

## Dissertation Proposal Defense

### UTILIZING MULTIDISCIPLINARY METHODS TO UNDERSTAND CONTAMINANT ACCUMULATION IN CETACEANS: CASE STUDIES IN THE GULF OF MEXICO AND NEW ZEALAND

Meaghan McCormack

Major Advisor: Dr. Jessica Dutton (Department of Biology – Texas State University)

Committee Members: Dr. Weston Nowlin, Department of Biology - Texas State University Dr. Floyd Weckerly, Department of Biology - Texas State University Dr. Todd Swannack, Integrated Ecological Modeling US Army ERDC Dr. Aaron Roberts, Department of Biological Sciences - University of North Texas

Wednesday, November 28, 2018, 9:00 a.m., Freeman Aquatic Biology 102

Cetaceans are long-lived top predators that can accumulate high concentrations of contaminants, including Hg, Cd, PCBs (polychlorinated biphenyls), and DDT (dichloro-diphenyl-trichloroethane) in their tissues. However, studying cetaceans can be difficult due to logistical and legal constraints. As a result of these challenges, contaminant studies are often limited by sample size and therefore a mixed methodological approach is the most effective way to advance our understanding of contaminant body burdens in cetaceans. My proposed research will use tissues, teeth, and computer modeling to understand the accumulation of contaminants in cetaceans from the Gulf of Mexico and New Zealand. The recent northern Gulf of Mexico (GoM) Cetacean Unusual Mortality Event (2010-2014) provided a unique opportunity to obtain tissue samples (e.g., skin, blubber, muscle, kidney, liver, and brain) from over 300 individual cetaceans [primarily bottlenose dolphins (*Tursiops truncatus*), but also less commonly sampled cetacean species] to assess the bioaccumulation patterns of essential (e.g., Cu, Se, Zn) and nonessential (e.g., As, Cd, Hg, Pb) trace elements in relation to body length/age, sex, food source ( $\delta^{13}C$ ), trophic position ( $\delta^{15}N$ ), and habitat ( $\delta^{34}S$ ). Using Laser Ablation Inductively Coupled Plasma Mass Spectrometry (ICP-MS) and Scanning Electron Microscopy equipped with Energy Disrupting X-ray Spectroscopy (SEM-EDX) I will determine trace element concentrations in the annual growth layers of GoM bottlenose dolphin teeth to determine if changes in environmental exposure to trace elements can be reflected within an individual's lifetime. Finally, I will incorporate organic pollutants into a previously developed computer model based on the behavioral interactions of dusky dolphins (*Lagenorhynchus obscurus*) and killer whales (*Orcinus orca*) off New Zealand to comprehend the interactions between energetics and the bioavailability of PCBs and DDT. Due to the inherent challenges associated with studying cetaceans in the wild, a multidisciplinary approach using toxicology, stable isotope analysis and ecological modeling is necessary to better understand the accumulation of contaminants in cetacean populations.

Bio: Meaghan McCormack is originally from Long Island, New York. She holds a B.A. in Biology from Adelphi University and an M.S. in Marine Affairs and Policy from the University of Miami. Her interest in marine mammal science stems from an appreciation of the evolutionary adaptations required of cetaceans, the ability of charismatic megafauna to generate interest in science, and the role cetaceans play as sentinel species. Meaghan started in the Ph.D. Program in Aquatic Resources at Texas State University in 2016.

## Dissertation Proposal Defense

ALL IN THE FAMILY: THE AFFECTS OF URBANIZATION AND CLIMATE CHANGE ON THE BEHAVIOR, SOCIALITY, AND POPULATION DYNAMICS OF A KIN-STRUCTURED PASSERINE, THE BLACK-CRESTED TITMOUSE (*BAEOLOPHUS ATRICRISTATUS*)

Rebekah J. Rylander

Major Advisor: Dr. Sarah Fritts (Department of Biology – Texas State University)

Committee Members: Dr. Butch Weckerly and Dr. Andrea Aspbury (Department of Biology - Texas State University), Dr. Thomas R. Simpson (Texas State University – Professor Emeritus), Dr. Michael Patten (Department of Biology - Oklahoma University)

Friday, November 16, 2018, 9:30 a.m., Ingram Hall (IGRM) 3207

Climate change and habitat fragmentation through urbanization pose a threat to avian biodiversity on a global scale. Though many species are capable of co-existing in anthropogenic landscapes, there often are compromises in species' survivorship, fecundity, and/or dispersal mechanisms. Avian species that are social can be even more affected by altered climate and urbanization due to additional challenges of maintaining familial bonds. A residential species of central Texas, the black-crested titmouse (*Baeolophus atricristatus*, BCTI), is a social songbird that forms kin-structured neighborhoods in rural, less-disturbed regions of its range. However, the titmouse also is regularly encountered in areas of high anthropogenic influence, but it is unknown how this altered landscape affects BCTI demographics, behaviors, and sociality. Thus, the focus of my dissertation research is three-fold: 1) assess the influence of urbanization on BCTI kin-structured neighborhood formation; 2) examine fitness costs and benefits associated with BCTI familial-living through resource sharing behaviors; and 3) compare BCTI population demographics and dynamics across varying levels of anthropogenic disturbance and seasonal weather patterns. I will perform this study in urban San Marcos, Texas and the Freeman Center of Texas State University. In both locations, I will capture, color-band, and monitor BCTI families that utilize nestboxes during the breeding season. Through focal observation and territory mapping, I will determine dispersal patterns, annual fecundity, survivorship, and kin-structure behaviors in locations with varying degrees of urbanization. With the use of passive integrated transponder (PIT) tag technology on the Freeman Center, I will examine the potential fitness benefits that BCTI receive through sharing behavior by residing next to relatives. Because this study will span seven years, I will assess the possible effects of weather patterns, in addition to urbanization, on the population dynamics of this species. Therefore, a thorough investigation of the BCTI could lead to better-focused conservation practices for socially-oriented species, especially in the face of inevitable habitat fragmentation and climate change.

Bio: Rebekah Rylander grew up in central Texas where she fell in love with avifauna during her bachelor's degree from UT Austin. After a whirlwind of travel and exciting field experience, Rebekah settled into Texas State University where she earned her master's degree studying social flocking dynamics of the black-crested titmouse. Because of the questions that surfaced after degree completion, Rebekah decided to continue working with titmice and their unique behaviors. During her limited spare time, Rebekah enjoys assisting undergraduates in research projects, performing banding station demos, and monitoring a local population of golden-cheeked warblers.

Dissertation Defense

AN INTEGRATIVE APPROACH TO THE ECOLOGY AND EVOLUTION OF ALTERNATIVE REPRODUCTIVE TACTICS IN MALE SAILFIN MOLLIES, *POECILIA LATIPINNA*

Diana Kim

Major Advisor: Dr. Caitlin Gabor

Dr. Chris Nice, Texas State University

Dr. Ryan Earley, University of Alabama, Tuscaloosa

Dr. Felix Breden, Simon Fraser University

Tuesday, November 13, 2018 - 2:00 p.m., Ingram Hall, 03203

Understanding the sources of variation that make up complex phenotypes has been a long-standing goal of evolutionary biology. Sexually-selected polymorphisms such as those found in alternative reproductive tactics (ARTs) are an example of complex phenotypes that show extreme variation among multiple traits. Males often show phenotypic traits that vary in size, ornamentation, coloration, and behavior. For my dissertation, I used an integrative approach to investigate aspects of the social, hormonal and genetic effects that contribute to alternative reproductive tactics using male sailfin mollies, *Poecilia latipinna*, a live-bearing fish species. Complex phenotypes have both genetic and environmental sources of variation, and hormones often mediate the interaction between these two sources. Maternal effects and the presence of rival males are two such social environmental factors that can affect male phenotypes. First, I examined the effects of other rival males on male mate choice for conspecific females, and on the changes in circulating levels of the androgen 11-ketotestosterone (KT) and cortisol within a mate choice context. Although rival males did not affect male mate choice, these potential competitors did affect the KT release rates of focal males and females. Further, males released more KT with increasing size of the rival male. Then, I investigated how cortisol release rates varied in female sailfin mollies during gestation to identify the potential effects of maternal stress on son phenotype. I conducted an adrenocorticotrophic hormone (ACTH)-challenge to determine the natural range of cortisol by gestating and non-gestating females and whether within and among individual variation (repeatability) contributed to female cortisol release rates. Gestational status did not correlate with cortisol but females showed high repeatability in cortisol release rates which suggests that variation in maternal stress may affect offspring and that cortisol release rates may be heritable. Lastly, I identified the genetic basis of male phenotypic variation using a genome-wide association study. Using a Bayesian sparse linear mixed model approach, I characterize the underlying genomic architecture of relevant morphological traits that define ARTs in male sailfin such as body size. Together, these chapters provide greater understanding of the genetic and physiological mechanisms for the variation in male phenotypes of sailfin mollies.

Bio: Diana was born in Pusan, South Korea but raised in Monticello, NY. Diana earned her B.A. degree in Biology from Wesleyan University in Middletown, CT and a M.S. degree from University of Wisconsin-Milwaukee

## Dissertation Proposal Defense

Assessing population dynamics of threatened and endemic aquatic species using genetic and mark-recapture analyses

Alex Sotola

Major Advisor: Dr. Noland Martin

Committee Members:

Dr. Timothy Bonner, Texas State University

Dr. Chris Nice, Texas State University

Dr. Daniel Stich, SUNY Oneonta

Dr. Jess Jones, Virginia Tech

Wednesday November 14, 2018, 12:00 p.m., Freeman Aquatic Building 102

Anthropogenic influences on our ecosystems have increased in the last 100 years and will continue to do so. In the aquatic world, it is apparent how humans are influencing populations, whether it be by blocking migratory routes with dams, turning a lotic system into a more lentic system, or altering water quality or flows. As human influences continue to increase, our ability to assess and manage populations of conservation concern is increasing as well. Two powerful techniques that can be used to assess population dynamics and help manage threatened and endemic species are the use of genotyping-by-sequencing and mark-recapture methods. Not only can these techniques help with managing species of concern, but they can also help to better understand their biology (e.g., environmental influences, historical processes, or population dynamics). The three chapters of my dissertation proposal will provide valuable information about endemic species of conservation concern with regards to their population dynamics from a molecular and population level. My first chapter assesses hybridization dynamics between the endemic and threatened prairie chub (*Macrhybopsis australis*) and the widespread shoal chub (*M. hyostoma*) in the Red River basin of Texas. My second chapter is a biogeographical assessment of the *Macrhybopsis* species complex within Texas using molecular techniques. The complex consists of five species (potentially six), of which four (potentially five) are endemic to Texas or the basins surrounding Texas. My third and final chapter is a Pollock's Closed Robust Design mark-capture study of two endemic freshwater mussels, which are also species of concern, the Texas pimpleback (*Cyclonaias petrina*) and smooth pimpleback (*C. houstonensis*). These three chapters will provide valuable information about the hybridization dynamics of fishes in the wild, historical biogeography of fishes within Texas, and population dynamics of freshwater mussels in Texas.

Bio: Alex was born and raised in upstate New York. He graduated from Plattsburgh State University in 2012 with a B.S. in Ecology. Subsequently worked for two years at the University of Vermont as a fisheries research technician. Completed his master's degree in 2016 at Eastern Illinois University in Biological Sciences focusing on fisheries genetics. Started his PhD here in 2016 in Aquatic Resources.

## Thesis Defense

Population structure and gene flow in the Louisiana Irises

Alex Zalmat

Major Advisor: Dr. Noland Martin

Committee Members: Dr. Chris Nice (Biology) and Dr. James Ott (Biology)

Tuesday, November 6, 2018, 2 p.m., IGRM 3203

Identifying the distribution of genetic variation and gene flow is fundamental to understanding the evolutionary history and dynamics of populations undergoing divergence. Natural selection and genetic drift shape the distribution of population structure and gene flow throughout the ranges of species and can drive the divergence of taxa. With the advent of next generation DNA sequencing techniques, it is now possible to explore population structure and gene flow at a genomic level throughout the range of such ecologically divergent taxa. The Louisiana Irises (*Iris*, series *Hexagonae*) comprise a group of three or more ecologically and reproductively divergent lineages that occasionally still produce hybrids in nature, giving us an opportunity to explore the process of speciation as it happens. Here we sampled populations of Louisiana *Iris* spp. in an attempt to characterize population structure and gene flow throughout their respective ranges. We discovered evidence for gene flow in some parts of the range and tested several standing hypotheses of nominal taxonomy accepted by Louisiana *Iris* enthusiasts. We also quantified introgression in a newly discovered hybrid zone between *Iris hexagona* and *I. brevicaulis* using a Bayesian Genomic Cline analysis. We also tested the hypothesis that a purportedly hybrid species, *I. nelsonii*, indeed shows ancestry from two or more of the hypothesized parental species. We discovered that a relatively small proportion of the loci we sampled in the hybrid zone are experiencing extreme patterns of introgression in the studied hybrid zone. We found evidence that population structure appears to be more complex than previous taxonomic designations suggest. It was also discovered that *I. nelsonii* only appeared to share ancestry with only one of the purported parent species, *I. fulva*. This study provides a foundation for future exploration of evolutionary dynamics affecting these taxa.

