



Texas Tech 7th Annual Biological Sciences Symposium



TEXAS TECH UNIVERSITY
DEPARTMENT OF BIOLOGICAL SCIENCES
LUBBOCK, TEXAS
APRIL 1-2, 2016

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TEXAS TECH UNIVERSITY
Department of Natural
Resources Management™



TEXAS TECH UNIVERSITY
Department of
Biological Sciences™



Research and Testing
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Welcome Note:

It is with great honor and my pleasure to welcome everyone to the 7th Texas Tech Annual Biological Sciences Symposium (TTABSS), which is held this year of 2016, on April 1st and 2nd. This year the Biological Sciences Symposium is hosted at the Jones AT&T Stadium (Friday, April 1st) and at the Biological Sciences & Experimental Sciences buildings (Saturday, April 2nd). Since the first Texas Tech Annual Biological Symposium in 2009, the Association of Biologists and the Department of Biological Sciences have been planning this annual symposium every year. Today, three graduate student organizations, (TTUAB, ANRS, and ASM) work closely with both Departments of Biological Sciences and Natural Resources Management to make this symposium possible.

Our goal as a scientific community is to provide a platform to share scientific findings and explore the diverse world of Biological Sciences, by exchanging ideas among peers and gain experiences from academic advisors. TTABSS comes to help in achieving that.

This year the symposium has a total of 150 undergraduate, graduate and faculty participation from 10 academic institutions. Our program will have 71 research presentations that include 27 poster presentations and 4 parallel oral sessions. For the first time, we would like to announce the invitation of two distinguished guest speakers, Dr. Christopher A. Brochu and Dr. José F. González–Maya, respectively. Both are renowned scientists in their prospective fields from the University of Iowa and ProCAT Colombia/Sierra to Sea Institute. We are excited to have such incredible speakers to donate their time for our event and cause.

As a chairperson of the TTABSS committee, I would like to thank all the members of the committee team for their hard work and dedication. To our advisors for their advice and suggestions on organizing the program and to our event sponsors who had helped us to with the costs of TTABSS 2016 for all participants. I would like to express my 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!

Brandon A. Gross
Local Committee Chairperson President
TTUAB 2014–2016

EVENT HOSTS

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

EVENT COLLABORATORS

Department of Plant and Soil Science, Texas Tech University
CISER/HHMI at Texas Tech University
The Institute for Environmental and Human Health (TIEHH)

PARTICIPATING INSTITUTIONS

Texas Tech University
University of Iowa
Hardin-Simmons University
McMurry University
Midland College
Museum of Texas Tech University
South Plains College
Institute of Environmental and Human Health, Texas Tech University
Texas Tech Health Science Center
Wayland Baptist University

A SPECIAL NOTE

With the blessings of his wife, Heather Whitlaw, the Department of Natural Resources Management and the Association of Natural Resource Scientists; 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 2016 would not have been possible.

TTU ADMINISTRATORS & DEPARTMENT OF BIOLOGICAL SCIENCES STAFF

Robert Duncan - Chancellor, TTU
John Opperman- Interim President, TTU
Lawrence Schovanec- Provost and Senior Vice President, TTU
Robert Duncan- Vice President for Research, TTU
Mark Sheridan- Dean of Graduate School, TTU
Michael San Francisco- Dean of Honors College, TTU
Jeffrey Williams – Dean, College of Arts & Sciences, TTU
Clifford Fedler- Associate Dean of Graduate School, TTU
John Zak – Associate Dean of Research, TTU
Lou Densmore – Graduate Student Advisor, Biological Sciences, TTU
Ron Chesser – Chair, Biological Sciences, TTU
Lauren Gollahon – Associate Professor, Biological Sciences, TTU
Mark Wallace – Chair, Natural Resources Management, TTU
Richard E. Zartman – Chair, Plant & Soil Sciences, TTU
Todd Anderson – Chair, The Institute of Environmental and Human Health, TTU
Cameron Saffell- Museum of Texas Tech University
Julie S. Isom- Associate Director, TTU/HHMI (CISER)
Lanita Ladd – Business Manager, Biological Sciences, TTU
Carol Espinosa – Senior Business Assistant, Biological Sciences, TTU
Charles Barnes – Unit Manager, Biology Building, TTU
Vina Khan – Specialist II, Dept. of Biological Sciences, TTU
Kunyu Li – IT Support, Biological Sciences, TTU
Jennifer Smith – Unit Manager, Biology Greenhouse, TTU
Pat Moore – Senior Office Assistant, Biological Sciences, TTU
Jacqueline Miralles-Salazar – Senior Technician, Biological Sciences, TTU
Lisa Torres – Lead Account Processor, Biological Sciences, TTU
Janie Vasquez – Sr. Business Assistant, Biological Sciences, TTU

Judges

Rhonda Boros – Biological Sciences, TTU
T. J. Boyle – Biological Sciences, McMurry University
Robert Bradley – Biological Sciences, TTU
Joel Brant - Biological Sciences, McMurry University
Christopher Brochu – Earth and Environmental, University of Iowa
José González-Maya - BioCAT Colombia, Sierra to Sea Institute
Lou Densmore - Biological Sciences, TTU
Arun Ghosh - Biological Sciences, West Texas A&M University
Kerry Griffis-Kyle - Natural Resources Management, TTU
Ruth Serra-Moreno - Biological Sciences, TTU
Stephen Karaganis - Biological Sciences, West Texas A&M University
Wendi Wolfram - Hardin-Simmons University

Anna Gibson - Department of Environmental Toxicology, TTU
Julie Parlos - Biological Sciences, TTU
Stephanie Lockwood - Department of Biological Sciences, TTU
Nicky Ladkin - Museum of Texas Tech University
Caleb Phillips - Biological Sciences, TTU
Brandon A. Gross – Biological Sciences, TTU
Daniela Pereira-Derderian - Biological Sciences, Wayland Baptist University
Neal Platt – Biological Sciences, TTU
Megan Keith - Biological Sciences, South Plains College
Michael Dini - Biological Sciences, TTU

Moderators

Nicté Ordóñez-Garza – Biological Sciences, TTU
Kayla Bounds - Biological Sciences, TTU/TTUHSC
Christopher Dunn - Biological Sciences, TTU
Gage Rowden - Biological Sciences, TTU
Taylor Soniat, Biological Sciences, TTU
Mark Lee - Biological Sciences, TTU
Caroline Schuster - Biological Sciences, TTU
Katherine Crocco - Biological Sciences, TTU

Thanks to the following businesses and individuals for their contributions:

Texas Tech Red Raider Club	Starbucks	McPherson Winery
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Red and Black Bookstore	Red Raider Club	Jovenal Arañes
Texas Tech University Press		



Texas Tech 7th Annual Biological Sciences Symposium

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ASSOCIATION OF BIOLOGISTS AT TEXAS TECH UNIVERSITY

FACULTY ADVISOR/DEPARTMENT OF BIOLOGICAL SCIENCES CHAIR

Dr. Ron Chesser

FACULTY CO-ADVISOR

Dr. Lou Densmore

Dr. Robert Bradley

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LOCAL COMMITTEE

Chairperson

Brandon A. Gross

Poster Competition & Public Relations

Kayla Bounds & Christopher Dunn

Registration

Laramie Lindsey

Silent Auction

Caroline Schuster

Abstract & Program Book

Emma K. Roberts

Brandon A. Gross

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Judge Solicitation

Brandon A. Gross

Award Banquet

Emma K. Roberts

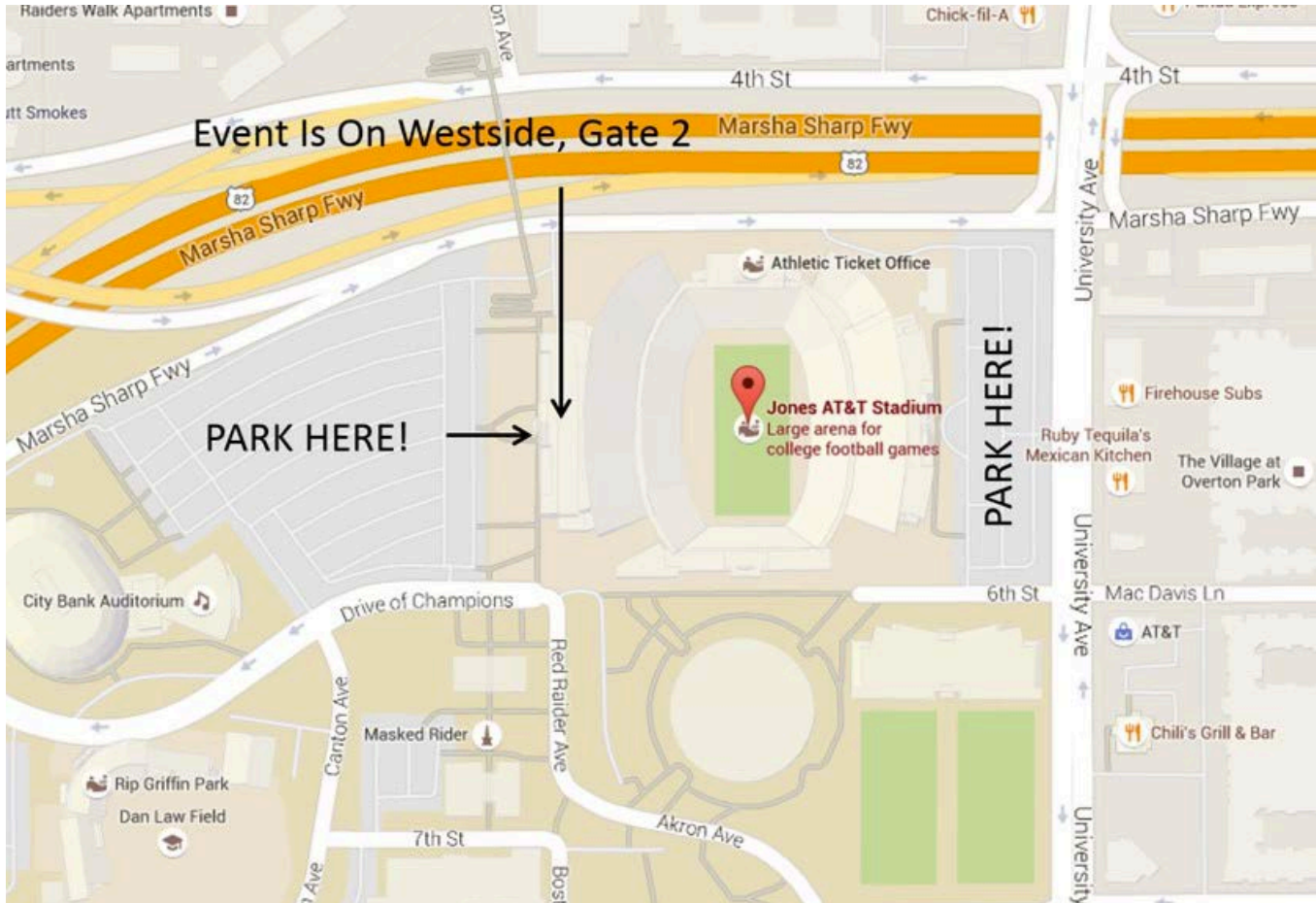
IT/Website

Kunyu Li

EVENT LOCATION - POSTER SESSION

April 1, 2016

Jones AT&T Stadium - Texas Tech University
2526 Mac Davis Lane
Lubbock, TX 79409
806-742-4496



LOCAL RESTAURANTS

SHORT DRIVING DISTANCE (within 2 miles)

Name	Address	Phone
Blue Sky Texas Burgers	3216 4 th St (Right Across from Museum)	(806) 368-0750
Jumbo Joe's Burgers	3310 4 th St (Right Across from Museum)	(806) 747-7900
Rosa's Cafe	4407 4 th St	(806) 785-5334
Sonic	4401 4 th St	(806) 771-0117
McDonald's	5201 4 th 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
Dion's	905 University Avenue	(806) 747-4800
Firehouse Subs	411 University Avenue	(806) 747-9600
Freebirds World Burrito	1201 University Avenue	(806) 741-0900
Jimmy John's	2413 Broadway Avenue	(806) 740-0002
Little Panda	1221 University Avenue	(806) 722-0888
Mesquites Sports Grill	2419 Broadway	(806) 744-9277
One Guy's Pizza	1101 University Avenue	(806) 747-1226
Raising Canes Chicken	907 University Avenue	(806) 744-8552
Rocky LaRues	2420 Broadway #B	(806) 747-6366
Ruby Tequila's	413 University Avenue	(806) 747-7829
Sazon Restaurant	1205 University Avenue	(806) 687-2572
Spanky's	811 University Avenue	(806) 744-5677
Starbucks	801 University Avenue	(806) 744-8234
Subway	1109 University Avenue	(806) 744-1535
Which Wich Sandwich	1021 University Avenue	(806) 472-9424

DRIVING DISTANCE (INSIDE LOOP 289)

Name	Address	Phone
Arby's	2422 19th Street, Suite 6037	(806) 744-2535
Burger King	2405 19th Street	(806) 762-2282
Fuzzy's Taco Shop	2102 Broadway	(806) 740-8226
Josie's Authentic Mexican Food	2332 19th Street	(806) 796-0192
McCallister's Deli	2415 19th Street	(806) 740-0022
McDonald's	2339 19th Street	(806) 747-5536
Quizno's	2312 19th Street #100	(806) 771-7827
Schlotzsky's Deli	3719 19th Street	(806) 793-5542
Skooner's Grill & Bar	1617 University Avenue	(806) 749-7625
Wendy's	2401 19th Street	(806) 741-0955

**7th Texas Tech Annual Biological Sciences Symposium
April 1-2, 2016**

**Venues:
Jones AT&T Stadium
Texas Tech University
2526 Mac Davis Lane
Lubbock, TX 79409**

**Department of Biological Sciences
Main & Flint Avenue
Texas Tech University**

PROGRAM AT A GLANCE

Friday, April 1st

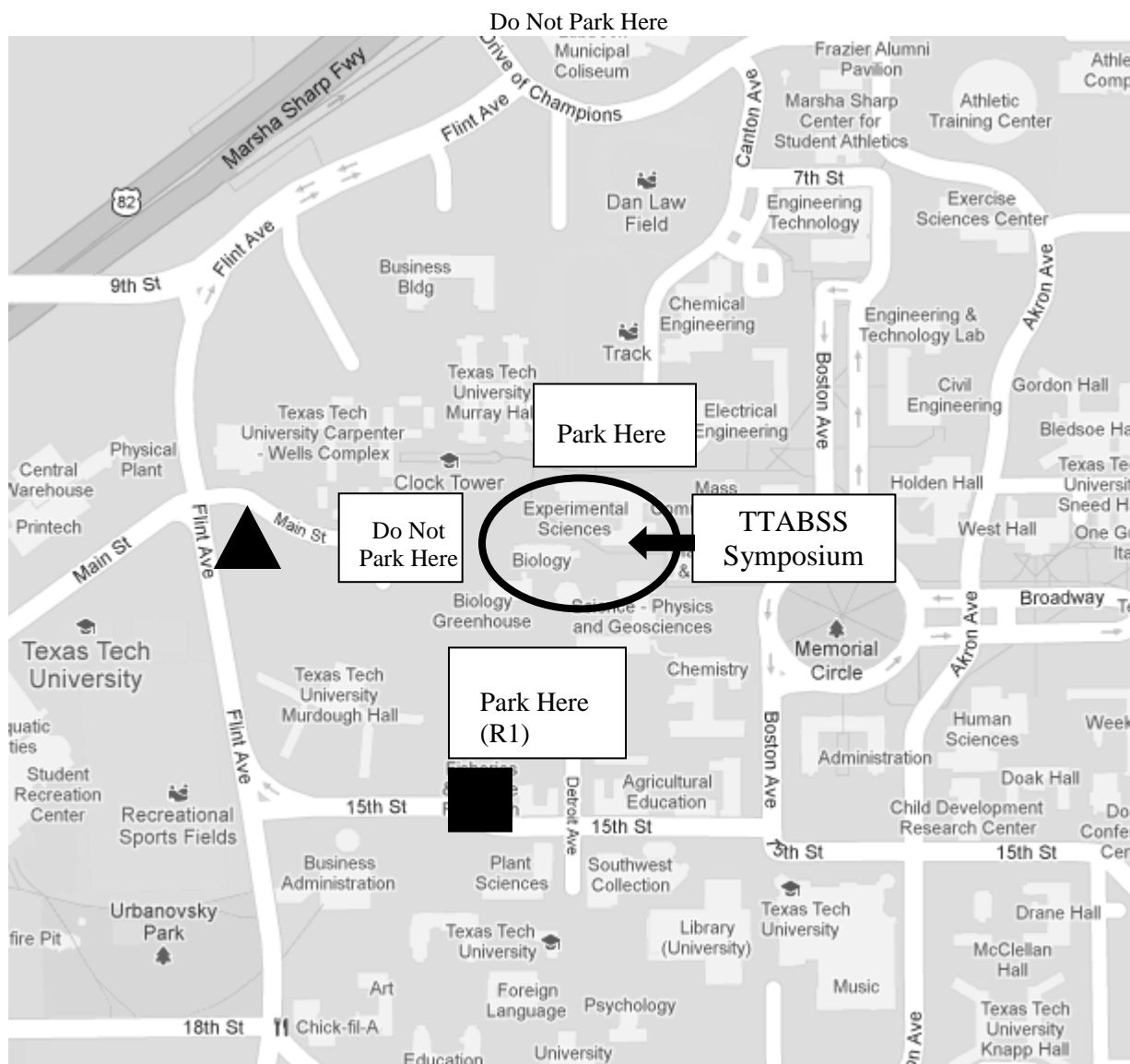
- 5:00 pm – 8:00 pm** Registration – Jones AT&T Stadium Club Level (West Side – Gate 2 Entrance)
- 6:00 pm – 6:10 pm** TTABSS 2015 kick off by Dr. Lou Densmore, Faculty Advisor
- 6:00 pm – 10:00 pm** Opening Mixer & Vendor Show – Jones AT&T Stadium Club Level
- 6:10 pm – 8:30 pm** Poster Session– Jones AT&T Stadium Club Level
- Poster Hanging 5:30 – 6:00 pm
Poster Judging 6:10 – 8:30 pm

