native, or are migratory will be associated with more natural environments. By studying effects of urbanization on avian communities, we can better understand how species and traits are influenced by increasing development.

83. EVALUATING THE EFFECTIVENESS OF UAV-BASED REMOTE SENSING SYSTEMS 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 plant distribution and track wildlife habitat. Recent advancements in the fields of remote sensing, UAVs (Unmanned Aerial Vehicles), and data processing offer land managers more efficient ways of evaluating rangeland health and diversity. A study was completed in 2017-2018 at the Texas Tech Native Rangeland using a Phantom 3 Professional UAV mounted with a Parrot Sequoia multispectral camera to test the viability of mapping distinct plant species on rangeland sites. This study focused on two problematic species found at the study site and on Texas rangelands, Honey Mesquite (*Prosopis glandulosa*) and non-native Yellow Bluestem (*Bothriochloa ischaemum*). The impact of seasonality was tested by conducting UAV flights during four different growth stages throughout the year. The effect of pixel size in UAV-based, high resolution imagery was tested by flying the UAV at different altitudes in each of those stages. New image classification tools in ArcGIS were also compared to determine their viability of mapping distinct plant species on rangelands. The resulting classified images were evaluated using a pixel-based accuracy assessment method to determine how well the species were mapped. The results show that mapping accuracy of Honey Mesquite and Yellow

Bluestem are impacted by the time of year imagery is collected and the altitude of UAV flights. This study also provides guidance in the use of UAV's in assessments on rangeland sites and how specific techniques can generate more reliable data for land managers.

84. CO-OCCURRENCE PATTERNS OF BATS IN THE TRANS-PECOS REGION OF TEXAS

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Roosts can be limiting resources for bats and therefore might cause deterministic patterns of distribution and abundance. In addition to natural roosts, bats regularly use man-made structures such as bridges and culverts. However, little is known about why bats choose to roost in these structures and whether interactions between species influence patterns of co-occurrence. Co-occurrence is the frequency at which species occur together in the same place and time. Studying trends of bat assemblage structure and co-occurrence patterns among day roosts can illuminate roost occupation patterns observed in highways structures and provide better understanding the ecology of this unique group of organisms. We examined co-occurrence patterns among bat species roosting in bridges in the Trans-Pecos region of Texas, which has the highest bat diversity within the state and spans a variety of habitat types. This study encompasses 37 occupied bridges in the Trans-Pecos. We predicted non-random segregations of species at the landscape level because of high variety of habitat types within the landscape and potential avoidance of competition among specialized bat species. We also hypothesized significantly different co-occurrences patterns of species habitats, because more moist and vegetated habitats may provide more abundant and easily accessible resources for bats and would therefore have greater aggregations of bat species. Furthermore, we hypothesized larger bridges would have more species aggregations than smaller bridges, due to greater area of roosting habitat available. The results of these tests will provide valuable information regarding biodiversity and ecology of bats in a highly diverse region of Texas.

85. SPATIAL AND TEMPORAL VARIATION IN BAT ACTIVITY DURING WINTER

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While communities generally remain static over short durations, some ecological contexts can cause dynamic changes in composition. In North America, winter provides a unique opportunity to study this assembly as conditions can rapidly fluctuate leading to changes in resource availability. Since temperature is a driving force behind insect abundance, insectivores such as bats must alter their activity patterns to limit energy lost when resource availability is low. While many bats at northern latitudes combat the absence of insects by hibernating or

migrating south, those at southern latitudes remain active throughout winter as more favorable conditions prompt increased insect activity. Individuals in these regions must decide between foraging on these limited resources and remaining torpid to preserve accumulated energy stores. We investigated how species-specific activity changes through space and time in response to fluctuating temperatures and predicted a dynamic community structure as different species implemented varying physiological strategies to survive. We also hypothesized that bats would reduce interspecific competition by becoming active at different times of night and foraging in unique habitats to maximize resource acquisition. In 2018 and 2019, we deployed acoustic detectors in managed conifer forests of central Louisiana and eastern Texas, recording over 35,000 bat passes. Initial observations suggest that variation in activity occurs as some species are active year-round, while others are rare or inactive until late winter when temperatures are consistently warmer. Statistical analyses will be used to determine the spatial and temporal trends in activity. Employment of different physiological strategies leads to a dynamic community structure, allowing multiple species to coexist during times of limited resource availability.

86. COMPETITORS VERSUS FILTERS: DRIVERS OF NON-RANDOM STRUCTURE IN FOREST INTERIOR INSECTIVOROUS BAT ASSEMBLAGES ALONG ELEVATIONAL GRADIENTS

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Non-random assemblage structure in species-rich resource-based assemblages are driven independently or simultaneously by competition and environmental filtering leading to trait dissimilarity or similarity respectively. Monotonic decline in bat species richness along forested Afrotropical elevational gradients is resource driven, yet the relative roles of competition and environmental filtering remains unclear. Ecomorphological traits such as bite force and wing morphology are essential for dietary resource partitioning, and respond to environmental conditions, providing opportunities to answer such questions. We hypothesize that if competition is driving assemblage structure along elevation gradients then species should be less similar in trait space, but conversely more similar under environmental filtering. Along two forested elevational gradients in southeastern Nigeria, we trapped bats using five harp traps set every 50 m along four 200 m long transects, at sites established on elevational strata ca. 250 – 400 m apart. We measured vegetation structure within four 2 m^2 plots around each harp trap and collected insects using light traps at each transect. For captured bats, we recorded forearm length and body mass, and measured bite force using bite plates attached to a Kitzler force transducer and photographed wings of bats restrained to a gridded board. Wing morphology parameters were measured from photographs of bat wings using imageJ and mean nightly counts of insect conducted. We establish trait-environment relationships and assess trait dispersion and changes in trait volume of bat assemblages along elevational gradients. The results of these analysis will uncover the functional basis of the bat assemblage structure along elevational gradients.

GENETICS & GENOMICS

87. CRISPR – ANGEL OR DEVIL?

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A few years ago, the researchers invented a new technology for editing genomes. It's called CRISPR-Cas9. The CRISPR technology allows scientists to make changes to the DNA in cells that could allow us to cure genetic disease. You might be interested to know that the CRISPR technology came about through a basic research project that was aimed at discovering how bacteria fight viral infections. Bacteria have to deal with viruses in their environment, and we can think about a viral infection like a ticking time bomb—a bacterium has only a few minutes to defuse the bomb before it gets destroyed. So, many bacteria have in their cells an adaptive immune system called CRISPR, that allows them to detect viral DNA and destroy it. The CRISPR technology has already been used to change the DNA in the cells of mice and monkeys, other organisms as well. The opportunity to do this kind of genome editing also raises various ethical issues that we have to consider, because this technology can be employed not only in adult cells, but also in the embryo of organisms, including our own species. And so, the researches, called for a global conversation about the technology, so that we can consider all the ethical and societal implications of a technology like this.