Bio: Alex grew up in Dallas, TX and received his bachelor's degree in biology from Texas State University in 2014. He joined the biology graduate program at Texas State in Fall of 2014 and now lives in San Marcos, TX. He enjoys hiking with his dog Morgan, rock climbing, and fly-fishing on the San Marcos River. He hopes to use his bioinformatics skills in his professional life post graduation.

## Thesis Defense

Investigating the Nocturnal Nest Box use of the Black-crested Titmouse (*Baeolophus atricristatus*)

Christina Farrell

Major Advisor: Dr. M. Clay Green, Department of Biology, Texas State University

Committee Members: Dr. Thomas R. Simpson, and Dr. Andrea Aspbury, Department of Biology, Texas State University

Tuesday, November 6, 2018, 2:00 p.m., Supple Norris Room

Nest boxes are used during the breeding season by many cavity-nesting birds, however less is known about the use of nest boxes as sites for roosting during the winter non-breeding season. The Black-crested Titmouse (*Baeolophus atricristatus*; hereafter BCTI) is a member of the family Paridae, which is a family containing birds known to utilize nest boxes during the winter seasons. However, the BCTI is a species with undocumented or unknown roosting behavior. For this study, possible factors influencing the propensity for winter roosting in the BCTI were examined. I conducted nocturnal surveys on nest boxes with the use of a wireless infrared cavity inspection camera across two winter field seasons. I analyzed the influence of nightly weather conditions and vegetation on winter roosting. For the weather variables affecting the probability of roosting, a decrease in temperature was found to increase BCTI roosting. Vegetation density surrounding nest boxes was also found to influence roosting with an increase in vegetation leading to an increase in roosting frequency. This study has shown nest boxes are of use to BCTI during the non-breeding season and has shed light on some of the factors influencing their winter roosting behavior. Future analyses should further explore the effect of wind conditions on roosting, as wind speeds were not found to influence roosting probability. The specifics of habitat and vegetation preference on roosting site selection should also be further assessed to determine how habitat species composition affects nocturnal winter roosting.

Bio: Christina obtained a B.S. in Geography from Texas State University in Fall 2013 and began her M.S. in Wildlife Ecology at Texas State in Spring 2016. She recently accepted a position as the Biodiversity Researcher and Collections Curator at the Selah, Bamberger Ranch Preserve in Blanco, Texas.

## Dissertation Defense

An analysis of the effects of photosynthetically active radiation and recreation induced turbidity in the San Marcos River on the vegetative growth of Texas wild rice (*Zizania texana* Hitchc.)

Michele L. Crawford-Reynolds

Major Advisor: Thomas B. Hardy, Department of Biology, Texas State University

Committee Members: Tina M. Cade, Department of Agriculture, Texas State University, Robert D. Doyle, Department of Biology, Baylor University, David E. Lemke, Department of Biology, Texas State University, Weston H. Nowlin, Department of Biology, Texas State University, Paula S. Williamson, Department of Biology, Texas State University

Tuesday, November 6, 2018, 8:30 a.m., Freeman Aquatic Biology Building, Room 130

Texas wild rice (TWR) is an endangered perennial macrophyte known to occur only in the San Marcos River, Hays County, Texas. Availability of photosynthetically active radiation (PAR) is an important abiotic factor affecting a plant's biomass. The San Marcos River is impacted on a seasonal, weekly and diel basis by contact water recreation. Recreational activities can cause increases in suspended sediment induced turbidity resulting in a decrease in water clarity and reduction in ambient PAR. Studies were conducted to test the effect of a reduction in PAR on the vegetative growth of TWR. Results of ex situ experiments involving a reduction in PAR through shade frames (0%, 10%, 20%, 40%, and 80% PAR reductions) found that with only 20% ambient PAR (80% PAR reduction), above ground biomass, below ground biomass, above/below ground biomass, total biomass, shoot number, root number, and total leaf surface area of TWR plants were significantly reduced in two of three experimental periods. The second study focused on periods of low and high contact recreational use, the suspended sediment induced turbidity response, and the impact on TWR biomass production. Results showed that differences in TWR biomass production existed along a longitudinal gradient in the river. The Eastern Spillway study site, which had very limited upstream recreational activity, was compared to downstream treatment sites located at Sewell Park, Bicentennial Park, and Ramon Lucio, which all had substantial upstream recreational activity. Greater growth was found in TWR plants at the upstream Eastern Spillway site. Differences in biomass production are likely the result of lower levels of suspended sediment in the water column at the Eastern Spillway site, allowing for higher levels of PAR. No difference in the amount of periphyton on the leaf surface of plants at the different study sites under either low or high contact recreational use was found. Therefore, periphyton does not account for observed differences in TWR growth. Findings from this study suggest that locations in the river receiving more than 20% ambient PAR provide optimum habitat for the reintroduction of TWR. Predicted model trends in percent PAR reduction at various depths in the river showed 20% ambient light could be reached at 60cm. Turbidity levels and depth are important factors to consider when selecting sites for reintroduction of TWR. The results of these studies inform future conservation and management efforts to restore TWR to once historical habitat and increase areal coverage in the San Marcos River.

Bio: Michele received a B.S. in Biology in 1991 and M.A. in Biology in 1993 from the University of Incarnate Word. She completed a M.Ed. degree in Education from Sul Ross University in 1998. Michele is currently a tenured Biology Professor at Southwest Texas Junior College.

## Thesis Defense

### STOMACH CONTENT ANALYSIS OF THE INVASIVE SMALL INDIAN MONGOOSE (*HERPESTES AUROPUNCTATUS*) FROM PUERTO RICO

Candice M. Rodriguez

Major Advisor: Iván Castro-Arellano

Committee Members: Thomas R. Simpson and Christopher Serenari

Monday Nov. 5, 2018, 2:00 p.m., Norris Room

Since their introduction to Puerto Rico as a form of biological pest control in the late 1800's, the small Indian mongoose (*Herpestes auro-punctatus*) has been identified as a reservoir for several zoonotic diseases and has been suggested as a factor affecting native fauna. Mongooses are considered generalist predators that readily switch prey consumption depending on prey availability. Puerto Rico is home to a diverse fauna with multiple endemic species. There are 7 ecological zones in Puerto Rico that vary in rainfall, elevation, and vegetation thus creating heterogeneous environments that likely differ in prey abundance which presumably results in diverging prey use by mongooses in distinct ecological zones. Prior dietary analyses conducted on introduced mongooses in Puerto Rico have focused on individual ecological zones. For the present study I contrasted mongoose diets from the subtropical moist forest zone and subtropical dry forest zones. Stomach content was separated and analyzed to determine aggregate percentages of prey remain compositions for 5 categories (Invertebrate, reptile, mammal, vegetation, and other). Of 51 mongoose stomachs analyzed (Dry, n=22, Moist, n=29) there was a difference in category compositions across all mongooses but there was no difference in compositions of prey remains between ecological sites. Invertebrates conformed the largest category of prey (Dry=13.7%, Wet=9.4%) used by mongooses at both ecological zones. Despite their large ecological differences, these zones proximity to each other likely allows prey distributions to overlap across both zones. Future studies on prey abundance per ecological zone would provide insights into whether mongooses are selecting or using prey based on their availability.

Bio: Candice was raised in San Antonio, Texas. She received her Bachelor of Science Degree in Biology with a minor in Chemistry from Texas State University in Fall of 2015 where she then stayed to continue her Master of Science in Wildlife Ecology. She plans to apply the College of Veterinary Medicine at Michigan State University in the Spring of 2019.

## Thesis Defense

Exploring Latino Parent Attitudes Toward Science, Involvement in Science, and Perceptions of Value and Comfort of Family Science Events

Izzy De Leon

Major Advisor: Dr. Julie F. Westerlund

Committee Members: Dr. Kristy Daniel and Dr. Ruben Garza

November 5, 2018, 8:45 a.m. in Supple 257

Diversity within teams and organizations guards against groupthink and overconfidence, and improves their ability to problem solve and make predictions. Even though efforts have been made to increase diversity within the Science, Technology, Engineering, and Mathematics (STEM) fields, marginalized groups are still largely underrepresented in the STEM workforce. This study focused on the Latino population gap in representation within the STEM fields. Most programs aimed at increasing Latino representation in science focus on directly encouraging students to pursue STEM careers. This study explored Latino parents' attitudes toward science and what types of informal science activities parents engage in with their children. I organized 15 family science events in San Marcos, Texas, in which parents completed a pre- and post-event attitude toward science survey and an additional parental involvement survey to find out their attitudes towards science and what types of informal science activities they are involved in with their children. The activities and experiments performed during the family science events utilized common household items or items that were inexpensive. Twenty-two Latino parents participated in the study and 15 completed both the pre- and post-attitude toward science survey. The attitude toward science survey had 14 items and was scored using a Likert-type scale with a minimum and maximum score of 14 and 70 respectively. Latino parent's pre- and post-event attitude toward science means were 60.1 and 62.2 respectively for attending at least one family science event. On the parental involvement survey, Latino parents identified 27 science activities that they have performed with their children, with 67% of those being discovery-based indoor activities and 59% being free activities. In terms of parent participation, the majority of Latino parents (73%) preferred free activities. This study can help inform school districts, principals, teachers, and informal science education organizations on strategies for changing Latino parent's' attitudes toward science and increasing their involvement in their children's science education.

Bio: Izzy De Leon was born and raised in San Antonio, TX. He received a Bachelor's of Music in Violin Performance from Texas State University as well as a Bachelor's of Science in Biology in 2016. During his undergraduate tenure, he studied the violin with Dr. Lynn F Ledbetter and was part of Dr. Kristy L Daniel's research lab. In Spring of 2017 he began his Master's of Science in Biology at Texas State University where he joined the lab of Dr. Julie F. Westerlund. While working on his Master's, Izzy has had the opportunity to work with the Mentoring Matters program and HSI STEM IMPACT program on giving support and professional development to students that are underrepresented in STEM. Izzy has also had the privilege of attending a week long professional development at NASA's Johnson Space Center to improve his teaching in science. In his spare time, Izzy likes to read and re-watch The Office, sometimes at the same time. He also maintains his fiddle chops by playing with the Starlight Symphony

Orchestra and performing throughout the Austin-San Antonio corridor. Izzy can be reached at [izzydeleon@txstate.edu](mailto:izzydeleon@txstate.edu).

## Thesis Defense

### Mercury Concentrations in Fish from the Guadalupe River, Texas: Relationships with Body Length and Trophic Position

Taylor Gold Quiros

Major Advisor: Dr. Jessica Dutton

Committee Members: Dr. Tim Bonner (Biology), Dr. Weston Nowlin (Biology), Clint Robertson (Texas Parks and Wildlife Department - Inland Fisheries)

Monday November 5, 2018, 2 p.m., FAB 130

Mercury (Hg) is a nonessential trace element that is toxic to aquatic life at low concentrations. Mercury is known to bioaccumulate over time in freshwater fish and biomagnify up freshwater food webs, so top predatory fish have the highest Hg body burden. Within Texas, Hg studies in freshwater fish have primarily focused on the northern half of the state and south Texas is relatively understudied. This study investigated the concentration of Hg in muscle tissue from 41 species of trophically diverse fish ( $n = 1,772$ ) in relation to body length and trophic position at five sites on the Guadalupe River (Flat Rock Lake, Canyon Lake, Lake Dunlap, Gonzales, and Victoria) using a direct mercury analyzer and stable isotope analysis ( $\delta^{13}C$ ,  $\delta^{15}N$ ). The majority of species showed a positive relationship between body length and Hg concentration ( $p < 0.05$ ), indicating that Hg was bioaccumulating over time. Striped mullet was the only species that displayed an inverse relationship due to growth dilution. Mercury concentrations were highest in top predators including longnose gar, flathead catfish, and striped bass, and lowest in moderate and low trophic level species, including Mexican tetra, threadfin shad, and suckermouth catfish. Within the five sites examined, the average Hg concentration in each species was higher in reservoir sites than riverine sites. There was a positive relationship ( $p < 0.05$ ) between  $\delta^{15}N$  and Hg concentration at all sites except Victoria, indicating Hg biomagnification between trophic levels. Five species (flathead catfish, channel catfish, white bass, striped bass, and longnose gar) had at least one individual that exceeded the Texas Department of State Health Services (TDSHS) human health criterion for Hg ( $0.7 \mu\text{g/g}$  wet weight), with at least one species at each site exceeding the guideline. Based on this data, the current Hg advisory for Canyon Lake needs to be reevaluated and the other 4 investigated sites may need to have Hg advisories issued.

