

Thesis Defense

The role of birds as hosts for ticks, vectors of *Borrelia burgdorferi*, in eastern Texas

Brian Gold

Major Advisor: Dr. Ivan Castro-Arellano

Committee Members: Dr. Clay Green & Dr. Maria Esteve-Gassent

November 6, 2017, 3:30 PM, Supple Science Building 376-A (Norris Room)

The bacterial spirochete *Borrelia burgdorferi*, the etiological agent of Lyme disease, an emerging infectious disease in the United States [US], has been detected in previous surveys in Texas. However, the northeastern and midwestern US are currently the areas with the highest abundance of cases of Lyme disease reported. Ticks infected with *Borrelia* of the genus *Ixodes* are solely responsible for transmission to humans, though other tick species maintain its persistence in the environment. The distribution of the black-legged tick, *Ixodes scapularis*, the primary vector of *Borrelia* to humans in the US includes most of the eastern portion of Texas. While adult *I. scapularis* ticks feed primarily on large mammals (e.g. deer), the larval and nymphal stages are generalists that will feed on numerous taxa, including small mammals, birds, and reptiles. This project, along with associated tick flagging, mammal, and reptile surveys in eastern Texas were implemented to ascertain how the *Borrelia* life cycle is structured at the local level in eastern Texas. The focus of my research was on the role that ground-dwelling and foraging birds had on the abundance and distribution of ticks in eastern Texas. The study sites chosen for this project were disturbed and more pristine sylvan habitats at Gus Engeling Wildlife Management Area [GEWMA] and Big Thicket National Preserve [BTNP]. A reference infestation rate of 5.1% was chosen to compare the observed infestation rate. In total, 211 birds were captured over two field seasons, 4 of which were found infested with Ixodid ticks (1.9%). This suggests that birds are not an important vertebrate host group for maintaining tick density at the local level in eastern Texas. Several migratory bird species that have been found in other studies to be important in translocating ticks were captured at each site. A comparison of the alpha and beta diversity at and among each site revealed that the habitats at GEWMA were most similar in composition, though the disturbed habitat at BTNP was the most diverse ($H' = 2.4840$).

Bio: Brian is originally from Durham, North Carolina and has lived in Texas for the last 20 years. He attended Collin College in Plano, TX and transferred to Texas State University, where he earned a B.S. in wildlife biology in 2014. As an undergrad Brian assisted with small mammal trapping and processing for grad students in Dr. Castro's disease ecology lab. Brian joined Dr. Castro's lab in 2015 as a graduate student (M.S. wildlife ecology) seeking to combine his interest in bird community structure and conservation with the lab's focus on wildlife disease systems. Brian has worked as a bird survey technician for the American Bird Conservancy (Texas), US Forest Service (Oregon), and most recently at Fort Hood, Texas for the University of Illinois-Urbana where he was part of a team that won the USFWS Conservation Partnership Award in June, 2017.

Thesis Defense

Reproductive Ecology of *Lampsilis bracteata* (BIVALVIA: UNIONIDAE)

Name: L. Ashley Seagroves

Major Advisor: Dr. Astrid N. Schwalb

Committee Members: Dr. Weston Nowlin & Dr. Thom Hardy

November 6, 2017, 1:00 PM, Freeman Aquatic Biology (FAB) 130 (Seminar Room)

Lampsilis bracteata (Texas Fatmucket) is one of fifteen threatened mussel species in Texas. A better knowledge of their reproductive ecology is needed to develop conservation and management strategies. The purpose of my study was to investigate differences in mussel host fish relationships between populations of *Lampsilis bracteata* and fish originating from the San Saba and Llano River in Central Texas, and to monitor and compare gamete production, gravidity period and viability of their larvae (glochidia) between the rivers. Gamete production, gravidity, and glochidia viability varied with season and were significantly higher in the San Saba compared to the Llano River. Transformation success of glochidia to juveniles differed significantly between host fish species, and on some fish species glochidia tended to transform better when they originated from the same river. The results of this study suggest that propagation efforts that are currently initiated in Texas should consider ecological differences between populations. Further investigations of the life-history strategies of *Lampsilis bracteata* and other mussels are warranted before augmentation and reintroduction efforts are initiated.

Bio: Ashley is a proud native to central Texas who developed a love for water at a young age. She graduated in 2014 with a B.S. in Wildlife Biology from Texas State University after dipping her toe into the world of aquatic ecology by working as an undergraduate researcher. She went on to use her knowledge of wildlife and fisheries as a research technician before beginning her Master's degree. In her time at Texas State University she was selected as a recipient of the Chuck Nash Aquatic Studies Scholarship in 2016 and 2017, and was awarded Best Student Poster at the 2017 annual meeting of the Texas Chapter of the American Fisheries Society. She would now like to pursue a career in freshwater ecology, and cannot get enough of these crazy critters that we call freshwater mussels. She would like to thank all of her friends and family for their support—including her trusty and snuggly dog friend, Mr. Jack.

Thesis Defense

Development of a rapid diagnostic test for detection of *Streptococcus mutans* in saliva for dental caries diagnosis

Name: Kelly L. Braddock

Major Advisor: Dr. Shannon Weigum

Committee Members: Dr. Robert McLean, Dr. John Carrano

Monday, November 6, 2017, 8:00 AM, Supple Science Building 257

The personal and financial impact of common and often overlooked oral diseases, such as dental caries, is sizable and prevalent throughout the world. Rapid diagnostic tools continue to be developed to prevent, diagnose and monitor treatment responses of a variety of diseases including, dental caries. This assay, like many other point-of-care diagnostics, is based on the lateral flow immunoassay design. Initial development required identification of two antibodies that specifically recognize antigens on the surface of *Streptococcus mutans*, and are compatible as a matched pair. To identify a matched pair, antibodies were first purified from hybridoma cell culture supernatant, by affinity chromatography, and screened against two *S. mutans* strains of differing serotypes. The two hybridoma cell lines for which antibody was successfully purified, were screened and both indicated activity against one *S. mutans* strain of the most common serotype, serotype c. However, only one of the purified antibodies was able to recognize the non-serotype c strain. Further assay development focused only on the strain of *S. mutans* recognized by both antibodies. Conjugation to biotin allows the detection antibody to form a complex with the reporter molecule HRP, which is conjugated to streptavidin. A portion of both antibody stocks were conjugated to biotin and each of them was tested in both the detecting and capture positions, in order to determine the optimal orientation of the matched pair. Only one orientation recognized *S. mutans* within the lateral flow assay. Initial experiments indicated that the lower limit for *S. mutans* detection was within the clinically relevant range, for which concentration of salivary *S. mutans* can be used to diagnose dental caries. After identifying a matched pair, detergent concentration as well as blocking conditions were optimized. To assess analytical performance within a realistic matrix, a dose response curve was created from samples made in human pooled saliva. The dose response indicated results of the assay at varying concentrations were reproducible, but detection of *S. mutans* occurred only at concentrations much higher than in previous testing. This discrepancy is likely due to matrix effects within saliva, including presence of endogenous proteins and high viscosity. Future testing to optimize the assay within saliva, may improve its detection capabilities by mitigating some of these matrix effects, through addition of detergents or mucolytic agents.

Bio: Kelly was born in Louisiana and raised in Central Texas where she spent most of her childhood playing soccer. After earning a B.S. in Biology from Texas State University in San Marcos, she decided to pursue a M.S. focusing on microbiology and their detection by point-of-care diagnostics. Kelly hopes to continue her career in the point-of-care diagnostics field.

Dissertation Defense

Epigenetic regulation of the defense gene induction in *Arabidopsis thaliana* in response to *Pseudomonas syringae*

Name: Yogendra Bordiya

Major Advisor: Dr. Hong-Gu Kang

Committee Members: Dr. Nihal Dharmasiri (Dept. of Biology, Texas State University)

Dr. Sunethra Dharmasiri (Dept. of Biology, Texas State University)

Dr. Daniel F. Klessig (Boyce Thompson Institute, Cornell University)

Dr. Ping He (Department of Biochemistry, Texas A&M University)

November 3, 2017, 2:00 PM, Supple 116

Plants and animals respond to ever changing environment by making changes in the physiological level of various proteins and metabolites. The rapid physiological change to the environment is achieved by massive transcriptional reprogramming. Therefore, switching the large number of genes on and off at the right time in the right place requires highly sophisticated transcriptional regulation and is very important in mounting responses appropriate for the environmental change/stress. Recent studies begin to suggest that epigenetics is one of the critical components in the regulation of transcription to help responding and adapting to environmental changes/stresses. The epigenetic regulation of transcription is achieved through the modification of the chromatin structure, which is generally mediated by DNA/histone modifications, small RNAs (sRNAs), long non-coding RNA, and nucleosome positioning. In my dissertation, I have studied the role of epigenetic components which regulate defense responses in *Arabidopsis thaliana* in response to *Pseudomonas syringae*. To this end, I assessed biotic-stress-triggered changes in chromatin accessibility and characterized several epigenetic mutants in gene silencing in *Arabidopsis*. From these assessments, I particularly focused on testing the hypothesis that these epigenetic changes are important in the induction kinetics of defense genes triggered by infection. Intriguingly, I found that biotic-stress-triggered chromatin changes were frequently associated with transposable elements (TEs) proximal to defense genes, some of which functioned as transcriptional enhancers. This observation suggested that a TE controlling mechanism(s) might be important in defense responses. Indeed, I found that more than a hundred of TEs become transcriptionally induced under biotic stress, which justified further characterization of mutants involved in RNA-dependent DNA methylation (RdDM), the best characterized regulatory mechanism for TEs. I chose to characterize four DCL (dicer-like) genes that are important in the biogenesis of sRNAs, critical modulators for TEs and chromatin remodeling. Among these dcl mutants, dcl1 displayed the most compromised resistance and induction of defense genes against avirulent *P. syringae*, suggesting that some sRNAs may be necessary for the rapid defense responses. In contrast, dcl2 and dcl3 showed marginally enhanced resistance and elevated expression of defense genes to the avirulent pathogen. In particular, dcl2 and dcl3 showed substantially increased expression of defense genes without pathogen challenges, suggesting that DCL2/3-generated sRNAs are important in suppressing defense genes. Note that the expression analysis of defense genes was performed using a novel targeted RNA-seq known as RASL-seq (RNA-mediated oligonucleotide Annealing, Selection, and Ligation with next-generation sequencing) on defense genes.