88. DECIPHERING THE WHOLE GENOME STRUCTURE OF THE NIGHTSHADE SPECIES *SOLANUM LYCOPERSICOIDES*

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S. lycopersicoides is a diploid nightshade relative of tomato that has been reported to have resistance to Lepidopteran pests and a broad group of pathogens, as well as tolerance to cold, drought and salinity. To efficiently utilize the potential of *S. lycopersicoides* as a genetic resource for cultivated tomato improvement, it is imperative that the genomic structure of the species is first understood. This study aims to analyze the whole genome structure of *S. lycopersicoides* and use the generated genome sequence information to build a marker resource for the species. Whole genome sequencing of *S. lycopersicoides* was carried out using the Illumina platform. Sequence assembly and analysis were performed using publicly available software including ABySS, PAGIT, AUGUSTUS, RepeatMasker and GMATA. The sequenced region estimated a 1.45 Gb genome size for *S. lycopersicoides*, with 34.27% GC content. An estimated 39,918 genes were detected across the 12 *S. lycopersicoides* chromosomes which is 22.67% more than the number of genes in tomato. Repeats were detected in the form of LINEs, SINEs, LTRs and SSRs. Based on sequence alignments between *S. lycopersicoides* and tomato, a total of 366 indel and SSR markers were designed. All markers amplified targets not only in *S. lycopersicoides* but also in tomato and silverleaf nightshade. Knowledge of *S. lycopersicoides* genome will be useful in studying the genomic similarities between the nightshade species and cultivated tomato. Results of this study will also have applications in leveraging research on other nightshade species sharing the same genome as *S. lycopersicoides.*

89. DIFFERENT SEX DETERMINATION SYSTEM IN NARROWLEAF WILLOW (*SALIX EXIGUA*) COMPARED WITH OTHER SHRUB WILLOW SPECIES

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Dioecy is found in many plant lineages, but overall only ~6% of angiosperms have evolved dioecy. The *Salicaceae* family is unique in angiosperms because all species are dioecious. Studies of the genes controlling sex determination in this family have found that *Populus trichocarpa* has an XY sex determination system located on chromosome 19, whereas the closely related species *Salix purpurea, S. suchowensis*, and *S. viminalis* have a ZW system located on chromosome 15. We investigated the location of the sex determination system in *S. exigua*, which resides in a different section of the *Salix* phylogeny. To map the sex determination region (SDR), we randomly sequenced 24 males and 24 females from a natural population of Salix *exigua*. SDRs are characterized by increased genetic diversity (heterozygosity) and can be identified using Fst statistics comparing male and female genotypes. We called polymorphisms and calculated Fst using GATK and vcftools. Our results demonstrated that the sex chromosome of S. *exigua* is located on Chr15 and includes many of the same genes as *S. purpurea*, however heterozygosity evidence indicated that S. *exigua* has a XY system, which differs from *S. purpurea*. The speciation history of the *Salicaceae* family indicates that the SDR likely first shifted from Chr 19 to Chr 15, then shifted from XY to ZW. Accordingly, detailed comparisons between the XY SDR in *S. exigua* and the ZW SDR in *S. purpurea* will aid in understanding the mechanisms and dynamics causing the shift of sex determination system from XY to ZW.

90. TRANSPOSON ACTIVITY AND MUTATIONAL IMPACTS IN *MYOTIS*

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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. *Myotis* is one genus within vespertilionid bats which has experienced an unorthodox TE history. For example, their genomes are unique among mammals in containing many active DNA transposons, which continue to shape their genomic landscapes. Recent data suggests that, in addition to the indel mutations normally associated with TE activity, these genetic elements may also contribute to higher mutation rates via 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 extent of mutations in nearby genes that are associated with DNA repair after transposon insertions and excisions. These increased mutation rates could correlate to differences in orthologous genes between closely related *Myotis* species and contribute to our understanding of this exceptionally diverse clade.

91. MACROECOLOGY OF BUTTERFLY GENOMES

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Macroecology attempts to understand intra- and inter-specific relationships at large taxonomic, spatial, and/or temporal scales. While conventionally focused on species within communities, macroecological concepts could also be applied to smaller levels of biological organization such as transposable elements (TEs) within genomes. TEs are mobile segments of DNA that can move from one location to another and might compete for transcriptional machinery or space in the genome. If TEs interact with one another similarly to species occupying ecological communities, then we may be able to apply ecological analyses to better understand patterns of TE insertion and accumulation. Nonrandom patterns of co-occurrence within genomes may result from interactions among TEs. If interactions among TEs influence their distribution. For example, segregation has been used as evidence of competition, although other processes can give rise to similar patterns such as dispersal limitation. We analyzed co-occurrence patterns of TEs in ten butterfly species. Additionally, we examined rank-abundance distributions which describe the abundances of species within communities. Our preliminary data suggests TEs exhibit segregated patterns of co-occurrence that could result from interactions within the genome. Rank-abundance patterns displayed few dominant TE families with the majority being rare. This research could have a broad range of implications including clarification of TE preferential insertion, stronger predictions in how TE families will expand, shrink, and accumulate over time, and how we view TEs within genomes.

92. EXAMINING TRANSPOSABLE ELEMENT CONTRIBUTIONS TO BAT DIVERSITY AND EXTENDED AGING PHENOTYPES

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The Bat1k project is a bioinformatic collaboration to eventually sequence every bat species at very high quality standards. This endeavor will be important for phylogenetics, conservation efforts, understanding genome organization, and uncovering genomic mechanisms behind traits such as echolocation, diet, and aging. The lattermost point will be a prime focus, as several bats live up to 10x longer than expected given their body size. One aspect of bat biology that requires more scrutiny is their transposable elements (TEs). These genome components

have significant impacts on genome structure and function. The currently published bat genomes show their TE landscapes can be much different than that of a typical mammal. Their mutational effects on gene expression have been confirmed in several sequenced genomes to date and speciation events have been linked to increases in TE activity. Here, we will describe TE data on the first six Bat1k genomes comparing the landscapes and activity in different yangochiropteran and yinterochiropteran lineages. Additionally, we will compare TE enrichment around genes associated with increased longevity to determine if higher levels of TEs may have led to an adaptive breakthrough in bat aging.

93. A NOVEL METHOD TO CHARACTERIZE RESISTANCE EVOLUTION USING SPATIAL PROXIMITY FOR MEDICAL POLYMICROBIAL BIOFILMS

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Hi-C, an established molecular tool, identifies 3D chromatin structure in a cell. By adding an initial lysis step, spatial information and a mutational profile may be obtained concurrently by using next generation sequencing (NGS). Employing this technique to study biofilms could reveal genomic mutations in biofilms specifically arising from modified environmental conditions. Polymicrobial infections can form incurable biofilms that exacerbate health issues like chronic wounds (CW), cystic fibrosis (CF) and many others associated with microorganism infections. NGS 16s amplicon studies demonstrate that culturing techniques, the previous standard to study biofilms, underrepresent microbial diversity. Furthermore, cultured microorganisms grown in isolation fail to replicate the complex interactions in biofilms. Our study develops and tests a new NGS method for biofilms that will overcome such limitations by jointly yielding mutational information and micro- geography that may provide information on cell-cell interactions. Experimentation focused on a manufactured pseudo-polymicrobial community of *Staphylococcus aureus* and *Pseudomonas aeruginosa* – focal species in CF and CW – and *Escherichia coli*. We tested the method using mixed bacterial suspensions of *P. aeruginosa S. aureus* and *E. coli* at 3 lysis times. As secondary confirmation of the extracellular DNA (eDNA) linkage, we bioinformatically designed FISH probes specific to repeated genomic regions of our target microbes to detect eDNA intermingling. Through microscopy we aim to demonstrate successful cell lysis – a key step in our new procedure – by observing neighboring chromatin associating. This technique seeks to characterize spatial proximity of compensatory and complementary mutations in biofilms.