Bio: Bio: Taylor is a native of Seguin, Texas and earned her B.S. in Biology and Environmental Science from Trinity University in San Antonio in 2016. She enjoys hiking with her dog, Lily, and genuinely believes that Jurassic Park should be taught in public schools. She plans to start a PhD in fall 2019.

Thesis Defense

ASSESSMENT OF THE SMALL INDIAN MONGOOSE (*HERPESTES AUROPUNCTATUS*) IN SUSTAINING CATTLE FEVER TICK POPULATIONS IN PUERTO RICO

Madison Torres

Major Advisor: Dr. Ivan Castro-Arellano

Committee Members: Dr. Sarah Fritts and Dr. Thomas R. Simpson

Monday, November 5, 2018, 9:00 a.m., Supple 153

The ectoparasite *Rhiphicephalus* (*Boophilus*) *microplus*, also referred as Cattle Fever Tick (CFT), serves as the primary vector for the protozoan pathogen *Babesia* which causes bovine babesiosis in livestock and other wildlife hosts. Current management practices in Puerto Rico have failed to control CFT prevalence resulting in major economic loss. One factor that has not been directly addressed is the high pervasiveness of invasive Small Indian Mongoose (*Herpestes auropunctatus*) in Puerto Rico and their potential to serve as an alternate Cattle Fever Tick host. For this study, radio-telemetry and ectoparasite sampling was conducted on mongooses at five farm sites in Puerto Rico to estimate habitat use and ectoparasite prevalence. I estimated the overlap of mongoose home ranges within cattle pastures and compared utilized versus available habitat types. Mongooses were found to nonrandomly select for grasslands and a portion of all mongoose home range estimates overlapped with corresponding farm sites. *R. microplus* was not found on sampled mongooses, suggesting the mongoose is not serving as a host for CFT populations in Puerto Rico. These results show continued research is needed to evaluate all potential CFT hosts to implement improved management practices. This study also provides insight on movement patterns and habitat use for a highly invasive species prevalent throughout many Caribbean islands.

Bio: Madison obtained a Bachelor of Science degree in Wildlife Biology from Texas State University in Spring 2013 and began her Masters in Wildlife Ecology at Texas State in Fall 2013. For the last year and a half, she worked for the United States Department of Agriculture Wildlife Services conducting wildlife management throughout New York City. She is currently a Wildlife Biologist for an environmental consulting firm based in Austin, TX.

Dissertation Defense

Influence of Bacterial Outer Membrane Vesicles on Struvite Crystal Growth

Ashley Summers

Major Advisor: Dr. Robert JC McLean

Committee Members: Dr. Manish Kumar and Dr. Jeffery W Schertzler, Binghamton University

Friday, November 2, 10:00 a.m., Supple 257

Urinary tract infections (UTIs) are a very serious health concern, affecting millions of people each year. They lead to almost 10 million doctor's visits and hundreds of thousands of hospital admissions every year in the United States (Mittal 2009). One of the common causatives of UTIs is *Pseudomonas aeruginosa*, a gram negative, aerobic, rod-shaped bacterium (Balcht 1994). As a potential way to deliver virulence factors, *P. aeruginosa* secrete outer membrane vesicles (OMV), which are formed through direct interaction of *Pseudomonas* quinolone signal (pqs) with the lipopolysaccharide component of the outer membrane (Wessel 2013). Strains used in this research have mutations in these genes in the pathway that result in the inhibition of the formation of OMV. Commonly seen in bacterial urinary tract infections is the presence of struvite crystals. These crystals precipitate in alkaline urine, and eventually form larger stones. Alkaline urine is caused by the hydrolysis of urea to ammonia via the enzyme urease (Le Corre 2005). The purpose of this research is to study if the presence of outer membrane vesicles produced in *P. aeruginosa* induce struvite crystal formation. Various strains of *P. aeruginosa*, with and without OMV, were grown in BHI (blood heart infused agar) and suspended in artificial urine. Since *P. aeruginosa* lacks urease, the urease action was mimicked by titrating artificial urine with ammonium hydroxide, inducing struvite crystal formation. The presence and shape (crystal habit) of struvite crystals was confirmed via phase contrast microscopy. Transmission electron microscopy (TEM) was used to confirm the presence of OMV. When crystals were measured using imaging flow cytometry, there was no significant difference in crystal numbers in intact and fragmented *P. aeruginosa* cells regardless of the presence or absence of OMV; although the number of crystals formed was elevated in controls lacking bacteria. This *in vitro* data suggests that *P. aeruginosa*, regardless of OMV production, does not enhance struvite formation in artificial urine.

Bio: Ashley was born in South Texas where she grew up working on a farm that focused on the production of corn and cotton. She received a Bachelor of Science in Microbiology from Texas State University with a double minor in biochemistry and honors studies. Ashley aims to attend medical school to become a pediatric cardiologist. She also hopes to continue doing research and provide access to medical resources to areas that lack any basic healthcare infrastructure. She thanks her family for all their love and support.

## Dissertation Proposal

ALL IN THE FAMILY: THE AFFECTS OF URBANIZATION AND CLIMATE CHANGE ON THE BEHAVIOR, SOCIALITY, AND POPULATION DYNAMICS OF A KIN-STRUCTURED PASSERINE, THE BLACK-CRESTED TITMOUSE (*BAEOLOPHUS ATRICRISTATUS*)

Rebekah J. Rylander

Major Advisor: Dr. Sarah Fritts (Department of Biology – Texas State University)

Committee Members: Dr. Butch Weckerly and Dr. Andrea Aspbury (Department of Biology - Texas State University), Dr. Thomas R. Simpson (Texas State University – Professor Emeritus), Dr. Michael Patten (Department of Biology - Oklahoma University)

Friday, November 2, 2018, 9 a.m., Supple 153

Climate change and habitat fragmentation through urbanization pose a threat to avian biodiversity on a global scale. Though many species are capable of co-existing in anthropogenic landscapes, there often are compromises in species' survivorship, fecundity, and/or dispersal mechanisms. Avian species that are social can be even more affected by altered climate and urbanization due to additional challenges of maintaining familial bonds. A residential species of central Texas, the black-crested titmouse (*Baeolophus atricristatus*, BCTI), is a social songbird that forms kin-structured neighborhoods in rural, less-disturbed regions of its range. However, the titmouse also is regularly encountered in areas of high anthropogenic influence, but it is unknown how this altered landscape affects BCTI demographics, behaviors, and sociality. Thus, the focus of my dissertation research is three-fold: 1) assess the influence of urbanization on BCTI kin-structured neighborhood formation; 2) examine fitness costs and benefits associated with BCTI familial-living through resource sharing behaviors; and 3) compare BCTI population demographics and dynamics across varying levels of anthropogenic disturbance and seasonal weather patterns. I will perform this study in urban San Marcos, Texas and the Freeman Center of Texas State University. In both locations, I will capture, color-band, and monitor BCTI families that utilize nestboxes during the breeding season. Through focal observation and territory mapping, I will determine dispersal patterns, annual fecundity, survivorship, and kin-structure behaviors in locations with varying degrees of urbanization. With the use of passive integrated transponder (PIT) tag technology on the Freeman Center, I will examine the potential fitness benefits that BCTI receive through sharing behavior by residing next to relatives. Because this study will span seven years, I will assess the possible effects of weather patterns, in addition to urbanization, on the population dynamics of this species. Therefore, a thorough investigation of the BCTI could lead to better-focused conservation practices for socially-oriented species, especially in the face of inevitable habitat fragmentation and climate change.

Bio: Rebekah Rylander grew up in central Texas where she fell in love with avifauna during her bachelor's degree from the UT Austin. After a whirlwind of travel and exciting field experience, Rebekah settled into Texas State University where she earned her master's degree studying social flocking dynamics of the black-crested titmouse. Because of the questions that surfaced after degree completion, Rebekah decided to continue working with titmice and their unique behaviors. During her limited spare time, Rebekah enjoys assisting undergraduates in research projects, performing banding station demos, and monitoring a local population of golden-cheeked warblers.

## Thesis Defense

### Classification of Small-Mammal Metacommunity Structures Along Elevational Gradients With Connections to Metacommunity Networks

Emily M. Javan

Major Advisor: Ivan Castro-Arellano

Committee Members: Ivan Castro-Arellano, Joseph Veech, Daniela Ferrero, Michael Willig Friday, Nov. 2, 2018, 1:00 pm, Supple 257

Small-mammals host a wide variety of zoonotic pathogens and thus their ecological patterns are intricately tied to the emergence of infectious diseases. They also serve an important role in ecosystem function by being prey and sources of seed dispersal. To assess the interaction structure, or metacommunity structure, of small-mammal assemblages, presence-absence surveys along elevational gradients were collected from the literature at both local and regional scales. In total, fifty-nine sources were used to create 337 species incidence matrices based on 104 study sites. Each incidence matrix was organized by six relatedness groupings: genus, family, suborder, order, superorder, and multiple superorders. Metacommunity structures changed due to the choice of relatedness grouping, but was independent of the size of the input matrix. Random metacommunity structures were rare and often reflected disconnected metacommunity networks. Metacommunity networks treat species as nodes with connecting edges weighted by species co-occurrence at elevational bands. Nestedness metrics did not depend on maximum elevation, average annual mean temperature, average annual precipitation, or the number of species clusters as determined by the Louvain method and Spinglass algorithm. Relativized nestedness did increase as the novel nestedness metric, species deletion ratio, increased at both local and regional scales. Further analyses should explore the use of geographical information system software and clustering algorithms that allow species to be in multiple clusters. The habitat preference and temporal niche of each species should also be assessed to determine to what extent co-occurrence implies species interactions and potential transmission of infectious pathogens.

Bio: Emily received her Bachelor of Science degree in Applied Mathematics with a minor in Ecology, Evolution, and Biodiversity from UC Davis in Spring 2014. She began her Masters in Population and Conservation Biology at Texas State University in the Fall of 2016. She plans to start at PhD in Mathematical Epidemiology with an emphasis on network science in Fall 2019.

## Thesis Defense

### INITIAL RESPONSES OF AQUATIC BENTHIC MACROINVERTEBRATE COMMUNITIES TO LARGE FLOW PULSES IN THE GUADALUPE, SAN ANTONIO AND BRAZOS RIVER BASINS OF TEXAS

Jeremy Maikoetter

Major Advisor: Dr. Timothy Bonner

Committee Members: Dr. Caitlin Gabor (Biology), Dr. Archis Grubh (TPWD)

Thursday, November 1, 2018, 3:30 p.m., FAB 130

Riverine benthic macroinvertebrates (BMI) communities are regulated, in part, by the dynamic character of the river's flow regime. Purpose of this study was to assess the influence of a flow regime component (i.e., large flow pulse) on BMI riffle communities. Predictions were that BMI richness and density would decrease with large flow pulses, ranging between 1 in 2 year events (340 m<sup>3</sup>/s) to 1 in 5 year events (331 to 886 m<sup>3</sup>/s), but that density reductions would differ among taxa categorized as swiftwater, moderate, and slackwater forms. BMI communities were monitored at 11 sites located in three river basins and distributed among upper and lower reaches of major rivers and tributary streams. A total of 93,400 aquatic macroinvertebrates were identified to family and used to estimate BMI richness and BMI density among 102 riffles (61 riffles pre-flood and 41 riffles post-flood) between 2014 and 2017. Physical and chemical aspects of riffle habitats were similar between pre-flood and post-flood, except that post-flood riffles had less sand and gravel than pre-flood. BMI communities were similar among river basins and were segregated along environmental gradients related to physical and chemical (16%), season (6%), flood (2%) effects. Overall BMI richness decreased between pre-flood and post-flood at two sites. Changes in density were not detected at any of the 11 sites. Densities of swift and moderate BMI taxa increased at two sites; changes in slack BMI density were not detected at any sites. My initial predictions were largely unsupported, but continued monitoring of these communities will add to the current knowledge of flow pulse effects on BMI. Resistance and resiliency of the BMI communities were attributed to several factors and have implications to state-wide environmental flow standards and future water quantity biomonitoring.

Bio: Jeremy lives in New Braunfels, Texas with his wife Michelle and son Collin. He returned to Texas State University to complete his B.S. in Aquatic Biology in 2015 with a minor in Chemistry while assisting in the Bonner Aquatic Ecology Lab prior to starting the M.S. Aquatic Resources program in 2016. Throughout his time at Texas State University, he has studied several aspects of Aquatic Ecology, including fishes, aquatic insects, and freshwater mussels. Jeremy is currently a biologist for Zara Environmental and upon completion of his M.S. degree plans on continuing to study and monitor rare and imperiled aquatic and terrestrial species in Texas.