Saturday, April 2nd

- 08:00 am – 11:30 am** Registration – Department of Biological Sciences Building
- 08:00 am – 08:45 am** Breakfast – Department of Biological Sciences Building
- 08:45 am – 08:55 am** Welcome – Dr. Ron Chesser, Chairman, Dept. of Biology, TTU
Department of Biological Sciences Building
- 09:00 am – 10:00 am** Oral Presentations – BIOL 106, BIOL 023, BIOL 101, ESB 120
Biological Sciences Building (BIOL)/Experimental Sciences
Building (ESB)
- 10:00 am – 10:15 am** Break – Department of Biological Sciences Building

10:15 am – 11:15 am	Oral Presentations – BIOL 106, BIOL 023, BIOL 101, ESB 120 Biological Sciences Building (BIOL)/Experimental Sciences Building (ESB)
11:15 am – 12:15 pm	Plenary talk – Dr. Christopher Brochu – BIOL 101 – Biological Sciences
12:15 pm – 01:45 pm	Lunch break (On Your Own)
01:45 pm – 02:15 pm	Oral Presentations – BIOL 106, BIOL 023, BIOL 101, ESB 120 - Biological Sciences Building (BIOL)/Experimental Sciences Building (ESB)
02:30 pm – 02:45 pm	Break – Biological Sciences Building
02:45 pm – 03:45 pm	Oral Presentations – BIOL 106, BIOL 023, BIOL 101, ESB 120 Biological Sciences Building (BIOL)/Experimental Sciences Building (ESB)
03:45 pm – 04:00 pm	Break - Biological Sciences Building
04:00 pm – 05:00 pm	Plenary talk – José F. González-Maya – BIOL 101 – Biological Sciences
07:00 pm – 09:00 pm	Jones AT&T Stadium Suite Level 1, West Side – Gate 2 Entrance Silent Auction
07:00pm – 10:00 pm	Awards Banquet – Jones AT&T Stadium Suite Level 1

BIOLOGICAL AND EXPERIMENTAL SCIENCES BUILDINGS – SYMPOSIUM APRIL 2, 2016



DETAILED SCHEDULE OF EVENTS
POSTER SESSION
FRIDAY, APRIL 1st

REGISTRATION 5:00–8:00 PM

Jones AT&T Stadium Club Level (West Side – Gate 2 Entrance)

OPENING MIXER & VENDOR SHOW 6:00–10:00 PM

Jones AT&T Stadium Club Level (West Side – Gate 2 Entrance)

TTABSS 2016 KICK OFF BY DR. LOU DENSMORE 6:00-6:10 PM

Jones AT&T Stadium Club Level (West Side – Gate 2 Entrance)

POSTER SESSION 6:10–8:30 PM

Jones AT&T Stadium Club Level (West Side – Gate 2 Entrance)

UNDERGRADUATE POSTERS

- 1. SURFACE-WATER DYNAMICS OF SALT PLAYAS IN TEXAS OVER A 27-YEAR SPAN**
Caroline L. Claassen^{1*}, Lucas J. Heintzman², Scott M. Starr², and Nancy E. McIntyre²
- 2. COMPONENTS OF EQUISETUM ARVENSE CYTOTOXIC TO CULTURED 4T1 MURINE BREAST CANCER CELLS**
Jake A. Brozek^{1*}, Sarah Kelly¹, Adam J. Reinhart¹, and Gary O. Gray¹
- 3. ESTABLISHING A CIRCADIAN MODEL OF GASTROINTESTINAL PHYSIOLOGY IN RODENTS**
Tyler R. Humphreys¹, Dario Pajic¹, Michael R. Stebbins^{1*}, and Stephen P. Karaganis¹
- 4. GENETIC PRESERVATION OF MUSEUM SPECIMENS FOR THE AMERICAN ALLIGATOR (*ALLIGATOR MISSISSIPPIENSIS*) FROM VARIOUS CLEANING METHODS**
Brandon A. Gross^{1,4}, Travis J. Stieb^{1*}, Robert D. Bradley¹, Ruth M. Elsey^{2,4}, Ray E. Willis³, and Llewellyn D. Densmore III^{1,4}
- 5. EFFECTS OF INDEPENDENCE CREEK INFLOW ON PECOS RIVER WATER QUALITY, TERRELL AND CROCKETT COUNTIES, TEXAS**
Greg L. Larson¹, Daniel K. Dalager^{1*}, and Jordan T. Middleton^{1*}
- 6. INFLUENCE OF SMOKE ON GERMINATION OF GRASSES IN NORTH AMERICA**
Ian G. Smith^{1*} and Robert Cox²
- 7. HABITAT USE BY LADDER-BACKED WOODPECKER (*PICOIDES SCALARIS*) IN THE CAPROCK CANYONLANDS IN FLOYD COUNTY, TEXAS**
Victoria K. Solis^{1*} and Andrew C. Kasner¹
- 8. OBSERVATIONS OF POTENTIAL SYMBIOTIC RELATIONSHIP BETWEEN FERAL HOGS (*SUS SCROFA*) AND RACCOONS (*PROCYON LOTOR*)**
Tracina Maiden^{1,2*}, Phillip Seiwert³, Stephanie McMillan-Randell², and Stephanie Lockwood¹
- 9. OVARIAN CANCER EARLY DETECTION: AN OVERVIEW OF BIOMARKERS AND DEVICES**
Brooke Walterscheid^{1,2*}, Maruzio Chiriva-Internati¹, and Jose Figueroa¹
- 10. PATTERNS OF GENETIC DIVERSIFICATION IN A WIDELY DISTRIBUTED SPECIES OF BAT, *MOLOSSUS MOLOSSUS*, BASED ON A NUCLEAR MARKER**
Kelsey B. Donckels^{1*}, Laramie L. Lindsey¹, Loren K. Ammerman², and Robert D. Bradley^{1,3}
- 11. NEST BOX USE AND PRODUCTIVITY OF AMERICAN KESTRELS ON THE HIGH PLAINS OF TEXAS**
Christopher K. Gulick^{1*} and Clint W. Boal²

12. FUNCTIONAL AMYLOIDS: A LINK BETWEEN YEAST MATING AND MAMMALIAN FERTILIZATION

Gage R. Rowden^{1*} and Gail A. Cornwall¹

13. SALT ADDICTION IN MALE SATISFIED ATHLETE MAY BE EXPLAINED BY THE PREPARATION OF HOME-MADE FOOD LESS SALTY THAN RESTAURANT AND PROCESSED FOOD

Sharon M. Robinson^{1*}, Whitney M. Phillips^{1*}, and Daniela T.B. Pereira-Derderian¹

14. PHYLOGENY OF BATS OF GENUS *MONOPHYLLUS*. A STUDY OF GENETIC AND MORPHOLOGICAL DIVERGENCE BASED ON MITOCHONDRIAL CYTOCHROME-*b* GENE

Marilyn Mathew^{1*}, Dayana P. Bolzan¹, Julie A. Parlos¹, James Q. Francis¹, and Robert J. Baker¹

GRADUATE POSTERS

15. USING REMOTELY SENSED IMAGERY TO DOCUMENT HOW LAND USE DRIVES TURBIDITY OF PLAYA WATERS IN TEXAS

Scott M. Starr^{1*}, Lucas J. Heintzman¹, Kevin R. Mulligan², Lucia S. Barbato², and Nancy E. McIntyre¹

16. INVESTIGATING THE EFFECTS OF ESTROGEN AND TRICLOSAN MIXTURE ON SOIL MICROBIAL DIVERSITY

Ezinne Osuji^{1*} and Deborah Carr¹

17. MICROSCOPIC ASSESSMENT OF INDOOR AIR QUALITY (IAQ) USING AHPCO NANO-TECHNOLOGY AND AIR-O-CELL SAMPLERS

Chandini Revanna^{1,2*}, Mahin Bastamian¹, Mitsy Veloz¹, Jeff Bennert³, Jim Rogers¹ and Nabarun Ghosh¹

18. EVALUATING MODELS OF NUTRITIONAL CARRYING CAPACITY FOR WINTERING MOOSE ON THE COPPER RIVER DELTA, AK

Sharon E. Smythe^{1,2*}, Dana M. Sanchez¹, and Clinton W. Epps¹

19. QUALITATIVE AND QUANTITATIVE DRUG RESIDUE ANALYSES: FLORFENICOL IN WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) AND SUPERMARKET MEAT BY LIQUID CHROMATOGRAPHY TANDEM-MASS SPECTROMETRY

Shanoy C Anderson^{1*}, Seenivasan Subbiah¹, Angella Gentles¹, Galen Austin¹, Paul Stonum², Tiffanie A. Brooks^{2,3}, Chance Brooks³, Ernest E. Smith¹

20. SPATIAL AND TEMPORAL VARIATION IN MYCORRHIZAL ASSOCIATIONS IN A RARE NORTH AMERICAN ORCHID

Pablo A. Tovar-Ballen^{1*}

21. IDENTIFYING SURROGATE BIOMARKERS FOR OPHTHALMIC DISEASE IN NORTHERN BOBWHITE QUAIL (*COLINUS VIRGINIANUS*) INFECTED BY *OXYSPIRURA PETROWI*

Jordan W Hunter^{1*} and Steven M Presley¹

22. INFLUENCE OF NPY ON PREY CAPTURE AND PREDATOR AVOIDANCE RESPONSE IN THE AFRICAN CLAWED FROG, *XENOPUS LAEVIS*

Ranakul Islam^{1*} and James A. Carr¹

23. MOLECULAR PHYLOGENETICS OF THE *PEROMYSCUS MEXICANUS* SPECIES GROUP

Taylor J. Soniat^{1*}, Nicté Ordóñez-Garza¹, and Robert D. Bradley^{1,2}

**24. MOSQUITO SURVEILLANCE FOR WEST NILE VIRUS FROM 2012 TO 2015 IN LUBBOCK, TEXAS,
UNITED STATES**

Steven T. Peper^{1*}, Daniel E. Dawson¹, Jordan Hunter¹, Grant E. Sorensen¹, Francis Loko¹, Sadia Almas¹, Kevan Athanasiou¹, Anna G. Gibson¹,
and Steven M. Presley¹

**25. PROPOSED RESEARCH: FUNCTIONAL DIVERSITY OF AQUATIC COMMUNITIES AT TRIBUTARY
CONFLUENCES OF THE PECOS RIVER**

Kelbi D. Delaune^{1*} and Allison A. Pease¹

26. PROTEOMIC STUDY OF POLYSTYRENE DEGRADATION BY MEALWORMS

Anisha Navlekar^{1*} and Deborah Carr¹

DETAILED SCHEDULE OF EVENTS

Saturday, APRIL 2nd

REGISTRATION 8:00-11:30 AM

Department of Biological Sciences Main Lobby

BREAKFAST 8:00-8:45 AM

Department of Biological Sciences Main Lobby

WELCOME BY DR. RON CHESSER 8:45-8:55 AM

Department of Biological Sciences Main Lobby

ORAL PRESENTATIONS 9:00-10:00 AM

Department of Biological Sciences 106, 101, 023, and Experimental Sciences 120

BREAK

Department of Biological Sciences Lobby

ORAL PRESENTATIONS 10:15-11:15 AM

Department of Biological Sciences 106, 101, 023, and Experimental Sciences 120

PLENARY TALK #1: 11:15-12:15 PM

DR. CHRISTOPHER BROCHU

Biology 101

LUNCH (ON YOUR OWN) 12:15-1:45 PM

ORAL PRESENTATIONS 1:45-2:15 PM

Department of Biological Sciences 106, 101, 023, and Experimental Sciences 120

BREAK 2:30-2:45 PM

Department of Biological Sciences Lobby

ORAL PRESENTATIONS 2:45-3:45 PM

Department of Biological Sciences 106, 101, 023, and Experimental Sciences 120

BREAK 3:45-4:00 PM

Department of Biological Sciences Lobby

PLENARY TALK #2: 4:00-5:00 PM

DR. JOSÉ GONZÁLEZ-MAYA

Biology 101

SILENT AUCTION 7:00-9:00 PM

Jones AT&T Stadium Suite Level 1, West Side - Gate 2 Entrance

AWARDS BANQUET 7:00-10:00 PM

Jones AT&T Stadium Suite Level 1, West Side - Gate 2 Entrance

DATE PRINTED: 02/12/13 DWG LOCATION: I:\Shared\Biology - 271\CAD Floor Plan\Biology.dwg



FIRST FLOOR PLAN

SCALE: 1" = 40'-0"



PROJECT MANAGER:

PROJECT#:

DATE: 01/12/10

TEXAS TECH UNIVERSITY

BIOLOGY
FLOOR PLAN

Physical Plant Engineering Services

Physical Plant Building - Suite 3
 Texas Tech University
 (P) (806) 742-2761
 (F) (806) 742-0147

Mailing Address:
 PO BOX 43142
 LUBBOCK, TX 79409
 on campus: M53142

REVISIONS:

SHEET
A-3
OF 09

	UNDERGRADUATE (BIOL 101)	NATURAL RESOURCES MANAGEMENT (ESB 120)	CELL & MOLECULAR BIOLOGY (BIOL 106)	MICROBIOLOGY (BIOL 023)
9:00 AM	AN ANALYSIS OF THE IMPACT OF BIOMETEOROLOGY ON GREY WOLF (<i>CANIS LUPUS</i>) AND RED WOLF (<i>CANIS RUFUS</i>) SCENT-MARKING BEHAVIOR (27) Hannah M. Jones ^{1*} and Wendi K. Wolfram ¹	ELEVATED HUMIDITY AND BUNCHING DECREASE DESICCATION RATE AND INCREASE SURVIVAL OF AIR-EXPOSED FRAGMENTS OF THE AQUATIC INVASIVE PLANT (<i>HYDRILLA VERTICILLATA</i>) (54) Sasha D. Soto ^{1*} and Matthew A. Barnes ¹	MOLECULAR DETERMINANTS FOR HYSTERESIS IN POTASSIUM CHANNELS: A SPECTROSCOPIC AND CRYSTALLOGRAPHIC APPROACH (34) Cholpon Tilegenova ^{1*} , D. Marien Cortes ¹ , and Luis G. Cuello ¹	BCA2 PREVENTS THE NUCLEAR TRANSLOCATION OF NF- κ B, RESTRICTING HIV-1 TRANSCRIPTION (50) Marta Colomer-Lluch ^{1*} and Ruth Serra-Moreno ¹
9:15 AM	SPATIAL BIAS IN BAT SAMPLING LOCALITIES IS INDEPENDENT OF FAMILY AND ECOLOGICAL GROUPING (28) Rebecca Smith ^{1*} , Marina Fisher-Phelps ¹ , and Tigga Kingston ¹	THE INFLUENCE OF WEATHER PARAMETERS ON LESSER PRAIRIE-CHICKEN RANGEWIDE NEST SURVIVAL (55) Alixandra J. Godar ^{1*} , Blake A. Grisham ¹ , Cody Griffin ¹ , Sarah Fritts ¹ , Clint W. Boal ² , David A. Haukos ³ , Jim C. Pitman ⁴ , Christian A. Hagen ⁵ , and Michael A. Patten ⁶	OVEREXPRESSING MULTIPLE GENES IN ARABIDOPSIS ENHANCES PLANT RESISTANCE TO MULTIPLE STRESSES (35) Nardana Esmaeili ^{1*} , Li Sun ¹ , Hong Zhang ¹	INTERACTION OF THE FUNGUS <i>BATRACHOCHYTRIUM DENDROBATIDIS</i> WITH <i>STAPHYLOCOCCUS AUREUS</i> AND <i>ESCHERICHIA COLI</i> (51) Amanda M. Starr ^{1*} , Susan San Francisco ² , John Zak ¹ , Abdul Hamood ³ , Louise Rollins-Smith ⁴ , and Michael J. San Francisco ¹
9:30 AM	SALT ADDICTION IS MEDIATED BY ENCEPHALIC VASOPRESSIN (33) Mayra H. Gonzales ^{1*} , Jake A. Brozek ¹ , Janlyn Jerome ¹ , Chanda J. Smith ¹ , Whitney Phillips ¹ , Sharon M. Robinson ¹ , and Daniela T.B. Pereira-Derderian ¹	ASSOCIATION BETWEEN SALINITY AND GROWTH OF GOLDEN ALGA IN THE LABORATORY – IS ENVIRONMENTAL SALINITY A BARRIER TO ITS EXPANSION INTO COASTAL HABITATS? (56) Rakib H. Rashe ^{1*} and Reynaldo Patiño ²	TRANSPOSABLE ELEMENT ANNOTATION USING <i>DE NOVO</i> BASE REPEAT IDENTIFICATION (36) Laura Blanco-Berdugo ¹ , Roy N. Platt II ¹ , and David Ray ¹	EFFECTS OF TWO POLYPHENOLS ON THE GUT MICROBIOME AND ASSOCIATED WEIGHT GAIN IN MICE (52) Jeremy E. Wilkinson ^{1,2*} , J. Delton Hanson ² , Caleb D. Phillips ³ , Mike R. Wages ¹ , Eric J. Rees ² , and Greg D. Mayer ¹
9:45 AM	USING GENOMICS AND BIOINFORMATICS TO DETERMINE THE ORIGIN AND PHYLOGENETIC SIGNIFICANCE OF THE ZONADHESIN GENE IN RODENTIA (30) Emma K. Roberts ¹ , Whitney N. Watson ^{1*} , Daniel M. Hardy ² , and Robert D. Bradley ^{1,3}	AVIAN RESPONSE TO BRUSH MANAGEMENT ON THE WELDER WILDLIFE REFUGE (57) Olivia A. Kost ^{1*} , Clint W. Boal ² , and Terry L. Blankenship ³	NOVEL METHOD FOR TRANSPOSABLE ELEMENT ANNOTATION ACROSS MULTIPLE TAXA (37) Austin B. Osmanski ^{1*} , Roy N. Platt ¹ , and David A. Ray ¹	INFLUENCE OF DAILY SOIL TEMPERATURE RANGE ON MICROBIAL COMMUNITY DYNAMICS IN DRYLAND AGRICULTURE (53) Diana L Vargas-Gutierrez ^{1*} , John C. Zak ² , and Veronica Acosta-Martinez ³
10:00 AM	BREAK			