94. TRANSPOSABLE ELEMENTS AND LINEAGE SORTING WITHIN THE GENUS *HELICONIUS*

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The genus *Heliconius* is a colorful, diverse, well-studied collection of butterfly species. Prior studies have found several examples of hybrid speciation within the genus as well as high levels of introgression. The abundance of mimicry and hybridization within the genus has complicated the process of reconstructing an accurate phylogeny for *Heliconius* with single-gene and multi-gene phylogenies. The recent availability of whole-genome alignments of 24

Heliconius butterflies makes it possible to investigate the forces driving the phylogenetic conflict in this genus. Several factors, such as hybridization, phylogenetic error, and incomplete lineage sorting can drive conflict between markers and make phylogenetic inference difficult. 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 tested the application of novel software packages (n-way and 2-way) to identify differential insertion patterns an abundant SINE (Metulj) in each species. Preliminary results suggest that these novel software packages will enable further investigation into the history of introgression and lineage sorting within the genus *Heliconius*.

95. ANCIENT HYBRIDIZATION DETECTION WITHIN *CROCODYLUS*

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Interspecific hybridization can have lasting effects on genome architecture and the evolutionary trajectory of a species. The charismatic genus *Crocodylus* contains the most species, boasts the largest distribution, and utilizes more ecologically diverse habitats than any other extant group of Crocodilian. Previous work has recognized multiple cases of hybridization events between *Crocodylus* species with relatively deep diverges (~10mya), an uncommon observation among vertebrates. Here, we investigate ancient hybridization among members of *Crocodylus* by assessing the phylogenetic discordance and SNP variation across their genomes. Light-to-medium coverage Illumina data was used to construct 18 reference-guided assemblies of crocodilians. ABBA-BABA comparisons and D-statistics were calculated for each 100kb sliding-window along the assemblies. We also present the most robust dated phylogeny of *Crocodylus*. Evidence of phylogenetic discordance was abundant in our analyses with possible indications of ancient hybridization events.

MICROBIOLOGY & MEDICINE

96. HIV NEF COUNTERACTS AUTOPHAGY BY PROMOTING THE INTERACTION BETWEEN THE AUTOPHAGY INITIATOR BECN1 AND ITS INHIBITOR BCL-2

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Human immunodeficiency virus (HIV) is the causative agent of AIDS (acquired immunodeficiency syndrome), a pandemic that causes more than 1 million deaths per year. Although current treatments delay the progression to AIDS, they cannot eliminate HIV from affected individuals. Therefore, new avenues for therapeutic intervention are strongly needed. In this regard, the enhancement of different host immune barriers represents a promising strategy to block HIV. Among these defenses, autophagy stands out for its two-hit antiviral

activity. Autophagy is able to degrade intracellular pathogens which in turn, will also assists mounting an adaptive immune response against them. Although autophagy is very effective at clearing important human pathogens such as Zika virus or flu, its interrelation with HIV replication still remains unclear and requires further investigation. In this study, we show that the pharmacological activation of autophagy restricts HIV replication, causing a significant defect in virion production. However, HIV has evolved its virulence factor Nef to protect from autophagy. A thorough analysis of the interactions between HIV Nef and the autophagy machinery revealed that Nef is able to increase the association of the initiator of autophagy BECN1 with its inhibitor Bcl-2. Nef achieves this by affecting the post-translational modification patterns of Bcl-2. More precisely increasing the mono-ubiquitination levels of Bcl-2, a post-translational modification that makes this protein more stable and therefore, enhances its inhibitory effect over BECN1. Currently, we are in the process of further characterizing Nef's ability to counteract autophagy, due to its potential to become a target for new antiretroviral drugs.

97. PREDICTING METAGENOME-MEDICATION INTERACTIONS

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Over recent decades, there has been a revolution in sequencing and characterization of human and environmental metagenomes. Different research groups documented the effects of human-associated microbiome and their enzymes on the bioavailability and toxicity of different medications. Glucuronidation is a major metabolic pathway that improves the elimination of many medications. Bacterial β-glucuronidases in the gut break down drug-glucuronide conjugates and reactivate the drugs or their metabolites, causing metagenome-medication interaction. Characterizing the gut microbiome in terms of their capacity to interfere with drug metabolism is necessary for achieve drug efficacy and safety. Using publicly available cheminformatics and bioinformatics tools, we found that the metabolism of a hundred drugs could be affected by gut microbial β-glucuronidase. By studying the structural similarity of these medications, the commonly occurring drug scaffolds were estrogen and morphine. However, the variability in the level of β-glucuronidase has not been described before. Thus, Magic-BLAST was used to achieve this, and we found a wide variability in the β-glucuronidase level in the female gut metagenome samples based on the abundance of β-glucuronidase sequences. We also observed that β-glucuronidase sequences were more abundant in the infant gut metagenomes compared to those of adults. Here, we used β-glucuronidase in the human gut microbiome to present a novel and fast approach to characterize and compare different human metagenomes for their capacity to harbor known bacterial enzymes involved in drug metabolism. This research approach is able to predict metagenome-medication interactions, hopefully avoiding such potential interactions, and presenting new hypotheses that need experimental testing.

98. PATIENT GENETICS SHAPE CHRONIC WOUND MICROBIOME COMPOSITION AND IS ASSOCIATED WITH HEALING

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The clinical importance of microbiomes to the chronicity of wounds is widely appreciated, yet little is understood about the processes determining wound microbial community composition. Here, a two cohort microbiome-genome wide association study (mbGWAS) is presented through which patient genomic loci significantly associating with chronic wound microbiome diversity were identified. Further investigation revealed that alternative genotypes at single nucleotide polymorphisms located in ZNF521 and TLN2 significantly explained inter-patient variation in relative abundance of *Pseudomonas aeruginosa* and *Staphylococcus epidermidis*. Wound diversity was lowest in *Pseudomonas aeruginosa* infected wounds, and decreasing wound diversity had a significant negative linear relationship with healing rate. Whereas ZNF521 is a broadly implicated transcription factor that includes regulation of innate immunity, TLN2 is an important component of focal adhesions which are exploited by bacteria during attachment and invasion. Other loci exhibiting suggestive associations with wound microbiome diversity were significantly enriched for protein-protein interactions and are known to function in cellular adhesion processes. This study is the first to identify patient genetic determinants for wound microbiomes which influence healing and implicates patient variation in cellular adhesion phenotypes as important drivers of infection type.

99. SYNTHESIS OF STEROLS AND SPHINGOLIPIDS PROTECTS *LEISHMANIA* AGAINST MEMBRANE PERTURBING AGENTS, OSMOSTRESS AND STARVATION

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Leishmania promastigotes reside in the sandfly midgut where they are exposed to 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 differentiate 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, despite being dispensable in normal in vitro culture conditions, become crucial during *Leishmania's* complex life cycle and 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 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. Sterol and sphingolipid mutants also differed in uptake and endocytosis of lipophilic and hydrophilic dye, suggesting difference in plasma membrane composition, binding affinity and permeability to small molecules.

MOLECULAR BIOLOGY & BIOCHEMISTRY

100. DO CATEGORICALLY DISTINCT STRESSORS AFFECT VISUAL ATTENTION TO FOOD IN HUMANS?

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Neuroanatomical, endocrinological and neurological studies have revealed two major pathways for initiating stress, induces the release of CRF in the PVN. Both anticipatory and reactive stressors have been shown to influence food intake, however, there has been little work on whether anticipatory and reactive stressors impact the eating behavior in humans to the same degree. A total of sixty participants were randomly divided into one of control, TSST, or CPT group. We measured salivary cortisol and salivary alpha-amylase before and after the stressor, and then, all the participants performed an eye-tracking test. We analyzed saccade latency, gaze duration, and saccade bouts in balanced pairs of food and non-food images. We did find both TSST and CPT stress groups showed a considerable and statistically significant tendency for less attention time toward the food pictures than the control group, and there was a significant reducing effect for the CPT group when comparing the count number of looking at food images than the control group ($p=0.037$). The gaze duration reflects that both TSST and CPT stress groups showed a statistically significant tendency for spending less time looking at high - palatability foods images than on the control group. Thus far, both the anticipatory and reactive stressors spent less time looking at food images on fixation duration time. Only reactive stressor causes a preference for high satiability images on saccade latency.