Dissertation Defense

The Genomics of Speciation

Katherine Bell

Major Advisor: Dr. Chris Nice

Committee Members: Dr. Noland Martin, Texas State University

Dr. Jim Ott, Texas State University

Dr. Jim Fordyce, University of Tennessee

Dr. Darrin C. Hulsey, University of Konstanz

Monday October 29, 2018, 9am, Supple Science Building, Room 153

Speciation, the process by which reproductive isolation evolves between diverging lineages, is pivotal to our understanding of evolution. Across multiple wild populations I explored the genetic architecture of reproductive isolation and adaptive traits, the interaction between gene flow and genetic architecture of traits and their impact on the process of speciation, and finally I assessed the repeatability of genetic differentiation and absolute diversity across the genome, across multiple species pair comparisons. My dissertation includes investigations of hybridization between pitcher plants (*Sarracenia* sp.), a repeated trophic polymorphism within the Cuatro Ciénegas cichlid fish (*Herichthys minckleyi*), and a species complex of blue butterflies (*Lycaeides* sp.) that have a complicated evolutionary history that includes repeated, independent evolution of hybrid species. I generated genome-wide population genetic data to quantify patterns of genomic differentiation in all of these case studies. I used a combination of analyses to dissect the relationships between trait architecture, adaptation, and reproductive isolation. Bayesian clustering was used to describe patterns of variation and identify areas of admixture. Bayesian Sparse Linear Mixed Models (BSLMM) were used to map the genetic architecture of a variety of traits and I compared estimates of introgression for genomic regions that contribute to trait variation to understand if these traits are associated with fitness in admixed individuals. Bayesian Genomic Cline models were used to identify patterns of introgression and excess ancestry in admixed individuals. Patterns of differentiation measured along chromosomes was used to assess the repeatability of differentiation and potential adaptation. I found remarkable variation in trait architecture, ranging from very simple to highly complex. Many genomic regions were associated both with trait variation and patterns of strong selection, though this was not universal. Repeatable patterns were detected in some regions of the genome which suggests that evolution can be predictable, yet there are also instances of unrepeated differentiation suggesting a role for historical contingency. Overall, my results contribute to our understanding of the process of speciation and highlight the power of genome-wide data to resolve important questions in evolution.

Bio: Kate was raised in Dorset, in southern England. In 2009 she obtained a Bachelor of Science degree with Honors in Zoology from Queen Mary, University of London. In 2012 she completed a Master of Science in Population and Conservation Biology from Texas State University. She stayed at Texas State and begun a Ph.D. in 2012 in Aquatic Resources.

## Thesis Defense

The use of 23S ribotyping to detect harmful and nuisance phytoplankton in a large, subtropical reservoir during an extended drought period

Tatiana Gámez

Major Advisor: Dr. Alan Groeger

Committee Members: Dr. Schonna Manning (University of Texas), Dr. Vicente Lopes (Texas State University)

Friday, October 19, 2018, 9:00 a.m., Freeman Aquatic Building Room 102

Inland subtropical water bodies are highly susceptible to freshwater harmful algal blooms (HABs). Still, there remains a lack of studies on this subject and the conditions encouraging blooms in this climate. Central Texas, USA, went through an extended drought from 2011-2015 – a phenomenon common in the subtropics. Lake Buchanan, a large inland reservoir, experienced rapid shifts in the phytoplankton community during this period as the lake transitioned to more eutrophic conditions, and serves as an excellent model for subtropical lakes due to its location and size. Samples were taken bimonthly and included measuring water quality parameters, nutrients and phytoplankton, along with the identification of living and preserved phytoplankton to assess the impacts of the transition. The phytoplankton community was evaluated by cell counts and DNA barcoding using 23S ribotyping to verify the presence and abundance of different strains. Abiotic and biotic factors were evaluated to determine which variables contributed to the formation of HABs. DNA sequencing analysis confirmed the presence of known bloom-forming cyanobacteria. Overall, this study shows that the saxitoxin-producers *Planktothrix*, *Aphanizomenon*, and *Cylindrospermopsis* thrived in drought conditions ( $p < 0.001$ ) whereas *Limnothrix* and *Pseudanabaena* did not. The diatoms *Fragilaria* and *Lindavia* increased in terms of community dominance after the end of the drought. Following the drought period, *Aphanizomenon ovalisporum*, *Phormidium tenue*, and *Planktothrix* sp. were present along with additional potentially harmful yet rarely studied species. These results suggest that drought-induced eutrophication lead to the dominance of harmful cyanobacteria in Lake Buchanan. Thus, subtropical reservoirs should be monitored closely during extended drought periods, as the risks associated with eutrophication and HABs are predicted to be higher.

Bio: Tatiana earned her Bachelor of Science degree from the University of North Texas in Spring 2015 with an Ecology major and Chemistry minor. She joined the Aquatic Biology program at Texas State in Fall 2016.

## Dissertation Proposal Defense

Descriptions, classifications, and explanations of processes and patterns structuring and maintaining inland fish communities

Cody A. Craig

Major Advisor: Timothy H. Bonner, Department of Biology, Texas State University

Committee Members:

Emmanuel Frimpong, Department of Fish and Wildlife Conservation, Virginia Tech

Keith B. Gido, Division of Biology, Kansas State University

Noland H. Martin, Department of Biology, Texas State University

Chris C. Nice, Department of Biology, Texas State University

Tuesday, October 2, 2018, 2:00 p.m., Freeman Aquatic Biology Building, Room 102

Factors influencing fish community structure are numerous, complex, and interdependent. Structuring mechanisms of aquatic communities fall within four broad classes (i.e., zoogeography and deep-evolution, local abiotic and biotic phenomena, autecology of individual species, and biotic interactions among fishes) and explain why fishes are found in local and regional communities. The common theme among chapters is identification of patterns that aid in understanding contributions of the four broad classes in regulating fish community structure. A unique contribution of my work is the application of theoretical community ecology framework across multiple scales, from individuals to ecoregions, using descriptive and manipulative field and laboratory experiments. Chapter 1 provides drainage basin keys for Texas inland fishes, which provides accurate identification of study organisms. Chapter 2 quantifies habitat associations and guilds of western gulf slope fishes ( $S = 146$ ) to describe autecology and ecological niches within fish communities. Remaining chapters focus on identification of mechanisms that maintain fish community structure, including water quantity within riverine environments (Chapter 3-- Responses of the Brazos, Guadalupe, and San Antonio rivers to environmental flows), water quantity and water quality within spring complexes (Chapter 4--Nueces historical and current fish community, Chapter 5--San Antonio historical and current fish community), and biotic factors (Chapter 6--Temperature-mediated feeding between spring-associated and riverine-associated congeners, with implications for community segregation).

Bio: Cody is from Longview, Texas. He graduated with his B.S.-Wildlife and Fisheries Management from Texas Tech University in 2012. Cody completed his M.S.-Aquatic Resources in December 2014 studying the relationship between spring flow magnitude and fish communities. He began as a PhD student in 2016 and plans to complete his PhD in 2020.

## Thesis Defense

Detectability affects the performance of survey methods - a comparison of sampling methods of freshwater mussels in Central Texas

Brittney Sanchez

Major Advisor: Dr. Astrid Schwalb

Committee Members: Dr. Weston Nowlin (Biology), Dr. David Rodriguez (Biology)

Friday, August 24, 2018, 1:30 p.m., Freeman Aquatic Biology 130

Designing effective surveys for freshwater mussels (Unionidae) is a challenge, because they are spatially clustered and often found in low densities. The objective of this study was to examine how the effectiveness of three different survey methods (timed searches, transect method, and adaptive cluster method) varied between different habitats at six sites in the San Saba, Guadalupe, and San Antonio Rivers in Central Texas. Species richness, the total number of mussels per search effort, species composition and size distribution obtained with different survey methods were compared between sites. Timed searches were generally the most effective method in detecting species especially when densities were low ( $\leq 0.2$  individuals per  $m^2$ ) or mussels were highly clustered. The adaptive cluster method, however, was as effective as timed searches in detecting species when densities were moderate or higher ( $>2$  ind. per  $m^2$ ) and detected more species than timed searches at a site at which habitat conditions hindered searches. The performance of adaptive cluster in respect to number of mussels found per unit search effort seemed to be enhanced by sandy substrate facilitating detection of mussels, whereas timed searches were less effective at sites at which habitat conditions hindered the detectability of mussels. Differences in detectability of mussels was not only associated with habitat conditions, but also with the size of mussels, their behavior and morphology. Timed searches detected a larger proportion of larger mussels that tended to be less burrowed and that had shells with more sculpturing compared to quantitative methods. In addition, surveyors with more search experience detected a larger number of mussels. Our results suggest that to design effective surveys variation in detectability of mussels must be considered which depends on local habitat conditions, experience of surveyor, behavior, size and morphology of mussels.

Bio: Brittney is from Uvalde, Texas. She moved here in August of 2010 to begin her undergraduate degree in Biology. In 2016 she began the graduate program and has been juggling a variety of responsibilities such as teaching Biology as a high school teacher in San Antonio, teaching as a graduate instructional assistant in San Marcos, and finishing up her research in the Schwalb lab. She is passionate about working hard, science, health, and helping others. She is thankful and grateful for the experience and research she has conducted in the Schwalb lab. She hopes to continue research in her future endeavors.

## Thesis Defense

Interspecific Spacing between Harvester Ant (*Pogonomyrmex barbatus*) and Red Imported Fire Ant (*Solenopsis invicta*) Colonies along the Invasion Gradient in Texas

Skyler Flaska

Major Advisor: Dr. Joseph Veech

Committee Members: Dr. Sarah Fritts (Biology), Dr. Todd Swannack (USACE and Dept. of Biology)

Friday, August 3, 2018, 1:00 p.m., Supple 153

Invasive species can be devastating to ecosystems and their impacts on native species are innumerable. The red imported fire ant (*Solenopsis invicta*) invasion is a threat to many native species and is one hypothesized explanation for the observed decrease in the red harvester ant (*Pogonomyrmex barbatus*). Understanding how *S. invicta* affects harvester ants is important given harvester ants' beneficial role in ecosystems and as a prey base for certain species. In this study I performed a "space for time substitution" to investigate if the ecological interactions between these two species has changed over time. Using data on the interspecific spacing between *P. barbatus* and *S. invicta* colonies and density of *S. invicta* colonies in the vicinity of *P. barbatus* colonies (compared to neighboring random points), the goal of my study was to quantitatively characterize these interactions and test if they differ across the invasion gradient of *S. invicta* in Texas. I predicted that interspecific spacing might increase with time since first contact if *P. barbatus* colonies have developed an avoidance response. I obtained data for 125 *P. barbatus* colonies at 24 study sites. I did not find a significant difference in the spatial interaction between the two species along the invasion gradient. However, my study provided some evidence for the possibility of coexistence without an adaptive avoidance response by *P. barbatus*. The size of *P. barbatus* colonies becomes significantly larger as the distance to nearest fire ant mound decreases but colony size becomes smaller as density of fire ant mounds increases. This result might represent a relatively intricate interaction worthy of future research. Overall my results indicate that *S. invicta* may not negatively impact *P. barbatus* to the extent commonly thought, although *S. invicta* likely remains a threat to other native species.

Bio: Skyler is from Mineral Wells, Texas, and moved to San Marcos in the fall of 2016 when he joined the Wildlife Ecology graduate program. He graduated cum laude from Tarleton State University with his Bachelor of Science degree in Biology with an emphasis on Environmental Science and a minor in Chemistry in May 2015. Upon successful completion of his master's Skyler will be attending the University of Louisiana in Lafayette to pursue a Ph.D. in Biology focusing on assimilation wetland ecology.

## Thesis Defense

### EXPERIMENTAL TESTS OF THE EFFECTS OF EXOTIC HETEROPHYID METACERCARIAE ON THE SWIMMING ENDURANCE OF SMALL FISH HOSTS

Kelby Clements

Major Advisor: Dr. David Huffman

Committee Members: Dr. Timothy Bonner and Dr. Clay Green

Thursday, July 5, 2018, 2:00 p.m., FAB 130

An exotic snail from Asia (*Melanoides tuberculata*) has been introduced into many Texas springs and has become of great ecological concern due to harmful trematode parasites it harbors. The larvae of two of these parasites (*Centrocestus formosanus* and *Haplorchis pumilio*) infect many native fishes, some of which are listed species, and have become the most common trematodes in habitats they infest. Many studies have explored the pathology of *C. formosanus* in different host species, but after 20+ years and hundreds of thousands of dollars, conservation workers are still unable to quantify what effects the parasite is having on the relative fitness of affected fish, meanwhile, the effects of *H. pumilio* have been virtually ignored. Almost any task most fish must perform in order to compete for food, mates, spawning sites, or to escape from predators, relies on the ability of the fish to swim either at its maximum speed or at lower speeds for sustained time. Anything that negatively affects the swimming performance of such fish will reduce the individual's ability to thrive. We have developed a device to test the swimming performance of small fish to measure the reduction in performance caused by varying levels of infection with either *Centrocestus formosanus* or *Haplorchis pumilio*. Our findings indicate that high levels of infection with *Haplorchis pumilio* can cause mortality while non-lethal exposure has profound effects on the swimming performance of *Cyprinella venusta* and the threatened *Dionda diaboli*. Indeed, we can now specify the percent reduction in swimming performance that can be attributed to infection with *H. pumilio*. Interestingly, however, *C. formosanus* had virtually no measurable effects on swimming performance. We conclude that, except for the fountain darter, which is dramatically affected by *C. formosanus*, more research should be focused on studying *H. pumilio* as a greater threat to native fishes.