	UNDERGRADUATE (BIOL 101)	TOXICOLOGY (ESB 120)	ECOLOGY (BIOL 106)	PROPOSALS (BIOL 023)
10:15 AM	WINTER HABITAT USE OF LONGSPURS (<i>CALCARIUS SPP.</i>) AND OTHER WINTER GRASSLAND BIRDS IN HALE AND FLOYD COUNTY, TEXAS (31) Lauryn Bruggink ^{1*} , Andrew Kasner ² , and William Hahn ³	ANALYSIS OF LEAD IN AMERICAN WOODCOCK (<i>SCOLOPAX MINOR</i>) USING INDUCTIVELY-COUPLED PLASMA MASS SPECTROMETRY (ICP-MS) (66) Amanda D. French ^{1*} , Daniel S. Sullins ² , Warren C. Conway ³ , and David M. Klein ¹	PAST AGRICULTURAL LAND USE AND PRESENT-DAY FIRE REGIMES CAN INTERACT TO DETERMINE THE NATURE OF SEED PREDATION (38) John D. Stuhler ^{1*} and John L. Orrock ²	THE EFFECT OF BIODIESEL VS. PETRODIESEL ON SOIL MICROBIAL COMMUNITY-LEVEL PHYSIOLOGICAL PROFILING, DIVERSITY, FUNCTION AND PLANT GROWTH (58) Meijun Dong ^{1*} and Deborah L. Carr ¹
10:30 AM	THE EFFECTS OF SOCIAL INTERACTION AND SALT ADDICTION ON RENAL GENE EXPRESSION IN RATS (32) Catherine Wiechmann ^{1*} , Mayra Gonzales-Herrera ¹ , Jake A Brozek ¹ , Ashley M Rivera ¹ , Trevor Burrow ^{1,2} , Katie M Bennet ² , Erica C Hendrix ² , and Daniela Pereira-Derderian ¹	HYPOXIA SENSITIVITY AMONG TEXAS FISH AND INVERTEBRATES: THE EFFECT OF CENSORED DATA ON PROTECTIVE BENCHMARK VALUES (67) Jacob R. Carrick ^{1*} , Todd A. Anderson ¹ , and Jonathan D. Maul ¹	SMALL MAMMAL ABUNDANCE NOT DRIVEN BY LIANA PRESENCE IN A PANAMANIAN FOREST (39) Michaela K. Halsey ^{1-4*} , Thomas D. Lambert ¹ , Scott A. Mangan ² , Stefan A. Schnitzer ³	PHENOTYPIC FLEXIBILITY AND ENERGETIC DEMAND: INSECTIVOROUS BATS DURING THE SUMMER REPRODUCTIVE PERIOD (59) Amie S. Sommers ^{1*} and Liam P. McGuire ¹
10:45 AM	FISH BITE PREVALENCE AND YELLOW-BAND DISEASE ON <i>MONTASTRAEA</i> AND <i>ORBICELLA</i> COMPLEXES IN TOATAN, HONDURAS (29) Kara L. Schmidt ^{1,2*} , Traesha R. Robertson ¹ , Stephanie A. Lockwood ² , Donna E. Hamilton ³ , and Stephanie C. Randell ¹	SUBCELLULAR COMPARTMENTALIZATION OF CADMIUM IN THE FRESHWATER SNAIL <i>LYMNAEA STAGNALIS</i> (68) Evelyn G. Reátegui-Zirena ^{1*} , Amanda D. French ¹ , David M. Klein ¹ , and Christopher J. Salice ²	SPATIAL NETWORK APPROACHES TO CHARACTERIZE METACOMMUNITY STRUCTURE OF NEOTROPICAL BATS IN COLOMBIA (40) Cristina Rios-Blanco ^{1*} and Richard D. Stevens ¹	RESOLVING THE PHYLOGEOGRAPHY AND PHYLOGENETIC VARIATION PRESENT IN <i>PEROMYSCUS MANICULATUS</i> USING MOLECULAR SYSTEMATICS AND NEXT GENERATION SEQUENCING (60) Jack Q. Francis ^{1*} , Caleb D. Phillips ^{1,2} , and Robert D. Bradley ^{1,2}
11:00 AM		INCIDENCE OF VETERINARY PHARMACEUTICALS IN WEST TEXAS PLAYA WETLANDS (69) Melissa A. Sandoz ^{1*} , Loren L. Hensley ¹ , Kimberly J. Wooten ¹ , and Philip N. Smith ¹	SPATIAL ECOLOGY OF THE AMERICAN CROCODILE ON COIBA ISLAND, PANAMA (41) Sergio A. Balaguera-Reina ^{1*} , Miryam Venegas-Anaya ² , Andrés Sánchez ³ , Italo Arbelaez ⁴ , Harilaos A. Lessios ² , and Llewellyn D. Densmore III ¹	INCORPORATING A HETEROTHERMIC CONTINUUM INTO OPTICAL MIGRATION THEORY: RE-CONSIDERING COSTS, CURRENCIES, AND CONSTRAINTS (61) Jeff Clerc ^{1*} and Liam P. McGuire ¹
11:15 AM	PLENARY TALK 1: "The giant horned crocodiles that ate our ancestors: crocodylian diversity, phylogeny, and response to climate change in the Neogene of East Africa" By: Dr. Christopher Brochu			
12:15 PM	LUNCH BREAK 12:15-1:45 PM			

	EVOLUTIONARY BIOLOGY (BIOL 101)	TOXICOLOGY (ESB 120)	ECOLOGY (BIOL 106)	PROPOSALS (BIOL 023)
1:45 PM	<p>THE UTILITY OF ZONADHESIN IN EXAMINING A POTENTIAL REPRODUCTIVE ISOLATION MECHANISM IN RODENTS (44) Emma K. Roberts^{1*}, Daniel M. Hardy², and Robert D. Bradley^{1,3}</p>	<p>BIOACCUMULATION, STRESS, AND SWIMMING IMPAIRMENT IN <i>DAPHNIA MAGNA</i> EXPOSED TO MULTI-WALL CARBON NANOTUBES (70) Amanda M. Cano^{1*}, Jonathan D. Maul¹, Micah J. Green³, Mohammad Saed³, and Jaclyn E. Cañas-Carrell¹</p>	<p>SPATIAL AND TEMPORAL VARIATION IN DUCT INVESTMENTS FOR FIVE PINES (<i>Pinus</i>) FROM WEST TEXAS MOUNTAINS (42) Erik M. Lindberg^{1*}, Dylan W. Schwilk¹, and Scott Ferrenberg²</p>	<p>THE POWER OF ONE: INTRASPECIFIC VARIATION IN BAT POLLINATION SERVICES TO BAOBABS IN SOUTH AFRICA (62) Macy A. Madden^{1*} and Tigga Kingston¹</p>
2:00 PM	<p>HAMILTON'S RULE UNRAVELED: ADDING STOCHASTICITY AND NON-ADDITIVITY ARE EVOLUTIONARY GAME CHANGERS (45) Sarah E. Fumagalli^{1*} and Sean H. Rice¹</p>	<p>MERCURY CONTAMINATION IN BATS FROM THE CENTRAL UNITED STATES (71) Jennifer M. Korstian^{1,2*}, Matthew M. Chumchal¹, and Amanda M. Hale¹</p>	<p>DIET OF PREGNANT AND LACTATING SEBA'S SHORT-TAILED FRUIT BATS (<i>CAROLLIA PERSPICILLATA</i>) (43) Erin E. Bohlender^{1*}, Jairo Pérez-Torres², Natalia Borray², and Richard D. Stevens^{1,3}</p>	<p>EXPERIMENTAL INVESTIGATION OF FLAMMABILITY IN C3 AND C4 GRASS SPECIES IN KIOWA NATIONAL GRASSLAND (63) Xiulin Gao^{1*} and Dylan W. Schwilk¹</p>
2:15 PM	<p>A PHYLOGENETIC ANALYSIS OF FOURTEEN RODENT MITOCHONDRIAL GENOMES (46) Kevin A.M. Sullivan^{1*}, Roy N. Platt¹, Robert D. Bradley¹, and David A. Ray¹</p>			<p>SPECIATION PROCESSES WITHIN SIGMODONTINE RODENTS: THE GENUS <i>AKODON</i> AS A FIRST APPROXIMATION (64) Daniela Arenas-Viveros^{1*}</p>
2:30 PM	BREAK			
2:45 PM	<p>EVOLUTIONARY BIOLOGY (BIOL 101)</p>			<p>PROPOSALS (BIOL 023)</p>
3:00 PM	<p>PHYLOGENETIC RELATIONSHIPS BETWEEN THE MEMBERS OF THE GENUS <i>NOTROPIS</i> (FAMILY CYPRINIDAE) USING CYTOCHROME B AND CYTOCHROME C OXIDASE SUBUNIT I (47) Ryan R. Vazquez^{1*} and Gene R. Wilde¹</p>			<p>THE RANK/RANKL/OPG AXIS IN OSSEOUSLY METASTATIC BREAST CANCER (65) Caroline Schuster^{1*} and Lauren Gollahon¹</p>
3:15 PM	<p>RECENT POPULATION EXPANSION IN <i>CALOMYS TENER</i> (RODENTIA: SIGMODONTINAE) (48) Narayan P. Kandel^{1*} and J. Salazar-Bravo¹</p>			
3:30 PM	<p>ADDRESSING THE ADAPTIVE RADIATION IN <i>PEROMYSCUS</i> USING TRANSCRIPTOME DATA (49) Laramie L. Lindsey^{1*}, Roy N. Platt¹, Caleb D. Phillips^{1,2}, David A. Ray¹, and Robert D. Bradley^{1,2}</p>			
3:45 PM	BREAK			
4:00 PM	<p>PLENARY TALK 2: "Biodiversity conservation in the tropics: from global to local, a view from the south" By: José F. González-Maya</p>			

ABSTRACTS

POSTER (UNDERGRADUATE)

1. SURFACE-WATER DYNAMICS OF SALT PLAYAS IN TEXAS OVER A 27-YEAR SPAN

Caroline L. Claassen^{1*}, Lucas J. Heintzman², Scott M. Starr², and Nancy E. McIntyre²

¹Department of Mathematics and Statistics, Texas Tech University, Lubbock, TX 79409

²Department of Biological Sciences, Texas Tech University, Lubbock, TX 79409

Seasonal and interannual surface-water dynamics over the past 27 years in the 39 salt playas (salinas) occurring within a ~149,810 km² portion of Texas were examined. These groundwater- and precipitation-fed wetlands are regionally unique habitats with high salt concentrations and halophytic biota that may be vulnerable to changes from groundwater extraction for agriculture. Landsat imagery from four satellite scenes was used to detect water within the 39 salina basins over seven dates (comparing summer and winter, representing periods of high and low groundwater demand, respectively) from 1986-2013, comprising all of the cloud-free data available simultaneously for all four scenes. During this span for the study area, the saturated thickness of the underlying Ogallala Aquifer decreased by ~0.19%, and the amounts of total and irrigated cropland increased in area. There was individual variation in surface water area per salina, with two salina basins never holding water at all during the duration of the study. Most salinas went dry at least once (although not simultaneously or in the same region), slightly more frequently during the summer than in winter. These results suggest that these wetlands are being impacted by human changes to the landscape. Human activities are diminishing groundwater inputs to these wetlands, effectively creating novel wetlands that are now primarily or only supplied by precipitation and no longer by groundwater, thereby potentially altering water chemistry and biota. These novel wetlands no longer have the same hydrological or ecological dynamics and may exacerbate vulnerability to projected climate change.

2. COMPONENTS OF *EQUISETUM ARVENSE* CYTOTOXIC TO CULTURED 4T1 MURINE BREAST CANCER CELLS

Jake A. Brozek^{1*}, Sarah Kelly¹, Adam J. Reinhart¹, and Gary O. Gray¹

¹Department of Chemistry, Wayland Baptist University, Plainview, Texas 79072

The herb *Equisetum arvense* (horsetail) is commonly used in herbal remedies in cultures around the world. Strong antioxidant and anti-inflammatory effects have reported. Horsetail, however, has been scarcely explored as a potential anti-cancer treatment. It has shown promising results in the treatment of leukemia (Chaadaeva *et al.*). Previous studies in our lab have shown that extracts from several common herbs with anti-inflammatory activity have cellular components cytotoxic to cultured 4T1 murine breast cancer cells. In this study, extracts of horsetail were prepared by refluxing powered *Equisetum arvense* in ethanol (Soxhlet extraction, 1.5 hours). The ethanolic extracts were concentrated and then fractioned via Sephadex LH20 chromatography (50% ethanol mobile phase; eluate monitored 280 nm). The resulting fractions were assayed for cytotoxicity to cultured 4T1 cells, and the fractions pooled based upon cytotoxicity. Pooled fractions with strong cytotoxicity were further separated via HPLC (C₁₈, 75-100% methanol gradient over 40 min.). The HPLC peaks were collected, concentrated and again tested for cytotoxicity. All six collected peaks showed significant cytotoxicity (p<0.05) compared to the controls. Analysis of the physicochemical properties of the six collected peaks is ongoing.

3. ESTABLISHING A CIRCADIAN MODEL OF GASTROINTESTINAL PHYSIOLOGY IN RODENTS

Tyler R. Humphreys¹, Dario Pajic¹, Michael R. Stebbins^{1*}, and Stephen P. Karaganis¹

¹Department of Life, Earth, and Environmental Sciences, West Texas A&M University, Canyon, Texas 79016

The gastrointestinal (GI) tracts of humans and animals are regulated over a period of 24 hours. Recently, food entrainable circadian oscillators have been discovered throughout the gut wall of rodents. Circadian clocks within layers of the GI tract presumably coordinate their outputs to regulate rhythmic processes, such as gut motility and endocrine signaling. Here we present work demonstrating establishment of an animal model and analytical methods to study circadian regulation of gastric motility, hormone signaling and gene expression in the intestine of the mouse. Our preliminary results include a pilot study in which we compared the gastric motility phase shift of a restricted feeding (RF) paradigm against controls fed *ad libitum*. We used cosinor analysis to test for statistically significant rhythmicity and to quantify circadian parameters such as acrophase, amplitude, and mesor. We present both pilot and preliminary data from a follow up study in which tissue samples will be analyzed for 1) expression of canonical clock genes presumed to comprise the core oscillators; and 2) serotonin levels, an endocrine output of the GI circadian clock. In addition to the *in vivo* studies, we present preliminary work toward developing a model to study the circadian clocks of intestinal crypts *in vitro*. This model is essential for assessing the roles of circadian oscillators independent of neuroendocrine connections, which obfuscate their study *in vivo*. Developing these models will improve understanding of the physiology of the gut, which may improve understanding of human diseases linked to circadian dysregulation, including IBS and colon cancer.

4. GENETIC PRESERVATION OF MUSEUM SPECIMENS FOR THE AMERICAN ALLIGATOR (*ALLIGATOR MISSISSIPPIENSIS*) FROM VARIOUS CLEANING METHODS

Brandon A. Gross^{1,4}, Travis J. Stieb^{1*}, Robert D. Bradley¹, Ruth M. Elsey^{2,4}, Ray E. Willis³, and Llewellyn D. Densmore III^{1,4}

¹Texas Tech University, Lubbock, Texas, USA,

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³Midwestern State University, Wichita Falls, Texas, USA

⁴IUCN/SSC/Crocodile Specialist Group

Museum collections are vital to preserving research specimens for long term studies. Scientists travel around the globe to utilize collections and the DNA that museum specimen hold. Due to this, specimen preservation is paramount to future studies in multiple fields, this project will deduce which preservation and cleaning method is the most efficient. This project will use three distinct methods (burial method, dermestid beetle, and maceration) to clean and preserve pre-juvenile and adult American alligator (*Alligator mississippiensis*) skeletons. DNA will then be extracted from the skeletons (destructive and minimally-destructive extraction methods) to test which method of cleaning yields the best DNA results. With this information, museum curators, private collectors, and scientists can clean their specimens in the most efficient way for DNA removal and preservation. This will allow future scientists to be able to obtain the highest quality bone DNA while also causing the least amount of damage to the specimen. With this knowledge we can increase, as well as preserve, specimens for long term studies on climate change, animal habitats, population trends, and biodiversity. The findings of this project will also encourage curators to open up valuable specimens for DNA extraction by providing the cost and benefit frame of damage to DNA to justify the in-depth study of the specimen.

5. EFFECTS OF INDEPENDENCE CREEK INFLOW ON PECOS RIVER WATER QUALITY, TERRELL AND CROCKETT COUNTIES, TEXAS

Greg L. Larson¹, Daniel K. Dalager^{1*}, and Jordan T. Middleton^{1*}

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Water quality data were obtained from two Pecos River sites located on the Chandler Ranch upstream and downstream of the Independence Creek confluence in Terrell County, Texas. The data included site visits between May 6th, 2015 and February 27th, 2016 (7 visits) for field data, including 3 visits to collect samples for lab analyses. Additionally, historical water quality data were obtained at these Chandler Ranch sites, as well as established Pecos River monitoring sites (2) near Sheffield (upstream) and the Lower Pecos (2 sites) near Val Verde County (downstream) to assess regional trends in water quality.

Historical data for Independence Creek were also collected. Data collected during the site visits of this study, and from historical data at these two Pecos River Chandler Ranch sites, revealed through statistical t-test analyses, that Independence Creek significantly dilutes the Pecos River at the Chandler Ranch. Furthermore, from a regional standpoint, the river enters the Sheffield area under the saline influence of the Cenozoic Pecos Alluvium Aquifer where freshwater inflow from spring systems of the Edwards Trinity Plateau Aquifer, most notably Independence Creek, significantly dilute the Pecos River, enhancing its water quality.