101. FUNCTIONAL PVDF/VB2/TIO_2 NANOFIBER WEBS FOR DRUG DELIVERY

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Nanofiber webs produced by electrospinning method have been used for biomedical applications because of the nano-scale fiber size and pore size, high surface area and structure controllable (for example bio-mimic extracellular matrix). In this paper, polyvinyl alcohol (PVA) is chosen as raw polymer because of its flexibility, high tensile strength, and excellent nanofiber formation property. To provide functions for PVA nanofibers, inorganic nanoparticles and bioactive molecules are used to modify nanofiber morphology. Vitamin B2 (VB2) is chosen as the drug, because it is cheap, soluble in water, and no evidence of toxicity. In addition, anatase TiO_2 is used as coating material for VB2 to control the drug release rate.

Drug (vitamin B2, riboflavin, VB2)/nanoparticle (TiO_2, coated on drug surface) loaded poly(vinyl-alcohol) (PVA) nanofibers nanofiber webs were successfully fabricated. The characteristics of nanofiber structure, chemical composition, mechanical properties, and drug release properties were investigated. The morphology and diameter of nanofibers were

analyzed by scanning electron microscopy (SEM) and atomic force microscopy (AFM). The drug release properties of nanofiber webs were studied by liquid chromatography-mass spectrometry (LC-MS). The result showed the average retention time of VB2 was around 10.50 mins. Besides that, PVA/VB2/TiO_2 nanofiber webs with VB2/TiO_2 ratio of 4.5:1 exhibited a steady release rate and 50% of VB2 was released within a day. In addition, by coating VB2 with TiO_2, the burst release was effectively prevented for PVA/VB2/TiO_2 nanofiber webs with VB2/TiO_2 ratio of 4.5:1. The results in this study indicates drug-loaded and nanoparticle coated hydrophilic nanofiber webs are useful candidates in drug delivery application field.

102. COMPARING THE ANTI-CANCER EFFECTS ON MITOCHONDRIAL FUNCTION AND METABOLISM DISRUPTION IN BREAST CANCER CELLS BY A PLANT EXTRACT MIXTURE COMPARED TO THREE OF ITS COMPONENTS INDIVIDUALLY AND IN COMBINATION

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One of the major obstacles in current breast cancer treatment efficacy is the off-target cytotoxicity to normal cells, leading to debilitating side effects. Many of current chemotherapeutics target DNA (repair, replication, division). As a result, the bystander effect to normal cells is significant. One major difference between cancer and normal cells is their metabolism. Validation of the Warburg Effect shows that cancer cells prefer a glycolytic environment. Emerging studies have begun to delineate differences in mitochondrial function between cancer and normal cells. In this study, we sought to exploit this metabolic difference by investigating alternative breast cancer treatment options based on application of natural products. Previous studies from our lab demonstrated the efficacy of a mixture of plant extracts in killing cancer cells which showed significant mitochondrial disruption in cancer cells compared to normal cells. Here, we investigate three of the main components, namely arctigenin, chlorogenic acid, and cinnamaldehyde, to determine their anticancer properties. We hypothesize that each component causes breast cancer cell death by disruption of mitochondrial activity and metabolic shifts that is further amplified by combination treatment. Components were administered to MCF-7 breast cancer or normal MCF10A breast cells, either alone or in combination. To evaluate differences in cell response, mitochondrial integrity was evaluated by fluorescence microscopy and MTT. This study provides evidence that targeting the mitochondria may be a more effective anticancer treatment and that components of natural products or combinations thereof offer new approaches in treating breast cancer that significantly reduce off-target effects to normal cells.

PHYSIOLOGY & EVOLUTIONARY BIOLOGY

103. PATHOGEN EVOLUTION WHEN TRANSMISSION AND VIRULENCE ARE STOCHASTIC

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Evolutionary processes are inherently stochastic, since we can never know with certainty exactly how many descendants an individual will leave, or what the phenotypes of those descendants will be. Despite this, models of pathogen evolution have nearly all been deterministic, treating values such as transmission and virulence as parameters that can be known ahead of time.

We present a broadly applicable analytic approach for modeling pathogen evolution in which vital parameters such as transmission and virulence are treated as random variables, rather than as fixed values. Starting from a general stochastic model of evolution, we derive specific equations for the evolution of transmission and virulence. We show that adding stochasticity introduces new directional components to pathogen evolution. In particular, two kinds of covariation between traits emerge as important: covariance across the population (what is usually measured), and covariance between random variables within an individual. We show that these different kinds of trait covariation can be of opposite sign and contribute to evolution in very different ways. In particular, probability covariation between random variables within an individual is sometimes a better way to capture evolutionarily important tradeoffs than is covariation across a population.

104. MORPHOLOGY AND GENETICS OF *SIGMODON FULVIVENTER DALQUESTI* IN THE CHIHUAHUAN DESERT ECOREGION

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The tawny-bellied cotton rat, *Sigmodon fulviventer dalquesti*, is a Texas endemic subspecies reported only from a single sampling near Fort Davis in 1991. The current population, distribution and evolutionary origin of *S. f. dalquesti* is enigmatic. 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), 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. To inform an accurate conservation assessment, a more complete understanding of *S. f. dalquesti* biology is required. Here we present results of a morphometric analysis of 18 skull characters of *S. fulviventer* ssp. We also report preliminary results of a cytochrome *b* phylogenetic analysis.

105. PHYLOGENETIC INFORMATION IN SEED MORPHOLOGY AND SEED GERMINATION FOR SHORTGRASS PRAIRIE SPECIES

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Seed germination is critical for species survival and colonization of new habitat. Systematically obtaining some insights of seed germination could be beneficial for seeding in wildland restoration and agricultural practice. In this study, we seed germination rate and seed morphological measurements (seed mass and seed surface area) for 19 common shortgrass

prairie species. We tested the phylogenetic signal in each seed measurement using Pagel's lambda and Blomberg's K. We also applied phylogenetic comparative methods to explore potential patterns between seed germination rate and seed morphological traits. Our results show that seed morphology in shortgrass prairie species contains phylogenetic signal, and seed morphology is weakly correlated with seed germination. These findings support that phenotypic evolution plays a role in shortgrass prairie conservatism. To benefit the shortgrass prairie re-seeding restoration, the phylogenetic analysis of physiological seed traits is expected for future study.

PLANT & SOIL SCIENCE

106. MODELING OF ROOT WATER UPTAKE OF COTTON UNDER DEFICIT SUBSURFACE DRIP IRRIGATION

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An understanding of spatial and temporal patterns of root water uptake (RWU) of cotton (*Gossypium hirsutum* L.) under a semiarid deficit drip irrigation practices is of great importance for efficient use of irrigation water in groundwater-dependent agricultural production of Southern High Plains, where high rate of water extraction from the Ogallala aquifer to meet crop water requirements continues to be a major concern in cotton production in the region. Despite its importance, there remains a paucity of quantitative information on spatial and temporal patterns of RWU of cotton, particularly under deficit subsurface drip irrigation. Therefore, the objective of this study was to simulate patterns of multidimensional RWU in a semiarid subsurface drip-irrigated cotton field using the HYDRUS (2D/3D) numerical model. A field study consisted of four levels of deficit subsurface drip irrigation, was conducted over two consecutive growing seasons (2017-2018) to evaluate spatial and temporal RWU in a semi-arid cotton field. The HYDRUS, which agreed with the measured volumetric water content and soil temperature data at different soil depths in the cotton root zone during the model calibration period (2017 growing season), was used to simulate root zone soil water dynamics, and compensated and non-compensated RWU under four different levels of subsurface drip irrigation during the model validation (2018 growing season). Overall, the results of the simulation, validated against measured data in a cotton field, suggested that the use of the HYDRUS model could be an effective tool for managing the water use in a subsurface drip-irrigated cotton production system.