Bio: Kelby is from Gustine, Texas, and moved to San Marcos in 2016 when he joined the Biology graduate program. He earned his Bachelor of Science degree in Wildlife Management from Texas State University in 2012. Kelby enjoys backpacking trips, rock climbing, and winter sports and has plans to move to New Zealand to pursue a career in wildlife conservation.

## Thesis Defense

Modeling Detection and Density Using Distance Sampling for Three Priority Grassland Bird Species in Texas – Northern Bobwhite (*Colinus virginianus*), Eastern Meadowlark (*Sturnella magna*), and Painted Bunting (*Passerina ciris*)

Name: Anna Matthews

Major Advisor: Dr. M. Clay Green

Committee Members: Dr. Floyd Weckerly and Dr. Jennifer Jensen

Thursday, July 5, 2018, 10:00 a.m., Supple 153

Within Texas, three priority grassland species that have experienced declines due to loss of native grasslands are the Northern Bobwhite (*Colinus virginianus*), Eastern Meadowlark (*Sturnella magna*), and Painted Bunting (*Passerina ciris*). This 5-year study identified covariates that influence detection, availability, and density for these three species using data collected from 986 surveys across 11 Texas counties. Points were visited once per year from 2013 to 2017 in May and June, and 5-minute point counts were performed using distance sampling protocols. Models were fit using `gdistamp` from the package “unmarked” in R. Covariates that influenced detection for Northern Bobwhite were observer, ambient noise, time of day, and Julian date. Detection was higher later in the season, earlier in the morning, and at lower ambient noise levels. Julian date and observer influenced Eastern Meadowlark detection, with detection declining later in the season. Painted Bunting detection was influenced by ambient noise and observer, although the effect of ambient noise appears to be negligible. The proportion of individuals available for detection was influenced by year, showing trends that are likely influenced by precipitation from the preceding year. However, despite this, availability for all species was not influenced by the Palmer Drought Severity Index. Vegetative cover was selected in the top density model for all three species. Native grasslands positively influenced density of Northern Bobwhite and Eastern Meadowlarks, shrubland positively influenced bobwhite and Painted Bunting, and cropland positively influenced bobwhite. Overall, there was high variability in the effect of vegetative cover on density across the three species, indicating that management for one species may ignore vegetative cover needs of other grassland species. Finally, for all species, monitoring should emphasize observer training and attempt to survey only under low ambient noise conditions.

Bio: Anna was born and raised in Dallas, Texas. She left Texas for freezing weather to receive a Bachelor of Science in Fisheries and Wildlife from the University of Minnesota. While there, she discovered a passion for birds, grassland conservation, and education, and she has been fortunate to be able to continue to expand her knowledge and experience in these fields as a graduate student at Texas State University.

Thesis Defense

DETERMINING THE IMPACT OF A CORRELATED SCIENCE AND MATHEMATICS PROFESSIONAL DEVELOPMENT MODEL ON TEACHER LEADERSHIP

Ruby Hernandez

Major Advisor: Dr. Sandra West

Committee Members: Dr. Julie Westerlund, Dr. Emily Summers, and Dr. Sandra Browning

Friday, July 5, 2018, 7:30 a.m., Norris Room Supple 376

The mathematics and science national standards advocate for educational reform by implementing research-based strategies that includes recognizing the teacher's critical role in effective instruction. A school's success can be attributed to recognizing and fostering teacher leadership development. Teachers often feel empowered and become advocates for integration on their campus when they understand how to relate mathematics and science grade-level content in a meaningful way. The purpose of the Correlated Science and Math professional development model used in the Mix It Up project was to better enable science and mathematics integration by classroom teachers. My study aimed to determine the impact of the Mix It Up project on teacher leadership growth in a 2-year cohort (n=23). I investigated teacher leadership using a mixed-methods approach which allowed me to understand if and how teacher leadership growth is occurring. I selected a multiple case study (n=4) to gather enriched details of the process of teachers in MIX progressing into teacher leadership by attaining stage 3, the highest level of leadership, using the NCSM PRIME Leadership Framework. Overall, MIX teachers' reported they possessed teacher leadership characteristics while 91% reported taking on leadership roles outside their classrooms and stage 3 leaders in my case study attributed their leadership growth to their participation in the MIX PD program. Participants' reported they were not only implementing and impacting their own students, but were ultimately advocating for science and mathematics integration and the use of general best practices at the district and even state level

Bio: Ruby A. Hernandez is a former high school Biology teacher and plans to return to teaching science in middle or high school to broaden her experience in teacher leader progression. She was born in San Antonio, Texas where she earned her Bachelor of Arts degree in Biology with a minor in secondary education at the University of the Incarnate Word in 2014. She joined the Biology graduate program in Fall 2016.

## Thesis Defense

Variation in temperature tolerance of two invasive snails in Texas

Linus Ray Delices

Major Advisor: Astrid Schwalb, Department of Biology, Texas State University

Committee Members: Weston Nowlin, Department of Biology, Texas State University

Benjamin Schwartz, Department of Biology, Texas State University

Tuesday, July 3, 2018, 10:00 a.m., FAB 130

Invasive species are a major concern for aquatic ecosystems and tropical freshwater snails (Thiaridae) can be very successful invaders. *Melanoides tuberculata* and *Tarebia granifera* are two invasive snails in Central Texas that serve as intermediate hosts for several Asiatic trematode parasites of fishes, birds, and other organisms. A better understanding of their temperature tolerances is needed to better predict their spread in Texas and to inform management strategies. Therefore, the goal of my study was to determine the critical thermal minima of these species and to compare temperature tolerances between species, river segments, and different local morphotypes. Survival of snails were monitored in environmental tanks in which temperature was decreased by 0.1°C per hour from 23°C to 10°C. In addition, survival was monitored over time in environmental tanks in which temperature was held constant at 17°C, 15°C, 11°C and 10°C after acclimatization. *M. tuberculata* showed slightly higher survival at colder temperatures compared to *T. granifera*. There was no significant difference between local morphotypes of *M. tuberculata* found in Central Texas, and there were some differences in temperature tolerances of snails between river segments i.e. the upper and lower San Marcos and Guadalupe Rivers. My results show that *M. tuberculata* can tolerate colder temperatures down to 11°C for a few weeks, which will facilitate their dispersal in rivers of Central Texas farther away from thermally stable spring influenced reaches. Further research is need to examine differences in thermal preferenda and temperature tolerances of snails between rivers.

Bio: Linus grew up in the small town of Viuex-Fort, Saint. Lucia-West Indies. He earned his Bachelor of Science in Biology with a second major in Psychology at Grambling State University. He joined the Biology graduate program in Spring 2015. He is passionate about science and he willingly shared his gifts, talents, keen-eye, great personality and knowledge with others.

## Thesis Defense

Impact of Environmental Contaminants on the Threeridge mussel (*Amblema plicata*) in the Guadalupe River Basin, Texas

Name: Stacey Britton

Major Advisors: Dr. Jessica Dutton and Dr. Astrid Schwalb

Committee Members: Clint Robertson (Texas Parks and Wildlife Department- Inland Fisheries)

Tuesday, July 2, 2018, 10:00 a.m., Freeman Aquatic Biology 130

Aquatic pollution has contributed to the significant decline in unionid mussels in North America; however, toxicological studies on Texas unionids are limited. In this study, adult Threeridge (*Amblema plicata*) mussels were collected from 8 sites within the Guadalupe River basin and the concentration of 8 essential (Co, Cu, Fe, Mn, Mo, Ni, Se, Zn) and 8 nonessential (Ag, As, Cd, Cr, Hg, Pb, Sn, V) trace elements were determined in gill and foot tissues. Additionally, water samples from each site were analyzed for nutrient concentrations. Biomarker analysis (lipid peroxidation, total antioxidant capacity against peroxy radicals, and protein content) of gill tissue was used to quantify the physiological response of mussels to environmental stressors. Contrary to my expectations, trace element uptake, nutrient concentrations, and physiological stress responses were not necessarily higher at downstream sites. Hg and As concentration in gill tissue were observed to be highest in mussels at the uppermost sites on the San Marcos River and Guadalupe River, respectively. Trace element concentrations in gill tissue did not correlate with general physiological stress biomarkers in mussels; however, higher total nitrogen and total phosphorous concentrations at upstream sites correlated with a) higher lipid peroxidation and lower antioxidant capacity against free radicals, indicating greater oxidative stress, and b) lower protein concentration indicating reduced overall health of adult mussels. Future studies need to investigate the impact of these contaminants on glochidia and juvenile mussels, since early life stages are more sensitive to exposure.

Bio: Stacey has spent the last decade living between Austin and Seattle while pursuing an education in science and raising two bright young girls. Stacey earned her B.S. in Biology with a minor in Chemistry at Texas State University in 2016. She is passionate about science outreach and youth mentorship and hopes to encourage the next generation of environmentalists and ecologists to find their voice.

Thesis Defense

AN INVESTIGATION OF PRESERVICE TEACHERS' ENGAGEMENT AND PERCEPTIONS OF SCIENCE LEARNING  
IN OUTDOOR LEARNING ENVIRONMENTS

Sara Salisbury

Major Advisor: Dr. Kristy Daniel

Committee Members: Dr. Michelle Forsythe and Dr. Julie Westerlund

Friday, June 1, 2018, 1:30 p.m., SUPP 257

Science education programs that use both formal and informal instruction provide students with more engaging experiences than when only using traditional instruction. However, educators often do not know of, or are uncomfortable with using informal resources. Thus, understanding how educators view and experience science learning in informal environments is necessary for increasing the likelihood that these educators will integrate informal science resources into their curricula. The purpose of this study is to investigate relationships amongst preservice teacher engagement during informal, outdoor learning activities, and perceptions about using informal resources during their future teaching career. During this study, preservice teachers (n=5) took part in a one-day, nature-based fieldtrip as part of a General Science education course. During this fieldtrip, they learned science content and how to teach science in a fieldtrip setting. Using a four-dimensional framework of engagement (i.e., behavioral, cognitive, affective, agentic), I analyzed video, eye-tracking, and interview data to identify moments of engagement, preservice teachers' perceptions of the fieldtrip, and their integration ideas for using outdoor learning environments in their future teaching career. Overall, participants' actions indicated their engagement across all four dimensions. Participants thought highly of using outdoor learning environments as potential teaching tools, and could identify some way they could integrate them into future teaching practices. No clear relationship existed between observable engagement actions and preservice teachers' future integration ideas; However, participants' overall past experiences with informal learning environments (including the General Science fieldtrip) appeared to largely influence their perceptions and integration ideas. Participants who had no prior teaching experiences drew primarily on their experiences as a student, whereas participants with informal and formal teaching experiences drew upon their experiences as a teacher more than their experiences as a student. Observable engagement actions and interview responses also suggested some participants underwent personally meaningful learning experiences.

Bio: Sara is from New Jersey, and moved to San Marcos in 2016 when she joined the Biology graduate program. She earned her Bachelor's of Science degree in Environmental Science with a minor in studio art from Allegheny College in 2012. Sara is an avid rock climber, and hopes to someday become a Director of Research and Education at an outdoor education institution.

## Master's Thesis Defense

Bacterial community structure in soils of the oldest agronomic experiment fields in the United States, the Morrow Plots, and of the original tallgrass prairie

Abirama Sundari Ganesan

Major Advisor: Dr. Dittmar Hahn

Committee Members: Dr. Robert McLean and Dr. David Rodriguez

Wednesday, May 16, 2018, 10:00 a.m., Supple 257

New molecular techniques that focus on high throughput DNA sequencing techniques such as 454 pyrosequencing and the MiSeq sequencing platforms revolutionized the field of microbial diversity studies. These techniques are widely used in projects such as the Earth Microbiome Project (EMP), a collective attempt to establish microbial fingerprints in different environments of the planet. Additional applications include studies on long-term effects of crop rotation and different fertilization regimen on bacterial community structure. We tried to build on these studies and assess microbial community structure in the Morrow Plots, the oldest agronomic experimental fields in the United States, and adjacent tallgrass prairie with emphasis on members of the genus *Frankia*. The Morrow Plots were designed in 1876 on tallgrass prairie soils to evaluate the effects of different cropping systems and soil treatments on crop, and include the oldest continuous corn plots in the world. Illumina-based 16S rRNA V3 amplicon sequencing retrieved total of 26.47 M effective sequences obtained from 44 samples, i.e. 12 soils with different vegetation and fertilization, and 3 to 6 replicates per soil, with 313,695 to 906,328 reads per sample. At a sequencing depth of 300,000 sequences for each sample, Acidobacteria, Actinobacteria, Proteobacteria and Verrucomicrobia were the most abundant bacterial phyla present across all soil samples accounting for 74±4% of the reads. Crop rotation increased diversity of the bacterial community, which was also affected by the fertilization regimen. Reads representing frankiae accounted for 0.1 to 1.0% of all reads, with generally higher percentages in fertilized soils. Reads represented frankiae of clusters 1a, 2, 3, and 4, but also a group of frankiae that could not reliably be assigned to a cultured relative. The results provide evidence of long-term establishment of *Frankia* populations in soils under different management conditions.