Selection of the defense genes was based on my RNA-seq analysis, which identified rapid induced genes at different time points in response to avirulent *P. syringae* as compared to virulent counterpart. In addition to altered defense gene induction in the mutants, I also found that many RdDM genes including *morc1/2* were transcriptionally suppressed as early as 6 hr post infection, suggesting a dynamic nature of these epigenetic components in defense responses. Based on the presented observation, I have described a model how defense responses are epigenetically regulated and discussed the implication of this regulation in the evolution of resistance traits.

Bio: Yogendra received bachelor's degree in Agricultural Science in 2009 from the University of Agricultural Sciences Bangalore, master's degree in Crop Science and Biotechnology in 2012 from Seoul National University and started doctoral research with Dr. Hong-Gu Kang at Texas State University in August 2012.

Thesis Defense

Effects of urbanization on the relative abundance of hummingbirds (*Archilochus alexandri* and *Archilochus colubris*) as measured by

resource removal rates.

Name: Caley Zuzula

Major Advisor: Dr. Joe Veech

Committee Members: Dr. Jennifer Jensen (Geography), Dr. Jeff Troy (Temple College, Temple, TX)

November 3, 2017, 1:00 PM, Supple 153

Urbanization leads to loss of natural habitat, an increase in impervious surfaces, and sometimes an increase in the provisioning of artificial food sources for local wildlife. One common scenario of supplemental feeding includes artificial nectar feeders placed out for hummingbirds, typically within suburban neighborhoods. These can be so successful at attracting hummingbirds as to cause an increase in local density. Thus intermediate intensities of urbanization could have an indirect positive effect on hummingbirds. While previous studies have investigated persistence of hummingbird populations across an urban-rural gradient, my study is the first to examine removal rates of resource (sucrose solution) from hummingbird feeders as a proxy variable for relative hummingbird abundance. I deployed nectar feeders (N=27) in locations encompassing various intensities of imperviousness (percent impervious surface as an indicator of urbanization intensity) and canopy cover around San Marcos, Texas, USA, to determine whether these factors affect removal rates of sucrose solution by *Archilochus alexandri* and *Archilochus colubris* at 100, 200, and 400 m spatial scales. Canopy cover was presumed to roughly indicate the availability of habitat. Data were collected in Summer 2016 and 2017. Extraneous variables including Julian date, resource availability (ornithophilous plants), precipitation, and temperature were examined, but none of these individually had an effect on solution consumption ($p > 0.05$). Imperviousness had a significant negative linear effect on solution consumption across all three spatial scales, indicating that hummingbirds become increasingly less abundant with an increase in urban development ($p < 0.05$). Canopy cover had a non-significant effect ($p > 0.1$) on solution consumption at all spatial extents. In addition to developing a reliable method for surveying hummingbirds, my findings show that urbanization, despite warmer local temperatures and increased food provisioning, may negatively affect some hummingbird populations.

Bio: Caley was born and raised in San Antonio, Texas. She started appreciating wildlife in elementary school after catching some tadpoles and raising them to frogs. After high school, she attended Hendrix College in Conway, Arkansas, where she earned her Bachelor's degree in Biology. During college, she developed a deep interest in ecology and evolution through various experiences, including undertaking an animal care internship at the San Antonio Zoo, studying tropical ecology in Costa Rica, doing bioinformatics research on colorectal cancer, and learning about human evolution by studying Paleolithic caves in western Europe. Upon graduating college, she worked as a naturalist at the University of Georgia's satellite campus in Monteverde, Costa Rica, where she taught people from around the world about rainforest ecology. Before starting graduate school at Texas State, she worked as an education intern at the Bamberger Ranch in Johnson City, where she gained hands-on experience about ranch management. In addition to working on her Master's degree, she teaches undergraduate

labs and works at Texan by Nature, a wildlife nonprofit organization based out of Austin. In her free time, Caley enjoys hiking, birding, insect collecting, and cooking.

Thesis Defense

Characterization of the IBR5-PAD1 Interaction in Arabidopsis Auxin Response

Name: Nicholas Siefert

Major Advisor: Dr. Nihal Dharmasiri

Committee Members: Dr. Sunethra Dharmasiri, Dr. Hong-Gu Kang, & Dr. Dana Garcia

November 2, 2017, 5:00 PM, Supple Science Building 376-A (Norris Room)

Plant hormones utilize the ubiquitin-proteasome system (UPS) to modulate the expression of specific genes involved in various developmental processes as well as responses to environmental stress. In this process the target proteins are polyubiquitinated by a multi-subunit E3 ubiquitin ligase complex, essentially tagging the target proteins for degradation by the 26S proteasome. One specific type of E3 ligase, the SKP1-CULLIN1-F-BOX protein (SCF) complex, is utilized by several plant hormones to ubiquitinate target proteins. This process is highly specific and requires multiple levels of regulation which are not fully understood. Recent studies have shown that the INDOLE-3-BUTYRIC ACID RESPONSE5 (IBR5) gene, which encodes a dual specificity phosphatase, plays an important role in the auxin signaling pathway. IBR5 negatively regulates Aux/IAA repressor protein degradation, and has been shown to interact with the SKP1 (ASK1 in Arabidopsis) component of the SCF complex. Additionally, IBR5 has been shown to interact with a variety of stress response and signaling proteins such as HSP90 and MPK12. This research identifies and characterizes a novel interaction between IBR5 and PAD1, a subunit of the 20S core of the proteasome. The interaction between IBR5 and PAD1 was confirmed in vitro and in vivo. Additionally, specific domains or regions of each protein were identified to be crucial for this interaction. Characterization of the IBR5-PAD1 interaction provides new insights into the potential function of IBR5 in SCF E3 ligase-mediated protein degradation. Furthermore, IBR5 and PAD1 mutant analysis revealed similarities in auxin-related phenotypes, suggesting a functional connection between IBR5 and PAD1.

Bio: Nick grew up in central Texas, and was a member of the first graduating class of Manor New Technology High School. This school system focuses on project-based learning and preparing students for STEM fields. While attending Texas State University, Nick developed an interest in molecular biology and joined the Dharmasiri lab in the spring of 2014. He received the Francis Rose Undergraduate Award for Excellence in Biological Research to help fund his work. In the fall of 2014, Nick earned a B.S. in Biology with a minor in Biochemistry from Texas State University. He went on to join the M.S. program in Biology at Texas State University, continuing his research into plant hormone signaling. Nick is currently exploring job opportunities in the biotech industry.

Thesis Defense

DETECTING THE PRESENCE OR ABSENCE OF ALTERNATIVE SPLICING OF THE SUPERKDR LOCUS IN HORN FLIES, HAEMATOBIA IRRITANS

Name: Gabriela Solis

Major Advisor: Dr. Ivan Castro-Arellano

Co-Advisor: Dr. David Rodriguez

Committee Member: Dr. Dana Garcia

Wednesday, November 1, 2017, 9:00 am, SUPP 257

Changes to pest control efforts are dependent on interactions between insecticides and the pests they target. Horn flies (*Haematobia irritans*) are agricultural pests that cause economic losses owing to their effect on cattle and their resistance to insecticides. The Superkdr locus is a single nucleotide polymorphism from Thymine to Cytosine resulting in an amino acid change from Methionine to Threonine. This specific mutation has been associated with pyrethroid-resistance in horn flies. In the houseflies (*Musca domestica*), the superkdr locus was discovered to occur on mutually exclusive exons, exon C and exon D. The purpose of my research is to determine if alternative splicing is occurring at the superkdr locus of horn flies. I used two different methods to determine the presence or absence of alternative splicing. The first method involved sequence analysis of the sodium channel gene containing the superkdr locus. cDNA and genomic DNA were cloned, sequenced, and compared using MacVector. The second method used a single-nucleotide polymorphism (SNP) assay to perform genotyping via real-time PCR. The SNP assays allowed me to genotype the superkdr locus in cDNA and genomic DNA, and simultaneously detect alternative splicing if the locus was not detected in cDNA. I found no significance difference between the genotype of the superkdr locus in genomic DNA compared to cDNA. If alternative splicing of the superkdr locus is occurring, it seems to be rare.

Bio: Gabriela Solis was born and raised in Laredo, Texas. In 2015, she earned a B.Sc. in Biology with a minor in Chemistry from Texas State University. As an undergrad, Gabriela gained research experience by interning with USDA-ARS working with cattle fever ticks and Porcine Reproductive and Respiratory Syndrome. She decided to pursue a M.Sc., and in Fall 2015 joined the Castro and Rodriguez lab at Texas State. Gabriela hopes to continue her education by pursuing a dual degree in DVM and PhD.