107. GENETIC DIVERSITY ANALYSIS OF SILVERLEAF NIGHTSHADE POPULATIONS UNDER HERBICIDE STRESS

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Solanum elaegnifolium (silverleaf nightshade) is a member of the Solanaceae family and is native to central America. It is an aggressive, poisonous weed, that dramatically spreads from deep rootstocks with persistence. Silverleaf exhibits a large amount of morphological variation and harbors a high degree of resistance to several economically important pests, pathogens and herbicides. Increased infestations of weedy silverleaf nightshade have caused significant

reduction in major crop yield worldwide. The adaptability of noxious weeds has been attributed to both phenotypic plasticity and genetic variation. The goal of our study is to assess the genetic variation in two populations of silverleaf subjected to herbicide pressure. To this end, we need to establish the genetic diversity of the *S. elaegnifolium* by first distinguishing transferability of related SSR markers and second use the markers that are transferable to elucidate the genetic diversity. From the acquisition of polymorphism information content and the generation of a dendrogram model we were able to deduce that herbicide resistance was not the cause of individual clustering, but there was significant variation/divergence within both the populations. The observed significant variation/divergence in population germplasms found between the heterogenous populations is entirely the product of obligate outcrossing that has resulted in an innate degree of variability. Thus, this research propositions to elucidate molecular mechanisms that confer the genetic adaptability observed in *S. elaegnifolium* and then use the resulting information to create a simulation model that may better illustrate potential range expansion and population distribution of the species.

108. TRADE-OFF BETWEEN FORAGE QUALITY IMPROVEMENT AND CROP WATER USE FOR ALFALFA-GRASS SYSTEM

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Alfalfa (*Medicago sativa* L.) can potentially enhance the supply of high-quality forage when interseeded into native warm-season grassland in the Southern High Plains. Alfalfa is a high water-using species; therefore, a possible trade-off between soil-water depletion and forage quality of the sward merits study. The objective was to determine the effect of interseeding alfalfa on forage nutritive values, crude protein (CP) and digestible organic matter (DOM) yield, and to calculate the water footprint [WF, m^3 of evapotranspiration (ET) per kg of product] of CP and DOM yields at two planting densities. The ET was estimated as the difference between precipitation and the change in soil water storage in the root zone. Grass-legume mixture increased forage CP concentration and DOM over the grass-only control by 59 and 11% across 3 years whereas neutral and acid detergent fiber concentrations were reduced by 19 and 11%, respectively ($P < 0.001$). Alfalfa presence reduced the WF ($P < 0.001$) with respect to CP and DOM yields by 56 and 30%, respectively, relative to grass-only control, attributable to large increases in CP and DOM yields of the forage mixtures. Hay-type alfalfa cultivars NuMex Bill Melton and WL 440HQ enhanced the forage mixture quality to a greater extent than did the grazing-type Falcata-Rhizoma blend, mainly driven by greater alfalfa DM production. Managing alfalfa in wide rows (low planting density) in mixture with warm-season perennial grasses can increase the efficiency of water use (lower WF) by enhancing forage quality, thereby causing minimal trade-off in soil water consumption.

109. USING CROP RESIDUE AND NO-TILL TO MANAGE SOIL MICROBIAL DYNAMICS IN A DRYLAND COTTON SYSTEM IN WEST TEXAS

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Conventional agriculture practices and climate variability impact the Southern High Plains changing physical, chemical, and biological characteristics of the soil, which decline soil health. Thus, it is important to consider the use of conservation practices to increase microbial activities and soil health in drylands. We assessed the effects of crop residue in combination with no-till on soil microbial activities in a dryland cotton production system in West Texas. The research was carried out from 2014-2017 years. Three treatments were established 1) using erosion blankets (shade), 2) Sorghum residue or wheat residue (stubble) and 3) control (no stubble) with 6 replicates plots (8 x 7 m) in each treatment and control. In 2016-2017 shade treatment was not included. Soil samples were collected before planting and over the growth season to evaluate environmental, nutrients, and microbial parameters. Results showed over the four years that stubble reduced daily soil temperature range (DTR_{soil}) by approximately 6 °C on average at 0 cm and approximately 3 °C at 15 cm during the hottest months. The reduction in daily soil temperature range increased microbial activities. Overall, microbial biomass carbon increased by 35 % in the stubble with respect to the controls. Enzyme activities increased by 41 % in stubble on average with respect to the control and the proportion of fungi was higher in all years in comparison with bacteria under stubble. The implementation of conservation management practices mitigate climate variability with the reduction in (DTR_{soil}) and positively affect the dynamics of microbial communities and their contribution to soil productivity.

110. MANAGING PALMER AMARANTH (*AMARANTHUS PALMERI*) WITH SEQUENTIAL APPLICATIONS OF DICAMBA AND GLUFOSINATE WITH OR WITHOUT ACETOCHLOR

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Palmer amaranth (*Amaranthus palmeri* S. Wats.) is one of the most common weeds in west Texas. The management of Palmer amaranth has changed since the discovery of glyphosate resistant populations in 2005. Dicamba tolerant cotton systems that utilize XtendiMax® with VaporGrip Technology® were introduced in 2017 and provide a new opportunity to manage glyphosate resistant populations. The use of glufosinate (Liberty® 280 SL) tank-mixed with the postemergence residual herbicide acetochlor (Warrant®) in a dicamba-based system may improve the management of glyphosate-resistant Palmer amaranth and be proactive against new developments of herbicide resistance. A field study was conducted in a non-crop environment in Lubbock, Texas in 2018 to determine the influence of sequential order when applying dicamba and glufosinate on three different sized Palmer amaranth (<10 cm, 10-20 cm, and >30 cm) and examine the benefit of adding acetochlor in tank-mixture in one of the sequential postemergence applications. When evaluated 21 days after the sequential application, treatments of dicamba followed by (fb) dicamba and dicamba fb glufosinate controlled less than 10 cm Palmer amaranth >90%, which was greater than glufosinate fb dicamba and glufosinate fb glufosinate. When evaluated 21 days after the sequential application, glufosinate fb dicamba controlled 10 to 20 cm Palmer amaranth 74%, which was

greater than dicamba fb glufosinate. No treatment controlled 30+ cm Palmer amaranth more than 55%. Acetochlor improved weed control when added to several tank-mixes, such as glufosinate + acetochlor fb glufosinate (91%) compared to glufosinate fb glufosinate (<90%) for less than 10 cm weeds.

PROPOSAL

111. UNEARTHING PROXY DETERMINANTS OF THE SUBTERRANEAN NICHE FOR SPECIES DISTRIBUTION MODELS

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A common objective in biogeographical studies is to determine which, and to what extent, environmental factors influence patterns of species diversity and distributions. Species distribution models (SDMs) have been used for this objective across numerous taxa occupying a variety of realized niches. Nevertheless, a unique perspective that is underrepresented in SDM literature is the subterranean niche, whose paucity of information is likely due to the inaccessible nature of direct predictors such as illuminance, geohydrology or other underground measures. When a suitable variable is unavailable, it becomes customary to incorporate efficient proxy variables to accurately envelop the distribution of a species. Here, we propose to use three classes of environmental variables: historical, climate and habitat heterogeneity, which span a stability-variability gradient, to model the subterranean niche of the plains pocket gopher, *Geomys bursarius*. Within each environmental class, we will assess the explanatory power of each variable on species occurrence using generalized linear models. Significant variables will be used to construct overall species distribution models using Maxent. This model will be compared to similarly generated models that illustrate distributions of Merriam's kangaroo rat (*Dipodomys merriami*) and the Southern Plains woodrat (*Neotoma micropus*), two widespread rodents representing fossorial (i.e., digging) and non-fossorial lifestyles, respectively. We hypothesize that the environmental constancy captured by historical factors, namely geologic patterns, describes contemporary species distributions of subterranean rodents better than climate or aboveground habitat variables. Results from this study are essential for digging deeper into ecology and evolution of the understudied subterranean niche.

