Ecology and Evolutionary Biology
Undergraduate Research Colloquium 2020

April 27, 2020
1300-1600

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Program

13:00 - 13:15 Opening remarks. Pam Diggle, Head-designate, Department of Ecology and Evolutionary Biology

13:15 - 13:30 Are Predators and Pollution a Problem for Freshwater Ecosystems? Pastore, Amanda¹, Mark C. Urban², and Christopher Nadeau², ¹Ecology and Evolutionary Biology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology, University of Connecticut

13:30 - 13:45 Strategies to Improve Annotation and Assembly for Complex and Large Plant Genomes. Ferreira, Alyssa¹, Sumaira Zaman², Vera Velasco³, Madison Caballero², Jill Wegrzyn², ¹Pathbiology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology, University of Connecticut, ³Department of Biology, University of Toronto Mississauga, Mississauga, ON, Canada

13:45 - 14:00 Investigating Genetic Signatures Associated with Reduced Mortality Against Emerald Ash Borer in Green Ash. Fritz, Ava¹, Jeremy Bennett¹, Jeanne Romero-Severson², Megan Reid², Jennifer Koch³, Noah Reid⁴, Jill Wegrzyn⁴, ¹Biomedical Engineering B.S.E. (expected May 2020), ²Department of Biology, University of Notre Dame, Notre Dame, IN, ³USDA Northeastern Research Station, Delaware OH, ⁴Department of Ecology and Evolutionary Biology, University of Connecticut

14:00 - 14:15 Genetic components controlling flower size. Olsen, Lisa¹, Yaowu Yuan², ¹Molecular and Cell Biology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology.

14:15 - 14:30 Break
Program (cont’d)

14:30 - 14:45  A Change of Heart? Shifts in Juvenile Alewife Heart Size and Lipid Content Prior to Migration. Stephens, Jacqueline B.¹, Rebecca S. Colby², and Eric T. Schultz², ¹Biological Sciences B.S. (expected May 2020), Department of Ecology and Evolutionary Biology, University of Connecticut

14:45 - 15:00  Comparative Transcriptomic Analysis of Juvenile and Adult Leaf Morphologies in Conifers. Cynthia Webster¹, Laura Figueroa Corona², Alejandra Vázquez-Lobo², Jill Wegrzyn³, ¹Molecular and Cell Biology B.S. (expected December 2021), ²Department of Systematics and Evolution, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, Mexico, ³Department of Ecology and Evolutionary Biology, University of Connecticut

15:00 - 15:15  The impact of distance from a stream on color morph distribution of *Plethodon cinereus*, the Eastern Red-backed Salamander. Baker, Sarah E.¹, and Elizabeth L. Jockusch², ¹Ecology and Evolutionary Biology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology

15:15 - 15:30  Poster session:
Expert Swimmers and Tank Potatoes: Swimming Behavior of Alewives at Differing Migratory Stages. Shook, Erika¹, Rebecca S. Colby², Eric T. Schultz², ¹Animal Science B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology

The Shape of Things to Come: Morphological Shifts in Juvenile Alewife Body Shape Preceding Emigration to Saltwater. Smith, Brandon S.¹, Rebecca S. Colby², Eric T. Schultz², ¹Ecology and Evolutionary Biology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology
Abstracts of Oral Presentations

Baker, Sarah E.¹, and Elizabeth L. Jockusch² The impact of distance from a stream on color morph distribution of *Plethodon cinereus*, the Eastern Red-backed Salamander

¹Ecology and Evolutionary Biology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology

The Eastern Red-backed Salamander, *Plethodon cinereus*, has lead and red-striped color morphs that have persisted throughout millions of years. The morphs differ in physiology and diet. We investigated if morph ratio varies with distance from a stream, site, and soil moisture; if invertebrate community composition varies with site and distance from a stream, and if salamander condition is correlated with foraging opportunities. We designed transects extending from stream edges to survey for salamanders, measure soil moisture, and collect soil invertebrate samples at six sites in Tolland County, Connecticut, USA. We used generalized linear models to test if morph ratio varies with distance from a stream, site, and soil moisture for two datasets. The model that best fit the data was distance-only for the dataset including all salamanders, and site-only for the dataset containing salamanders associated with moisture data. We used nonparametric tests to assess variation in invertebrate abundance with distance from a stream, and site. Invertebrate abundance did not vary consistently with distance from a stream or site based on Kruskal-Wallace tests. Therefore, distance from a stream and site best explain morph distribution, and variability in invertebrate community composition did not differ with distance from a stream or site.