Abi received her Bachelor's degree in Microbiology from the Bharathidasan University, Tamilnadu, India, in 2006, and a Master's degree in Biotechnology from Bangalore University- Bangalore, India. She started her Master's degree in Biology in Dr. Hahn's lab in 2014, applying next generation sequencing methods and the corresponding bioinformatics tools to analyze microbial community structure in soils

Dissertation Defense

Differential selection pressure among duplicated genes in teleosts

Richard John Nuckels, Jr.

Major Advisor: Dana M. García

Committee Members: Dr. Chris Nice, Dr. Noland Martin, Dr. Karen Lewis & Dr. Jeff Gross

Friday, May 11, 2018, 10 a.m., 153 SUPP

Gene and genomic duplications provide organisms with new genetic material subject to selection. Using *myo5*, *rab11*, and *rab27* gene families as models, I examined the evolutionary rate differences among duplicated genes and whether selective forces (e.g. purifying selection or positive selection) could be identified in one or both duplicated gene clades. I used phylogenetic and syntenic analyses along with ancestral chromosomal mapping to identify each duplicate. I then analyzed the duplicates using tests for evolutionary selection at the molecular level. Using a branch site-random effects likelihood test, I found evolutionary rate values ( $\omega$ ) to fall into two or three rate classes along at least one branch for one duplicated gene clade for each of the gene trees created. One rate value ( $\omega_1$ ) for a percentage of codon sites was close to zero, representing purifying selection. A second rate value ( $\omega_2$ ) for a percentage of the codons was much greater than one ( $\omega_2 \gg 1$ ), signifying positive selection. The two rate classes were present in the teleost *myo5bb* branch for the motor domain and the cargo binding domain, and two rate classes were present in teleost *myo5ba* for the cargo binding domain. Also in teleosts, I found two rate classes for the *rab11a* branch, *rab11a1* branch, and *rab27bb*. Using sequences from 7-10 organisms that diverged from a common ancestor 140-440 million years ago, I found  $\omega$  values between 0.01 and 0.24 for the whole coding sequence for duplicated genes ranging in size from 200-220 codons. For longer coding sequences (1915 codons),  $\omega$  ranged from 0.26 to 0.41. I examined the percentage of invariant codons present in each of the gene clades and found the percentage of codons that were invariant to range from 6% for the highly variable neck region of *myo5* to more than 30% for some highly conserved duplicated *rab11* and *rab27* genes and some highly conserved regions for some *myo5* duplicates. I identified a highly conserved  $\omega$  for codons for amino acids that have previously been linked with the functionality of the Myo5 and Rab proteins. These data lead me to infer that the duplicated genes remain functional or have some modified, acquired functionality that remains to be identified.

Bio: Richard John Nuckels, Jr. was born and raised in Texas with brief stints in Wyoming and Colorado. Richard's research experience began as an undergraduate researcher using zebrafish as a model to understand the evolution and development of pigment cells. His research continued as a lab manager and graduate student using zebrafish as a model for vertebrate eye development. He completed a B.S. in Biochemistry from UT-Austin and an M.S. in Biology from Texas State University. Upon completing his Ph.D. degree, Richard will continue working as a lecturer and lab coordinator at UTSA where he hopes to continue his research while mentoring students in comparative genomics.

Thesis Defense

INFLUENCE OF VARIABLE PLANTING TIME ON THE PRODUCTIVITY OF A CORN-BEAN INTERCROPPING SYSTEM

Sarah Eisenmenger

Major Advisor: Dr. Susan Schwinning

Committee Members: Dr. Nihal Dharmasiri, Dr. Ken Mix

Thursday, April 5, 2018, 4:30 p.m., Supple Norris Room

Intercropping is an agricultural practice in which two or more crops are grown together. It is employed in many countries to increase yields relative to monoculture, especially when crops are grown without fertilizer and pesticide inputs. Previous research has focused on modifying planting densities and spatial arrangements to optimize intercropping yields. This project focused on optimizing the timing of component crop planting as an additional method for improving the overall yield of a corn-bean intercropping system. Corn-bean intercrops typically overyield (meaning they produce more yield grown together than grown separately), either because bean supports the growth of corn through biological nitrogen fixation, or because the two crops have weak competitive interactions and are less suppressed in the intercrop than if they competed intraspecifically in monoculture. I hypothesized that if the bean-corn interaction is facilitative, earlier planting of bean should increase the yields of both crops. Alternatively, if the interaction is competitive, earlier planting of bean would increase bean yield but lower corn yield with little effect on their combined yield. Beans were seeded 20 and 10 days before, simultaneously with, and 10 and 20 days after corn for a total of five intercropping treatments. Additionally, monocultures of each crop with matching planting dates were grown to calculate the yield advantage relative to monoculture. Final yield data supported the second hypothesis; the intercropping yield advantage was not significantly affected by the bean planting offset, but an earlier bean planting provided greater bean yields and slightly lower corn yields. The experiment suggested that, while it is possible tweek corn and bean yields in the intercrop by varying planting times, this does not appear to be an effective method for optimizing combined yield.

Bio: Sarah was born and raised in San Antonio, TX. She enjoys learning about animals, plants, and insects and grew up spending a lot of time outdoors. After starting out as an English major in college, she found that conservation and the environment were more important to her. She graduated from the University of the Incarnate Word in 2015 with a Bachelor of Science in Environmental Science. Sarah then joined the Population and Conservation Biology graduate program in Fall 2015 to study plant ecology. She has a German Shephard mix named Percy and a bearded dragon named Layla.

## Thesis Defense

Host plant affiliation and spatial autocorrelation as drivers of genetic differentiation among populations of a regionally host-specific insect herbivore

Name: Amanda L. Driscoe

Major Advisor: Dr. James R. Ott

Committee Members: Dr. Chris C. Nice and Dr. Noland H. Martin

Monday, April 2, 2018, 1:00 p.m., Norris Room

Disentangling the processes responsible for structuring patterns of biodiversity at all spatial scales challenges biologists as such patterns represent evolutionary and ecological processes coupled with spatial autocorrelation among sample units. The phytophagous insect, *Belonocnema treatae* (Hymenoptera: Cynipidae) exhibits regional specialization on three species of live oaks throughout its geographic range across the southern USA. Here I ask whether populations of *B. treatae* affiliated with each host plant exhibit genetic differentiation that parallels host plant phylogeography while controlling for spatial autocorrelation among sampling locations. I used next-generation genotyping-by-sequencing of 1,219 *B. treatae* collected from 58 sites distributed across the geographic ranges of the three host plants to identify 6,987 common, and 44,390 rare, single nucleotide variants. Population genomic structure was then investigated using a hierarchical Bayesian model to assign individuals to genetic clusters and estimate admixture proportions. To control for spatial autocorrelation when investigating the role of host plant affiliation in determining patterns of among-population genetic differentiation, Distance-based Moran's eigenvector maps was used to construct regression variables summarizing spatial structure inherent in the sampling design. Redundancy analysis (RDA) incorporating these spatial variables was then used to simultaneously examine the roles of host plant affiliation and spatial autocorrelation in determining patterns of among-population genetic differentiation. RDA confirmed host-associated lineages of *B. treatae* in the eastern portion of the species' range and clinal host-associated lineages in the west, independent of spatial autocorrelation. These results suggest a linkage between the history of genetic differentiation among host plants and genetic differentiation of the host-associated herbivore populations.

Bio: Amanda earned her Bachelor's of Science in Animal Science at University of Minnesota, Twin Cities. She joined the Population and Conservation Biology graduate program in Fall 2015.

Thesis Defense

CONSEQUENCES OF LONG-TERM CHANGES IN FISH COMMUNITY STRUCTURE ON ECOSYSTEM FUNCTIONING IN A SUBTROPICAL SPRING-FED RIVER

Aine Carroll

Major Advisor: Dr. Weston Nowlin

Committee Members: Dr. Thom Hardy, Dr. Josh Perkin

Monday, April 2, 2018, 12:00 p.m., FAB 130

Ecologists have examined and debated about the relationship between biodiversity and ecosystem functioning but have in general found that the functional roles of species within communities affect ecosystem functioning. Biological invasions are globally pervasive and can have potentially deleterious effects on ecosystems because some non-native taxa can establish dominance in biomass or abundance and have a detrimental impact on their introduced environment. Although the effects of non-native taxa have been examined for decades, few studies have utilized a longer-term perspective (> 10 years) to assess how non-native taxa affect ecosystem functioning. In this study, I examined long-term changes in fish community composition in the spring-influenced upper San Marcos River (central Texas, USA) and its ecosystem functioning implications, specifically how temporal changes in the composition and diversity of the fish community were related to changes in the rates and ratios of dissolved inorganic N (NH<sub>4</sub><sup>+</sup>) and P (PO<sub>4</sub><sup>3-</sup>) recycled by the fish community and the sequestration of nutrients into fish biomass. I assembled a 76-year data set (1938 – 2016) of fish collections for the upper San Marcos River and linked it to contemporaneous estimates of species-specific nutrient content and dissolved nutrient excretion rates from the upper San Marcos River. Analysis of the fish community indicated three distinct time periods with notable shifts in fish community composition between time periods: 1938 – 1959 (Period I), 1960-1989 (Period II), and 1990 – 2016 (Period III). Patterns in occurrence-weighted biomass indicated that there were substantial shifts in which species had the larger contribution to community-wide biomass (as C, N and P) of the entire fish community, with the proportional contribution of non-native and non-spring associated fishes being the highest in Period II. However, the proportional contribution of non-native and riverine-associated fishes to the community-wide dissolved P and N recycling rates increased across the three periods. This study indicates that, although the upper San Marcos River contains a relatively diverse community containing a large number of native taxa, the relative importance of non-native species in ecosystem functioning has generally increased over time.

Bio: Aine is from Dallas, and moved to Austin in 2007. She earned her bachelor's degree in English Writing with a minor in Environmental Science and Policy from St. Edward's University in 2011. She joined the Aquatic Resources graduate program in Fall 2015.

## Thesis Defense

### Host Plant and Spatial Influences on the Natural Enemy Community Structure of a Host Specific Herbivore

Name: Robert Busbee

Major Advisor: Dr. James Ott, Department of Biology, Texas State University

Committee Members: Dr. Chris Nice, Department of Biology, Texas State University, Dr. Noland Martin, Department of Biology, Texas State University

Monday, April 2, 2018, 10:00 a.m., Supple Science Building, Room 257

Both environmental variation and spatial autocorrelation play roles in structuring communities at all spatial scales. However, untangling the respective contributions of these sources of variation represents a long-standing, complex, and methodologically ever-evolving question for community ecology. Here I investigate the structure of the insect natural enemy community centered on galls produced by *Belonocnema treatae* (Hymenoptera: Cynipidae) on the leaves of its host plants across the gall former's geographic range while controlling for spatial autocorrelation among sample sites. *Belonocnema treatae* exhibits regional host plant specialization across the southern US on three live oak species, *Quercus fusiformis* (Qf), *Q. virginiana* (Qv), and *Q. geminata* (Qg). I sampled the natural enemy community at 118 sites by rearing natural enemies that emerged from galls collected at each site. I identified 32,722 natural enemies representing  $\geq 30$  taxa from 126,812 galls. I hypothesized that richness and diversity on Qv would exceed that on Qf and Qg since the geographic range of Qv bridges that of Qf to the west and Qg to the east. Contrary to my hypothesis one-way ANOVA followed by a Tukey's HSD showed that both richness and Shannon-Wiener diversity was greatest on Qf. To disentangle the role of host plant affiliation from spatial autocorrelation among sample sites I conducted a Redundancy Analysis (RDA). I first used Principal Coordinates of Neighbor Matrices (PCNM) to generate explanatory variables representing orthogonal aspects of spatial structure within the sampling frame. The set of PCNM vectors that were significant were then included in a RDA along with the host plant species from which each natural enemy was reared to examine the respective roles of host plant affiliation and spatial structure in determining abundance and species composition of the natural enemy community. This study establishes a significant role for both alternative host plants and geography in structuring the diversity of the natural enemy community of *B. treatae* and illustrates the advantages of the PCNM & RDA approach.

Bio: Robert earned his Bachelors of Science in Ecology and Evolutionary Biology at Angelo State University. He joined the Population and Conservation Biology graduate program in Fall 2015.