6. INFLUENCE OF SMOKE ON GERMINATION OF GRASSES IN NORTH AMERICA

Ian G. Smith^{1*} and Dr. Robert Cox²

¹Department of Natural Resource Management, Texas Tech University, Lubbock, Texas 79409

²Department of Natural Resource Management, Texas Tech University, Lubbock, Texas 79409

Smoke exposure is known to influence germination of a wide variety of species. However, the influence of smoke on germination of grasses is poorly studied. In order to investigate the influence of smoke on grasses native to North America, we tested six species for their germination response to smoke exposure. Species tested were: sideoats grama (*Bouteloua curtipendula*), blue grama (*Bouteloua gracilis*), Thurber's needlegrass (*Acnatherum thurberianum*), bluebunch wheatgrass (*Pseudoroegneria spicata*), and Sandberg's bluegrass (*Poa secunda*). Seeds were treated with one of four dilutions of smoke-water and distilled water: 0:1 (no smoke), 1:10 (high smoke), 1:100 (medium smoke), and 1:1000 (low smoke). Seeds were soaked in the smoke treatment for 20 hrs, then placed in a germination chamber programmed to 35 degrees Celsius on the high end and 20 degrees Celsius on the low end, with the lights programmed to cycle every 12 hrs per day. We then monitored the seeds daily for germination. We found that germination was inhibited in some species and promoted in others. For example, germination of bluebunch wheatgrass was stimulated at the medium smoke level, while Thurber's needlegrass was non-responsive to all levels of smoke. On the other hand, blue grama was inhibited at only the low smoke level, while sideoats grama was inhibited by all levels of smoke. It is apparent that smoke does have a significant effect on germination of many grass species in North America.

7. HABITAT USE BY LADDER-BACKED WOODPECKER (*PICOIDES SCALARIS*) IN THE CAPROCK CANYONLANDS IN FLOYD COUNTY, TEXAS

Victoria K. Solis^{1*} and Andrew C. Kasner¹

¹Department of Math and Science, Wayland Baptist University, Plainview, Texas 79072

Observations of Ladder-backed Woodpeckers (*Picoides scalaris*) in various tree species were recorded in Floyd County at a site located in Blanco Canyon, near Floydada, TX to determine the habitat associations of males and females. Transects were established and observation data was collected during spring 2015 from March 13th to April 8th and winter 2015/2016 from January 22nd to February 22nd with a total of 16 female sightings and 13 male sightings. Association with certain tree species and perch locations on trees were recorded for males and females to determine any differences in foraging habitat use. For male observations, 46% were in hackberry trees (*Celtis*), 31% were in mesquite trees (*Prosopis*), 23% were in elm trees (*Ulmus*), and 0% were in chinaberry (*Melia*) or cottonwood (*Populus*) trees. For female observations, 62% were in mesquite trees, 13% were in cottonwood trees, 19% were in hackberry trees, 6% were in chinaberry trees, and 0% were in elm trees. For perch location in males, 46% were on secondary limbs, 23% were on tertiary limbs, 15% were on canopy limbs, and 16% were on primary limbs. For female locations, 31% were on primary limbs, 37% were on tertiary limbs, 19% were on secondary limbs, and 13% on canopy limbs. Males were found primarily in hackberry trees on secondary limbs, while females were found mostly in mesquite trees on primary limbs.

8. OBSERVATIONS OF POTENTIAL SYMBIOTIC RELATIONSHIP BETWEEN FERAL HOGS (*SUS SCROFA*) AND RACCOONS (*PROCYON LOTOR*)

Tracina Maiden^{1,2*}, Phillip Seiwert³, Stephanie McMillan-Randell², and Stephanie Lockwood¹

¹Department of Biological Sciences, Texas Tech University at Waco, a Higher Education Teaching Site, Waco, Texas

²Department of Biology, McLennan Community College, Waco, Texas

³Department of Natural Resources Management, Texas Tech University, Lubbock, Texas

Feral hogs, *Sus scrofa*, are an invasive species, brought in by early Spanish explorers in the 1500s, but were eradicated and reintroduced in the early 1900s. Raccoons, *Procyon lotor*, are small mammals that were first identified in the 1600s in North America. Due to the recent introduction and range expansion, these species' relationships are novel. In fall of 2013, game cameras were set up in Aquilla, Texas to observe feral hogs for two weeks to determine a latency to detection and obtain a population density in Hill County, Texas. During this study, one particular feral hog was observed providing protection for a band of raccoons from other feral hogs, who was then rewarded for this behavior. Very little research has been identified documenting the relationship between feral hogs and any other species; however, an internet search identified multiple pictures of this relationship. One picture demonstrated a raccoon sitting on the back of a feral hog, cleaning parasites out of the hog's fur. In 2015, game cameras were set up in the same location as 2013; however, no feral hog sightings were documented at that time. These findings demonstrate a mutualistic relationship between these two species, which is rarely observed. A better understanding of the relationship between raccoons and feral hogs could assist researchers to identify potential ways to control feral hog damage and population expansion. The close relationship between feral hogs and raccoons could allow for the transmission of diseases between the species and could lead to novel diseases.

9. OVARIAN CANCER EARLY DETECTION: AN OVERVIEW OF BIOMARKERS AND DEVICES

Brooke Walterscheid^{1,2*}, Maruizio Chiriva-Internati¹, and Jose Figueroa¹

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²Texas Tech University Honors College

As survival rates steadily decrease with the respective stage of epithelial ovarian cancer (EOC), it is crucial to identify EOC at its earliest stages when the chances of response to treatment are higher. In addition to catching the disease in early and generally treatable stages, early detection devices also allow for more time available for treatments. These tests are typically inexpensive and noninvasive. Recently, diagnostics have shifted to point-of-care devices, which allow for bedside, clinical testing using microRNA analysis, microfluidic technology, nanodevices, multimarker assays, and multiplexed panels. These methods are designed to detect various types of cancer biomarkers with high sensitivity and specificity. However, these new diagnostic devices must be able to discriminate malignant tumors from benign neoplasias, inflammation, and other environmental factors. To improve upon present early detection devices for EOC, the current market must be overviewed to evaluate the strengths and weakness of each device, and how the future of early detection devices can aim to solve present challenges.

10. PATTERNS OF GENETIC DIVERSIFICATION IN A WIDELY DISTRIBUTED SPECIES OF BAT, *MOLOSSUS MOLOSSUS*, BASED ON A NUCLEAR MARKER

Kelsey B. Donckels^{1*}, Laramie L. Lindsey¹, Loren K. Ammerman², and Robert D. Bradley^{1,3}

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²Department of Biology, Angelo State University, San Angelo, Texas 76909

³Natural Science Research Laboratory, Texas Tech University, Lubbock, Texas 79409

The taxonomy and evolutionary relationships of the velvety free-tailed bat, *Molossus molossus*, from Central and South America long has been debated. Within this species, and for the entire genus *Molossus*, specimens have been difficult to identify and have presented several taxonomic challenges. DNA

sequencing data can be used to compare and propose evolutionary relationships between different organisms. The objective of this project was to characterize the genetic relationship among individuals representing subspecies of the widely distributed species, *M. molossus*, based on the nuclear marker beta fibrinogen (β -fib). To obtain these results, we extracted DNA from *Molossus* tissues using a lysis buffer, and then amplified the intron 7 of β -fib using Polymerase Chain Reaction. Once the DNA was amplified, we performed traditional Sanger cycle sequencing. A Bayesian analysis was conducted with *M. rufus* as an outgroup and genetic divergence was estimated. Our results indicate that some currently recognized subspecies of *M. molossus* are consistent with the lineages recovered, and are consistent with lineages recovered in a mitochondrial gene tree (cytochrome *b*) from previous work. However, not all recognized subspecies of *M. molossus* were recovered by this analysis suggesting that several taxonomic revisions are needed. Overall there was low average genetic divergence across all specimens.

11. NEST BOX USE AND PRODUCTIVITY OF AMERICAN KESTRELS ON THE HIGH PLAINS OF TEXAS

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²U.S. Geological Survey, Texas Cooperative Fish and Wildlife Research Unit, Texas Tech University, Lubbock, TX 79409, USA

The American kestrel (*Falco sparverius*) is a widely ranging falcon in North America. These raptors are secondary cavity nesters in that they rely on previously formed cavities in order to rear their young. This adaptation has aided their distribution across North America, especially in exurban environments where cavities within man-made structures are plentiful. However, despite their wide range, kestrel numbers have been declining throughout much of their distribution. In order to analyze factors affecting kestrel success in exurban environments, we constructed and monitored 29 kestrel nest boxes over the course of three years. Our study site has experienced an increase in both nest box use and reproductive success by kestrels in the years since its establishment. We will assess a suite of covariates including year, monthly precipitation, nest box orientation, land cover type, distance to other nest boxes, and categorical levels of human activity to evaluate their influence on the response variables of nest box use, success, and productivity. We will use these factors to create predictive models of American kestrel nest box use in exurban environments on the high plains of Texas. The model results will provide box placement guidance for expansion of the American kestrel nest box program in the region.

12. FUNCTIONAL AMYLOIDS: A LINK BETWEEN YEAST MATING AND MAMMALIAN FERTILIZATION

Gage R. Rowden^{1*} and Gail A. Cornwall¹

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Amyloids are self-aggregating proteins, which form cross- β sheet fibrils. They are typically considered pathogenic structures such as the A β aggregates and neurofibrillary tangles in Alzheimer's disease. However, amyloid can also carry out normal biological rolls in the absence of pathology. In a previous study we found that functional amyloids were present in the normal mouse sperm acrosomal matrix, and the zona pellucida (ZP) surrounding the mouse oocyte, suggesting amyloids may play a role in sperm-egg recognition. A sequence analysis of the mouse ZP3 protein using AmylPred 2, which predicts amyloidogenic sites, revealed an important hydrophobic region that is conserved in mollusk, fish, frog, quail, and human ZP3 proteins and is also present in the α -agglutinin/Sag1p protein in *Saccharomyces cerevisiae*, a protein known to be involved in sexual recognition between the Mat-A and Mat- α mating types. This suggests yeast sexual mating, as in mammalian fertilization, may be mediated through an amyloid-amyloid interaction. Discovering a similar mechanism for sexual recognition between complex multicellular animals and single-celled eukaryotes would illustrate remarkable conservation through hundreds of millions of years of evolution. Using Congo Red (CR) and Thioflavin-S (Th-S) and the

confirmation dependent antibodies, OC and A11, to selectively bind to cross- β sheets, we observed a concentration of amyloid at the shmoo (mating-specific cell wall extensions) in both mating types. The presence of a signal in these extensions would imply amyloid is involved in yeast sexual reproduction; however, further research is required to establish the interaction of amyloids during the formation of the mating bridge.

13. SALT ADDICTION IN MALE SATISFIED ATHLETE MAY BE EXPLAINED BY THE PREPARATION OF HOME-MADE FOOD LESS SALTY THAN RESTAURANT AND PROCESSED FOOD

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Previous results showed male satisfied athlete displaying signs of salt addiction while female satisfied athlete avoiding salty foods. We investigated dehydration level of WBU athletes versus non-athletes. Healthy college student volunteers (n=491) completed a food survey. Exercise frequency; subjective sweat degree; alcohol and caffeine consumption; enjoyment of fat, sugar, and salt in the food; and perceived saltiness of home-made food versus restaurant/processed food were analyzed. Female satisfied athlete (FSA) and female hungry athlete (FHA) exercises and sweats more than non-athlete, FSNA or FHNA. FSA and FHA consume less caffeine than FSNA or FHNA. FSA and FSNA or FHA and FHNA display similar pattern of alcohol consumption and enjoyment of fat, sugar, and salt in food. FSA perceives their home-made food saltier than restaurant/processed food compared to FSNA. However, FHA and FHNA does not see any difference in the saltiness of home-made food versus restaurant/processed food. Male satisfied athlete (MSA) and male hungry athlete (MHA) exercises and sweats more than MSNA or MHNA. MSA drink less alcohol but amount and type of alcoholic drinks intake is similar to MSNA. MHA display similar patterns of alcohol consumption than MHNA. MSA and MHA drink less caffeine than MSNA or MHNA. MSA and MHA display similar enjoyment of fat, sugar, and salt in food and perceived saltiness of home-made food versus restaurant/processed food. Preparation of home-made food saltier than restaurant and processed food may explain avoidance of salty foods by FSA while lack of proper sodium repletion may explain salt addiction in MSA.

14. PHYLOGENY OF BATS OF GENUS *MONOPHYLLUS*. A STUDY OF GENETIC AND MORPHOLOGICAL DIVERGENCE BASED ON MITOCHONDRIAL CYTOCHROME-*b* GENE

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The genus *Monophyllus* is distributed throughout the Caribbean Islands. Two species of *Monophyllus* are recognized, *M. redmani* and *M. plethodon*, and are sympatric in Puerto Rico. Two hypotheses were formed, first that *M. plethodon* has multiple species and second that there is more than one species of *M. redmani*; both hypotheses were based by evaluating morphological differences and application of the Morphological Species Concept. Molecular data, generated from the mitochondrial cytochrome-*b* gene, were used to test if genetic differentiation was congruent with morphological variation. Genetic distance between *M. redmani* and *M. plethodon* is approximately 11%. Considering the Genetic Species Concept, analysis of cytochrome-*b* does not support the hypothesis of more than one species of *M. plethodon* (genetic distance < 5%). The experimental data generated from analysis of *M. redmani* suggests that there could be an undescribed species on the island of Puerto Rico (genetic distance > 5%). Genetic distance values of the cytochrome-*b* gene are compatible with standards used to determine taxonomic status in mammals. Multiple species concepts exist, and not all can be applied. However, application of multiple species concepts provide more confidence in conclusions drawn from the data. Based on the sequence from *Monophyllus* from different islands, there is no indication for the existence of more than three species in the genus *Monophyllus*, however there is still a number of islands where specimens remain to be sequenced. Further research to analyze the cytochrome-*b* gene, by completing sequencing, is being

conducted. In addition, we plan to sequence a nuclear gene which could determine if gene flow is occurring among the two groups classified as *M. redmani*.

POSTER (GRADUATE)

15. USING REMOTELY SENSED IMAGERY TO DOCUMENT HOW LAND USE DRIVES TURBIDITY OF PLAYA WATERS IN TEXAS

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Sedimentation (primarily from human land use) is a major threat to runoff-fed wetlands of the Great Plains of North America (playas), but it is unknown how many playas are turbid, how prevalence of turbidity has changed over time, and how turbidity is related to surrounding land use. We used remotely sensed imagery to assess sedimentation in the waters of over 7700 playa basins in Texas on four dates during a 29-year span: 25 July 1986 (a regionally wet time), 3 May 2014 (during drought), 4 June 2014 (after the drought was broken), and 25 July 2015 (one year post-drought). Even on the wettest date examined, 64.0% of playa basins did not hold water. Turbidity varied over time, was already present in over half of the basins examined in 1986, and prevalence of turbidity was not simply proportional to overall wet playa abundance. There was an increase in total and irrigated cropland in our focal region and a statistically significant association between sedimentation and land use within 100 m of a playa: clear playas were associated with more urban development and pasture/grassland, and turbid playas were surrounded mostly by cropland.

16. INVESTIGATING THE EFFECTS OF ESTROGEN AND TRICLOSAN MIXTURE ON SOIL MICROBIAL DIVERSITY

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Pharmaceutical and personal care products (PPCPs) associated with land farming of municipal wastewater effluent may potentially, persist in the soil and alter soil microbial community processes. Estrone (E1) and the anti-microbial agent, Triclosan, were examined for their potential to persist and disrupt soil microbial community function. The community level physiological profile was examined using BIOLOG® EcoPlates™. Soil with 7decades-long exposure to these chemicals and naive soil (not previously exposed), was spiked with estrone, triclosan, and a 1:1 mixture of estrone: triclosan, incubated for 90 days and analyzed for the ability of their microflora to utilize ecologically relevant carbon sources. Control samples consisting of unspiked exposed and naive soil were included in the analysis. Over the 90-day incubation, there was a significant increase in substrate activity and substrate richness in all treatments except in the naive soil treated with the estrone: triclosan mixture. Principal component analysis (PCA) of the data showed the microbial community utilized different carbon substrates by day 90 whereas they had exhibited similar substrate utilization at day 0. Microbial communities in the previously exposed soil samples adapted more quickly to the contaminants by utilizing a greater variety of substrates earlier in the time course.

17. MICROSCOPIC ASSESSMENT OF INDOOR AIR QUALITY (IAQ) USING AHPCO NANO-TECHNOLOGY AND AIR-O-CELL SAMPLERS

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Global warming with increased CO₂ and early flowering are causing increased allergies and asthma by raising pollen and fungal spore counts¹. To improve the IAQ, we developed and assessed an Air Oasis air purifier that uses Advanced Hydrated Photocatalytic Oxidation Nanotechnology (AHPCO) for net reduction of the aerial microbiome to improve the IAQ. These air purifiers utilize AHPCO nanotechnology producing a blanket of redundant oxidizers that cleans the surrounding air and sanitizes surfaces by targeting the particulate matters. Air sampling was conducted in a room using two techniques. We exposed the petri-plates and collected data on microbial colonies formed with and without running the air purifier. Bacteria isolated from the room air exposure were gram positive bacilli, *Staphylococcus*, *Micrococcus* etc. Fungal colonies included *Alternaria alternata*, *Cladosporium* sp., *Drechslera*, *Stachybotrys* and *Curvularia* sp. There was a gradual reduction in the number of microbial colonies formed with the increased intervals on running an air purifier. We also used the *Air-O-Cell*® sampling equipment. It is designed for a rapid collection of airborne aerosols including mold spores, pollen, insect parts, skin cells, fibers and inorganic particulates. Samples using *Air-O-Cell*® cassettes analyses using digital microscopy reported the reduction of *Aspergillus* / *Penicillium* from 200 count/m³ to 0 count/m³ in a room. The Air Oasis air purifier AO3000 that applies AHPCO nanotechnology showed significant improvement of the IAQ². This experiment using AO3000 purifiers established that the use of a negative ion purification system is an effective means of eradicating the microbial aeroallergens from the indoor air.