Ferreira, Alyssa¹, Sumaira Zaman², Vera Velasco³, Madison Caballero², Jill Wegrzyn² Strategies to Improve Annotation and Assembly for Complex and Large Plant Genomes

¹Pathobiology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology, University of Connecticut, ³Department of Biology, University of Toronto Mississauga, Mississauga, ON, Canada.

A high quality reference genome and annotation for Douglas fir (*Pseudotsuga menziesii*) can contribute to maintaining healthy populations for forest health and timber production. This study examines methods for improving the Douglas fir genome annotation, resolving issues of gene fragmentation, pseudogene detection, and incorrect gene structures. The genome of Douglas Fir is immense (>15 Gb), with significant repeat content (> 85%), high pseudogene prevalence (>5%), and long introns (> 800Kb). These challenges impact *ab initio* gene prediction which uses the genome sequence to inform structural predictions. Recently, the transcriptome was sequenced with the PacBio Iso-Seq approach, assembled and aligned to the genome, providing more contiguous transcripts than previously available. Different annotation models were produced and compared to optimize the genome annotation strategy. A transcriptome alignment using Illumina short reads and Iso-Seq long read derived transcripts was compared to 19,000 filtered Maker *ab initio* predictions, and over 200,000 filtered Braker *ab initio* predictions (reliant on evidence from these transcriptomic resources). Annotation quality was assessed by gene structural statistics, completeness based on single copy orthologs, and a reciprocal BLAST evaluating protein level completeness. The final gene set shows improvement in quality and can be used for studying Douglas fir and its conservation.
Investigating Genetic Signatures Associated with Reduced Mortality Against Emerald Ash Borer in Green Ash

Emerald Ash Borer (*Agrilus planipennis*), an invasive pest that is threatening the sustainability of the entire North American ash tree population (*genus: Fraxinus*), can kill a susceptible tree within five years of detection. Efforts to prevent, treat, and remove afflicted trees are culminating to billions of dollars, and the eradication of this species is impacting all landscapes. Among impacted populations, individuals that survive longer are identified as “lingering,” though these account for less than 1% of the population. To complement breeding efforts, we conducted double-digest RAD-Seq across a phenotyped population of 87 green ash (*Fraxinus pennsylvanica*) and low-coverage whole-genome shotgun sequencing on 11 samples, representing 9 families. Variant detection conducted on the Illumina sequence provided 11,000 SNPs for analysis. The families were phenotyped with a greenhouse egg bioassay, where EAB larvae are applied to the stem and after six weeks the percentage of larvae killed (by the host) and the mean weight of surviving larvae are measured. QTL analysis was conducted with a reference genome to examine regions associated with partial resistance to EAB. The information gathered here will be used to improve conservation efforts and generate populations of green ash that are more resistant to EAB.

Genetic components controlling flower size

Flowers exhibit tremendous diversity in many traits, including their size, which is a key factor in reproductive success and evolution. In addition to interspecific flower size variation, many species have significant intraspecific differences in flower size. The aim of this study was to identify the genetic components involved in controlling flower size. To understand flower size variation, we looked at two species from the classic model system *Mimulus*. We analyzed a crossbreeding between the small *Mimulus parishii* flower and the closely related large *Mimulus cardinalis* flower. Our work suggests a gene on the seventh chromosome, near the six hundredth nucleotide, is a major component in flower size control. Identification of this gene advances our understanding of genetic controls of flower size, which in turn improves our understanding of mating system evolution and fitness.
Pastore, Amanda¹, Mark C. Urban², and Christopher Nadeau² Are Predators and Pollution a Problem for Freshwater Ecosystems?