Thesis Defense

Distribution of the Texas kangaroo rat (*Dipodomys elator*) in Texas, with comments on microhabitat, habitat, and habitat modeling

Name: Silas Ott

Advisor: Dr. Joe Veech and Dr. Randy Simpson (co-advisors)

Committee Members: Dr. Ivan Castro-Arellano, Dr. Clay Green

October 27, 2017, 9:00 AM, Supple 257

The Texas Kangaroo Rat (*Dipodomys elator*) is a species of conservation concern in Texas with sightings in only seven counties in the past 30 years. The decline of *D. elator* has been attributed to habitat loss, although its exact habitat requirements have not been determined. Habitat studies have focused on microhabitat and burrow associations but have failed to create an accurate landscape level habitat model. Multiple species within the genus *Dipodomys* have demonstrated strong associations with certain soil and land-cover types. My goal was to determine which soil and land-cover types are associated with *D. elator* and then use these associations to model potential habitat across their historic 11-county range. During the summers of 2016 and 2017, I surveyed with spotlights at night for *D. elator* on public roads throughout its historic range. I found the species at 75 and 63 locations in 2016 and 2017, respectively, among five counties. For analysis, random points were generated along the roads surveyed in 2016 to create a dataset of points representing species absence. A two-group randomization test was used to determine if percent composition of soil and land-cover types (within 150 m buffers surrounding the points) were significantly different between 2016 presence and absence points. Presence points had a significantly greater proportion of mixed grass/shortgrass prairie ($P < 0.1$), cropland ($P < 0.05$), clay loam and loam as the topmost soil layer ($P < 0.05$), and friable clay as the underlying soil layer ($P < 0.05$) than did absence points. Based on these results, a potential habitat model (map) was created using ArcGIS. This model portrays a much more restricted range than that shown by previous modeling efforts; $< 30\%$ of the 11-county area is potential habitat. Given its very limited range, habitat specificity, and potentially small population sizes, *D. elator* should be monitored carefully with the possibility of establishing populations in protected areas

Bio: Silas was born in Takoma Park, Maryland, but moved to Texas as soon as he could, growing up in the countryside of the Devil's Backbone. Since a young age, Silas has had a fascination with flora and fauna of all forms, naming plants and animals as soon as he started talking and reading every field guide he could get his hands on as soon as he learned to read. As a young adult, Silas knew his future career would involve biology in some aspect. As an undergraduate at Texas State, Silas worked in multiple labs assisting with both field and lab work in addition to being the instructional assistant for two senior level courses. He also has worked for the Lower Colorado River Authority as a nature education and recreation facilitator. As a graduate student, Silas has spent the last two summers chasing kangaroo rats around north Texas and has also worked as a biological survey contractor for multiple projects. Silas hopes to start his career as a field technician so that he can be paid to travel around the United States. and continue his adventures in the great outdoors.

Thesis Defense

EVALUATING THE DETECTION OF SEASONALLY PRESENT, POND-BREEDING AMPHIBIANS USING ENVIRONMENTAL DNA: A CASE STUDY WITH THE HOUSTON TOAD (*Bufo* [=Anaxyrus] *houstonensis*)

Name: William Keitt

Committee Members: Dr. Dittmar Hahn, Dr. David Rodriguez

Tuesday, October 31st, 2017, 8:00 AM, Supple Science Building 376-A (Norris Room)

Molecular survey techniques focusing on the detection of species via environmental DNA (eDNA) are increasingly being implemented for the detection of a wide breadth of animal taxa. Despite increasing use, relatively few studies have evaluated this method for seasonally present pond-breeding amphibians. This study seeks to provide an evaluation of the efficacy of eDNA surveys for the detection of one such species, the Houston toad (*Bufo* [=Anaxyrus] *houstonensis*). The Griffith League Ranch (GLR), a primary recovery site in Bastrop County Texas, was sampled weekly during the Houston toad breeding season from February to June of 2016 and sporadically in the spring of 2017. Nine perennial ponds on the GLR were surveyed and 557 water samples were collected for eDNA analysis, with 217 representing known positive controls collected from buckets containing each life stage of this amphibian. Samples were collected following a USGS approved protocol (Goldberg et al. 2011). Both PCR and nested PCR assays were used to assess Houston toad detection/non-detection based on positive amplification of a diagnostic fragment of mitochondrial DNA. PCR assays successfully showed amplification of Houston toad eDNA in 82% of known positive controls, while only 1.1% of eDNA samples from the sampled ponds, and none of the eDNA samples from known positive ponds showed amplification. Nested PCR assays proved more efficient, detecting Houston toad eDNA in 86% of all known positive control samples, 7.4% of all pond samples, and 14% of the known positive pond samples. Our results suggest that these PCR-based detection methodologies for eDNA incur false negative detections, and therefore, are likely less reliable than current survey approaches. The inability of eDNA surveys to accurately detect species presence may be impacted by a variety of factors ranging from environmental inhibitors to lack of assay sensitivity. Therefore, I offer many critical considerations for the implementation of this monitoring strategy in the detection of elusive, seasonally present, pond-breeding amphibians.

Bio: William Keitt was born in northern Virginia and moved to Corpus Christi, Texas at a young age. In 2014, he earned a B.Sc. (AG.) in Animal Science from Texas State University which he used to promptly get a job in a non-agricultural based field as a laboratory technician in Austin, Texas. He decided to pursue a M.Sc., focusing on molecular genetics, and returned to his Alma Mater, joining the Forstner lab in the Fall of 2015. William's career interests lie in the field of pharmacogenomics, where he hopes to continue developing his skills as a geneticist, and use biotechnology to improve patient care.

Thesis Defense

SURVEYING MIXED-SPECIES WATERBIRD COLONIES WITH UNMANNED AERIAL SYSTEMS (UAS): VISIBILITY BIAS, DISTURBANCE, AND PROTOCOL RECOMMENDATIONS

Jarred Barr

Major Advisor: Dr. M. Clay Green

Committee Members: Dr. Stephen J. DeMaso and Dr. Thomas B. Hardy

Thursday, 19 October 2017, 9:00AM, Supple Science Building 376-A (Norris Rm.)

Surveys of colonial-nesting waterbirds are necessary for assessing population trends, gaining insight into wetland ecosystem health, and even determining the impact of natural disasters and other environmental concerns. The popularity of unmanned aerial systems (UAS) for use as a survey tool has risen in the past decade, but little research has been conducted on the effectiveness of such technology. I investigated visibility bias and disturbance impacts associated with using UAS to survey waterbird colonies in Texas, specifically in cypress-tupelo watershed and coastal island habitats. I used a stratified random design to place “colonies” of four different decoy types in each habitat, and had six observers independently count decoys from aerial imagery obtained with a consumer-grade UAS (DJI Phantom quadcopter). I used generalized linear mixed-effects models (GLMMs) with a Poisson error distribution to estimate detection probabilities of each decoy type. Black skimmers were the only decoy type at the dredge-spoil island to have a detection probability of significantly less than 100% (0.54 [0.44–0.63 CI], $P \leq 0.001$). Detectability of both white- and dark-plumaged herons decreased considerably in the canopied cypress-tupelo habitat when compared to dredge-spoil island (by 80 and 84%, respectively). I investigated disturbance to waterbirds by setting up video cameras at the periphery of active nesting colonies while surveying with unmanned aircraft. I tested the effects of two UAS types on the behavioral reactions exhibited within four active colonies in Texas, and reactions were tallied in 1-minute sampling periods for each nesting colony. These data were used to estimate GLMMs for vigilance and flush behavior. I found that the DJI Phantom quadcopter significantly increased vigilance for 3 of the 4 survey altitudes tested. Vigilant reactions increased in magnitude by 72, 119, and 118% for survey altitudes of 91, 61, and 46 m, respectively. Flush reactions were not influenced by either UAS type or any altitude flown. My results suggest that managers should employ UAS surveys on clear days in high-visibility habitats, or otherwise use another survey method to supplement photographic counts obtained by UAS. In addition, surveys should be flown between 46–91 m only when high resolution imagery is needed (e.g. for abundance estimates) to mitigate disturbance. Even though the Phantom UAS caused increased vigilance, if surveys are done promptly and in back-and-forth transects, the impact of this increased behavior is likely negligible especially when considering the much more harmful effects of ground-based survey methods.

Bio: Jarred Barr was born and raised in Trabuco Canyon, California. In 2009, he earned a B.Sc. degree in Wildlife Biology from Humboldt State University, and shortly thereafter worked as a field biologist for various agencies. From 2012–2015 he worked as an Ecologist for US Geological Survey, helping monitor the nests of numerous waterbird species in the wake of a large-scale restoration project for the San Francisco Bay. He decided to pursue a M.Sc., and in Fall 2015 joined the Green lab at Texas State. Jarred

hopes to continue as a conservationist/ecologist in some capacity, and hey, if he can get paid while doing that, that'd be cool too.

Dissertation Proposal

Determining the status and distribution of the Eastern Black Rail (*Laterallus jamaicensis jamaicensis*) in Texas

Amanda Moore

Major Advisors: Floyd Weckerly and Clay Green, Department of Biology, Texas State University

Committee Members: Thom Hardy, Department of Biology, Texas State University; Chris Butler, Department of Biology, University of Central Oklahoma; Paul Leberg, Department of Biology, University of Louisiana Lafayette

Friday, September 1, 2017, 9:00 am, Supple 257

The enigmatic Black Rail (*Laterallus jamaicensis*) is often regarded as the most secretive marsh bird in North America. The Eastern Black Rail (*L. j. jamaicensis*) may be the most endangered bird species along the Atlantic and Gulf coasts of North America, as it is listed as endangered in six eastern states and is a candidate for federal listing. Texas represents a knowledge gap critical to the development of the species status assessment (SSA) needed for the proposed listing rule in the Federal Register (to be published September 2018). Determining the status of a species or its populations is an arduous task but there are some principles that can help inform conservation efforts: resiliency and redundancy. The objective of my research is to assess the current status of the Eastern Black Rail in the state of Texas, specifically in terms of resiliency and redundancy of rail populations. I hope to better understand Black Rail habitat requirements in Texas by examining home range size, movements, and habitat selection through the use of radio telemetry, and use occupancy-detection data obtained from standardized surveys to develop species distribution models for the Black Rail along the Texas coast.

Bio: Amanda spent her formative years in Illinois and moved to Texas at the ripe old age of 21. After attending UT San Antonio for two years she relocated to Dallas where she graduated from UT Dallas with a B.A. in art & technology. Working office jobs for the next few years led to a dull existence so she decided to follow her heart and peruse a graduate degree in wildlife ecology at Texas State and study birds.

Dissertation Proposal

"The impact of dispersal assessment methods on the resulting management interpretations of endangered species stewardship"

Shashwat Sirsi

Major Advisor: Michael R. J. Forstner, Department of Biology, Texas State University

Committee Members: David Rodriguez, M. Clay Green, Department of Biology, Texas State University.