18. EVALUATING MODELS OF NUTRITIONAL CARRYING CAPACITY FOR WINTERING MOOSE ON THE COPPER RIVER DELTA, AK

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Models of Nutritional Carrying Capacity (NCC; e.g., Ecological Carrying Capacity) produce estimates of idealized, sustainable resources to which further environmental, biological, or managerial factors can be added. Thus, estimates of NCC are often a first step when evaluating the need for further managerial actions or calculations. We compared results from five model structures to estimate the NCC for an isolated and locally-important moose (*Alces alces gigas*) population on the western Copper River Delta (CRD) of Alaska. Our models incorporated forage nutritional data and forage biomass available during the 2012–14 winters. Because of concerns of reduced forage availability due to snow burial and differences in moose winter range observations, we also incorporated a variety of winter (mild, moderate, and severe) and range (12,995–53,945 ha) scenarios into all model types. Estimates of NCC across all models, winter ranges, and scenarios ranged from 195–5,228 moose. These estimates allow for managerial flexibility in adjusting to variable winter ranges and potentially decreased winter severities with climate change. However the model and range most currently applicable produced estimates between 2,198–3,471 moose, depending on winter severity. Results from a sensitivity analysis (*Sx*) conducted on this model show lowest and highest *Sx* were attributed to digestible dry matter reduction resulting from lignin levels and snow depth, respectively. Our results will aid wildlife managers as they balance local needs and ecosystem diversity, while our NCC model structure can be applied to other ungulate populations with dynamic forage availability, ranges, or ecosystems.

19. QUALITATIVE AND QUANTITATIVE DRUG RESIDUE ANALYSES: FLORFENICOL IN WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) AND SUPERMARKET MEAT BY LIQUID CHROMATOGRAPHY TANDEM-MASS SPECTROMETRY

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Drug, residue and disease resistant microbe is a major public health focus area. The use of veterinary drugs is integral to raising food producing animals. It is possible that residues from the parent compounds may remain in the meat that is used for food. The consumption of deer meat is not regulated. The antibiotic florfenicol is used in white-tailed deer industry in an “off-label” status. To determine optimum withdrawal times it is necessary to optimize quantitative procedures for florfenicol in white-tailed deer tissue. This paper presents a confirmatory method that was developed for determining florfenicol amine concentration in white-tailed deer tissues. Qualitative and quantitative analyses were carried out using liquid chromatography - heated electrospray ionization and atmospheric pressure chemical ionization-tandem mass spectrometry. Ten days after a single injection, florfenicol drug residue in white-tailed deer tissue samples ranged from 0.4-0.6 $\mu\text{g/mL}$ for liver and 0.02-0.05 $\mu\text{g/mL}$ for muscle and a trace in blood samples. These concentrations of white-tailed deer florfenicol residue are lower than the established maximum residual limit for bovine tissues.

20. SPATIAL AND TEMPORAL VARIATION IN MYCORRHIZAL ASSOCIATIONS IN A RARE NORTH AMERICAN ORCHID

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Platanthera praeclara is a rare endemic orchid native to parts of the North American tallgrass prairie. Like other orchid species, its survival relies on mycorrhizal associations that remain through the rest of their life. This study assessed the mycorrhizal diversity from several sites to describe mycorrhizal communities of a rare orchid across its natural distribution. Mycorrhizal assessments were conducted by sampling plant roots at 11 sites in 2013 and 2014 and by using nuclear ribosomal internal transcribed spacer (nrITS) sequences in two consecutive years. Across the two years, 39 Operational Taxonomic Units (OTUs) in two fungal families, Ceratobasidiaceae and Tulasnellaceae, were observed in roots of *P. praeclara*. Ceratobasidiaceae was the dominant fungal family at majority of the sampled sites, and it was represented by 77% of the analyzed nrITS sequences. Short pairwise sequence distances ($\pi = 0.039 \pm 0.03$, N=238) between the sequences of Ceratobasidiaceae and phylogenetic clustering of the OTUs suggested specific associations from *P. praeclara* towards fungi from Ceratobasidiaceae. Broader pairwise sequence distances ($\pi = 0.135 \pm 0.06$, N=69) between sequences from Tulasnellaceae represented less specificity in its associations with *P. praeclara*. Fungal communities in roots tended to vary ($P < 0.05$) among a large majority of the sites. Mycorrhizal community composition changed from one year to the next ($P < 0.05$).

21. IDENTIFYING SURROGATE BIOMARKERS FOR OPHTHALMIC DISEASE IN NORTHERN BOBWHITE QUAIL (COLINUS VIRGINIANUS) INFECTED BY OXYSPIRURA PETROWI

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The frequent presence of the ocular parasitic nematode *Oxyspirura petrowi* in west Texas northern bobwhite quail (*Colinus virginianus*) is implicated in the population decline of this galliform. Parasites, including helminths are believed to elicit oxidative stress in host's tissues via a Type-2 (Th2) immune response mediating phagocytic proliferation of toxic reactive oxygen/nitrogen species (ROS/RNS), subsequently depleting the availability of endogenous antioxidants at the site of infection. Oxidative damage of ocular tissue, linked to eye disorders, may be further explained by the immunopathological response pathways generated by helminth infections of the avian host. We harvested ophthalmic tissue from wild adult northern bobwhite quail trapped within the region of west Texas and south west Oklahoma and performed histological analysis to identify pathology in proximity to the helminth infected tissue. In total (n=29), 14 males (8 infected, 6 uninfected) and 15 females (8 infected, 7 uninfected), have been used to compare the mean concentrations of glutathione (GSH) and thiobarbituric acid reactive substances (TBARS) across parasite infection status and sex. The gene expression of immune responses in infected

and uninfected quail will be assessed via qRT-PCR to provide relative quantification of expressed mRNA involved in the host's regulation of antioxidants (GPX7), uncoupling protein (avUCP), and Th1/Th2 associated cytokine and transcription factors (IL-4, IL-8, IL-10, IL-13, GATA-3).

22. INFLUENCE OF NPY ON PREY CAPTURE AND PREDATOR AVOIDANCE RESPONSE IN THE AFRICAN CLAWED FROG, *XENOPUS LAEVIS*

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Studies across several taxonomic groups have shown that under high predation risk situations, prey increase vigilance by reducing their foraging effort. These behavioral decisions increase immediate survival at the expense of decreased intake of food which may impose long-term costs on the individual's growth rate or reproductive output. Although the ecological and evolutionary consequences of foraging/predation tradeoffs have been widely investigated, less effort has been devoted to understand the physiological mechanisms mediating such decision making. How is the urge to eat quickly overridden by an urge to escape a predator? Here, we will address this important question in a genetically tractable animal model, African clawed frog *Xenopus laevis*. Accumulating evidence indicates that neuropeptide Y (NPY), an abundant peptide neurotransmitter in the brain, rapidly shuts off visual cues regarding prey, thereby decreasing foraging. My M.S. project aims to test whether NPY is critical for the coding of predator avoidance decisions by testing the central hypothesis: NPY neurons are responsible for detecting predator and inhibiting the recognition of prey in the presence of a visual threat. We predict that NPY acts on Y2 receptors in the OT, the subcortical visual processing center, to inhibit the visual recognition of prey. To test this hypothesis we will microinject different doses of NPY directly into the tectum in the presence or absence of Y2 receptor antagonists and observe the effect on prey-capture and predator avoidance behavior. Our results will contribute broadly to understanding how visually triggered fear affects food recognition.

23. MOLECULAR PHYLOGENETICS OF THE *PEROMYSCUS MEXICANUS* SPECIES GROUP

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The genus *Peromyscus* is divided into 13 species groups. The *Peromyscus mexicanus* species group is composed of seven species (*P. grandis*, *P. guatemalensis*, *P. gymnotis*, *P. mexicanus*, *P. nudipes*, *P. stirtoni*, and *P. zarhynchus*). In addition, several other species in the *Peromyscus* genus have been given indeterminate species group status and some of these show an affiliation with the *P. mexicanus* group. We analyzed all Cytochrome-*b* gene sequences of the seven species identified as being in this species group, as well as species with an indeterminate species group from GenBank and augmented the sample with recently collected specimens from Mesoamerica. Sequences were analyzed in PAUP using Maximum Likelihood and Bayesian methods.

24. MOSQUITO SURVEILLANCE FOR WEST NILE VIRUS FROM 2012 TO 2015 IN LUBBOCK, TEXAS, UNITED STATES

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West Nile virus (WNV) was first detected in the United States in 1999 and has since spread to all states except Alaska. WNV is an arbovirus in the genus *Flavivirus* (family *Flaviviridae*) and causes West Nile

fever and West Nile neuroinvasive disease. WNV is maintained in nature through a bird-mosquito-bird transmission cycle, most commonly in the western United States by *Culex tarsalis* and *Culex quinquefasciatus*. As part of a WNV surveillance program we trapped mosquitoes from around the city of Lubbock, TX, USA, and screened them for WNV using reverse transcription polymerase chain reaction (RT-PCR). During 2012-2015 we trapped a total of 914 trap nights over 120 weeks, resulting in 56,471 mosquitoes trapped, including 16,571 (29.3%) *C. tarsalis* and 1,500 (2.7%) *C. quinquefasciatus*. Each week, female *C. tarsalis* and *C. quinquefasciatus* were pooled by species and trap site, and RT-PCR was used to determine if mosquitoes were infected with *flavivirus* and WNV. Positive *flavivirus* and WNV results were detected in 21 (17.5%) and 16 (13.3%) of the 120 weeks, respectively. We successfully developed statistical models to help vector control programs make more informed cost-reducing decisions regarding their insecticidal spraying regime based on the average precipitation and low temperatures from previous weeks. These results demonstrate that WNV screening can be an important and versatile aspect of a vector control program.

25. PROPOSED RESEARCH: FUNCTIONAL DIVERSITY OF AQUATIC COMMUNITIES AT TRIBUTARY CONFLUENCES OF THE PECOS RIVER

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Tributary streams offer basal resources for aquatic food webs including macroinvertebrates, algae, nutrients, and organic matter. In addition to resources, they also offer unique habitats to fishes that differ from the mainstem of the river. Because of this, many stream tributaries are known to be biological “hot spots” for species diversity, making them of great conservation importance. This is especially true for rivers in arid regions where resources are limited and anthropogenic influences are often great, as stream tributaries may serve as refuge locations for biota. The Pecos River, which flows from New Mexico through Texas, has experienced extreme degradation within the Permian Basin region due to agricultural irrigation and oil and gas production. For this reason, the Pecos River offers an ideal study system to investigate diversity in stream tributary junctions across both natural and impacted conditions. For this study, I have chosen eight tributary streams of the Pecos River in New Mexico and Texas encompassing a broad range of habitat conditions. The purpose of this study will be to 1) determine how tributary confluences affect the functional diversity of macro-invertebrate assemblages on the Pecos River, 2) determine how tributary confluences affect the functional diversity of fish assemblages on the Pecos River and 3) investigate the effects that resource subsidies from tributary streams have on local food webs on the Pecos River. The results of this study will be useful in understanding the dynamics of tributaries as well as for identifying tributary junctions, which offer the greatest potential for conserving aquatic diversity in the Pecos River.

26. PROTEOMIC STUDY OF POLYSTYRENE DEGRADATION BY MEALWORMS

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In the last 50 years, there has been a rapid increase in plastic usage in almost every sphere of life (Yang et al., 2015). Polystyrene (PS) has been used in various products like cups, packing material and also as a raw material and solvent in the processing of polymers (Mooney et al., 2006). Until very recently, it was assumed that polystyrene was non-biodegradable. The past decade has documented a few micro-organisms shown to degrade PS such as *Pseudomonas putida* CA-3 (Ward et al., 2006), *Brevibacillus* sp. (Hwang et al., 2008) and *Azotobacter beijerinckii* HM121 (Nakamiya et al., 1997). A study conducted last year showed the ability of mealworms in degrading polystyrene; the ability was attributed to their gut microbiome (Yang et al., 2015). The researchers concluded that the degradation must occur due to the secretion of enzymes by the gut micro-organisms. In my proposed research, I will isolate the gut microbiota as a community and identify the proteins specific to the metabolism of PS. The protocol will

involve community proteomic techniques such as 2D protein fractionation, mass spectrometry and identification of the obtained peptides using online databases. Functional properties and regulation of the involved enzymes will also be characterized. Further, I will be identifying the metagenomic diversity of the gut microbiota to build an understanding of how this community functions in order to degrade PS successfully. Results from this study will contribute to future plastic recycling and disposal, which is one of the most intractable problems of human society today.

ORAL (UNDERGRADUATE)

27. AN ANALYSIS OF THE IMPACT OF BIOMETEOROLOGY ON GREY WOLF (*CANIS LUPUS*) AND RED WOLF (*CANIS RUFUS*) SCENT-MARKING BEHAVIOR

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The study of biometeorology analyzes an environment's impact on living organisms, and assists field biologists in identifying how abiotic conditions affect animal behavior. Many studies focusing on Grey wolf (*Canis lupus*) activity levels in correlation to time of day and lunar phase have been conducted, and a previous study has been conducted analyzing the impact of their impact along with temperature and barometric pressure on the endangered Red wolves (*Canis rufus*). Environmental factors such as time of day, lunar phase, temperature, and barometric pressure impact not only animal behavior but also species' chemosensory signals, which they use to communicate with one another. These signals can be modified by abiotic conditions, thus potentially altering an animal's behavior. Abiotic factors were analyzed to determine the impact on scent-marking behavior in wolves. We used time of day, lunar phase, temperature, and barometric pressure as environmental variables to determine optimal conditions for scent-marking behaviors in both Grey wolves and Red wolves individually and comparatively. Our results reveal a number of overlaps in preferred scent-marking conditions between the two canid species to include: times from 10am-3pm, the waxing gibbous and full moon lunar phases, from 70-79°F, and 30.20-30.39Hg barometric pressure range. By gaining an understanding of biometeorological factors' impact on the scent-marking behavior of Grey wolves and Red wolves can provide field biologists with valuable knowledge in identifying effective species management plans and breeding programs for canids.

28. SPATIAL BIAS IN BAT SAMPLING LOCALITIES IS INDEPENDENT OF FAMILY AND ECOLOGICAL GROUPING

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A species distribution model (SDM) predicts and maps the probable distribution of a species across a given area. It is necessary to account for spatial bias when producing SDMs so the maps represent the true distribution of a species. One common form of spatial bias occurs when data are clustered due to sampling effort or methodology and not species ecology. Currently, spatial biases are corrected in models without assessing for variations in the magnitude, extent, or cause of spatial bias. Variation in spatial bias should be expected because different taxa may exhibit differential capture success. We compared differences in spatial bias between bat localities first at the family and sub-family level and then between different ecological groupings relating to roosting and foraging ecology. There were 13,803 accurately georeferenced Southeast Asian bat locality data from the Global Biodiversity Information Facility (GBIF) that were used for analysis. We assessed differences in spatial clustering by comparing global Moran's I statistics. Our results show that all bat sampling localities exhibit a significantly high level of spatial clustering, but that this was independent of family or ecological grouping. It is beneficial for researchers to know how locality data are biased so that the most accurate SDMs can be built. While no global bias differences were detected it is highly likely that clustering will exhibit a different spatial pattern when examined at the local level, which will be a direction for future analysis.

29. FISH BITE PREVALENCE AND YELLOW-BAND DISEASE ON *MONTASTRAEA* AND *ORBICELLA* COMPLEXES IN ROATAN, HONDURAS

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Yellow-band Disease (YBD), is a widespread coral disease primarily attacking the zooxanthellae of the *Montastraea* and *Orbicella* complexes. The causative agent for YBD is still unknown; however, various bacteria and viruses have been implicated. Increasing water temperatures, tourism, fish predation, variations in coral growth, and opportunistic pathogens are all contributing factors to coral disease and reef decline. Corallivorous fish may transmit the pathogen or increase coral susceptibility to infection due to bite wounds as they represent a biotic stressor. This study has assessed the relationship between fish bite and disease area as well as coral status frequencies affected by YBD. Research was conducted yearly between May 2013 and 2015. Area measurements were taken by using a 0.5x0.5 meter quadrat. *Orbicella annularis* had greater area of fish bites in relation to other evaluated star coral species. In relation to star corals species, *O. annularis* and *O. faveolata* were found to be the most affected by YBD. Recently, 2015 data shows that 70 percent of the *Montastraea* and *Orbicella* complexes in Roatán, Honduras are affected by disease. Variability in average fish bite area is high among dive sites and years; however, average YBD area shows low variability among dive sites. These data suggest coral disease area is not directly correlated to fish bite area; however, differences in fish feeding behaviors may still play a role in transmission of YBD. Future research should compare species diversity of reef fishes with diseased coral species at different geographical locations to identify potential vectors of disease.

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

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

31. WINTER HABITAT USE OF LONGSPURS (*Calcarius spp.*) AND OTHER WINTER GRASSLAND BIRDS IN HALE AND FLOYD COUNTY, TEXAS

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Longspur species (*Calcarius spp.*) populations are declining from habitat loss, however, there is no current literature on this species wintering habitat. Understanding their wintering habitat use would benefit conservation efforts for this species. Roadside point count surveys were conducted from December 2014-March 2015 and November 2015-February 2016, to sample the presence of longspur species in both Hale and Floyd counties in the Southern High Plains of Texas and identify habitat associations. Sites were classified as having homogeneous, heterogeneous or unfarmed (highest level) habitat heterogeneity. In both seasons a total of 4,387 passerine grassland bird species were counted, of that 427 were Longspur species. Other grassland bird species counted include the Western Meadowlark, Horned Lark and Lark Bunting. This study has shown that the Western Meadowlark prefers heterogeneous and unfarmed habitats. Whereas the Longspur and Horned Lark numbers were highest in heterogeneous and unfarmed landscapes, although these differences were not statistically significant.

32. THE EFFECTS OF SOCIAL INTERACTION AND SALT ADDICTION ON RENAL GENE EXPRESSION IN RATS

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Social interaction between rats positively drives reward behavior. Salt intake enhancement is a behavioral sensitization due to repeated sodium deficiency adaptation, like water deprivation–partial rehydration (WD-PR). Individually-housed (IH) rats develop salt addiction when exposed to repeated WD-PR cycles, whereas group-housed (GH) rats do not develop a dependency on salt. However, a ceiling effect of high salt intake is seen in GH animals. This study investigated if social interaction and WD-PR-induced salt dependency would have an effect on renal transcripts that regulates renal sodium balance. Forty adult male Sprague-Dawley rats had access to chow, water, and 1.8% NaCl solution. The kidneys were harvested from IH (one animal/cage) and GH (five animals/cage) that underwent either zero WD-PR (IH non-dep or GH non-dep) or three (IH dep or GH dep) cycles at 1-week intervals. The kidneys were homogenized, RNA extracted, cDNA synthesized, and quantitative real time-polymerase chain reaction was performed for vasopressin (Avp), non-voltage-gated sodium channel 1- β subunit (Scnn1 β), and Avp receptor type-2 (Avpr2). Similar β -actin-relative mRNA expression from IH non-dep, IH dep, GH non-dep, and GH dep for Avp (1.0 \pm 0.5, 1.5 \pm 0.8, 1.0 \pm 0.5, 0.3 \pm 0.2, respectively), Scnn1 β (1.0 \pm 0.5, 1.3 \pm 0.7, 1.3 \pm 0.8, 0.4 \pm 0.2), and Avpr2 (1.0 \pm 0.5, 1.0 \pm 0.4, 1.4 \pm 0.7, 0.5 \pm 0.3) was observed. Thus, renal Avp, Avp receptor type-2, and non-voltage-gated sodium channel 1- β subunit were not influenced by reward-seeking salt dependency amongst housing conditions. These results lead us to further investigate other transcripts (Scnn1 α , Scnn1 γ , Avpr1a, Avpr1b, Aqp2, Nedd4l, Drd1, Drd2, and Drd5) that could be affecting sodium regulation in the kidneys.