112. WINTER MOVEMENT AND ENERGETIC DEMANDS OF THE BLACK FLYING FOX IN QUEENSLAND, AUSTRALIA

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Hendra virus is a zoonotic paramyxovirus endemic to eastern Australia carried by a nomadic bat species, the black flying fox (Pteropus alecto). These bats transmit the virus to horses which can then be contracted by humans. Increased urbanization and habitat destruction have significantly decreased native winter flowering habitat resulting in an increased frequency of contact between bats and horses. In order to better understand the transmission of Hendra, more targeted studies are needed to examine the movement and physiology of *P. alecto*. This

study aims to understand how limited food supply during the winter months impacts the movement and feeding patterns of *P. alecto* populations. We hypothesize that limited food supply during winter causes populations to become immunocompromised, initiating changes in the movement patterns of these bats which leads to increased interactions with horses and spillover occurrences. This project will include active and passive sampling of resident and nomadic camps during winter by measuring body condition through bioelectric impedance analysis and using GPS tags to track individual movements. Understanding how food limitations impact the movement ecology of *P. alecto* can help identify regions where flying fox and horse populations overlap and provide insight into how initial transmission of Hendra to horses occurs. As we develop a comprehensive understanding of the system, we will use this information to develop better narrative framework, public communication, and guidance for habitat restoration efforts that may break the vicious cycle of human-wildlife conflict in this system.

113. THE INFLUENCE OF MICROBIAL SYMBIOSES ON LEAF- AND WHOLE-PLANT ACCLIMATION TO ELEVATED CARBON DIOXIDE

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The Intergovernmental Panel on Climate Change predicts that global atmospheric carbon dioxide (CO_2) concentrations could exceed 1000 parts per million by 2100. Plants are expected to acclimate to elevated CO_2 (eCO_2) by increasing whole-plant demand for soil resources, giving individuals capable of forming strong symbiotic relationships with fungi and bacteria a possible competitive advantage over those who do not form these relationships. However, plants are also expected to acclimate to eCO_2 by decreasing demand for foliar nitrogen and phosphorus as a result of reduced Rubisco carboxylation rates, which could eliminate any competitive advantage in microbial association. The role of microbial symbiosis in plant eCO_2 acclimation, given differences in nutrient demand at leaf- and whole plant-levels, is relatively unexplored. As such, there is a need to conduct additional studies to understand impacts of below-ground symbioses on plant acclimation, nutrient acquisition, and allocation under eCO_2.

I propose to investigate impacts of microbial symbioses on plant responses to different CO_2 concentrations. First, I will evaluate how nitrogen and phosphorus demand at leaf- and whole plant-levels affect below-ground carbon allocation under ambient and elevated CO_2. Next, I will determine plant symbiosis preference under different nutrient concentrations. Finally, I will evaluate any effects of competition between plants who associate with different symbiotic types on nutrient and carbon flux under ambient and elevated CO_2. These projects will provide important empirical data needed to evaluate robustness and reliability of Earth system models that predict plant responses to eCO_2, helping us better understand biosphere-atmosphere feedbacks to climate change.

114. CHARACTERIZING RETROTRANSPON ACTIVITY ACROSS RECENT HISTORY: A CASE STUDY IN THE NORTHERN FLICKER SPECIES COMPLEX

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The disproportionate prevalence of Transposable Elements (TEs) across vertebrate genomes is well known. By some estimates, for example, TEs comprise up to as much as 45 % of the human genome. Recent advances in sequencing have begun to uncover some of the effects TEs have had on genomes, with their being associated with diversification, adaptation, disease, chromosome evolution, etc. Birds contain a relative dearth of TEs , which comprise roughly 10 percent of their genomes. Recent work, however, has demonstrated that the Downy Woodpecker is a notable exception, containing a nearly two-fold increase in TEs relative to other birds. In large part, this is due to the expansion of chicken-repeat 1 (CR1), a non-long terminal repeat (LTR) retrotransposon that has been recently active in this species. In spite of this proliferation, Downy Woodpeckers have not experienced a substantial increase in genome size, suggesting that negative selection has been counteracting CR1 expansions. Here, we propose to test this hypothesis by identifying and assessing polymorphisms in four subfamilies (J2_pass, J3_pass, E_pass and Y4) of CR1 across four closely related lineages of the Northern Flicker (*Colaptes auratus*) complex. Using a *de novo* long-read genome assembly of *Colaptes auratus* as a reference, we will identify CR1 polymorphisms that are segregating across these lineages and assess their frequencies relative to single nucleotide polymorphisms (SNPs).

115. INFLUENCE OF GRASS FUEL LOAD AND CANOPY ARCHITECTURE ON FIRE BEHAVIOR AND FIRE RESPONSE OF *JUNIPERUS VIRGINIANA* IN SOUTHEASTERN MISSOURI

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If grass species differ in flammability, species composition could alter fire behavior and in turn influence post fire response. Recent work demonstrated that different grass species indeed vary in fire behavior, and grass canopy architecture affects soil heating: species with more biomass being concentrated near ground will produce more heat at soil surface. Such canopy effects can potentially influence both grass meristem survival and damage to tree stems. We propose to examine the influences of fuel load and canopy architecture on grass fire behave and fire effects in field.

This work will occur in tallgrass prairies in southeastern Missouri, where the dominant tree species is *Juniperus virginiana* L. Fire effects on trees will be determined by stratified sampling of 80 individuals of *Juniperus virginiana* in burning units. Tree traits, and local grass composition and biomass will be measured before fires. To mimic species-specific variation in grass fuels we will apply four fuel treatments: high(1000g/m^2) and low(430g/m^2) fuel load; two fuel partitions in vertical space (90% fuel concentrated below or above 10cm relative to ground). We will measure flame temperatures, rate of spread and biomass consumed. We will assess fire severity the day after fire, and check tree mortality and grass recovery 6 months after burning.

The study will provide a better mechanistic understanding in fire-mediated tree-grass interactions by linking species effects on grass fire behavior to tree stem and canopy damage. The outcome will also contribute to the fire managements in grass dominant ecosystems where grass composition varies across space.

116. NOSY NEIGHBORS EAVESDROP ON COMPLEMENTARY INFORMATION

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Why does the zebra follow the giraffe? It does so because the giraffe is tall. More specifically, their height and high vigilance make them adept at detecting predators. This information is then relayed to the surrounding herd through visible postural changes[1]. Because each species perceives its world in unique ways and accesses unique information, heterospecific eavesdropping may be beneficial if one associates with a community which perceives and communicates risk differently than you do. Being a nosy neighbor can have an adaptive advantage in that your neighbors may yield complementary information. This phenomenon we have dubbed, The Complementary Eavesdropper Hypothesis (CEH).