## Thesis Defense

Assessing seasonal diets of waterbuck (*Kobus ellipsiprymnus*) in central Texas

Kaitlin Lopez

Major Advisor: Dr. Thomas R. Simpson

Committee Members: Dr. Dittmar Hahn (Co-Chair), Dr. David Rodriguez, Dr. James Gallagher (Texas Parks and Wildlife)

Monday, April 2, 2018, 9:00 a.m., Supple 153

It is important to understand how different species use food resources when developing wildlife management strategies. This is particularly relevant in Texas where exotic ungulates are frequently stocked outside their native range with other species with which they did not coevolve. To date, no food habit studies have been conducted in Texas for waterbuck (*Kobus ellipsiprymnus*), a large antelope native to Africa. I investigated the seasonal diets of waterbuck located on Mason Mountain Wildlife Management Area in Mason County, Texas from June 2016 to March 2017. The objectives of my research were to 1) determine the seasonal diets of waterbuck by using microhistological analysis to identify and quantify plant fragments found in fecal material, 2) determine if waterbuck forage selectively, and if so, which foods were used more or less than their availability, 3) use DNA analysis to identify plant DNA extracted from fecal material, and 4) compare the results from both diet analysis techniques. In each meteorological season, I collected 20 freshly deposited fecal samples for diet analyses. To determine if waterbuck were selectivity foraging, I conducted vegetation surveys simultaneously with fecal sample collection to estimate availability of plants. I used the Daubenmire method to quantify available herbaceous vegetation and the line-intercept method to quantify available woody vegetation at 10 different points occupied by waterbuck. DNA analysis targeted the c to h region of the chloroplast trnL (UAA) intron. DNA was not successfully amplified and sequenced from fecal samples. Using microhistological analysis I quantified 47 unique plant species in the diet of waterbuck. To construct the diet, I looked at the number of fragments detected for each species compared to the total number of fragments examined (N = 2000, 500 per season). To determine if plants were utilized more than their estimated availability I performed a log-likelihood chi square test. To further determine forage selectivity, I used Manly's alpha index of selectivity and constructed 95% confidence intervals around estimate proportions of use for each species consumed. In all seasons, plants were not used proportional to their availability in the environment and waterbuck actively selected their food resources. The bulk of the diet consisted of grasses, most of which occurred in wetlands. My results suggest that resource competition between waterbuck and upland grazers such as gemsbok, sable antelope, and scimitar-horned oryx is minimal. However, competition needs to be considered when stocking waterbuck with cattle or other grazers that regularly utilize riparian species.

Bio: Kaitlin was born in Maryland but moved to McKinney, Texas at the age of two where her passion for animals, bugs, and all things outdoors flourished. In December 2014, she graduated cum laude from Texas State University with her Bachelor of Science degree in Wildlife Biology. Following a brief break from academia, Kaitlin returned to Texas State University to join the Wildlife Ecology graduate program in Fall 2015.

## Thesis Defense

Paleoclimate of the Two Medicine Formation based of leaf physiognomy

Ann Marie Prue

Major Advisor: Dr. Gary Upchurch

Committee Members: Dr. Karen Chin (University of Colorado), Dr. Julie Westerlund, and Dr. Noland Martin

Friday, March 30, 2018, 10:00 a.m., Supple 326

In the last 50 years, methods to study ancient warm climates, like those of the Cretaceous, have yielded new information on climates and their interaction with flora and fauna. One of the effective ways to reconstruct paleoclimates in terrestrial environments is to study the external features of plant leaves, or leaf physiognomy. Features of leaves from different climates have been correlated to mean annual temperature (MAT) and mean annual precipitation (MAP). There are several methods to determine paleoclimates that are based on the modern-day correlations between leaf features and climate parameters. These methods include the univariate methods of leaf margin analysis (LMA) and leaf area analysis (LAA), and the multivariate methods of Climate Leaf Analysis Multivariate Program (CLAMP) and Digital Leaf Physiognomy (DiLP). This study uses these paleoclimate proxies to study the Two Medicine Formation, a famous formation in northern Montana that contains both dinosaur and paleobotanical remains. In addition, the research examines the congruence of different physiognomic methods with each other and with other climate proxies for the Two Medicine Formation and surrounding formations of similar age. This study concludes that the univariate methods give generated temperature estimates that are too low, and a precipitation estimate that is too high. Of the two multivariate methods, CLAMP gives slightly lower temperature estimates and has inconsistencies based on classification of leaf features. DiLP, on the other hand, gives more reasonable estimates based on congruence with other paleoclimate proxies. However, the DiLP image processing of the leaves is more complex and time consuming than that of the other methods. In order to cut the leaf image processing time, a new modified technique of doubling the leaf halves from partial fossil specimens was implemented in this study. Preliminary results from the doubling halves technique indicates that climate parameter estimates are nearly the same as those described in the original DiLP method.

Bio: Ann Marie is a born and raised Cheesehead from Green Bay, WI. She got her bachelor's degree in Geology and a minor in Horticulture from the University of Wisconsin-River Falls in 2015. While participating in UNAVCO's NSF funded summer internship, RESESS, she was introduced to using fossilized leaves to infer paleoclimate by Dr. Gary Upchurch. She joined Dr. Upchurch's lab in the fall of 2015 to work on a project that combined her two passions: rocks and plants. Upon graduating, Ann Marie plans on returning to Wisconsin to weed her gardens, whack rocks, and join the work force. She eventually plans to continue her education to fulfill her dream of getting a PhD. in Geology.

## Thesis Defense

Prevalence of endoparasitic helminths of the small Indian mongoose (*Herpestes auropunctatus*) on the island of Puerto Rico

Name: Jose A. Martinez III

Major Advisor: Dr. Iván Castro-Arellano

Committee Members: Dr. Thomas R. Simpson (Co-Chair), Dr. David Huffman

Friday, March 30, 2018, 1:00 p.m., Supple 153

The small Indian mongoose (*Herpestes auropunctatus*; heretofore mongoose) has been widely introduced to islands around the world as a biological control agent. Species targeted for control were various rodents and venomous snakes. Follow-up research has been conducted on the mongoose's role as a potential reservoir of diseases that might affect man and economically important animals. However, most of previous studies have focused on detecting rabies and leptospirosis, with reports related to endoparasitic helminthes being largely incidental. The only study conducted on Puerto Rico reported no endoparasitic helminths from an examination of 210 mongoose visceral organs. From May 22 to August 12, 2015 I trapped mongoose from 5 sites (cattle farms) on Puerto Rico and conducted standard necropsy techniques to survey for endoparasitic helminthes in the viscera. Each site was trapped for a minimum of 2 weeks, logistics and farm operating hours permitting. Each transect consisted of approximately 50 Tomahawk live traps (20x7x7", Model #204, Tomahawk Live Trap Co, Hazelhurst, WI). Transect checks took place daily starting at 08:00 for regular intervals of 2 hours (depending on heat every hour) until approximately 1700. Using standard necropsy techniques, the visceral organs and tissues collected from 60 mongooses were: Lungs with attached trachea, heart, liver with attached gallbladder, gastrointestinal tract (esophagus to rectum) with associated mesenteric tissues, and bladder. There were no observable signs of parasitism in the major organs (Heart, liver, lungs, bladder, and gallbladder). My examinations of the gastrointestinal tracts yielded two species of nematodes and one Acanthocephalan. The nematode *Skrjabinocapillaria caballeroi* was found infecting 65 percent of mongoose stomachs while *Physaloptera* spp. were recovered from 18 percent of gastrointestinal tracts. The Acanthocephalan *Oncicola venezuelensis* was recovered from the greater and lesser omentum, fascia of the skin and muscle, small intestine tissues, and the connective tissues of the liver to the diaphragm of 36.6 percent of examined mongooses.

Bio: Jose was born in California but has moved over 30 times since including living and graduating High School in Italy. In 2002 he joined the United States Marine Corps where a passion for wildlife and the outdoors was deeply fostered. In December 2013, he graduated from Texas State University with his Bachelors of Science in Wildlife Biology. Following a short break in South Africa working with large African predators, Jose returned to Texas State and joined the Wildlife Ecology graduate program in Fall 2014.

Thesis Defense

ROOSEVELT ELK RESPONSE TO A NEWLY AVAILABLE FORAGING PATCH

Aaron McGuire

Major Advisor: Dr. Floyd Weckerly

Committee Members: Dr. Clay Green, Dr. Mark Ricca

March 30, 2018, 11:00 a.m., Supple 153

According to optimal foraging theory, herbivores will use a new foraging patch intensely to become familiar with a new resource. To better understand how herbivores incorporate new habitat into their home range, I examined use by a Roosevelt elk (*Cervus elaphus roosevelti*) herd in Redwood National and State Parks, California, that was recently given access to a nearby, new foraging patch, the cattle pasture. Cattle and predators, both of which can negatively affect elk spatial patterns, also used the cattle pasture. My study objectives were to examine monthly elk use in the cattle pasture, assess cattle and predator influence on herd use of the pasture, analyze summer and winter movement patterns to assess if forage biomass was more limited in one season, and determine if the herd was using the cattle pasture intensely to become familiar with the resources. I placed six infrared, motion sensitive cameras throughout the cattle pasture from August, 2016, to November, 2017. I followed the herd from dawn to dusk, recorded elk activity, movement (step length), and forage biomass in January, 2017 and 2018. Herd movement was also recorded in July, 2017. I found avoidance between elk and cattle and elk and predators at short temporal and small spatial scales in the cattle pasture. Step lengths were similar between summer and winter months. The herd used the cattle pasture more in January, 2018, than in January, 2017. My findings were inconsistent with optimal foraging theory.

Aaron grew up in Roswell, New Mexico where he found his passion for wildlife and working in the outdoors. He graduated from New Mexico State University in 2010 with his bachelor's degree in Fish, Wildlife, and Conservation Ecology with a double emphasis in wildlife and fisheries. After getting his bachelor's degree, Aaron moved to Northwest Wyoming where he worked for the Wyoming Game and Fish Department as a fisheries technician, a wildlife damage technician, and a hunt management coordinator. In 2014, Aaron moved to Bozeman, Montana where he worked for Montana State University as a fisheries technician and a wildlife capture technician. He also worked for Montana Fish, Wildlife, and Parks as a wildlife disease technician and a hunt management coordinator. Aaron moved to San Marcos in the fall of 2016 to pursue his master's degree in wildlife ecology. Aaron plans to move back up north and become a regional wildlife management biologist for a state agency.

## Thesis Defense

### Population Viability of Reddish Egrets (*Egretta rufescens*) in Texas: A System Dynamics Approach to Conservation and Management of North America's Rarest Heron

Sarah Durham

Major Advisor: Dr. Clay Green

Committee Members: Dr. Floyd Weckerly and Dr. Steve DeMaso

March 28, 2018, 11:00 a.m., Norris Room

Reddish egrets are a threatened waterbird species that inhabit the Gulf Coast of the U.S. and Mexico, as well as, the Bahamas, Cuba, the Mexican Pacific Coast, and the Yucatan peninsula. The plume trade of the late 1800s drastically reduced global population numbers of reddish egrets. By the 20th century, the species was decimated and possibly extirpated in many parts of its range. While much of the historical range has been recolonized, the reddish egret remains North America's least abundant heron species. An estimated one-third to one-half of the global reddish egret population occurs in the United States, with Texas having approximately 75% of the breeding pairs. While egret population numbers may be stable or increasing in portions of the range, many factors continue to threaten the persistence of the species. Population viability analyses (PVAs) are a common method of predicting a species' persistence into some future time. The purpose of developing a population viability analysis for *E. rufescens* is to identify possible factors impeding the growth of Texas populations. By assessing the relative threat of each contributing factor and identifying vulnerable life stages, a robust PVA can estimate how different management actions may affect population demographics. I found that four-year-old female survivorship during the non-breeding and breeding seasons to be the most influential model parameters. My findings are similar to other studies that have found adult survivorship to be the most influential factor to population growth in other long-lived avian species that mature late. Additionally, I found that both the total and breeding populations are projected to remain stable over the next 50 years. While these results are encouraging, it is important to note that the model does not incorporate habitat or spatial information. These findings suggest that management actions focusing on increasing adult survivorship, such as habitat protection, would be most beneficial to population growth and persistence of reddish egrets in Texas.

Bio: Sarah grew up in the rough and tumble corn fields of central Illinois. She moved to Texas in 2011 and began the Wildlife Biology undergraduate program at Texas State University in the Fall of 2012. Sarah graduated summa cum laude from Texas State University in 2015. She began her master's work in the Fall of 2015 studying reddish egrets. Her hobbies include knitting and cats.