Yongmei Lu, Department of Geography, Texas State University

Michael L. Morrison, Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas

Brian J. Halstead, U.S. Geological Survey, Western Ecological Research Center, Dixon, California

Wednesday, August 23, 2017, 2:00 pm, Supple 257

Movement in animals play a major role in determining the fate of individual organisms as well as the structure and dynamics of populations. Effective stewardship of animal populations needs to be cognizant of an accurate determination of individual movement rates. A large array of techniques are available to determine movements of individual organisms and thereby, the connectivity between groups of interbreeding individuals. However, it is not clear that the limitations or benefits to management decisions among the techniques have been synthetically analyzed. This is critical given the pace of modern urbanization and the increasing pressures placed on animal populations by human infrastructure impacts requires management decisions for mitigation. Three major frameworks enable the determination of movement rates, i.e. capture-mark-recapture, telemetry, and population genetics. The central theme that underpins this research is that a comparison of dispersal ranges from different data sources will likely reveal biases in consequent management or regulatory approaches. My research will first attempt an analytical review across taxa to demonstrate such biases and differences inherent to each study framework. I will then attempt to establish evidence of framework-specific differences in comparing estimates of movements for the Rio Grande Cooter (*Pseudemys gorzugi*) and in using potentially disparate framework-specific movement estimates in a broad-scale determination of availability, suitability, and connectivity of habitat for the endangered Houston Toad (*Bufo* [=*Anaxyrus*] *houstonensis*). Both species occur in highly-modified landscapes and approximating true individual-level dispersal increases chances of recovery through management decisions applied at an appropriate scale.

Bio: Shash is from Bangalore in southern India. He graduated with a Bachelor's degree in Environmental Sciences and subsequently earned a Master's Degree from the University of Kent at Canterbury, UK. He worked for an NGO that attempted freshwater turtle recovery for over 8 years. This short stint at attempting conservation without a true understanding of research and study design led him to pursue a PhD at Texas State University.

Thesis Defense

BRIDGING THE GAP: ATTEMPTING TO INCREASE LANDSCAPE CONNECTIVITY USING WILDLIFE
CORRIDORS IN THE LOST PINES ECOLOGICAL AREA OF TEXAS

Payton Prather

Major Advisor: Dr. Michael R. J. Forstner

Committee Member: Dr. Shawn F. McCracken & Dr. Thomas R. Simpson

Thursday, August 3, 2017, 2:00 pm, Norris Room

Artificial wildlife corridors are a potential solution to mitigating wildlife-motorist collisions and maintaining habitat connectivity. Such structures are components toward conservation stewardship of both species and landscapes. The Lost Pines region is home to the endemic, and endangered, Houston Toad. These structures serve as mitigation efforts to allow the Houston Toad and other wildlife a safe passage among habitat patches despite barriers to dispersal. Highway 290 in Bastrop County bisects critical habitat of the endangered Houston Toad. Wildlife corridors have now been installed (December 2016) at locations based on previous data indicating areas of high wildlife traffic. My study applies a suite of monitoring techniques to determine usage of artificial wildlife corridors along section the roadway. Monitoring techniques include camera trapping and wildlife mortality surveys (walking and driving). In order to determine usage of these corridors, camera traps were placed at the opening of each culvert. Wildlife mortality surveys along the roadway seek to determine areas of high density, and examine mortality densities post-installation of corridors. I compared wildlife mortality observations found in the construction area during construction and post-construction. These results show no difference in mortality observations between treatments. However, there is a significant difference in observations between survey methods (walking vs driving). I also monitored each wildlife-crossing structure and remaining culverts for usage by wildlife. Camera traps at the both WCS resulted in low observations of utilization by small mammals with high usage outside each structure. Track pads yielded similar results with both small and large species currently utilizing these structures. Continued monitoring is imperative in order to determine long term impacts of WCS and their resulting potential change on wildlife mortalities along this highway system.

Bio: Payton is originally from El Campo, Texas and received a B.S. in Wildlife Biology from Texas State University. Payton began working in the Forstner lab in the pursuit of his undergraduate degree assisting with management projects for the endangered Houston Toad. Upon completion Payton began his Master's of Science in Wildlife Ecology at Texas State University in the Forstner lab in the Fall of 2016. His research interests involve conservation management and stewardship of endangered and threatened species. Payton is supported by his wife Lauren and daughter Freya.

Thesis Defense

INFLUENCE OF INDOLE AND MIXED CULTURE GROWTH ON PSEUDOMONAS AERUGINOSA BIOFILM STRUCTURE

Name: Ernesto Valenzuela, Jr.

Major Advisor: Robert JC McLean

Committee Members: Gary M Aron, Stacie Brown (Southwestern University)

Date: Thursday July 6, 2017, 10:00am, Supple 153

When microorganisms are studied within their natural environments, they are not commonly found as single species. Microbes are usually found as clusters or multitudes of aggregates within surface-attached biofilm communities. The discovery of this sessile lifestyle has had a resounding effect on the scientific community and the approach toward studying anti-microbial resistance (AMR). Past studies showed that quorum sensing (QS) mutants of *Pseudomonas aeruginosa*, unable to produce N-acylated homoserine lactone (AHL) signals had altered biofilm structure. During mixed culture growth of *P. aeruginosa* with *Escherichia coli*, we found that *E. coli* production of the organic compound, indole, inhibited AHL-regulated genes in *P. aeruginosa*. The current study was conducted to see if mixed culture growth of *P. aeruginosa* with indole-producing *E. coli* affected biofilm structure. Two wt *Pseudomonas aeruginosa* strains, PA14 and PAO1 were co-cultured with wt *Escherichia coli* BW25113 (indole producing), and *E. coli* tryptophanase mutant *tnaA* (non-indole producing). Comparably, exogenous indole was added in multiple concentrations (mM) in order to try and monitor the response of the *P. aeruginosa* strains. *P. aeruginosa* *pqs* mutant strains were also studied in order to see if indole induced similar effects in a non-AHL mediated QS system. At lower concentrations (0.1mM), indole induced a spike in growth rates and genes geared toward virulence mechanism of *P. aeruginosa*. In contrast, higher concentrations (0.5 or 1mM), overall induced downregulation of virulence mechanisms controlling, pyocyanin, rhamnolipids, and elastase production, inhibiting quorum sensing. However, there was no obvious change in biofilm structure at any of the indole concentrations tested.

Bio: Ernesto Valenzuela, Jr. was born October 13, 1979 in Caldwell, Texas. Also known as the "Original Kolache Capital of Texas". He relocated to Little Rock, Arkansas where he attended The University of Arkansas at Little Rock, while working as a research technician in Biochemistry and Molecular Genetics at The University of Arkansas for Medical Sciences. He would graduate with honors as a Ronald E. McNair Scholar, completing a bachelors in Biology with a minor in Environmental Health Sciences. Upon graduation he managed a medical-based research laboratory in Toxicology & Pharmacology at The University of Arkansas for Medical Sciences before deciding to pursue graduate work at Texas State University under Professor R.J.C McLean.

Thesis Defense

MAMMALIAN ASSEMBLAGE STRUCTURE AND HOST-USE PATTERNS OF *I. SCAPULARIS* ACROSS ANTHROPOGENIC DISTURBANCES IN EAST TEXAS

Name: Bradford J. Westrich

Major Advisor: Dr. Iván Castro-Arellano – Texas State University

Committee Member: Dr. Maria Esteve-Gassent – Texas A&M University

Dr. Thomas R. Simpson – Texas State University

Tuesday, July 11, 2017, 2:00 pm, Supple 153

Borrelia burgdorferi, the causative agent of Lyme disease, is responsible for infecting more than 30,000 people annually in the United States (US), with 95% of cases reported in the Northeastern US. However, human risk for contracting Lyme disease in Texas is much lower, with only 54 cases reported in 2015. Understanding the composition of mammalian reservoir host assemblages is commonly used to predict areas of greatest concern for human risk of Lyme disease. Community dynamic factors such as predation and competition greatly influence the composition of hosts present at any given time; however, anthropogenically-disturbed habitats are positively correlated to increased densities of highly competent *B. burgdorferi* reservoirs and vectors. My research objectives were to 1) assess if mammal assemblages differed across habitat disturbances; 2) determine if tick intensities were greater in disturbed habitats; 3) assess host-use patterns of tick vectors across East Texas; and 4) identify whether known vectors are associated with competent reservoirs of *B. burgdorferi*. I found that mammalian assemblages share high degrees of richness and evenness (Hurlbert's PIE = 0.77 – 0.84), although disturbed habitats have greater proportions of rare species comprising 26 – 39% of assemblages. Average individual tick intensity differed across ecoregions in sylvan habitats with 634 ticks collected from mammals at Gus Engeling Wildlife Management Area (GEWMA) and 159 ticks collected from mammals at Big Thicket National Preserve (BTNP). I suspect this difference to be the result of a 13% increase in meso mammal species with greater tick intensities captured at GEWMA. Furthermore, host-use patterns were observed for all *Ixodes scapularis* adults utilizing meso mammal hosts and approximately 99% of *Dermacentor variabilis* nymphs selecting small mammal hosts. These results indicate that across evenly distributed mammalian assemblages in East Texas the prevalence of *B. burgdorferi* is expected to be low due to the rarity of competent reservoirs and association of known vectors with poor tick hosts.

Bio: Bradford J. Westrich received his B.S. in conservation ecology (2010) from New Mexico State University where he was first introduced to mammal sampling. He then went on to study scarlet macaws in Central America before monitoring threatened and endangered species with the Utah Department of Natural Resources. Prior to joining the Master's program at Texas State he captained a fleet of airboats charged with monitoring endangered raptors in Florida.