While eavesdropping has received extensive attention[2–6], the interaction of multiple informants influencing behavior in concert has not been explored. This work represents a continuation of my doctoral work testing the CEH by quantifying fear associated with foraging under perceived risk. Initial data supports previous work showing heterospecific alarms may influence perceived risk. However, individuals are capable of risk management by adjusting behavior based on time or location of risk[7]. I briefly propose additional experimentation to address these concerns. Specifically, if complementary information allows individuals to better determine acute periods of risk, then they should forage more intensively in periods of safety, than allowed through a single informant. Additionally, a spatial assay will assess spatial perception of risk in response to complementary eavesdropping. Lastly, I propose theoretical work to explore possible implications of complementary information, such as possible influence on niche partitioning, and as a mechanism of coexistence.

117. MULTI-OMICS DATA ANALYSIS OF FOUR GENOTYPES OF BANANA MICROBIOME USING A MODIFIED ENRICHMENT METHOD

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Banana is one of the most important agricultural products in the world (Cauthen et al., 2019). Vegetative propagation of banana cultivars has had several negative impacts such as transmission of diseases and lack of genetic differentiation (Kumar et al., 2019). Due to the challenge of culturing most plant-associated microbes, investigation of microbial diversity has lagged behind; therefore, little is known about detrimental or beneficial microbiome diversity within bananas (Köberl et al., 2016). Several studies have indicated the presence of potentially beneficial microbes with activity against banana pathogens (Ting et al., 2008). Characterization of microbes from bananas is possible with amplicon sequencing, but this provides little information compared with shotgun metagenomics or metatranscriptomics. However, these methods are costly with whole plant extractions due to the large genomes of plants. Our goal is to isolate whole microbial cells to enable detailed functional characterization of the banana microbiome. To achieve this, we have used a modified Cell Enrichment Method previously used for separation of bacteria from genetic materials of soybean and applied it to banana plant. During this culture-free method, we eliminated host cellular material resulting in successful isolation of a layer of bacteria. In the following step, using quantitative PCR, we will assess the presence and location of fungal cells in these layers targeting 18S rRNA. In the next step, we propose three procedures including; 1) long-read shotgun metagenomics, 2) coding mRNA metatranscriptomics and microRNomics, and 3) metabolomics to characterize microbiome diversity, function, and identify critical synergies that may strengthen defensive microbiomes.

TOXICOLOGY

118. SORPTION OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS (NSAIDs) TO MICROPLASTICS UNDER FRESHWATER, SEAWATER AND ACIDIFIED WATER CONDITIONS

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High disposability, high durability, and indiscriminate use have led to the accumulation of plastics at uncontrolled rates in the environment. Studies have found that microplastics are able to sorb and accumulate waterborne contaminants. Nonsteroidal anti-inflammatory drugs (NSAIDs), are a group of pharmaceuticals highly consumed in the market due to a low price and over-the-counter accessibility. NSAIDs are frequently detected in the environment at µg/L concentrations. In the present study, the sorption behavior of three NSAIDs (ibuprofen, naproxen, diclofenac) was examined with four types of microplastics (polystyrene (PS), ultra-high molecular weight polyethylene (UHMWPE), average molecular weight medium density polyethylene (MDPE), and polypropylene (PP)) under varying water conditions. Linear, Freundlich, and Langmuir isotherms were constructed using the batch equilibrium approach. Salinity and pH had significant effects on the sorption of NSAIDs to microplastics with increased sorption at low pH. Ionic strength also affected sorption behavior, but it varied among polymer type and NSAID. Among the NSAIDs tested, diclofenac exhibited the highest partition coefficient to microplastics. Among microplastics, AMWPE and UHMWPE exhibited the highest affinity to sorb NSAIDs and PP had the lowest sorption capacity. In general, NSAIDs exhibited a moderate sorption onto microplastics under environmentally relevant conditions. Understand the sorption behavior of pollutants on microplastics is relevant in the environmental toxicology field; due to its small size, appealing color and buoyancy, plastics debris can be ingested by aquatic organisms acting as vectors of pollutants and increasing the potential risk of toxic harmful effects on the organisms that ingest them.

119. DIETARY NUTRIENTS (C:P) MODULATE CADMIUM TOXICITY IN AQUATIC SYSTEMS AT TWO TROPHIC LEVELS

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Effective ecological risk assessment requires the understanding of complex ecological interactions, elemental cycling, and the interactive effect of natural stressors such as resource limitations and contaminants. The development of ecotoxicological models that incorporate such data would significantly contribute to interpreting how contaminants impact organisms and food webs in such a dynamic system. This study seeks to develop and analyze a series of empirically testable and robust mathematical models of population dynamics subject to stoichiometric nutrient modulation and contaminant stressors. Specific empirical measurements include: physiological traits-(growth, survival, reproduction, respiration, heartrate), behavioral-(distance moved, velocity), elemental-(C:P) and toxicant-(Cadmium-Cd)

uptake in primary producer, Algae (*Scenedesmus acutus*) and primary consumer, *Daphnia pulex*. *S. acutus* and *D. pulex* were cultured in Cd-containing (25%, 50% and 100% of daphnia-exposed LC_{50} values) media with varying P-nutrient ratios [Low P and COMBO (control)] media for acute (24 h and 96 h) and chronic (21 d) durations, according to USEPA methods. Acute toxicity results showed a concentration-dependent increase in the toxicity of Cd against *S. acutus* with higher in Low P media compared to the control. The survival of *D. pulex* reduced temporally with Cd exposure and Low P media further reduced the survival. Other toxicological endpoints (respiration, heartrate, growth, reproduction, and behavior) were also impacted by Cd exposure with enhanced impact in the Low P media, compared to control. Studies are currently underway to determine the effects of the stoichiometric modulation of the mineral nutrients (C:P) on the toxicities of Arsenic and Copper against *S. acutus* and *D. pulex*.

WILDLIFE & FISHERIES CONSERVATION

120. DATA COLLECTION METHODS AND SPECIES TRAITS INFLUENCE SPECIES DISTRIBUTION MODEL PREDICTIONS

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For effective conservation, managers first must understand where species occur. A useful tool for understanding ranges are species distribution models (SDMs), which predict potential ranges by relating known occurrences with environmental factors. SDMs assume that occurrence data provide an accurate representation of a species range; however, SDMs commonly use museum specimens or self-reported data, which may not meet this assumption. Therefore, we assessed the influence of data collection methods on SDM performance and further evaluated whether performance differed between taxa with different life history and physical traits. We used a suite of fish species found in the Texas Gulf representing a variety of characteristics that could influence SDM performance. We compared the systematic and random sampling data provided by the Coastal Fisheries Division of Texas Parks and Wildlife (TPWD) and the opportunistic sampling data provided by the Fishes of Texas Database (FoTx). SDMs of the Gulf fishes demonstrated that both data source and species traits affected model predictions. The AUC values (indicators of model strength) for FoTx were higher than TPWD for all fish species, indicating strong predictive performance. However, these data were more haphazardly collected than TPWD, likely causing model overfitting. Model performance was highest for species with longer lifespans, lower dispersal ability, and ones that were less common. Overall, our research demonstrated the impact of data collection method and species traits on SDM performance. Thus, consideration of these factors will improve the effectiveness of predictions from SDMs for conservation, management, and research.