33. SALT ADDICTION IS MEDIATED BY ENCEPHALIC VASOPRESSIN

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Repeated cycles of water deprivation–partial rehydration (WD-PR) induce body-fluid-associated behavioral changes, like sodium intake enhancement. Salt addiction is a behavioral adaptation to repeated sodium deficiency, unrelated to fluid-electrolyte imbalances, and thus, may be due to neuroplastic actions of the natural salt reward. Enhanced vasopressin (Avp) transcripts were found in the hypothalamus of salt addicted animals. This study investigated the effects of intracerebroventricular injection of Avp receptor type-1a/1b/2 antagonists (AAVPR) on WD-PR-induced salt intake sensitization. Twenty male Sprague-Dawley rats had access to chow, water, and 1.8% NaCl. Daily intake was recorded for three weeks. Guide cannulas were stereotaxically placed into the lateral ventricles and after five postsurgical days, animals underwent two WD-PR cycles at 1-week interval. During the cycles, AAVPR administration was performed after 12h of WD and 1h before sodium appetite test (SAT). β -mercapto- β , β -cyclopentamethylenepropionyl O-Et-Tyr², Val⁴, Arg⁸-Vasopressin (100 ng/3 μ l saline) for type-1a/2 and SSR149415 Nelivaptan (100 ng/ μ l DMSO) for type-1b. Deprived control animals did not receive any drug treatment. AAVPR treatment abolished daily sodium intake enhancement (2.9 \pm 0.7, 6.23 \pm 1.7, 4.7 \pm 1.9⁺ ml/week, respectively; ⁺p<0.05 vs. control) compared to control (4.1 \pm 0.5, 11.0 \pm 2.0*, 14.6 \pm 3.6* ml, *p<0.05 vs 1st week). AAVPR treatment blunted sodium appetite enhancement (4.1 \pm 1.2⁺; 5.6 \pm 0.6⁺ ml/SAT, respectively) compared to control (7.0 \pm 0.8; 10.0 \pm 0.1 ml, #p<0.05 vs 1st SAT). AAVPR treatment prevented daily chow intake enhancement (24.3 \pm 1.0, 23.3 \pm 2.5⁺, 22.7 \pm 0.9⁺ g/week, respectively) compared to control (22.2 \pm 1.1, 26.8 \pm 0.8*, 29.5 \pm 1.0* g). Our results suggest that encephalic vasopressin may be enrolled in the reward-mediated salt seeking behavior induced by repetitions of the WD-PR cycle.

ORAL (GRADUATE)

CELL & MOLECULAR BIOLOGY

34. MOLECULAR DETERMINANTS FOR HYSTERESIS IN POTASSIUM CHANNELS: A SPECTROSCOPIC AND CRYSTALLOGRAPHIC APPROACH

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Hysteresis has been observed in cyclic nucleotide-gated, transient receptor potential vanilloid, N-methyl-D-aspartate, human Ether-à-go-go-Related Gene⁶, human HCN4, mouse HCN1 channels. Voltage shift for QV (gating charge vs voltage) curve is well documented for voltage-gated cation channels, which was considered an intrinsic property of the voltage-sensing domain (VSD). However, it was showed recently that uncoupling the VSD from the pore domain of the Shaker K⁺ channel, eliminated the VSD's hysteretic gating behavior. It was suggested that the pore domain imposes a mechanical load on the VSD due to stabilization of an open state, which causes the hysteresis². Since open-state stabilization occur at the channels' pore domain, it is important to study the pore domain gating mechanism in isolation. We intend to use the archetypal pore domain of a K⁺ channel, KcsA, as a functional and structural surrogate, to elucidate the molecular basis of hysteretic gating behavior in ion channels. Recently, we have unveiled a novel hysteretic gating behavior in KcsA by electrophysiology and continuous wave electron paramagnetic resonance spectroscopy, which faithfully measure the pH dependent conformational changes associated to activation⁷ and deactivation gating. *We hypothesize that structural changes of the KcsA's selectivity filter associated to C-type inactivation underlie the molecular mechanism of hysteretic gating in KcsA and by extension in other ion channels.* The long-term goal of this project is to determine the molecular basis for hysteretic gating in ion channels, which can be useful for the development of drugs that can correct several channelopathies.

35. OVEREXPRESSING MULTIPLE GENES IN ARABIDOPSIS ENHANCES PLANT RESISTANCE TO MULTIPLE STRESSES

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Salt, drought, and heat are the most important environmental stresses that negatively affect plant growth, development and productivity. In response to these environmental challenges, we have introduced a two-gene construct, *SIZI-AVP*, in to Arabidopsis plant using an *Agrobacterium* mediated transformation to generate plants with higher resistance capability to multiple stresses. It has been reported that, overexpression of *AVPI*, the Arabidopsis vacuolar H⁺-pyrophosphatase gene 1, dramatically increases salt and drought tolerance in plants. Overexpression of *OsSIZI*, the rice SUMO E3 ligase gene, makes plants more resistant to heat and drought stresses. We hypothesize that co-overexpression of *SIZI* and *AVPI* in transgenic plants will likely increase tolerance to drought, Salt and heat stresses simultaneously. Homozygous lines with high expression of transgenes have been identified using segregation analysis, RT-PCR analysis, and RNA blot analysis. Physiological experiments such as water-deficit test, salt tolerance test and heat stress analysis have been pursued. Noticeably an enhanced tolerance was observed with *SIZI/AVPI* co-overexpressing plants under multiple stress conditions in comparing to non-transgenic, single gene overexpressing lines.

36. TRANSPOSABLE ELEMENT ANNOTATION USING *DE NOVO* BASE REPEAT IDENTIFICATION

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Transposable elements (TEs) are genetic elements that have the ability to replicate and relocate themselves around the host genome. The number of reference genomes has increased at a faster rate than the effort to annotate transposable elements from non-model species, methods of identification of these elements vary significantly from project to project, increasing the variation in TE annotation when less than optimal methods are used. It was found that across a variety of taxa, it becomes more difficult to identify TEs based only on homology as the phylogenetic distance between the queried genome and the reference genome increased. We annotated the repeats using both homology alone, as it is usually done with new genome analyses, and a combination of homology and the *de novo* methods as well as an additional manual curation step. The use of this methods showed a substantial number of new TE subfamilies in genomes that were previously characterized, recognized a higher proportion of the genome as repetitive, and decreased the average genetic distance within TE families, implying recent TE accumulation. Lastly, the findings were confirmed via analysis of the postman butterfly (*Heliconius Melpomene*). These observations imply that complete TE annotation relies on a combination of homology and *de novo* base repeat identification, manual curation and classification and that relying on simple, homology-based methods is insufficient to accurately describe the TE landscape of newly sequenced genome.

37. NOVEL METHOD FOR TRANSPOSABLE ELEMENT ANNOTATION ACROSS MULTIPLE TAXA

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Transposable elements (TEs) are sequences of DNA that can mobilize themselves through cut-&-paste or copy-&-paste mechanisms in host genomes. Increased TE activity can lead to expansion of genome size and massive amounts of genetic variation. TEs comprise more than half of the typical mammalian genome. In-depth TE analyses for a single genome have traditionally taken weeks to compile. Today, novel reference genomes are published more frequently than ever before as whole genome sequencing technology becomes progressively affordable. The surge in the number of available genomes has surpassed the efforts of in-depth TE annotation analyses. Here we present a novel method for in-depth TE annotation of closely related species. Our analyses included the six currently available genomes of cetaceans on the National Center for Biotechnology Information database (NCBI), Minke Whale (*Balaenoptera acutorostrata*), Baiji (*Lipotes vexillifer*), Killer Whale (*Orcinus orca*), Sperm Whale (*Physeter catodon*),

Antarctic Minke Whale (*Balaenoptera bonaerensis*), and Common Bottlenose Dolphin (*Tursiops truncatus*). The program faSplit was used to generate a fasta file of 500 million base pairs (bp) from each Cetacean genomes. All six 500 million bp sample genomes were then concatenated together to create a 3 billion bp “polycetacean” genome. Traditional in-depth TE annotation methods were then used to analyze the new polycetacean genome. Combining the genomes allowed for rapid TE identification simultaneously across six taxa. This method saves time and computational resources while attempting to mitigate the problem of TE annotation lagging behind the accelerated publication of non-model genomes.

ECOLOGY

38. PAST AGRICULTURAL LAND USE AND PRESENT-DAY FIRE REGIMES CAN INTERACT TO DETERMINE THE NATURE OF SEED PREDATION

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Historical agriculture and present-day fire regimes can have significant effects on contemporary ecosystems. Although past agricultural land use can lead to long-term changes in plant communities, it remains unclear whether these persistent land-use legacies alter plant-consumer interactions, such as seed predation, and whether contemporary disturbance (e.g., fire) alters the effects of historical agriculture on these interactions. We conducted a study at 27 sites distributed across 80,300 hectares in post-agricultural and non-agricultural longleaf pine woodlands with different degrees of fire frequency to test the hypothesis that past and present-day disturbances that alter plant communities can subsequently alter seed predation. We quantified seed removal by arthropods and rodents for *Tephrosia virginiana* and *Vernonia angustifolia*, species of conservation interest. We found that the effects of land-use history and fire frequency on seed removal were contingent on granivore guild and microhabitat characteristics. *Tephrosia virginiana* removal was greater in low fire frequency sites, due to greater seed removal by rodents. Although overall removal of *V. angustifolia* did not differ among habitats, rodents removed more seeds than arthropods at post-agricultural sites and non-agricultural sites with low fire frequencies, but not at non-agricultural sites with high fire frequencies. Land-use history and fire frequency also affected the relationship between microhabitat characteristics and removal of *V. angustifolia*. Our results suggest that historical agriculture and present-day fire regimes may alter seed predation by shifting the impact of rodent and arthropod seed predators among habitats, with potential consequences for the establishment of rare plant species consumed by one or both predators.

39. SMALL MAMMAL ABUNDANCE NOT DRIVEN BY LIANA PRESENCE IN A PANAMANIAN FOREST

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Small mammal abundance has been shown to correlate positively with liana abundance in tropical forests. Lianas provide three main resources for small mammals: as conduits for traveling through the forest, as cover structures along the ground and in gaps, and as a food resource. When hyperabundant, small mammals can suppress tree recruitment, thus negatively impacting forest regeneration. Here we examined whether the established relationship between small mammal abundance and lianas is causal or simply correlative. In Central Panama, 16 liana plots were established in 2010. In March 2011, lianas were cut and left to decay in 8 randomly selected plots. In over 30,000 trap nights, we live-trapped 345 individuals from 10 different species. To determine the effects of the liana removal, we conducted a profile analysis on each

of the three most abundant species: *Proechimys semispinosus*, *Marmosa robinsoni*, and *Didelphis marsupialis*. Our results indicate that liana presence is not the primary driver of small mammal increase in disturbed tropical habitat. However, liana presence adds structural complexity to a forest, thereby attracting terrestrial small mammals. Even so, this increase in small mammals could lead to the suppression of forest regeneration and the subsequent loss of biodiversity in the tropics.

40. SPATIAL NETWORK APPROACHES TO CHARACTERIZE METACOMMUNITY STRUCTURE OF NEOTROPICAL BATS IN COLOMBIA

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How species assemble into communities depends on environmental factors, biotic interactions and species dispersal abilities. The metacommunity approach evaluates the degree to which these three determinants integrate to produce spatial variation in species composition at regional scales. Typically, spatial proximity is used as a proxy for dispersal; however, such measures do not provide estimates of variability of species dispersal abilities. A network approach may be better to assess dispersal and its implications to metacommunity patterns. A common characteristic of metacommunities is that they are composed of compartments (i.e., distinct groups of sites with similar species composition) that may correspond to modules (i.e., a group of sites with more connections among themselves than with other sites) within a network framework. Moreover, we were interested in whether metacommunities exhibit network modularity and whether modules correspond to environmental gradients. We examined a bat metacommunity from the Colombian coffee-growing ecoregion to evaluate whether modules correspond to elevation or different kinds of land cover. We assessed modularity with an agglomerative hierarchical clustering analysis and related these results to elevation and land cover attributes. Modules were most associated with elevation. Common species exhibited a pattern similar to the overall network, whereas rare species exhibited a more fragmented network with fewer connections among sites. Determining if communities form modules within metacommunities and which environmental characteristic corresponds to those modules will help elucidate the mechanistic determinants governing metacommunity assembly, such as dispersal potential, physiological constraints, or habitat selection.

41. SPATIAL ECOLOGY OF THE AMERICAN CROCODILE ON COIBA ISLAND, PANAMA

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The limited information on the ecology of the American crocodile (*Crocodylus acutus*) has had a major impact on the recovery of this species over time, even though most of the 18 countries in which it is found have banned hunting. The last decade has made it clear that to implement sound conservation and management programs, we must understand crocodile spatial ecology. Telemetry has been the method of choice; however, in only two countries where the species occurs have telemetry studies been published. We characterized the spatial ecology of *C. acutus* by tracking 24 individuals at the southeastern tip of Coiba Island, between 2010 and 2013 to determine movement patterns, home range, and habitat use. Females showed a higher average movement distance (AMD) than males; similarly, adults showed a higher AMD than sub-adults and juveniles. However, males exhibited larger home ranges than females, and sub-adults had larger home ranges than juveniles, hatchlings, and adults. There was a relationship between precipitation seasons and AMD, with increased AMD in the dry and “low-wet” seasons, and a

reduced AMD during the actual wet season. We found disaggregate distributions according to age groups throughout the 9 habitat types in the study area; adults and hatchlings inhabited fewer habitat types than juveniles and sub-adults. These sex- and age-group discrepancies in movement are likely due to the influences of reproductive events and Coiba's precipitation cycle. Juveniles also showed distinct movement patterns and home ranges; however, with sexual maturation and development, these behaviors were becoming more characteristic of adults and sub-adults.

42. SPATIAL AND TEMPORAL VARIATION IN DUCT INVESTMENTS FOR FIVE PINES (*PINUS*) FROM WEST TEXAS MOUNTAINS

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Pines are affected by a variety of disturbances (pathogens, insects, and fire) and have developed a suite of defensive traits to cope with them. Bark beetle attack is among the most deadly threats to pines, and major bark beetle outbreaks have caused widespread tree mortality over the past decade. The predominant defense against bark beetles is resin production, for which resin duct size and density can serve as relative estimates. This study aims to understand how investment in resin ducts varies with microhabitat and tree age in three major mountain ranges in west Texas (Chisos, Davis, and Guadalupe mountains). A total of 159 individuals from five different pine species (*P. arizonica*, *P. cembroides*, *P. edulis*, *P. ponderosa*, and *P. strobiformis*) were sampled across each mountain range where they were present. 17-24 geo-referenced individuals per species were collected representing a range of ages (12 - 228 years). Using a 12mm diameter increment borer, tree cores were extracted, mounted and sanded to expose resin ducts. These were then scanned to produce a high resolution image, annual rings were marked, and resin ducts per ring counted. Topographic information for each tree was obtained by intersecting location information with a 3 m resolution digital elevation model. Preliminary results are being evaluated at present time. Information specific to this geographic area and tree species will aid foresters to better determine trees that have higher susceptibility to insect attacks.

43. DIET OF PREGNANT AND LACTATING SEBA'S SHORT-TAILED FRUIT BATS (*CAROLLIA PERSPICILLATA*)

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Optimal foraging theory is based on the premise that an individual will efficiently collect and handle food while maintaining a diet that maximizes fitness. Dietary choices are influenced by extrinsic and intrinsic factors such as reproductive status (e.g. pregnant or lactating). Pregnancy and lactation in females can be energetically expensive. Whereas energy availability may be one of the main precursors to reproductive success, nutrients such as calcium and nitrogen can also limit reproduction. Since energy and nutrient costs are high during reproduction, choices of foraging strategies or diet may be critical for survival of both mother and young. Our research analyzed dietary characteristics of Seba's short-tailed fruit bat (*Carollia perspicillata*) during reproduction. Dietary analysis was done on fecal samples from males and non-pregnant, pregnant, and lactating females at the Macaregua Cave in Santander, Colombia. We hypothesized three outcomes. Firstly, with pregnancy and lactation being energetically expensive and reproductive periods occurring during high fruiting periods, we predicted that reproductive females will have a more generalist diet compared to males and non-reproductive females. Secondly, to fulfill calcium demand associated with skeletal growth, we predicted that lactating female *C. perspicillata* will consume fruits that are richer in calcium than non-reproductive females and males. Thirdly, due to the importance of nitrogen in the development of tissues, we predicted that pregnant bats will consume a greater amount of

fruits that are nitrogen-rich compared to males and non-reproductive females.

EVOLUTIONARY BIOLOGY

44. THE UTILITY OF ZONADHESIN IN EXAMINING A POTENTIAL REPRODUCTIVE ISOLATION MECHANISM IN RODENTS

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

45. HAMILTON'S RULE UNRAVELED: ADDING STOCHASTICITY AND NON-ADDITIVITY ARE EVOLUTIONARY GAME CHANGERS

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Selection and transmission – at all levels – are inherently stochastic processes, meaning that there is a distribution of possible numbers of offspring that an individual could produce, and a distribution of possible phenotypes for each offspring. Despite this, the majority of research on the evolution of cooperation has treated evolution as a deterministic process – assigning fixed values to variables. For example, an “expected fitness” is typically used when estimating the number of offspring that an individual will produce. This narrowly defines an individual's range of lifetime reproductive success to one single value, ignoring the impacts of environmental and genetic stochasticity. Another issue that is not often addressed is the effect of non-linearity. For example, an individual's fitness is frequently modeled as the sum of benefits and costs that it can amass over its lifetime. This implies that each altruistic interaction increases fitness by an equal proportion. A number of experimental studies, though, have shown that this is not always the case, and that we should not assume linearity of any variable. In this study, we model the evolution of cooperation with stochastic variation and non-linear fitness effects. Our results show that stochasticity can no longer be an afterthought and that the Hamilton equation unravels as a rule of thumb.