¹Ecology and Evolutionary Biology B.S. (expected May 2020), ²Department of Ecology and Evolutionary Biology

The water flea, known as Daphnia, is a genus of crustaceous zooplankton that consist of many keystone species. As primary consumers, they maintain freshwater quality and serve as food for a variety of secondary consumers. To combat predation, Daphnia develop morphological defenses that include neckteeth, helmets, and tail spines upon sensing danger. One species at Acadia National Park, Daphnia magna, develops a tail spine to reduce the risk of predation from the predacious diving beetle. However, recent research suggests that increased CO₂ in freshwater systems could disrupt the chemosensory abilities of Daphnia, leaving them potentially unable to develop their defenses. Our research focused on the predator-prey interaction of Daphnia magna and predacious diving beetle larvae in order to understand whether the tail spine contributes to fitness, and if CO₂ increases will change the fitness of Daphnia magna. Unlike previous research, we used projected levels of CO₂ in our experiment and exposed both predator and prey to the same environment. If CO₂ increases inhibit the development of morphological defenses in Daphnia, then their populations could be severely impacted in the coming decades. The collapse of Daphnia populations would have a rippling effect on the freshwater communities they inhabit, therefore it is imperative that the effect of CO₂ is well studied.

Stephens, Jacqueline B.¹, Rebecca S. Colby², and Eric T. Schultz² A Change of Heart? Shifts in Juvenile Alewife Heart Size and Lipid Content Prior to Migration

¹Biological Sciences B.S. (expected May 2020), Department of Ecology and Evolutionary Biology, University of Connecticut

Migrating to a new location requires a large amount of energetic input. This is especially true for diadromous species, whose lives consist of cycling between freshwater and seawater environments. Some diadromous species show distinct morphological changes in preparation for migration; a key example being juvenile Atlantic Salmon (Salmo salar) parr marks transitioning into silver scales before heading to sea. However, obvious external changes are not present in all diadromous fishes. In Alewife (Alosa pseudoharengus) juveniles show only subtle changes in body size and shape prior to migration. The purpose of this study was to look beneath the surface to find internal changes occurring in preparation for migration. Two physical attributes and one performance assessment of migrant (actively-migrating) and resident (pre-migration) alewives were investigated: lipid content, ventricle mass, and swimming speed. I hypothesized that (1) migrants will have a larger lipid content for increased energy storage, (2) migrant ventricles will have greater mass than those of residents for higher cardiac function, and (3) larger hearts and increased energy storage will lead to better whole-body performance (i.e. swimming speed). Fish were collected in summer 2019 from the natal freshwater environment, exposed to seawater for 24 hrs, measured for swimming performance, and dissected for organ and tissue composition analysis. Hearts were excised and weighed pre- and post-drying, and a soxhlet extractor was used for lipid analyses. The results of this study will contribute to our knowledge of migratory ecology by increasing our understanding of key shifts in juvenile morphology and performance of Alewife, a species that has experienced drastic population decline since the 1960s and is currently listed as a Species of Concern.
Comparative Transcriptomic Analysis of Juvenile and Adult Leaf Morphologies in Conifers

Molecular and Cell Biology B.S. (expected December 2021), Department of Systematics and Evolution, Universidad Autónoma del Estado de Morelos, Cuernavaca, Morelos, Mexico,

Department of Ecology and Evolutionary Biology, University of Connecticut

Juniperus flaccida (drooping juniper) and Pinus cembroides (pinyon pine) are conifers native to North America, spanning Mexico and the Southwestern region of the United States. Although from two different lineages, both species exhibit heteroblastic growth. Morphologically, their leaves undergo a change between the juvenile and adult life stage. J. flaccida leaves appear needle-like at youth and awl-shaped at maturity, whereas the P. cembroides will maintain the needle-shape but develop a waxy coat with age. The objective was to perform a comparative transcriptomic analysis to quantify and examine differential expression in juvenile and adult individuals from both species. RNA from twelve samples was sequenced on HiSeq 4000 (100bp PE) and analyzed with available software. Because there are no reference genomes for these species, they were assembled de novo from the RNA-Seq reads. Following assembly, the coding regions were identified and redundant transcripts were removed. Quality filtered reads were aligned to the reference transcriptomes (one for each species), counts were generated from the alignment files, and differential expression analysis was performed with DESeq2 via Kallisto. Up and down-regulated genes (padj<0.1) across both age classes (juvenile vs adult) were observed in each species and compared. Overall, there were 531 up-regulated and 93 down-regulated genes in the juvenile condition of P. cembroides and 21 up-regulated and 24 down-regulated in J. flaccida.