121. REPRODUCTIVE BIOLOGY OF RIO GRANDE COOTER (*PSEUDEMYS GORZUGI*) ON THE BLACK RIVER, NEW MEXICO

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Rio Grande Cooter, *Pseudemys gorzugi*, is one of the least-studied species of freshwater turtles in North America. The species is listed as threatened in New Mexico and the Species of Greatest Conservation Need in Texas. Currently, the United States Fish and Wildlife Service is reviewing its status for potential federal protection. Little is known about *P. gorzugi* ecology making assessment of its conservation status and implementation of proper conservation and management practices challenging. In 2018, we studied reproductive ecology of Rio Grande Cooters on the Black River, New Mexico. From mid-May to mid-August, we surveyed *P. gorzugi* using traditional hoop net traps. Females (n=159) were x-rayed and ultrasounded to assess their reproductive status. We found 16 females containing shelled-eggs and 27 females containing oviductal follicles. High proportions of gravid females were observed at the end of May and mid-June. The size of the smallest gravid female was 185 mm in plastron length. Mean clutch size (n=15) and egg width (n=144) were 9.33±2.89 and 30.07±1.72 mm, respectively. In addition, we also used X-radiograph to assess the prevalence of fish hook ingestion and recreational shooting as potential threats to the species. Out of 228 x-rayed individuals, we found only 2% of turtles with ingested fish hooks and bullet fragments. Overall, our study significantly contributes to the existing knowledge of the *P. gorzugi* reproductive biology in New Mexico, which can aid in projecting future population dynamics and implementing sound management practices.

122. REVIEW OF BAT DIVERSITY, DISTRIBUTION AND CONSERVATION STATUS IN MALAYSIAN BORNEO: HOW MUCH DO WE KNOW?

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There are 100 species of bats in Borneo, harbouring about 30% and 74% of the bats of Southeast Asia and Malaysia, respectively. The international Union for Conservation of Nature (IUCN) Red List assessment revealed at least 31% of Bornean bats are considered threatened or data deficient, and about a third have decreasing population trends. Primary threats are human-led landscape modification that destroys roosts and foraging habitats, and overexploitation from hunting. Furthermore, there is a substantial lack of information on the diversity, distribution, ecology and biology of Bornean bats, which may impede the conservation of some of the most threatened bat species on the island. Results from various surveys conducted in the Malaysian states of Borneo over the past 20 years were compiled to address the gap of information on the bat species. New information on the distribution, diversity, ecology, and conservation status of Borneo's bat diversity is presented, and priority areas where regional sampling effort should be concentrated identified.

123. THE CROCODYLIANS OF BOLIVIA: A REPORT ON THE CURRENT STATE OF KNOWLEDGE AND REGIONAL CONSERVATION PRIORITIES

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Management programs and economic incentives that crocodylians generate have become key elements for species and habitat conservation. To guarantee sustainability of management programs, they must be designed on a scientific basis. Adapted from other species conservation strategies, we present a conservation planning model based on prioritization of critical habitats for crocodylians using spatial distribution information available in Bolivia. We carried out a literature search and spatial data compilation to estimate the distribution range (Extent of Occurrence - EOO), characterize it country range-wide by ecoregion (Crocodylian Geographic Region - CGR), and delineate areas with species occurrence or population surveys (Crocodylian Study Units – CSU). Finally, ecoregions inside CSU were defined as Crocodylian Conservation Units (CCU) for which we developed a weighting scheme to prioritize them as critical areas to protect, and/or if there is sufficient knowledge to implement management programs (Regional Habitat Priorities), and areas to implement research and monitoring programs due to the insufficiency of biological information (Regional Research Priorities). We reviewed 105 documents written from 1977 to 2017 and used spatial data from 44 documents. We estimated an EOO of 654873.943 km^2, defined 17 CGR, 98 CSU, and 167 CCU, out of which 29 were categorized as RHP and 138 as RRP. This analysis resulted in a weighting scheme that prioritizes areas where crocodylians potentially inhabit. This research will help develop a baseline and provide decision-makers the information needed to prioritize future research, habitat protection, and sustainable management programs to achieve the effective conservation of crocodylians in Bolivia.

EMERGING PROFESSIONALS

124. HOW MUCH DOES MICROCLIMATE MATTER? DECOUPLING THE EFFECTS OF TEMPERATURE AND HUMIDITY ON BAT HIBERNATION PHYSIOLOGY

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Knowledge of bat hibernation physiology has greatly increased in the past few decades with microclimate emerging as an important influential factor. Based on conventional observations, we expect bats to prefer colder, more humid conditions, which maximize torpor bout duration and minimize evaporative water loss. However, little research has been conducted to parse out the confounding effects of temperature and humidity, which is of increasing relevance in light of white-nose syndrome (WNS). We performed a captive hibernation study using 98 wild-caught tri-colored bats, *Perimyotis subflavus*, from central Mississippi. Bats were inoculated with the WNS causative agent*, Pseudogymnoascus destructans*, and placed in environmental

chambers at three different temperature and evaporative water loss treatments. We monitored bat activity and tracked arousal frequency for each individual over the course of 87 days. We measured body composition at the beginning of the experiment and performed respirometry on a subset of bats immediately following their removal from treatment conditions. In this presentation, we will address the independent effects of temperature and humidity on torpor arousal frequency, percent body mass loss, and evaporative water loss, while also accounting for other confounding variables, such as starting fat mass and sex. This study represents the first of its kind and provides valuable information about the relationships between microclimate and bat hibernation physiology in the context of a WNS system. Our research also contributes to baseline understanding that will be beneficial in informing conservation efforts and future studies directed at understanding the microclimate influences in other species and regions.

125. CONNECTING PATTERNS OF MIGRATION TO FUNCTIONAL MOTIVATIONS

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Each year billions of animals migrate between seasonally disconnected habitats, influencing the ecological properties of their temporary habitats and filling important ecological roles. Some species make ‘to-and-fro’ migrations, where all individuals move between seasonal habitats. But, for many species, migration patterns are more complex, involving partial and/or differential migration. Landscape-level patterns of migration are the cumulative result of the collective behaviors of individual migrants (migration is a characteristic of individuals, not species). Thus, to understand the adaptive drivers of population level migratory patterns, we must consider the functional motivations (i.e., the current fitness utility of a behavior) of migrating individuals, and how varied functional motivations within populations give rise to the observed diversity of landscape-level patterns of migration. In this talk we will first describe a conceptual framework linking the functional motivations of migrants to landscape-level patterns of migration. The framework includes considerations of varied migration strategies that result in different flight and stopover behaviors throughout migration. We apply the framework to a system of long-distance migratory Hoary bats (*Lasiurus cinereus*) that exhibit both partial and differential patterns of migration. We find that differences in reproductive contribution throughout the annual cycle between hoary bat sexes are a primary driver of the observed migratory diversity; demonstrating the influence of life history traits on migration. We conclude that our conceptual model is a useful framework for identifying critical natural history gaps, setting meaningful research trajectories for migration conservation, and understanding the evolution of migratory diversity.

126. *AEDES ALBOPICTUS* AND *AEDES AEGYPTI* INSECTICIDE RESISTANCE IN TEXAS

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The spread of vector-borne pathogens, such as West Nile, dengue, and Zika viruses, is constantly threatening public health. To mitigate the risk, vector control programs implement the use of a variety of insecticides. Consequently, the continued use of the same insecticides leads to the development of insecticide resistance, minimizing the effectiveness of their control capabilities. In an effort to investigate potential resistance throughout the state, we tested F_1

generation *Aedes albopictus* and *Aedes aegypti* mosquitoes from sixteen jurisdictions throughout the state of Texas using CDC bottle bioassays. Thirty-six total bioassays were performed testing resistance to permethrin, malathion, and deltamethrin, three commonly used insecticides. Sixty-nine percent (25/36) of bioassays performed revealed insecticide resistance, 11.1% (4/36) revealed possible resistance, and 19.4% (7/36) of all bioassays performed revealed susceptibility to the insecticides. This study provides valuable information relative to the potential of insecticide resistance development in the state of Texas. Future work will examine the mechanisms responsible for resistance.

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