46. A PHYLOGENETIC ANALYSIS OF FOURTEEN RODENT MITOCHONDRIAL GENOMES

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Mitochondrial markers have been an important data source in the study of *Peromyscus* phylogenetics. All current phylogenies are based in part on mitochondrial data. The question of, “What is *Peromyscus*?” remains in an open topic of discussion, as there are three contrasting hypotheses for the genus’ phylogeny. Current phylogenies lack support at nodes reflecting critical points in the *Peromyscus* radiation. The addition of more sequence data may be capable of providing resolution where other markers have failed. Here, we present fourteen rodent mitochondrial genomes, all of which exhibit archetypal gene composition and synteny. In addition to providing valued molecular data, they allow us to undergo a phylogenetic analysis of the genus with the largest data source to date. Bayesian and maximum likelihood trees of concatenated protein coding genes, along with a *cytb* tree to ensure the accurate identification of our gene sequences, were generated, showing similar phylogenetic relationships and improved support at prominent nodes.

47. PHYLOGENETIC RELATIONSHIPS BETWEEN THE MEMBERS OF THE GENUS *NOTROPIS* (FAMILY CYPRINIDAE) USING CYTOCHROME B AND CYTOCHROME C OXIDASE SUBUNIT I

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Notropis is an ecologically diverse genus in the family Cyprinidae. The genus is speciose with over 91 species. Currently, a phylogeny for the entire genus has not been completed. Therefore, I used data available on GenBank to perform the most complete phylogenetic analysis on *Notropis*. I accumulated 77 cytochrome *b* sequences (1140 bp, *cytb*) and 69 cytochrome *c* oxidase subunit I (654 bp, COI) sequences. I performed phylogenetic analyses using maximum parsimony and maximum-likelihood analyses. The *cytb* and COI gene trees showed different groupings for some of the species in the genus *Notropis*. Many of the groupings however, aligned with many of the smaller published phylogenies of *Notropis*.

48. RECENT POPULATION EXPANSION IN *CALOMYS TENER* (RODENTIA: SIGMODONTINAE)

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Calomys tener ranges broadly in the planalto of central Brazil and eastern Bolivia and has recently been reported from Paraguay, Argentina, and southeastern Brazil. It is unknown whether or not the species is expanding into new regions, maybe as a result of the expansion of the agricultural frontier, or if these new records correspond to geographic locations not previously sampled. In this study, we obtained sequence data for 30 samples of *Calomys tener* from different geographical localities from throughout the currently known distribution of the species to test for the signature of recent population expansion. We found a high diversity of haplotypes, which in combination with summary statistics, results of AMOVA, mismatch distribution, and BSP, support the hypothesis of a recent and/or ongoing population expansion in *C. tener*. Since, it is known that this species serves as a reservoir of the pathogenic Araraquara Hantavirus in Brazil, there is a possibility that the virus may be dispersing to new areas and into other countries of South America.

49. ADDRESSING THE ADAPTIVE RADIATION IN *PEROMYSCUS* USING TRANSCRIPTOME DATA

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Adaptive radiations are described by the origin of multiple new species over a short period of time. These

new species are often cryptic, with little or no morphological variation and display low levels of sequence divergence as measured by comparison of mitochondrial and nuclear genes. The genus *Peromyscus* represents such a scenario with approximately 70+ species arising in the last 5-6my. Over the years, evolutionary biologists and systematists have attempted to resolve species boundaries of *Peromyscus* through morphological and genetic analyses. However, the proposed evolutionary tree still contains unresolved relationships reflecting the rapidly radiating characteristic of *Peromyscus*. Advances in sequencing through-put and computational biology have provided biologists the opportunity to utilize more comprehensive datasets including genomic, transcriptomic, and whole exome approaches. Based on karyotypic convergence, we hypothesize that a suite of genes was repeatedly selected during the rapid radiation that resulted in the numerous species of *Peromyscus*. The rapid divergence suggests a role for selection of genes involved in reproductive isolation in the evolution of extant lineages. For this study, liver and testes transcriptomes of four taxa within *Peromyscus* were analyzed. To identify genes with putative testes-specific functions, transcriptomes were compared to determine if genes exhibited differential expression levels in testes versus liver transcriptomes. Preliminary results suggest that testes transcriptomes for the four species expressed higher levels of similar genes when compared to liver transcriptomes. Further analyses will determine what genes are differentially expressed among testes samples to identify which genes are subjected to directional selection in independent *Peromyscus* lineages.

MICROBIOLOGY

50. BCA2 PREVENTS THE NUCLEAR TRANSLOCATION OF NF- κ B, RESTRICTING HIV-1 TRANSCRIPTION

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BCA2 (breast cancer-associated gene 2) is an anti-HIV factor that prevents HIV-1 virion assembly and release. Since many HIV-1 restriction factors are connected to the innate sensing system through the NF- κ B pathway, we here sought to explore if BCA2 is associated to this cascade, and if this association causes any effects on HIV-1 replication.

Our gene expression and luciferase-based studies show that *BCA2* is induced by NF- κ B-activating pro-inflammatory cytokines, and that up-regulation of *BCA2* provides a regulatory negative feedback on this pathway. In particular, *BCA2* acts as an E3 SUMO-ligase in the SUMOylation of I κ B α . I κ B α is normally associated to NF- κ B in the cytoplasm. Under certain stimuli, I κ B α becomes phosphorylated, and this modification promotes its ubiquitination and degradation, which in turn facilitates the nuclear translocation of NF- κ B. However, if I κ B α is SUMOylated it becomes less susceptible to undergo phosphorylation. Thereby, the *BCA2*-mediated SUMOylation of I κ B α strongly inhibits NF- κ B signaling. In agreement with this, we observed a reduction of nuclear NF- κ B components in the presence of *BCA2*. Since HIV-1 requires NF- κ B to enhance its replication, we next examined the biological implication of the *BCA2*-dependent inhibition of NF- κ B in HIV-1 infectivity. Remarkably, *BCA2* has detrimental effects on HIV-1 transcription activity. Therefore, our findings indicate that *BCA2* represents an important barrier to HIV-1 by affecting multiple steps of its replication cycle: not only *BCA2* prevents assembly and release of nascent virions, but also significantly impairs the transcription capacity of HIV-1 by repressing the NF- κ B pathway.

51. INTERACTION OF THE FUNGUS *BATRACHOCHYTRIUM DENDROBATIDIS* WITH *STAPHYLOCOCCUS AUREUS* AND *ESCHERICHIA COLI*

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The decline of amphibians worldwide has been accredited to the fungus *Batrachochytrium dendrobatidis* (*Bd*). This fungus disrupts the osmotic balance of amphibian skin cells leading to cardiac arrest. The epidermis consists of a keratin rich layer, coated with mucous, antimicrobial peptides, immunoglobulins, and the microflora of the amphibian. Previous studies have shown that bacteria are capable of inhibiting growth of *Bd* through the production of antifungal substances. The interaction of *Bd* with commensal amphibian epidermal bacteria may increase the virulence of *Bd* through the up-regulation of toxin specific genes and production of germ tubes which would aid in invasion of host cells. Using Basic Local Alignment Search Tool we have identified the presence of 13 genes in *Bd* needed to produce a toxin-like compound and have studied their expression. Increased gene expression was observed using reverse transcriptase-PCR and Real Time PCR. Germ tubes were induced when *Bd* was grown in the presence of heat killed *S. aureus* but not *E. coli* cells. Heat killed bacteria do not affect the overall growth or chemotactic ability of *Bd*. Interactions of *Bd* with specific bacterial components would allow us to understand which bacteria or group of bacteria contribute the most to increased pathogenicity. These studies will contribute to our understanding of the mechanism(s) by which *Bd* is able to infect and kill amphibians and aid in the development of novel strategies for treating infections.

52. EFFECTS OF TWO POLYPHENOLS ON THE GUT MICROBIOME AND ASSOCIATED WEIGHT GAIN IN MICE

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Recently, changes in gut microbial assemblages are being investigated as underlying causes of many health issues. Even minuscule changes have been correlated to conditions such as glucose intolerance, diabetes, and autism. We studied two polyphenols that are regularly consumed by humans and examined their effects on the gut microbiome and weight gain, using mice as a model. Natural sweeteners (Stevioside) are derived from plants (*Stevia rebaudiana*), and have sweetening effects ~300-fold greater than sucrose. Sugar substitutes are known to play a pivotal role in both obesity and diabetes and are consumed regularly as an alternative to sugar. Epigallocatechin-3-gallate (EGCG) is a polyphenol found in green tea that has been reported to impact health, including involvement in gut microbial metabolism and weight loss. However, no DNA sequencing studies to date have documented the gut microbial composition after the regular consumption of Stevioside or EGCG. C57BL/6J mice were divided into 5 groups: control, EGCG treatment, and 3 Stevioside treatments. We observed shifts in Firmicutes and Bacteroidetes ratios. Differences were noted between fecal and colon samples. Trends in weight gain were present between groups, and between sexes within groups. We also observed a shift in OTU numbers from arrival until day 30, even in controls. Our results indicate that both polyphenols affect the gut microbiome and weight gain. Notably, change of habitat from arrival until baseline altered the gut bacterial composition. These results will inform people of potential health effects of these two polyphenols, and provide researchers knowledge of how acclimation and change in habitat affect gut microbial communities of mice.

53. INFLUENCE OF DAILY SOIL TEMPERATURE RANGE ON MICROBIAL COMMUNITY DYNAMICS IN DRYLAND AGRICULTURE

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Global mean temperature has increased in the last decade from 0.10 to 0.16 °C, leading to a decrease in the daily temperature range ($DTR = T_{max} - T_{min}$) where the night time minimum temperature (T_{min}) is increasing

at a faster rate. Changes in daily T_{\min} and T_{\max} have a positive or negative consequences to agriculture production depending upon crop type and location, but little is known about the possible effects of DTR_{soil} on microbial community. The main goal of this research is to evaluate the impacts of daily temperature range (DTR_{soil}) on microbial community size, structure and functional diversity in a dryland cotton production system on the South High Plains. Cotton was planted into flat beds and 3 treatments were established 1) Control 2) Reduced DTR_{soil} using erosion blankets 3) Reduced DTR_{soil} using sorghum residue as stubble, with 6 replicates in each treatment. Soil samples were collected before planting and over the growing season 2014-2015 from each set of plots and analyzed to evaluate microbial biomass carbon, carbon usage, enzyme activity and characterization of microbial community. There is a reduction in the DTR_{soil} under the erosion blankets and the Sorghum residue in comparison with the controls plots during the growing season, this reduction in DTR_{soil} leads to an increase in microbial biomass and soil moisture. The reduction in DTR_{soil} will positive affect the dynamics of microbial communities and its relationship with plant which can lead to a well crop development. Besides it can mitigate the effects of rising temperatures due to climate change.

NATURAL RESOURCES MANAGEMENT CONSERVATION

54. ELEVATED HUMIDITY AND BUNCHING DECREASE DESICCATION RATE AND INCREASE SURVIVAL OF AIR-EXPOSED FRAGMENTS OF THE AQUATIC INVASIVE PLANT (*HYDRILLA VERTICILLATA*)

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Aquatic invasive plants can become entangled on trailered boats and other recreational equipment and hitchhike to new locations, thus increasing invaded distributions and potential for negative environmental and economic impacts. However, extended periods of air exposure during overland dispersal result in prolonged periods of stress and hinder the likelihood of plant survival and growth once they are returned to aquatic environments. Atmospheric conditions, such as humidity, temperature, or light intensity, may contribute to the rate of desiccation and the viability of hitchhiking plant fragments. Additionally, when fragments travel in bunches such as wrapped around a boat propeller, they may self-insulate and resist desiccation. Using the aquatic invasive weed *Hydrilla verticillata* as a case study, we observed desiccation response of coiled (simulating entanglement around a boat propeller) or flat fragments under low and high humidity conditions, and then returned them to a common aquatic environment to further monitor survival and growth following desiccation. Coiled fragments and fragments exposed to high-humidity conditions lost less mass than flat fragments and fragments exposed to low-humidity conditions over the same amount of time (ANOVA $p < 0.0001$). Furthermore, fragments that experienced relatively lower mass loss during air exposure exhibited increased survival upon return to a common aquatic environment ($p = 0.005$; AUC = 0.9351). Overall, these results suggest that consideration of vegetative bunching as well as humidity or precipitation can improve estimates of how far plant fragments may disperse, benefiting efforts to slow their spread.

55. THE INFLUENCE OF WEATHER PARAMETERS ON LESSER PRAIRIE-CHICKEN RANGEWIDE NEST SURVIVAL

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Abstract: Lesser prairie-chicken (*Tympanuchus pallidicinctus*; LEPC) populations exist along a diverse climatic gradient. Temperature and precipitation impact survival in the sand shinnery oak (*Quercus havardii*) prairie in the southern extent of the range, but the potential impact remains unexplored across the extent of the range. To assess the impact of environmental conditions on nest survival across the distribution of the species, we collected data in the short-grass prairie (SGP; 2013–2015), the sand sagebrush (*Artemisia filifolia*) prairie (SSP; 1998–2002), the sand shinnery oak prairie (SSOP; 2000–2011), and the mixed-grass prairie (MGP; 2013–2015). We used the nest survival model in Program MARK to assess effect sizes of biologically relevant weather variables on nest survival for each ecoregion. In the SSOP and MGP, there was model selection uncertainty ($AIC_c w_i \leq 0.90$) but there was no model selection uncertainty in the SGP and SSBP. The same top model of total precipitation during incubation + hot days + cold days had the most support in three of the four ecoregions and SSOP's model of winter precipitation + hot days + total precipitation during incubation had the most support. Our models suggest that weather conditions during nesting are good predictors of nest survival, and precipitation and extreme temperatures influenced nest survival across the range of the lesser prairie-chicken.

56. ASSOCIATION BETWEEN SALINITY AND GROWTH OF GOLDEN ALGA IN THE LABORATORY – IS ENVIRONMENTAL SALINITY A BARRIER TO ITS EXPANSION INTO COASTAL HABITATS?

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Golden alga (*Prymnesium parvum*) is a harmful species presumed native to coastal environments worldwide that has become established in inland brackish waters of the USA. Inland toxic blooms typically occur during the cooler months of the year ($\leq 13^\circ\text{C}$). In Texas, however, golden alga has not produced toxic blooms in coastal aquatic habitats. An understanding of why golden alga has not bloomed along the Texas coastline may support efforts to reduce the risk of coastal invasions and prevent its further spread inland. This study determined the effects of salinity, temperature, and genetic background on growth of golden alga in laboratory cultures. The maximum cell density reached by the most common strain of golden alga found in Texas (Scottish strain) increased as salinity increased from 5 to 15 ppt, but thereafter decreased up to 30 ppt regardless of incubation temperature (13 or 22°C). A genetically distinct strain (English strain) also achieved maximum cell density at the low-to-mid range of brackish salinity (5-10 ppt). While this study was conducted in the laboratory where conditions may not fully mimic those of natural habitats, results indicate that the optimal salinity for golden alga growth is well below coastal/marine levels. The ecological relevance of this finding remains to be clarified.

57. AVIAN RESPONSE TO BRUSH MANAGEMENT ON THE WELDER WILDLIFE REFUGE

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Grassland obligate birds are experiencing population declines across North America, and anthropogenic actions have been identified as the primary driver of these declines. Among these actions, fire suppression and grazing management have facilitated encroachment by native and introduced woody species, resulting in altered grassland habitat. Considerable attention has been focused on prairie restoration and avian conservation in the Great Plains region of North America; far less attention has been given to the Gulf

Coast prairies. We are assessing avian community response to prairie restoration efforts on the Welder Wildlife Refuge. We have established 58 variable circle survey points in a 355-acre treatment plot and a 533-acre control plot. We began conducting point count surveys and vegetation surveys during the breeding season prior to herbicide application in October 2014, and will continue to do so for the breeding and wintering seasons of 2015 and 2016. Our preliminary results indicated a high avian diversity prior to treatment, but this was ultimately dominated by 5 species: Northern Cardinal, Painted Bunting, White-eyed Vireo, Northern Bobwhite, and Yellow-billed Cuckoo. We observed novel species during the breeding season of 2015, including an influx of Dickcissels and Red-winged Blackbirds. We are currently conducting density estimates based on species-specific detection probabilities in Program DISTANCE. We also sampled vegetation with 30 m line transects at each survey point. These data will provide a baseline of avian community composition and densities, and vegetation composition, in each study plot for comparisons of effects following brush removal efforts.

PROPOSAL

58. THE EFFECT OF BIODIESEL VS. PETRODIESEL ON SOIL MICROBIAL COMMUNITY-LEVEL PHYSIOLOGICAL PROFILING, DIVERSITY, FUNCTION AND PLANT GROWTH

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This study compares the effects of petroleum diesel with three biodiesels on soil health. In this study, the effects of petroleum diesel are compared with three biodiesels (castor ethyl ester, castor methyl ester and safflower methyl ester) in three soil types (sandy loam, sandy clay loam and silt loam). Soils are sieved to 2mm and are spiked with water, petroleum diesel, castor ethyl ester, castor methyl ester and safflower methyl ester at 2% w/w (w=weight). 11 time points are selected during a 180 days' laboratory incubation period (0, 3, 5, 7, 14, 21, 30, 90 and 180 Day). After 180 days' incubation, two types of environmentally relevant plant species, Alfalfa and Northern Wheatgrass, are planted in no contaminated soils and contaminated soils. Their germination rate and growth parameters are evaluated over 35 days. GC-FID is used to determine the degradation rate of contaminants. Commercial Biolog EcoPlates™ are used to test the microbial community level physiology profile. Soil microbial diversity and function are addressed by 16s rRNA gene sequencing and metaproteomics.