## Thesis Defense

Exploring tradeoffs in alternative life history strategies

Amara Lee Garza

Major Advisor: Chris C. Nice, Department of Biology, Texas State University

Committee Members: Jim R. Ott, Department of Biology, Texas State University

Susan Schwinning, Department of Biology, Texas State University

Friday, March 23, 2018, 9:00 a.m., Supple Science Building, Room 153

The evolution of gregarious feeding is an intriguing problem in ecology. It occurs in many phytophagous insects and typically coincides with eggs laid in large clutches. Despite many benefits to gregarious feeding, including accelerated larval growth rates, not all species feed gregariously suggesting disadvantages to gregariousness. To investigate the advantages and disadvantages, I studied a system of two sympatric, congeneric butterfly taxa that employ drastically different oviposition and larval feeding strategies. The Emperor butterflies both lay eggs on Hackberry trees (*Celtis laevigata*, *C. reticulata*); the Hackberry Emperor (*Asterocampa celtis*) lays a single egg and caterpillars feed alone, while the Tawny Emperor (*A. clyton*) lays a large clutch and caterpillars feed gregariously. To explore whether gregarious feeding drives clutch size differentiation while simultaneously filling in natural history information on *Asterocampa* butterflies this research addressed the following questions: 1) Is there a difference in emergence in terms of relative abundance of *Asterocampa* between sexes or species? 2) Do *Asterocampa* species have an oviposition preference between *Celtis* (Hackberry) host plants? 3) Do *Asterocampa* larvae experience enhanced performance in gregarious feeding groups? I predicted that the advantage of gregarious feeding would be realized for *A. clyton*, where females lay large clusters of eggs. Fruit baited traps were used to capture females. Phenological variation in relative abundance was analyzed with partial correlation coefficients. Female oviposition preference was assessed with a choice experiment with leaves of both host trees. Caterpillar group sizes were manipulated across the two host plant species. The group sizes approximated ranges from nature. Caterpillar performance was measured by average weight gained and proportion of caterpillars reaching their second instar. Oviposition preference was quantified using a Bayesian hierarchical model. Caterpillar performance was analyzed using an ANOVA in R. There were no differences in relative abundance across time. Females of both butterfly species preferred to oviposit on *C. laevigata*. I found significant differences in weight gained between group size treatments and caterpillar species but not between host species. I also found a significant difference in proportion reaching second instar between group size treatments, caterpillar species and host species. My results indicate a disadvantage to being gregarious and demonstrate that solitary feeding can enhance caterpillar performance; thus, the predicted benefits of gregariousness for caterpillar performance were not observed. The advantages of gregarious feeding were not realized in terms of caterpillar performance but might be related to defense against natural enemies.

Bio: Amara earned her Bachelors of Science in Biology at Saint Edward's University. She joined the Population and Conservation Biology graduate program in Spring 2014.

Dissertation Proposal Defense

Competition of Frankia populations for nodulation and development in soils

Spandana Vemulapally

Major Advisor: Dittmar Hahn

Committee Members: Mark Paschke (Colorado State University)

Jeffrey O. Dawson (University of Illinois, Urbana-Champaign)

Robert McLean

David Rodriguez

Monday, March 5, 2018, 1:00 p.m., Norris Room

Actinorhizal plants exist in symbiotic associations with root-nodule forming Gram-positive actinobacteria of genus Frankia. These filamentous heterotrophic bacteria provide the plants with reduced nitrogen resources through nitrogen fixation. Recent studies in our lab using molecular tools like qPCR and Illumina sequencing to quantify Frankia populations in soil and root nodules suggested large differences between detectable Frankia populations in soil and those in root nodules. The data suggested that root nodule formation was not a function of abundance or relative diversity of specific Frankia populations in soils. Our hypothesis was that the differences were due to alternative traits of the Frankia populations, one of which could be competition between strains in which one strain outcompetes the other for nodule formation even at low abundance. An alternative hypothesis was that it could be growth appearance, in which one strain producing many small fragments with small numbers of cells could provide more nodulation units than another one developing few large colonies with comparatively more cells. We took advantage of the availability of specific pure cultures representing individual clusters or sub-clusters within the genus Frankia and then developed specific quantification methods that allowed us to distinguish and quantify these strains after inoculating in different concentrations and combinations in microcosm studies under controlled conditions. Quantification and characterization of populations in soil and rhizosphere as well as in nodules of the host plant species were done using qPCR and in situ hybridization techniques targeting specific Frankia populations. Using the same techniques, we were also studying host plant effects on competition for nodule formation by representative strains of different Frankia clusters.

Bio: Spandana Vemulapally was born in Andhra Pradesh, India. She graduated with a Master of Science degree in Biotechnology from Texas Tech University in 2012 and a Master of Science degree in Biomedical Sciences from Texas Tech University Health Sciences Center in 2015. She enrolled in the PhD program at Texas State University in Spring 2016.

Dissertation Defense

Plant effects on the dynamics of Frankia populations in soil

Seifeddine Ben Tekaya

Major Advisor: Dittmar Hahn

Committee Members: David Rodriguez

Robert McLean

Jeffrey O. Dawson (UIUC)

Mark Paschke (CSU)

March 5, 2018, 8:00 a.m., Supple 153

Frankiae are slow growing actinobacteria that are able to form root nodules with some woody non-leguminous plants. Studies on the ecology of these bacteria are hampered by difficulties to isolate them into pure cultures which was a prerequisite for quantitative analyses in the past. We have therefore focused on the development of molecular approaches that allowed us to retrieve quantitative data from environmental samples unbiased by the limitations of culturability. A first objective of the current study was to develop qPCR based methods to distinguish groups within the genus and quantify their populations in soil. Additional attempts were made to distinguish and quantify typical, nitrogen-fixing frankiae from atypical, generally non-nitrogen fixing frankiae. Both SybrGreen- and Taqman-based qPCR methods were subsequently evaluated for the quantification of these populations in different soils. These methods are then used to study long term effects of agricultural management practices on abundance and diversity of frankiae. Data from these analyses were contrasted with Illumina sequencing data. Both qPCR and Illumina sequencing methods were also applied in analyses of microcosm experiments aiming to investigate the effects of plants species on indigenous populations of Frankia and relate abundance/diversity in soils to root nodule populations.

Bio: Seif was born in Carthage, Tunisia, in May 13, 1984. He completed a BS degree in Biological Sciences at the University of Tunis el Manar in 2007, and earned an MS degree in microbiology from the same university with a research thesis that focused on the diversity of ascomycetes in high saline lakes in 2009. In 2014, he joined the Ph.D. program in Aquatic Resources at Texas State University.

## Dissertation Proposal Defense

Consequences of Artificial Light at Night on the Physiology and Behavior of Amphibians

Zachery R. Forsburg

Major Advisor: Caitlin R. Gabor, Department of Biology, Texas State University, USA

Committee Members:

Andrea Aspbury, Department of Biology, Texas State University, USA

Mar Huertas, Department of Biology, Texas State University, USA

Jenny Ouyang, Department of Biology, University of Nevada, Reno, USA

Edward Narayan, Department of Natural Sciences, Western Sydney University, Australia

Wednesday, February 28, 2018, 4:00 p.m., Supple Science Building, Room 376

Artificial light at night (ALAN) is defined as artificial light that alters the natural light dark patterns in ecosystems. ALAN is a growing problem globally as 40% of the World's population lives in areas continually illuminated. ALAN can have a suite of effects on community structure and is a driver of evolutionary processes. ALAN has been shown to affect the behavior and physiology of many taxa, yet research on how ALAN may affect behavior and physiology in amphibians, the most imperiled vertebrate class, is lacking. ALAN may contribute to stress and ultimately declines of amphibian populations, particularly in urban areas. I propose to examine, through laboratory and semi-natural mesocosm studies, if ALAN is contributing to physiological stress and altering behaviors in amphibians. I will also explore whether exposure to ALAN is affecting growth and survival in tadpoles and potential carry-over effects of ALAN exposure on juvenile frogs. Further, in a mesocosm setting, I will investigate if other variables such as predation and pesticide exposure have synergistic effects with ALAN by measuring growth, behavior, and physiology in tadpoles. Employing a non-invasive water-borne hormone collection protocol will facilitate a repeated measures protocol allowing me to use a reaction norm approach to analyze how hormonal and behavioral traits change over time and environmental gradients. Together, this research will provide new insights into the consequences of ALAN on amphibian populations, and if hormonal responses can evolve in response to rapid human change such as light at night.

Bio: Zach Forsburg grew up in Central Pennsylvania and earned his B.S. and M.S. in Biology from Shippensburg University. Seeking warmer weather, Zach moved to South Florida after graduate school to work at Archbold Biological Station in Venus, Florida, where he collected data on habitat use and movements of gopher tortoises and federally threatened Eastern indigo snakes. Zach was a member of the 2015 Florida Wildlife Corridor Expedition team, a 70-day, 1,000-mile, journey across Florida to bring awareness of conservation needs in Florida. He ended his 6 years at Archbold as the Director of Development and began his PhD studies in 2015. He hopes to be the next Richard Archbold.

## Dissertation Proposal Defense

Factors influencing riverine community structure of aquatic organisms: implications for imperiled species management

David S. Ruppel

Major Advisor: Timothy H. Bonner, Department of Biology, Texas State University

Committee Members;

Noland H. Martin, Department of Biology, Texas State University

Kenneth Ostrand, U.S. Fish and Wildlife Service, San Marcos, Texas

Jim A. Stoeckel, School of Fisheries, Aquaculture, and Aquatic Sciences, Auburn University

Joseph A. Veech, Department of Biology, Texas State University

Thursday, February 15, 2018, 2:00 p.m., Freeman Aquatics Building, Room 102

Aquatic communities are structured by selection, drift, dispersal, and speciation processes. Processes collectively interact to generate a diversity in community patterns among riverscapes. Aquatic community patterns and processes can be disrupted by anthropogenic alterations, such as changes in water quality and quantity, introductions of exotics species, and habitat fragmentation. The common theme among the chapters of my dissertation is the identification of patterns that aid in understanding processes (e.g., selection, drift, and dispersal) and conservation status (resiliency, representation, and redundancy) of riverine communities and species. Dissertation chapters will address gaps in existing information necessary to inform individual, population, and range-wide responses to natural and anthropogenic influences using the USFWS Special Status Assessment (SSA) framework for establishing species viability through demonstrated or predicted redundancy, representation, and resiliency. Chapter I will be a fish-habitat community assessment within the upper Red River of Texas and Oklahoma (2-year survey). Chapter II and III will assess life history characteristics and factors influencing instream movement of USFWS candidate species (Prairie Chub), a SGCN species (Red River Shiner), and an endemic species (Plains Killifish). Chapter IV will be mussel distributions and habitat associations, including habitat assessments for several USFWS candidate species, within the Colorado River. Unique contribution of my work is the application of the theoretical community ecology framework to understanding redundancy, representation, and resiliency of local systems with multiple species of conservation concern.

Bio: David was born in Saginaw, Michigan but lived in the quaint town of Ishpeming in Michigan's upper peninsula for most his childhood. He graduated cum laude with his B.S. in Zoology from Northern Michigan University in 2012. David completed his M.S. in Aquatic Resources in August 2014 studying the effects of instream flow recommendation on larval fish diets in the San Antonio and Guadalupe Rivers. He began as a PhD student in 2015 and plans to complete his PhD in December 2018. Long term goals include obtaining a tenure-track professor position.

Dissertation Proposal Defense

Biofilm Growth and Control in Spaceflight

Starla Thornhill

Major Advisor: Dr. Robert “Bob” McLean Texas State University

Committee Members: Dr. Cheryl Nickerson Arizona State University

Dr. C. Mark Ott -NASA Johnson Space Center

Dr. David Rodriguez Texas State University

Dr. Dana Garcia – Texas State University

February 02, 2018, 8:00 a.m. Norris Conference Room, Supple 376

Biofilm formation in microgravity is largely understudied. At this time, only a few studies of biofilms in microgravity have been published, and in those cases only monoculture biofilms. Environmental biofilms, including those on spacecraft, are polymicrobial communities. The Potable Water Dispenser on the International Space Station (ISS) is host to a persistent biofilm that is resistant to long-term disinfection. Since biofilms cause microbiologically-induced corrosion and release cells into the environment, their presence is a potential risk to the ISS crew. To investigate mixed species biofilms in microgravity environments, biofilms of *Escherichia coli* and *Pseudomonas aeruginosa* will be grown in coculture on stainless steel coupons using microgravity modeling high-aspect ratio vessels (HARVs). These bacteria can be differentiated using inserted mCherry (into *E. coli*) and *gfp* (into *P. aeruginosa*) genes. Biofilm structure will be analyzed using confocal microscopy and species composition by qPCR. Boric acid, a biofilm dispersant agent, will be investigated in concert with disinfectants currently in use on ISS to determine their disinfection capability. Microbiologically-induced corrosion on stainless steel will also be investigated using analytical electron microscopy and energy dispersive X-ray spectroscopy. Additionally, an experiment investigating growth, Ag-based disinfection, and corrosion will be sent to ISS for investigation in true microgravity. While in flight, biofilms will be analyzed using epifluorescence microscopy and post-flight analytical electron microscopy. This will allow for a better understanding of the growth and treatment of biofilms on ISS, providing a safer environment for long-term habitation of humans in spaceflight.

Bio: Starla Thornhill earned her BS (Microbiology) and MS (Biology) at Texas State University in 2014 and 2016, respectively. She grew up in Austin, TX. She loves cats and video games. Her research interest is microbiology in spaceflight. She won People’s Choice Award at the University Final 3MT Competition in 2017.