Thesis Defense

SPRINGSHEDED DELINEATION AT CAVE WITHOUT A NAME, TX: DYE TRACING IN THE LOWER GLEN ROSE LIMESTONE

Mark D. Hiler

Major Advisor: Benjamin F. Schwartz

Committee Member: Weston H. Nowlin and Thom B. Hardy

Thursday, July 6, 1:00 pm, Freeman Aquatic Building 130

Cave Without a Name (CWAN) in Kendall County, TX contains ~5.5 km of active stream conduits formed in the karstic Lower Glen Rose Limestone which forms part of the Trinity Aquifer System. The primarily rural Kendall County lies just northwest of San Antonio in the Texas Hill Country. The Trinity Aquifer is the primary source of freshwater for this and many other Hill Country counties, although its yields are relatively low compared to the adjacent Edwards Aquifer. Springsheds contribute water via recharge features to a spring and are similar to watersheds, except that their boundaries are not constrained by topography. To delineate a springshed for Cave Without a Name, dye tracing was performed by injecting dyes into recharge features in the land surface. Dye tracing utilizes conservative tracers (non-toxic dyes) to trace recharging waters from direct recharge sites to a point of discharge (e.g., springs). For this project, multiple traces were performed from direct recharge sites (sinkholes and/or caves). Regional flow near CWAN is to the Southeast while local flow is towards springs and streams. The Guadalupe River, Spring Creek, and Sabinas Creek are assumed to act as local discharge boundaries, along which a number of known springs occur. Prior work by Veni (1994) and this work suggests that there may be several adjacent springsheds in the area, which is near a large oxbow in the Guadalupe River, just upstream from the confluence with Spring Creek. Results showed groundwater flow velocities in the area ranging from high velocity flow (~0.36 km/day) through preferential flowpaths to diffuse flow through the epikarst with low velocity flow (~0.02 km/day). Type of recharge feature, injection method, and hydrologic conditions were found to play significant roles in the behavior of each dye trace. Results may help with future efforts to manage water quality in the area.

Bio: Mark Hiler graduated magna cum laude with a B.S. in Geography from Texas State University in San Marcos, Texas. Before going back to graduate school, Mark joined the Student Conservation Association and participated in two internships with the National Park Service's Inventory & Monitoring Program where he collected hydrologic data in West Texas, New Mexico, and Arizona. Currently, he is looking for various water resource jobs to join the professional sector of work.

Thesis Defense

COMPARISON OF FINE SCALE VEGETATIVE PARAMETERS AT ACTIVE AND INACTIVE GULF COAST KANGAROO RAT BURROW SITES

Name: Meagan Marie Bell

Major Advisor: Dr. Thomas R. Simpson

Committee Members: Dr. Joseph Veech

Dr. Todd Swannack

Wednesday, June 28, 2017, 9:00 AM, Supple 153

The Texas endemic Gulf Coast kangaroo rat (*Dipodomys compactus*) is listed as vulnerable on Texas Parks and Wildlife Conservation Action Plan; however, few ecological studies have focused on Gulf Coast kangaroo rats. From April 2016 to March 2017, I have seasonally monitored burrowing activity of Gulf Coast kangaroo rats and recorded vegetative parameters at 63 randomly selected sites on a working cattle and wildlife ranch located in Guadalupe County, Texas. Sites with active burrows or a history of occupancy were monitored monthly. Within a 10-m radius plot at each site and using the Daubenmire frame cover estimate technique, I recorded percent cover of the following cover classes: bare ground, standing dead vegetation, litter, living grass, and living forbs. Additionally, I identified to the lowest taxonomic level the dominant live green grass and forb species in each Daubenmire frame and recorded the height of the tallest live grass, live forb, and standing dead vegetation. Using a spherical densitometer, I determined the percent woody canopy coverage at each Daubenmire frame. Twenty-two of 63 sites were occupied. Using Nested ANOVA, I found significantly greater cover of litter, taller standing dead, and taller grass ($p < 0.001$) at unoccupied sites, while percent cover of forbs, percent cover of bare ground, and distance to the nearest woody canopy was significantly greater ($p < 0.001$) at occupied sites. Using AICc model selection, the favored logistic model to predict the probability of site occupancy was positively influenced by percent bare ground and forb coverage. Percent woody canopy cover, litter, and grass negatively affected this probability of Gulf Coast kangaroo rat occupancy. This model can aid with future efforts to determine areas to protect Gulf Coast kangaroo rats or other similar species. Comparing the dominant plants at occupied and unoccupied sites, I found greater percentages of plantain (*Plantago* spp.), rosette grass (*Dichanthelium* spp.), paspalum (*Paspalum* spp.), sand bur (*Cenchrus spinifex*), and hogwort (*Croton capitatus*) at occupied sites. Except for plantain, these large seeded species are known colonizers of disturbed habitats and which may offer rich food sources. Together, these results suggest Gulf Coast kangaroo rats select for open disturbed areas that can support plants that produce relatively large seeds that are easily extracted from sandy soils.

Bio: Meagan Bell received her B.A. from the University of Texas at San Antonio in Biology with a concentration in Ecology. Working underneath a graduate student at Bent Creek Experimental Forest in North Carolina, she worked as a field technician, looking the impacts of silviculture treatments on small mammals and herpetofauna communities. Since then she has volunteered at Texas Parks and Wildlife in her free time working on both natural resource projects and interpretation programs. She is looking forward to exploring the natural world with her new found freedom and her soon-to-be husband. Currently, she is looking for various wildlife biologist jobs to join the professional sector of work.

Thesis Defense

Rapid quantitative assessment to assist in identification of imperiled fishes

Name: Nicky M. Hahn

Major Advisor: Dr. Timothy H. Bonner

Committee Member: Dr. Clay Green, Dr. Mar Huertas

Monday, June 26, 2017, 2:00pm, FAB 130

Methodologies for ranking conservation status of fishes range from a rapid qualitative method (e.g., expert opinion) commonly used by state agencies to time-consuming quantitative method (i.e., Species Status Assessment; SSA) currently used by US Fish and Wildlife Service. Purpose of this study was to develop a rapid but quantitative methodology for ranking conservation status of freshwater fishes. Using parameters of SSA, redundancy (i.e., occurrence in numbers of independent drainages and semi-independent reaches, occurrences outside of the study area), representation (i.e., commonality within reaches), and resiliency (i.e., number of reaches with recently reported absences) were compiled for 50 species of fishes within the Edwards Plateau, Chihuahuan Desert, and South Texas Plains ecoregions of Texas. The 50 species represented 12 families of fishes and consisted of narrowly distributed fishes (i.e., occurring in one drainage) and widely-distributed fishes (i.e., occurring in up to six drainages) and among 1 to 50 reaches. Twenty-six percent ($N = 13$) of the fishes occur only within the study area. Parameters were analyzed with multivariate analysis. Principal component axis I described a redundancy gradient, contrasting narrowly distributed fishes from widely distributed fishes, and principal component axis II described resiliency and representation gradient, contrasting fishes with greater percent absence or percent rare from those with fewer percent absences and occasional to abundant in relative abundances. Weighted summation of species scores for axes I and II were sorted from least (i.e., towards low redundancy, representation, and resiliency) to greatest (i.e., towards high redundancy, representation, and resiliency), and species were ranked. Species ranks were similar to the list of Texas Species of Greatest Conservation (SGCN), which were developed from rapid qualitative method, but discrepancies highlighted limitations of qualitative methods and expert opinion. Most notably, charismatic and well-studied fishes with moderate redundancy, representation, and resiliency were listed as SGCN, whereas less known fishes with lower redundancy, representation, and resiliency were not listed as SGCN. Among life history traits, top 50% ranked fishes were small-bodied fishes associated with aquifer dependent surface waters. Reproductive and trophic guilds were similar between the top and bottom 50% ranked fishes.

Bio: Nicky Hahn, originally from Vicksburg, MS, graduated from Louisiana Tech University with a Bachelor of Science in Environmental Science in 2015. She fell in love with the fish world while working for the Fish Team at the USACE Engineer Research and Development Center during summers and holidays since 2010. She started the Aquatic Resource Master's program in 2015 and has enjoyed being part of 'Minnow U' and the Bonner crew ever since. After graduation, Nicky hopes to pursue a doctorate in fish ecology and explore the world with her soon-to-be husband.

Thesis Defense

CHANGES IN LEAF AREA AND NUTRIENT CONTENT OF CELTIS SPP. ACROSS A PRECIPITATION GRADIENT IN TEXAS

Name: Allison Bordini

Major Co-Advisors: Dr. Michael Huston and Dr. Susan Schwinning

Committee Member: Dr. David Lemke

Thursday, June 15, 2017, 9:00 AM, Supple 153

Precipitation affects plant nutrient quality and ecosystem dynamics both directly and indirectly. Nitrogen is a key nutrient for cell and protein function for both plants and herbivores, and the ratio of carbon to nitrogen is a good indicator of nutrient availability within an ecosystem. Studies have shown that an increase in precipitation increases plant biomass and the C/N ratio, decreasing the plants' Nitrogen concentration. Using the precipitation gradient occurring across Texas, I wanted to find if leaf quantity increases while leaf nutritional quality (using C/N) decreases with higher rainfall. I also wanted to determine if soil mineral nutrients showed a unimodal relationship, with mineral dissolution and leaching increasing with precipitation. For my study, I sampled three species of *Celtis* spp. (Family: Cannabaceae) across the longitudinal, precipitation gradient of Texas and measured their area and specific leaf area (SLA) to determine a change in leaf size and C/N using the Flash EA 1112 C/N Analyzer to study leaf nutritional quality. I also collected soil samples at each sampling site, dried and ground the soils, and used a Mehlich-3 analysis to determine relative concentrations of soil mineral nutrients at each sample site. Of the three species, *Celtis reticulata* was the only one that showed any statistically significant patterns, and regression analysis showed an increase in size and C/N ratio as precipitation increased. While not significant, I also found a general decrease in soil P, Na, K, Mg, Ca, and Mn with increased rainfall, and an increase in the more toxic soil Fe, Cu, Zn, and Al. The higher concentrations of these elements may contribute to a decrease in plant nutritional quality. My results for *C. reticulata* showed high variability between all samples, but I conclude that in general, leaf quantity (area, SLA) increased while the leaf nutritional quality decreased with precipitation. The decrease in nutritional quality may be due to the dilution of leaf nitrogen as leaf size increases and the increase in more toxic soil nutrients as beneficial nutrients are leached from soils.

