Abstract for consideration to present at BREW:

Researchers at the University of Washington and the University of Idaho have developed a series of connected and standards-aligned **yeast evolution lab modules, called “yEvo”**, for high school biology students. We worked with three classrooms in two states that implemented the evolution module and took part in pre- and post-activity surveys to assess our program goals. We measured changes in student conceptions of mutation and evolution, confidence in scientific practices, and STEM and biology career interests. Students who participated in this project showed improvements in their grasp of several activity-specific concepts, including the importance of variation in evolution and the random nature of mutation. They additionally report an increased confidence in their ability to design a valid biology experiment. Our surveys identify places where specific curricular interventions could improve student learning. Student experimental data replicated literature findings on mechanisms of azole resistance and has additionally led to new insights into this phenomenon. We hope that this collaborative endeavor can serve as a model for other university researchers interested in engaging with K-12 students.

Best,

Paul A. Rowley

Assistant Professor

Department of Biological Sciences,

The University of Idaho,

132 Gibb Hall,

875 Perimeter Drive MS 3051,

Moscow, ID 83844-3051, USA.

In the **Plant Biology class** students have used the TUBBY Transcription Factor gene family in version 4 of Maize when it was just sequenced. The goal of the project was to manually curate the structure of the genes by using available illumina RNA-Seq data as well as PacBio RNA-seq data including the alternative spliced modules. Students at Old Westbury had access to a gbrowser where they could see the automated called genes and they were manually correcting the gene annotation. Further on some students expressed their interest to work further on the project and they characterize the targets of the genes using bioinformatics as well as the expression of the genes in different developmental stages in maize.

Christos Noutsos

Assistant Professor

Biology

SUNY Old Westbury

Old Westbury NY 11568

**Abstract: Genetics CURE: Investigating the Cell Wall Integrity Pathway in *Candida glabrata***

The laboratory portion of the Genetics course at Georgetown University is designed as a CURE (course-based undergraduate research experience). There is a single lecture for all students, and five lab sections of ~24 students. The focus of the lab is currently on the cell-wall integrity pathway in *Candida glabrata*. *C. glabrata* was chosen specifically because it (1) has a haploid genome for easy genetics, (2) is closely related to *Saccharomyces cerevisiae* with a wealth of literature, and (3) is an opportunistic pathogen like *C. albicans,* the hook for pre-meds*.* The cell wall integrity pathway was chosen because it is the fungal MAP Kinase pathway (pathway conservation, appreciation of model organisms) that has many discrete steps for genetic dissection, there is much understood about this pathway from studies in *S. cerevisiae* and *C. albicans*. Importantly, in the first few years of offering, there were few papers on this pathway and these students were the first to construct knock-outs and investigate phenotypes. Students work in pairs or trios on one of eight steps from the PM to the nucleus. The organization of the CURE during the semester is that students knock-out an assigned gene in the pathway using homologous recombination during the first third, they confirm construction of the knock-out strain during the middle third, and assess phenotypes during the last third. They write up their research in a manuscript-style final paper and give a group presentation to the lab session.

Thank you,

Ronda

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*Ronda J. Rolfes (she/her/hers)*

*Professor, Department of Biology*

*Director of Graduate Studies*

*Georgetown University*

Joseph A. Ross, Ph.D.

Associate Professor of Biology California State University, Fresno

**A community-science approach identifies genetic variants associated with three color morphs in ball pythons (Python regius)**

Hannah S. Seidel

Department of Biology, Eastern Michigan University, Ypsilanti, MI, USA

Color morphs in ball pythons (Python regius) provide a unique and untapped resource for understanding the genetics of coloration in reptiles. Here I present a CURE in which students identify the genetic causes of three color morphs affecting production of the pigment melanin. Students recruit shed skins of pet ball pythons via social media, extract DNA from the skins, and search for putative loss-of-function variants in homologs of genes controlling melanin production in other vertebrates. Data collected by students that (i) the Albino morph is associated with missense and non-coding variants in the gene TYR, (ii) the Lavender Albino morph is associated with a deletion in the gene OCA2, and (iii) the Ultramel morph is associated with a missense variant and a putative deletion in the gene TYRP1. Skills taught include lab techniques in molecular biology, sequence analysis, association studies, reading of scientific literature, scientific writing, oral presentation, and communication of science to a lay audience. This CURE is one of the first studies to identify genetic variants associated with color morphs in ball pythons and shows that pet samples recruited from the community can provide a resource for discoveries in the undergraduate classroom.



Hannah S. Seidel, PhD

Assistant Professor / Pre-Med and Pre-Health Advisor

Department of Biology, Eastern Michigan University

441 Mark Jefferson Science Complex, Ypsilanti, MI 48197

(734) 487-1476

hseidel@emich.edu

Eric Spana

Associate Professor of the Practice

Department of Biology

Duke University

Durham, NC 27708

Brew Abstract

**An Introductory level course at Duke University in Molecular Biology, Genetics, and Evolution** required a semester-long CURE-based lab component that spanned as much of these three subjects as possible. I have developed a lab that uses local, wild-caught fruit fly species (mostly *Drosophila*) as the starting point for an experiment in phylogenetic footprinting. Students choose flies from the collection and use PCR and sequencing of the Cytochrome Oxidase I gene to identify the species via DNA barcoding analysis. After phylogenetic analysis of the collected species, students amplify a region of a second gene, the Tyrosine Hydroxylase gene (TH) using degenerate PCR primers. This PCR product is then ligated into vector and after transformation, mini-preps, and restriction digest analysis, the plasmid insert is sequenced. The region of TH that is being sequenced covers both introns and exons, and there are cis-regulatory element(s) in the introns that drive expression in dopaminergic neurons in *D. melanogaster*. Students annotate their cloned TH sequences for exons and introns and verify the reading frame. Alignment of the TH intron sequences identified a few highly conserved regions within the introns that might represent transcription factor binding sites. I have run this course at two different Universities so far: Duke University and Duke Kunshan University, and have identified >20 species in Durham, NC and 10 in Kunshan, China with an overlap of only four species and at least one unidentified species in each location. This laboratory gives students experience in many common molecular biology techniques: PCR, cloning, plasmid DNA isolation, restriction digests, agarose gels, and sequencing as well as analysis of their own data for gene structure, reading frames, codon usage, dN/dS ratio, MK test, and phylogenetic trees. In this past semester we were forced into an online lab setting. We used the time normally spent performing lab techniques with retrieval and analysis of the same TH region sequence from the genomes of >80 different fruit fly species.