59. PHENOTYPIC FLEXIBILITY AND ENERGETIC DEMAND: INSECTIVOROUS BATS DURING THE SUMMER REPRODUCTIVE PERIOD

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Organisms experience a variety of intrinsic and extrinsic factors that affect energetic demand throughout their lifetime (e.g., inclement weather, reproduction). However, organisms are not fixed in their ability to respond to energetic challenges. Phenotypic flexibility describes the reversible changes organisms make to cope with varying energetic demands. These changes include short-term behavioral responses (e.g., increased foraging), and longer-term physiological responses (e.g., increased digestive capacity). My research will address the temporal variation in phenotypic flexibility in response to intrinsic and extrinsic energetic demands. Brazilian free-tailed bats (*Tadarida brasiliensis*) are ideal for studying phenotypic flexibility as they are small, endothermic, and volant, incurring greater energetic demands than similarly sized ectotherms or larger, non-volant endotherms. Additionally, females undergo variable energetic demands due to reproduction while concurrent energetic demands of males are relatively stable. I hypothesize bats demonstrate phenotypic flexibility in response to variation in energetic demand by adjusting their foraging rate (behavior) and digestive capacity (physiology). Specifically, I predict the

period of highest energy demand, lactation, will be associated with the highest foraging rate and digestive capacity, indicated by high plasma triglyceride concentrations and enlarged digestive organs. Conversely, I predict periods of relatively low energy demand (e.g., post-lactation) will be associated with lower plasma triglyceride concentrations and smaller digestive organs. Overall, I predict greater phenotypic variation in females than males due to the sex difference in energetic demand. Quantifying the behavioral and physiological responses of insectivorous bats during periods of high energetic demand will further inform the variation in organismal phenotypic flexibility.

60. RESOLVING THE PHYLOGEOGRAPHY AND PHYLOGENETIC VARIATION PRESENT IN *PEROMYSCUS MANICULATUS* USING MOLECULAR SYSTEMATICS AND NEXT GENERATION SEQUENCING

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Peromyscus maniculatus is an abundant mammal species occupying a wide variety of habitats in North America, with close to 60 recognized subspecies. Despite the common occurrence of this species, and the numerous described subspecies, few wide spread phylogenetic studies have been conducted across multiple populations. Our attempt to understand the phylogeny and genetic variation within this species will be a two-fold process. In the first part of our investigation an examination of the relationship between populations of this species was undertaken, using both a Bayesian and RAxML analysis of the mitochondrial gene cytochrome-*b* (*Cytb*). The goal of these analyses was to obtain information concerning the genetic relationship of this species across the entire known geographic range. The genetic variation in *Cytb* sequences will be used to provide insight into the phylogeographic similarities and differences of *P. maniculatus* throughout the species' range. Our preliminary results indicate three strongly distinct clades of *P. maniculatus* were formed, each clade representing populations in specific geographic areas. The topology of these clades indicates that the genetic variation within *P. maniculatus* can, in part, be defined by the geographic distribution of the species. With the preliminary data complete, the next step is to attempt to understand the genetic variation present in this wide ranging species by utilizing next generation sequencing to examine a wide array of mitochondrial and nuclear genes.

61. INCORPORATING A HETEROTHERMIC CONTINUUM INTO OPTIMAL MIGRATION THEORY: RE-CONSIDERING COSTS, CURRENCIES, AND CONSTRAINTS

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For many organisms, seasonal migration is an integral part of life history. Understanding the migration ecology and physiology of these organisms is necessary for assessing the adaptive values associated with variable migration strategies and predicting behavioral responses to an ever-changing environment. Optimal migration theory is a theoretical framework for establishing quantitative relationships among optimization criteria (i.e., time, energy, and predation risk) and migratory behaviors (i.e., stopover duration, optimal fuel load, and fat deposition rate), and has been used to describe the adaptive value of various migratory strategies in birds and bats. Despite empirical support, a major limitation of optimal migration theory is that all models developed to date assume strict homeothermy. Yet, many bats and birds are heterothermic and can be extremely efficient migrators by turning potential thermoregulatory costs into energy savings by reducing the energetic demands of maintaining a stable internal body temperature during periods of rest. I propose to 1) generate new predictions about migratory behavior by incorporating the heterothermic continuum into optimal migration models and 2) test those predictions empirically by comparing the foraging behavior and body composition of migrating heterothermic and homeothermic bats and hummingbirds at stopover sites.

62. THE POWER OF ONE: INTRASPECIFIC VARIATION IN BAT POLLINATION SERVICES TO BAOBABS IN SOUTH AFRICA

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Studies of ecological interactions have recently focused on the role of individuals. Especially important are individual variations among pollinators, because pollinator movements directly affect plant fitness. In this study, I will explore how morphology affects pollination by individual bats (primarily *Rousettus aegyptiacus*) in a bat-baobab (*Adansonia digitata*) mutualism in southern Africa. In bats, individual variation in flight morphology may lead to differences among individuals in foraging behavior, particularly wing loading which correlates with flight speed. Adult male *R. aegyptiacus* range in body mass from 79g to 165g, resulting in flight speeds between 11.8 m/s and 14.3 m/s (from $V=26.2(M)^{0.316}$). Consequently, the largest bats could fly approximately 10 more kilometers per hour than the smallest. I will use wing loading values, influenced primarily by body mass, to quantify intraspecific phenotypic differences that could contribute to pollination ability. I hypothesize intraspecific variation in wing morphology influences foraging and pollinator behavior. I predict individuals with greater wing loading values (typically, heavier individuals) will be more effective pollinators, able to visit more baobabs and fly longer distances per night, thus connecting more of the baobab population. Using coded VHF radio transmitters, bats will be manually detected at trees using an array of receivers throughout the night. Radio tracking data combined with morphological data makes analysis of individual foraging behaviors possible. Understanding individual behavior in this system is important because bats face many threats across Africa (i.e., hunted for bushmeat) and implications of losing more effective individuals from a population of pollinators is currently unknown.

63. EXPERIMENTAL INVESTIGATION OF FLAMMABILITY IN C3 AND C4 GRASS SPECIES IN KIOWA NATIONAL GRASSLAND

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Grasses are highly flammable compared to most woody plants. Species-specific variation in flammability across grasses and what factors cause this variation are poorly understood. Many fire-maintained grasslands are dominated by C4 grasses, therefore some authors have proposed that grasses with the C4 photosynthetic pathway might exhibit more fire-adaptations and show increased flammability relative to C3 grasses. In the proposed research, I will examine the influence of canopy architecture on grass flammability at the full plant scale, as well as evaluate if any flammability differences across species are associated with photosynthetic strategy (C3/C4). Specimens will be collected in Kiowa National Grassland in New Mexico. Ten grass species are chosen based on their phylogenetic relatedness, evenly divided into C3 and C4 species belonging to 5 lineages. Plant traits measured will include several canopy architecture traits that relate to above ground biomass partitioning, leaf traits, biomass density and fuel moisture. Full plant flammability trials will be conducted to collect flammability parameters, which include maximum flame height, temperature, biomass loss rate, time to ignition, flaming and glowing duration. Study goals will be achieved by testing flammability components' response to various plant traits with geology and phylogenetic influence as random factors. This study will provide a better mechanistic understanding of the dynamics of grass flammability and fire behavior, which will provide insight into grass fire predictions at larger scales. The outcome will benefit grassland conservation and grass fire management.

64. SPECIATION PROCESSES WITHIN SIGMODONTINE RODENTS: THE GENUS AKODON AS A FIRST APPROXIMATION

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As part of the macroevolutionary theory, the question as to why some clades are more species-rich than others has been constantly assessed. Most hypotheses trying to answer this question, involve the

emergence of an ecological opportunity (EO) that arises when a lineage experiences novel and underutilized resources, leading to the diversification and adaptive radiation of a clade. One way to assess it is by means of species-level phylogenies and geographic distributions of recently formed sister species. Among the mammalian class, rodents represent the most diverse order and within it Sigmodontinae is the most diverse South American subfamily of Cricetidae. Its historical biogeography represents one of the colonizations that have been hypothesized to have facilitated adaptive radiation by means of EO. I will work with the genus *Akodon* as representative of Sigmodontinae. The main purpose of this research is to evaluate the hypothesis proposed by Schenk et al. (2013) in which a strong pattern consistent with EO was found only for the primary murid colonization of South America. To do so, sister species within the genus will be determined using phylogenies built with four molecular markers (Cyt B, IBP, THY and DMPH1), and geographic ranges will be converted into polygons using the mapping software ArcMap. Once this is completed, the age-range correlation model and the *r*ase model will be implemented to try to understand the historical biogeography of the genus, which will ultimately give us information about the speciation processes that gave rise to the diversity contained within the genus *Akodon*.

65. THE RANK/RANKL/OPG AXIS IN OSSEOUSLY METASTATIC BREAST CANCER

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Breast cancer is the second leading cause of death in women in the United States. Localized breast cancer is not fatal, however, once breast cancer metastasizes to distant organs, survival rates of patients decrease dramatically. While breast cancer can metastasize to the lungs, liver and brain, 70% of all metastatic breast cancers spread to the bone. Breast cancer bone metastasis is usually osteolytic in nature, resulting in the breakdown of the bone. The RANK/RANKL/OPG axis is a major axis seen in the normal bone turnover, regulating bone building osteoblasts and the differentiation of bone resorbing osteoclasts. When breast cancer cells metastasize to the bone, they perturb the expression of RANKL and OPG in osteoblasts, leading to a higher rate of osteoclast differentiation from precursors and the breakdown of bone matrix. Recent studies have shown that the RANK/RANKL/OPG axis might also play an important role in the carcinogenesis and metastasis of breast cancer itself. However, the exact role of each player in this triad has been controversial in the literature. Our research focuses on the role of the RANK/RANKL/OPG axis in the tumorigenesis and transformation of mammary epithelial cells into a cancerous cell type and their further development into metastatic breast cancer phenotypes that preferentially migrate to the bone. In our study we will modulate RANK, RANKL, and OPG expressions in breast cancer cells as well as in human mammary epithelial cells at different stages of induced tumorigenesis and examine their migratory abilities and invasiveness.

TOXICOLOGY

66. ANALYSIS OF LEAD IN AMERICAN WOODCOCK (*SCOLOPAX MINOR*) USING INDUCTIVELY-COUPLED PLASMA MASS SPECTROMETRY (ICP-MS)

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Lead (Pb) concentrations in American woodcock (*Scolopax minor*) have been studied for several years and remain a conservation concern throughout North America. Woodcock foraging behavior makes them particularly susceptible to Pb accumulation from spent Pb-shot. Thus far, there have been no studies on Pb concentrations throughout the woodcock's geographic range using individuals from known origins. This work will combine previous work using stable isotope (deuterium) analyses on feathers from hatch year

(HY) woodcock to predict natal origins and estimate migratory connectivity of woodcock throughout its geographic range. For this study, ICP-MS was used to determine Pb concentrations among wings of HY woodcock using (a) second primary (P2) feathers to reflect natal origin lead exposure and (b) fourteenth secondary (S14) feathers to reflect Pb exposure during fall migration. Preliminary data shows that approximately 14 % of all feathers analyzed exhibited elevated (> 4 ppm) Pb concentrations. Females had larger average feather-Pb concentrations than males, suggesting that females may absorb greater concentrations of Pb. Thus far, data supports the original hypothesis that woodcock have relatively high feather-Pb concentrations and females have higher Pb concentrations than males.

67. HYPOXIA SENSITIVITY AMONG TEXAS FISH AND INVERTEBRATES: THE EFFECT OF CENSORED DATA ON PROTECTIVE BENCHMARK VALUES

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Anthropogenic nutrient input has fueled the spread of hypoxia in the Gulf of Mexico, which now features a prominent low-oxygen “dead zone”. Species sensitivity distributions (SSDs) can be used to model the proportion of species affected as a function of hypoxia intensity. An important benchmark value obtained from SSDs is the HC5, which is the estimated concentration at which 95% of species are protected. Unfortunately, the construction of SSDs is complicated by the lack of abundant, standardized data. A partial solution to the issue of limited data is statistical accommodation for censored values, which allows for inclusion of otherwise unused data. Censored data, expressed as less-than, greater-than, or interval values, are typically converted to point values by some arbitrary means or omitted altogether, increasing the likelihood of obtaining under or over protective benchmark values. In order to investigate how the common practice of omitting censored data influences HC5 estimates, a comprehensive literature review was carried out to gather information on hypoxia sensitivity among fish and invertebrate species of Texas. A maximum likelihood method was used to fit both uncensored and censored LC50 data sets to parametric SSD models. HC5 estimates with bootstrap-estimated confidence intervals were calculated and compared in order to assess the effect of including censored values. The results may be useful, firstly, in risk assessment and in the establishment of water quality criteria for Texas waters. Secondly, the results provide some guidance as to whether the exclusion of censored data has a significant impact on HC5s.

68. SUBCELLULAR COMPARTMENTALIZATION OF CADMIUM IN THE FRESHWATER SNAIL *LYMNAEA STAGNALIS*

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In ecotoxicology, analytical compartmentalization analysis can be used to interpret metal sequestration and detoxification. There are two main compartments, biologically detoxified metal (BDM) and metal sensitive fractions (MSF) that can provide valuable information about metal toxicity and tolerance. The purpose of this study was to analyze the subcellular distribution pattern of cadmium (Cd) in *Lymnaea stagnalis*. Adult snails were exposed to 3 concentrations of cadmium for 8 weeks. At the end of the exposure, organisms were euthanized and then separated in two sections (viscera and food). Each section was divided by differential centrifugation, followed by metal analysis. Results showed a statistically significant higher bioaccumulation of Cd in the viscera section compared to the foot. Cadmium accumulation also increased with increasing exposure concentrations. The MSF compartment (~65%) was in higher proportion than the BDM (~30%), but only in the lowest Cd exposure concentration was there a significant difference between these compartments. This indicated that there was more efficient detoxification in the two higher cadmium concentrations. We found a positive correlation between the concentration of Cd in the whole tissue and

both compartments. This study emphasizes the importance of understanding the cellular mechanisms that are involved in gastropods' metal detoxification capacity and efficiency.

69. INCIDENCE OF VETERINARY PHARMACEUTICALS IN WEST TEXAS PLAYA WETLANDS

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Veterinary pharmaceuticals, such as antibiotics, steroid hormones, and β -adrenergic agonists, are commonly used to promote weight gain and increase feed efficiency at beef cattle feed yards. These veterinary pharmaceuticals have been found in surface water and groundwater downstream of cattle feed yards. Veterinary pharmaceuticals can also be transported via airborne particulate matter. However, it is unknown whether dust particles are a substantial transport mechanism for veterinary pharmaceuticals that enter adjacent surface waters. This study assessed the incidence of veterinary pharmaceuticals in playa wetlands of the Southern High Plains region of west Texas. Playa wetlands located approximately 1-10 miles away from a feed yard were included in this study due to the potential of their basins to be exposed to feed yard dust but not wastewater. Water and sediment samples were obtained from 34 individual playa wetlands and analyzed using LC-MS/MS to quantify veterinary pharmaceuticals indicative of feed yards: 5 antibiotics, 6 steroid hormones, and a β -adrenergic agonist (ractopamine). These chemicals have potential to disrupt endocrine function and alter microbial communities. Results of this study have implications for biological diversity and potentially human health in arid or semi-arid regions that contain beef cattle feed yards.

70. BIOACCUMULATION, STRESS, AND SWIMMING IMPAIRMENT IN *DAPHNIA MAGNA* EXPOSED TO MULTI-WALL CARBON NANOTUBES

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With their versatile physiochemical properties, multi-wall carbon nanotubes (MWCNTs) have increased in industries such as agriculture and wastewater treatment. Some of these procedures involve direct application to terrestrial and aquatic environments, in which the potential for MWCNT exposure to aquatic organisms is possible. Although methods are available to quantify MWCNTs, it is often difficult to measure MWCNTs in complex matrices due to their carbon content and size. In previous studies, microwave-induced heating has been used to determine MWCNTs in biological samples. In this study *Daphnia magna* (*D. magna*) were used to measure MWCNT sublethal effects and bioaccumulation in the aquatic benthic community. *D. magna* (10-15 d old) were exposed to 8-15 nm outer diameter (O.D.) or 20-30 nm O.D. MWCNTs at concentrations of 0.1 mg/L in moderately hard freshwater for 2 d. MWCNT concentrations were measured using a fitted calibration curve produced by a microwave-induced heating method ($R^2 = 0.992$). Reactive oxygen species (ROS) was measured using dichlorofluorescein diacetate fluorescent dye in 10 individual *D. magna*. *D. magna* were also recorded for 10 s to measure swimming velocity to address impairment caused by MWCNTs at time points 0, 12, 24, and 48 h. Studies are currently ongoing.

71. MERCURY CONTAMINATION IN BATS FROM THE CENTRAL UNITED STATES

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Mercury (Hg) is a highly toxic metal that has detrimental effects on wildlife; we surveyed Hg concentration in ten species of bats collected at wind farms in the central United States and found contamination in all species. Hg contamination in fur from the 10 species examined was highly variable both within and between species (range 1.08-10.52 $\mu\text{g/g}$) with the lowest concentrations found in highly migratory species. Despite the distance between sites (up to 1200 km), only 2 of the 5 species sampled at multiple locations showed Hg concentrations consistent with regional variation. Juvenile bats tended to have lower fur-Hg levels than adult bats and we found no significant effects of sex on fur-Hg levels. For a subset of two species, we measured Hg concentration in muscle tissue as well as fur; concentrations were much higher in fur than in muscle and the two tissue types were weakly correlated. Mercury concentrations of 22 bats (3.8%) we examined exceeded the 7.8 $\mu\text{g/g}$ threshold known to cause lethal effects; however, the non-lethal effects of lower concentrations of Hg in birds and mammals have not been well studied. Additional research is needed to understand the impact of the levels of Hg observed in the present study and how it may interact with other threats to negatively influence bat survival. Abundant wind farms and ongoing mortality surveys offer an underutilized opportunity to obtain tissue samples that can be utilized by a variety of disciplines -from genetics to toxicology and beyond- to study bat populations without capturing live bats.

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