Bio: Allison Bordini received her B.A. from Austin College in Sherman, TX in Environmental Studies with a minor in French and Biology. She studied the health of the endangered Littoral Forest in Madagascar using chameleons as an indicator species (2012), and has a strong background in environmental education. When she's not studying biology or educating the future, Ms. Bordini is usually with her precious dog, Colette. She is also an avid baker and thoroughly enjoys exercise.

Dissertation Defense

ECOLOGICAL FACTORS OF RODENT ASSEMBLAGE STRUCTURE AFFECTING HANTAVIRUS PREVALENCE AT VARYING SPATIAL SCALES

Name: Matthew T. Milholland

Major Advisor: Dr. Iván Castro-Arellano – Texas State University

Committee Members: Dr. Joe Veech – Texas State University

Dr. Rodney Rohde – Texas State University

Dr. Tom Lee – Abilene Christian University

Dr. Gerardo Suzán – Universidad Nacional Autónoma de México

Monday, 05 June 2017, 9:00 am SUPP-153

Zoonotic pathogens are the dominant cause of novel and reemerging infectious diseases. Hantaviruses (family Bunyviridae) and their associated human diseases occur globally and differ according to their geographic distribution and type of illness exhibited in humans. Prevention of these diseases requires surveillance of seroprevalence in animal populations. Small mammal assemblage structure and species richness are suggested as strong drivers for the maintenance and spread of hantavirus infections. Climatic factors, such as precipitation, can influence reservoir density and abundance by increasing available food resources. These fluctuations in rodent assemblage structure can contribute to the maintenance or reduction of hantavirus seroprevalence. My research objectives were to: 1) determine the ecological correlates of hantavirus prevalence in small mammal assemblages at the site, region, continent, and global levels; 2) to compare differences in prevalence found in sylvan and disturbed habitats; 3) investigate the relationship between phylogenetic diversity and prevalence; 4) develop predictive models for hantavirus prevalence in rodent assemblages using defined ecological correlates; and 5) to quantify transmission events and seroconversions between naïve and infected rodents. I found that of the currently recognized 681 Cricetid, 730 Murid, 61 Nesomyid, and 278 Sciurid species, approximately 11.3%, 2.1%, 1.6%, and 1.1% respectively, have known associations with hantaviruses. The diversity of hantaviruses hosted by rodents and their distribution among host species supports a reassessment of the paradigm that each virus is associated with a single host species. By considering reservoir host diversity and distribution patterns I holistically evaluate the symbiotic and pathogen-host associations between rodents and hantaviruses. I examine this association on a global taxonomic and geographical scale, model these associations, compare habitats (i.e. sylvan vs. peridomestic) across a latitudinal gradient from Texas through México with emphasis placed on the rodent host diversity and distribution, and quantify infection seroconversion rates of naïve, wild rodents from interactions with naturally infected conspecifics.

Bio: Matthew T. Milholland received his B.S. in biology (1996) from Abilene Christian University and studied physiology at UNT Health Science Center at Fort Worth before obtaining his M.S. in wildlife ecology from Texas State University in 2005. He has been a contract biologist throughout Texas and an adjunct instructor at Cisco College before beginning the Ph.D. Aquatic Resources program at Texas State in January 2013. He and his wife of 21 years, Megan, have two children, Noah (12) and Posey (8), of whom he is extremely proud.

Thesis Defense

Examining Genetic Variation and the History of Differentiation in the Pallid Dotted-Blue Butterfly (*Euphilotes pallescens*) Within the Great Basin

Name Sarah B. Bialik

Major Advisor: Dr. Chris Nice

Committee Members: Dr. Noland Martin and Dr. David Rodriguez

Wednesday, May 31st, 2017, 10:00 AM, Supple Science Building 153

Quantifying genomic variation provides information that can be used to understand the evolutionary history of populations. In this study, I focused on populations of *Euphilotes pallescens*, a species of butterfly that lives within the Great Basin of North America. I genotyped 376 butterflies at over 90,000 loci to address two major questions: 1. Has gene exchange occurred among lineages of *E. pallescens* or between *E. pallescens* and other geographically proximate *Euphilotes* species? and 2. If there is evidence of admixture, what are the relative contributions of historical and contemporary gene exchange in the history of these butterflies? I stratified loci into “common” and “rare” loci based on minor allele frequencies to investigate historical and contemporary genetic structure, respectively. I used a Bayesian hierarchical model to visualize and quantify genetic variation in two analyses: one included just *E. pallescens* lineages, while the second analysis was performed at the genus level. I found evidence of both historical and contemporary gene exchange among subspecies within *E. pallescens* and among *Euphilotes* species. However, there was little evidence of a history of admixture between the Great Basin populations of *E. pallescens* and other *Euphilotes* species. I also found conflict between the patterns of genomic differentiation in these butterflies and their nominal taxonomy. My investigation of the evolutionary history of these butterflies revealed complex relationships and patterns of gene exchange between lineages that suggest the organization of biological diversity is not always strictly hierarchical and the history of divergence is not always strictly bifurcating.

Sarah Bialik was raised on a farm in Williamstown, Kentucky. She attended Centre College in Danville, Kentucky where she did population genetics research on sea squirts and earned her B.S. in Biology and Environmental Studies in 2015. Sarah realized she loved doing research and joined the Nice Lab in 2015 to work on these wonderful butterflies and earn her M.S. in Population and Conservation Genetics. She enjoys baking, knitting, yoga, rock climbing and playing with her puppy, Telo. She will be moving up to Austin with her soon-to-be husband and plans to pursue a career in research.

Thesis Defense

POPULATION GENETICS OF A FUNGAL AMPHIBIAN PATHOGEN IN CENTRAL TEXAS

Thomas L. Marshall

Major Advisor: Dr. David Rodriguez

Committee Member: Dr. Michael R. J. Forstner and Dr. Dittmar Hahn

Thursday, May 25, 2017, 9:00 AM, Supple Science Building 112

Chytridiomycosis, an emerging infectious disease caused by the fungal pathogen *Batrachochytrium dendrobatidis* (Bd), is a major contributor to declines in amphibian populations worldwide. Bd was first described in the 1990s, and there is still much to learn about its regional diversity and origin. The Global Panzootic Lineage (Bd-GPL) has been responsible for devastating amphibian population declines and extinctions in Central and South America, Australia, and the western US. On the other hand, a few localized endemic lineages have been discovered in regions such as Brazil and Asia, which have not experienced such severe disease outbreaks. There are still several geographic sampling gaps in the global genetics of Bd, and relatively few studies have focused on regions in which Bd exhibits low virulence, thus creating a bias in our current knowledge of the pathogen's diversity. One such region that has not seen disease-associated declines is the state of Texas. This pathogen has been detected from amphibians in the state, although strains had not been characterized genetically prior to this study. Here, I isolated, cultured, and genotyped strains of Bd in Central Texas and compared them to a panel of previously genotyped strains distributed across the globe. My results support the hypothesis that Bd is an introduced pathogen in the region. I found a diversity of Bd genotypes yet did not detect genetic structure in Texas and across North America. Strains in Central Texas are genetically similar to those in the western U.S. that have caused amphibian population declines, which raises questions about the roles that climate and host resistance play in shaping Bd-amphibian disease dynamics in the region.

Bio: Thomas Marshall was born in Princeton, NJ and raised in Dallas, TX. He graduated with a B.A. in psychology from Vanderbilt University in 2003 and soon after relocated to Austin, TX where he spent his free time chasing after reptiles and amphibians along the Barton Creek Greenbelt. He returned to school to study biology at Texas State University as a post-grad and then joined the Rodriguez lab as a Master's student in the fall of 2015. He will begin his doctoral program this fall in the David Hillis lab at University of Texas at Austin and investigate the phylogenomics and evolution of snakes.

Dissertation Defense

"Reevaluating the reproductive ecology of the endangered Houston Toad (*Bufo* [=*Anaxyrus*] *houstonensis*) using automated audio and environmental monitoring techniques"

Andrew MacLaren

Major Advisor: Michael R. J. Forstner, Department of Biology, Texas State University

Committee Members: Shawn F. McCracken; Floyd Weckerly, Department of Biology, Texas State University.

Benjamin M. Bolker, Departments of Biology and Mathematics, McMasters University, Hamilton, Ontario, Canada.

J. Andrew Royle, United States Geological Survey, Patuxent Wildlife Research Center, Laurel, MD.

Tuesday, May 16, 2017, 1:00 pm, Supple 257

The Houston Toad (*Bufo* [=*Anaxyrus*] *houstonensis*) is an endangered species of anuran endemic to east central Texas. Many of the assumptions regarding the natural history of the Houston Toad are founded in documents that provide little or no statistical evidence for their conclusions. This dissertation is focused, in part, on testing these observations using data gathered from remote audio recording devices to either substantiate or refute them. These devices are used to capture the sounds of male anurans chorusing at potential breeding locations for Houston Toads. These devices record audio 10 minutes per hour, 12 hours per night, every night between January and July, providing presence/absence data for the Houston Toad and co-occurring species at a rate that is unable to be matched by human observers. In some instances, these data allow for new discoveries to be made that have gone undetected through less rigorous sampling regimes. In other instances, the regularity and long-term provenance of these data require several currently held paradigms concerning the chorusing behavior of the Houston Toad to be challenged or re-evaluated. Given that auditory cues alone inform regulatory policy and enforcement, improving methods of detection inherently have the greatest impact on the conservation of this species. I intend to use these data to re-characterize the call of the Houston Toad, which is often misrepresented in textbooks and field guides; to describe the climatic conditions correlated with chorusing, the annual variation in chorusing phenology, and determine whether forecasted long-term climate change will impact favorable chorusing (i.e. breeding) conditions; to investigate the interaction between chorusing Houston Toads and Coastal Plains Toads (*Bufo* [=*Incilius*] *nebulifer*); and finally, to utilize these data to determine whether currently in place protocols for acoustically monitoring this species are adequate, and improve them if possible.

Bio: Andrew comes from Northwest Houston (near where the Houston Toad was first described) where he graduated from Langham Creek High School, then attended Lone Star College. He then completed his bachelors in biology at Texas State University in Fall 2013. He then completed his Masters in August 2015 focused on the development of audio recognition tools for the Houston Toad. He has two guinea pigs whose names are Einstein and Newton.

Thesis Defense

SPECIFICITY OF TLS11a APTAMER TOWARDS HEPATOCELLULAR CARCINOMA AS A MEANS OF DETECTION AND TARGETED DRUG DELIVERY

Name: Katie A. Kendrick

Major Advisor: Dr. Shannon Weigum

Committee Members: Dr. Dana Garcia and Dr. Joe Koke

Tuesday, May 9, 2017, 8:30 am, Supple 257

Liver cancer is the sixth most common occurring cancer and second leading cause of cancer-related deaths worldwide. An estimated 75% of all liver malignancy cases are hepatocellular carcinoma (HCC), the most common and most lethal form of liver cancer. While the incidence rates for many cancers have slowly declined over the years, HCC incidence and death rates have continuously risen due to poor prognosis and late stage diagnoses. This suggests that there is a lack of existing biomarkers and diagnostic equipment sensitive enough to identify this disease and that more sophisticated methods are needed to specifically target HCC and detect it at its early stages. Recently, an HCC-specific aptamer was described and shown to effectively discriminate mouse HCC from normal liver in vitro. In this thesis, the specificity of TLS11a towards human HCC is addressed. Specifically, immunohistochemistry staining of human tissue microarrays (TMAs) were utilized to address what tissue types TLS11a can bind, if it can differentiate between normal liver and HCC and if binding is correlated with tumor grade. Staining of fresh frozen TMAs showed TLS11a could distinguish between human normal liver and HCC tissue ($p < 0.001$) with the mean integrated intensity increasing more than an average 10-fold in HCC tissues. TLS11a was also found to bind to HCC tissue with higher affinity than any other malignant tissue type ($p < 0.001$) other than testis ($p = 0.122$), and little to no binding to other normal tissue types ($p < 0.001$). These results signify that TLS11a is highly specific to human HCC tissues and show its ability to recognize its target epitope with high affinity when compared to other tissue types. Although follow up studies are needed to confirm, these findings suggest TLS11a would be an excellent candidate for use in human studies for new HCC-targeted diagnostic and therapeutic applications.

Katie Kendrick was born and raised in San Marcos, Texas. She graduated from Texas State University with a Bachelor of Science in 2014, and returned to join Dr. Weigum's lab and earn her MS. After graduation, Katie plans on applying to medical school in the hopes of becoming a physician. Outside of her graduate studies, Katie enjoys being a mom and spending time with her amazing son and daughter.

Dissertation Proposal Defense

A consideration into ways biology-based student organizations facilitate partition in STEM

Zachary L Nolen

Major Advisor: Dr. Kristy L Daniel

Committee Members: Dr. Carrie Bucklin, Dr. Ivan Castro-Arellano,

Dr. Eleanor Close, and Dr. Paula Williamson

April 21, 2017, 10:00 a.m., Norris Room

Abstract. The United States has fallen behind other developed countries in the field of science resulting in fewer students entering scientific careers. It is speculated that students are leaving the field during or immediately following their degree program because students have not developed a strong perceived attachment to the field of science. One way that students may build this perceived attachment to science is through participation in science-based social organizations. The purpose of my study is to investigate the ways and reasons students participate in biology-based student organizations and the relationship between those experiences and students' perceived attachment. I will recruit three biology-based student organizations (Beta Beta Beta Biological Honor Society, Wildlife Society, and Microbiology club) to identify the extent that they exhibit characteristics of affinity groups. Data sources will include member responses to an open ended questionnaire, field observations, relevant artifacts, and focus groups with student leadership. I will analyze these data to determine the process by which these student organizations plan and execute activities. Additionally, I will explore the relationship between participation in these activities and members' perceived attachment to their respective organizations and biology. My findings will highlight how student organizations may be shaping the scientific future of students in ways we do not yet understand.

Bio: Zach Nolen earned his B.S. in Biology from the University of North Alabama in Florence, Alabama in 2011 and his M.S. in Biology from the University of Alabama in Birmingham in 2014. He began studying under Dr. Kristy Daniel at the University of Southern Mississippi in 2014 before transferring with her to Texas State University where he joined the Aquatic Resources program. Upon completing his doctoral degree, Zach hopes to pursue his passion for teaching at the university level and remain on the cutting edge of science education research.

Thesis Defense

“CHARACTERIZING STREAM-AQUIFER INTERACTIONS OF THE PEDERNALES RIVER WATERSHED IN CENTRAL TEXAS”

Raddiete Ghion

Major Advisor: Dr. Vicente Lopes

Committee Members: Dr. Alan W Groeger and Mr. Rene Barker

Monday, April 24, 2017, 11:00 AM, Freeman Aquatic Building 130

Understanding of stream-aquifer interactions is relevant to determining and managing the hydrologic impact of river and groundwater usage. Traditional techniques to analyze stream-aquifer interaction are based on digital ground-water flow models, however, aquifer parameters for model calibrations are generally unavailable and difficult to obtain. Recession curve analysis is an alternative approach to determine stream-aquifer interaction in a watershed. Basic assumptions in recession curve analysis include: no regulation on the stream, stream fully penetrates the aquifer, the watershed is underlined by impermeable rocks, aquifer systems have uniform hydraulic conductivity and transmissivity, aquifer system that sustains stream flow is a one-dimensional system (neglects vertical interaction with deeper aquifers), and watershed has uniform storage and recharge. This study sought to investigate changes in precipitation, streamflow, baseflow, and hydrologic properties of the Pedernales watershed in central Texas, as well as identify the primary aquifer system contributing flow to the Pedernales river from 1940 to 2014. The USGS Ground Water Tool box RECESS program was used to extract recession segments and the slope (K) of each segment (recession curve index, RCI). Man-Kendall Monotonic trend (MK) test was used to assess changes in climatologic and the hydrologic parameters during the study period. Annual trend analysis of precipitation streamflow, baseflow and RCI showed no significant changes across the study period. Values of stream-aquifer property T/a^2s (where T is the transmissivity of the aquifer, a is the average distance from the river to the watershed dived, and S is the storage coefficient of the aquifer) was estimated as 0.0403 d⁻¹ and the watershed K value was 23.15 days/ log cycle. It is concluded that the Hensel formation of the Cretaceous aquifer is the primary source of baseflow in the Pedernales River above the Johnson City gage. Results of this study are relevant to water resources management in the study area to satisfy the needs of a growing population while maintaining the ecological integrity of the stream-aquifer system. The approach used in this study can be readily available to other watersheds as it only requires recession and streamflow hydrograph analysis, the assurance that the stream system under consideration is not regulated, and that linearity of the recession curve of the watershed is observed.

Bio: Raddiete Ghion obtained a BS in Biology (2014) from Texas State University. Upon graduation she wanted to complete a Master's degree, she entered the MS Biology program in Fall 2014 and joined Dr. Lopes lab where she became interested in groundwater hydrology. Raddiete aims to pursue a career in environmental planning and integrated watershed management in Austin, TX

Thesis Defense

An Investigation of Relationships Between Student Acceptance of Evolution, Tree-Thinking, and Eye Movement among different Instructional Interventions

Name: Austin Leone

Major Advisor: Dr. Kristy L. Daniel

Committee Members: Dr. Joseph A. Veech, Dr. Julie F. Westerlund

April 6, 2017, 8:30 AM, Norris Room

Evolution is the unifying theme for the field of biology and is one of the most well developed and supported scientific theories to date. Although overwhelming evidence exists supporting evolution, evolution is considered a socio-scientific issue. Socio-scientific issues are potentially controversial social issues stemming in science content. For example, climate change, stem cell research and the concept of life are also current socio-scientific issues. Unfortunately, given the potential controversy, a large amount of the public still rejects evolution. In attempt to counter the controversy, educate people, and communicate the scientific basis for evolution, biologists commonly use a diagram called the phylogenetic tree. These diagrams represent hypothesized evolutionary relationships and learning how to accurately interpret and generate phylogenetic trees, called tree-thinking, is a difficult task for learners. Previous studies have investigated the relationship between tree-thinking and evolution acceptance. But, these results were based on an instrument limited in reliability. Additionally, these studies only incorporated a single, integrated instruction method. Using a new instrument which quantitatively measures tree-thinking and a reliable instrument which measures evolution acceptance, I investigated the relationship between tree-thinking learning outcomes and evolution acceptance in 884 undergraduate students from five different instructional interventions. Students completed the instruments both before and after learning about trees for one week of instruction. I found a significant but weak correlation between evolution acceptance and student tree-thinking learning. I also found that in non-majors biology students, evolution acceptance only explains 1.4% of the variance found in learning about tree-thinking. Knowing that students hold numerous misconceptions when interpreting phylogenetic trees, I used eye-tracking technology to investigate how these students visually interacted with these diagrams. I found that students spend the most amount of time looking at the tips of trees that incorporate organisms more than trees that incorporate abstract letters. My findings suggest that evolution acceptance does not significantly explain how students learn about phylogenetic trees. Additionally, biometric data indicates that students do not interact with trees as expected, with visual interactions closely aligned with expectations of common misconceptions.

Bio: Austin Leone graduated from the University of Oklahoma in Norman, Oklahoma with a B.S. in Zoology (2014). He began studying under Dr. Kristy Daniel for his M.S. in Biology at Texas State University in Fall 2015, and will continue his education as a Ph.D. student in Oklahoma State University's Integrative Biology program. After participating in a recent study abroad program to Southeast Asia, Austin hopes to travel and continue learning about how evolution is accepted on a global scale. Ultimately, Austin aims for a career in higher education as a biology education researcher.

Thesis Defense

EASTERN BLACK RAIL (*LATERALLUS JAMAICENSIS JAMAICENSIS*) OCCUPANCY AND ABUNDANCE ESTIMATES ALONG THE TEXAS COAST WITH IMPLICATIONS FOR SURVEY PROTOCOLS

James D. M. Tolliver

Major Co-advisors: Dr. Floyd W. Weckerly and Dr. M. Clay Green

Committee Member: Dr. Joseph A. Veech

Monday, April 3, 2017, 2:30 pm, Supple Science Building 257

Eastern black rails (*Laterallus jamaicensis jamaicensis*) are a subspecies of conservation concern. These birds vocalize infrequently and inhabit dense vegetation making them difficult to detect. I conducted the first large scale study of black rail occupancy and abundance in Texas. I repeated point count surveys at 308 points spread across six study sites from mid-March to late-May in 2015 and 2016. Each survey at a survey point was a 6-minute call broadcast. My study sites were Anahuac, Brazoria, and San Bernard National Wildlife Refuges, Mad Island Wildlife Management Area, Clive Runnel's Mad Island Marsh Preserve, and Powderhorn Ranch Preserve. I estimated 19 occupancy and 19 abundance models that also accounted for imperfect detection. Black rail detection increased with moon phase and temperature but decreased with wind speed and ambient noise. Occupancy and abundance increased with herbaceous, woody, *Spartina*, and intermediate marsh cover. Black rail occupancy and abundance estimates were similar between years. From the estimated detection probabilities I determined that ~ 16 surveys could establish absence of the species at survey points. I reached two main conclusions. One, black rail management, during the breeding season in Texas, should focus on *Spartina* cover as occupancy and abundance estimates were highest when *Spartina* cover was high. Two, effort to establish black rail absence from naïve occupancy estimates is impractical. Monitoring efforts of black rails, in Texas, should design studies that estimate distribution and abundance while accounting for imperfect detection.

Bio: James Tolliver was born and raised in central Texas. He became interested in the natural sciences at a young age and decided to pursue a career in the wildlife sciences. James graduated from Arthur Temple College of Forestry and Agriculture, Stephen F. Austin State University in 2013 with a Bachelor of Science in Forestry and a major in wildlife management. He took various technician jobs until he was accepted into the M.S. program at Texas State University. James joined the program in 2015 to work, in Drs. Green's and Weckerly's labs, on black rails.

Thesis Defense

Predicting Groundwater Level using Data Mining Techniques: A Case Study of the Edwards Aquifer

Lenée A. Dedeaux

Major Co-Advisors: Dr. Benjamin F. Schwartz, Biology, and Dr. Yihong Yuan, Geography

Committee Member: Dr. Ronald T. Green, Southwest Research Institute

Thursday, March 23, 2017, 2:00 PM , Freeman Aquatic Bldg., room 130

Continuous groundwater level data collected from observation wells in the Edwards Aquifer provide large time-series datasets useful for predictive modeling of groundwater levels across a wide range of aquifer conditions. However, due to the complex hydrogeology of the Edwards Aquifer, groundwater wells exhibit varying degrees of spatiotemporal dependency and heterogeneity challenging accurate groundwater level predictions. In this study, the data mining techniques of hierarchical clustering, a method to rank data based on response, and artificial neural networks (ANNs) to predict groundwater levels, were applied in a two-step approach with the specific goal of increasing groundwater level prediction accuracy in wells in the Edwards Aquifer. In step-one, a hierarchical clustering analysis was conducted using the time-invariant Distance Time Warping (DTW) algorithm as a measure of similarity to identify groups of wells that exhibit similar responses across a wide range of hydrologic conditions. In step-two, the datasets of the wells that clustered together across all hydrologic conditions, along with precipitation and spring flow datasets, were used to train artificial neural networks (ANNs) to predict daily groundwater levels for each of the other wells in the cluster. The results of this study show that the data mining techniques of hierarchical clustering and artificial neural networks, applied in a two-step approach, can increase groundwater level prediction accuracies. This methodology is useful for predicting missing values in time series datasets, simulation of groundwater levels, and calibrating numeric models.

Bio: After graduating this spring with a MS in Aquatic Resources, Lenée hopes to research climate change while pursuing her PhD. When not busy being with graduate studies, Lenée is the mom to three wonderful daughters who are future scientists and wife to a very supportive and patient husband.

DISSERTATION PROPOSAL DEFENSE

EXAMINATION OF ECOPHYSIOLOGY AND TROPHIC ECOLOGY OF EPIGEAN AND HYPOGEAN INVERTEBRATES FROM EDWARDS AQUIFER

Name: Parvathi Nair

Major Advisor: Dr. Weston Nowlin, Department of Biology, Texas State University

Committee Members: Dr. Benjamin Schwartz, Department of Biology, Texas State University

Dr. Thom Hardy, Department of Biology, Texas State University

Dr. Benjamin Hutchins, Texas Park and Wildlife

Dr. Joe Tomasso, Auburn University

Monday, March 6, 2017, 9:00 am, Freeman Aquatic Building, Room 130

The Edward Aquifer (EA) in central Texas contains one of the most diverse communities of subterranean and spring-associated organisms in the world, but the ecophysiology and trophic ecology of many of these organisms are poorly understood. Most subterranean ecosystems are characterized by severe resource limitation due to spatiotemporal patchiness of food resources because of lack of autotrophic production and intermittent inputs of surface-generated organic matter (OM). A long-standing hypothesis in subterranean biology posits that organisms living in subsurface habitats can withstand long periods of resource shortages and have increased starvation resistance due to reduced metabolic rate. In the first portion of my dissertation, I will investigate the effects of food deprivation in several related groundwater-, spring-, and surface-associated macroinvertebrates from the EA. It is also thought that organisms living in environmentally stable environments, such as subterranean habitats and at surface springs should exhibit relatively small ranges in thermal and environmental tolerances; however, results from experiments examining this prediction are equivocal. In the second portion of my dissertation, I will evaluate this hypothesis by investigating responses of spring- and surface-associated macroinvertebrates to increasing water temperatures and decreasing DO concentrations. Lastly, some hypogean-adapted organisms exist in both belowground and in surface spring habitats; these spring openings serve as an ecotone between surface and subterranean environments and both surface and subsurface organisms can occupy this habitat. In spring systems where both subsurface and surface species coexist, it is unclear how these groups of species potentially occupy habitat space and utilize resources in what is thought to be a homogenous and resource poor environment. I will investigate potential resource and microhabitat partitioning in the invertebrate community located along springs in the Comal Spring system in the EA using stable isotopes. The information obtained through these studies will be beneficial for devising conservation strategies and captive breeding programs for EA invertebrate species and for habitat conservation and restoration measures.

Bio: Parvathi Nair was born in Kerala, India. She earned a B.S. in Zoology in 2008 and a M.S. in Fisheries Science in 2010 from the University of Mumbai, India. She came to the USA in 2011 and earned a M.S. in Environmental Science in 2013 from University of Houston Clear-Lake, TX. She entered the Aquatic Resources Ph.D. program at Texas State University in 2014, in Dr. Weston Nowlin's lab, to work on the conservation of endangered invertebrates in the Edward Aquifer.

Thesis Defense

INTEGRATION OF A LATERAL FLOW IMMUNOASSAY PANEL FOR GASTROENTERITIS WITH SWAB-BASED SAMPLE PREPARATION CARTRIDGE

Name: Zhenyuan Lu

Major Advisor: Dr. Shannon Weigum

Committee Members: Dr. John C. Carrano and Dr. Rodney Rohde

Thursday, March 2, 2017, 9:00 am, Norris room

Gastroenteritis is one of the most common and deadly diseases, causing a combination of diarrhea, vomiting, and abdominal pain. In developing countries, there is a lack of advanced medical instruments, well-trained medical personnel and funding to process complex diagnostic tests that inform treatment decisions. Therefore, there is a need to develop inexpensive, easy-to-use, rapid, portable and highly sensitive detection assays that do not require complex testing procedure or highly trained personnel. To address this need, we propose the development of a novel lateral flow immunoassay (LFIA) that uses colorimetric or chemiluminescent signal enhancement of gold nanoparticles (AuNP) that can be integrated with a point-of-care, swab-based sample preparation cartridge, known as the Paratus SDS[®] Cartridge (Paratus Diagnostics, LLC. Austin, TX). These LFIA devices will be fabricated using a combination of laser cutting and wax printing to create physical or hydrophobic barriers that direct metered volumes of sample fluids extracted from the Paratus SDS[®] Cartridge onto the LFIA test strip. Capillary action will draw fluids toward the reaction zone where embedded multiplex immunoassay reagents will be embedded in a 3 x 3 microarray spot pattern. If the target pathogen is present, a sandwich based immunoassay complex will form between the capture antibody, pathogen, and detecting antibody, yielding a spatially resolved colorimetric or chemiluminescent signal. Preliminary results using a single pathogen, Norovirus GII.4 virus-like particles (VLPs), yielded visible AuNP signals in the presence of as little as 50 pM VLPs using this integrated sample prep/detection system. Additional optimization and refinement of the LFIA is ongoing and will involve antibody characterization for multiplexed assays and built-in LFIA structures for seamless integration with the Paratus SDS[®] Cartridge.

Zhenyuan Lu was born in Shanghai, China and earned his B.E. from Southwest University of Science and Technology, China with a major in Bioengineering. After graduation, he became a gorilla keeper at an animal zoo; and then worked at a cosmetic company as a R&D engineer until he joined Dr. Weigum's Lab at Texas State University in 2015. Meanwhile, he is a freelanced photographer and owns a photography studio for weddings, portraits, chasing dogs...since 2013.