



CCURI
COMMUNITY COLLEGE UNDERGRADUATE
RESEARCH INITIATIVE

Spring 2016 Colloquium

Volunteer State Community College

April 11, 2016

"What we have to learn to do, we learn by doing."

~Aristotle

www.ccuri.org

Dear Colleagues and Friends,

I would like to personally welcome each of you to Nashville, TN and the CCURI Regional Conference and Poster Session. The student poster sessions are our signature events where our undergraduate researchers have the opportunity to share their work with the CCURI community. CCURI's mission is to support the development, implementation, and evaluation of undergraduate research programs at our Nation's community colleges. As many of you already know, CCURI is in its first of four years of funding under NSF's Improving Undergraduate STEM Education (IUSE) program. To date, the National Science Foundation has invested more than \$5.7M in the CCURI program and its network of community colleges.

In 2014-2015, a total of 6,207 students participated in undergraduate research with support of CCURI at our 38 partner and affiliate institutions. Each year, CCURI sponsors two regional student poster sessions to provide students with an opportunity to showcase their work to the CCURI network. Previous events were held in Philadelphia, Phoenix, Washington, Charlotte and Portland. This year, we are honored to be holding our event in the great city of Nashville, TN, with Volunteer State Community College as our gracious host.

On November 16, 2010 the U.S. House of Representatives declared the week of April 11, 2011 as "Undergraduate Research Week". Since that time, each year the Council on Undergraduate Research has designated a week in April as "Undergraduate Research Week". This CCURI event occurs on the first day of Undergraduate Research Week for 2016 and we plan to celebrate as we enjoy the amazing work being showcased by our students. To connect with other events occurring across the country, you can use #URW2016 on social media.

President Obama has been consistent in his commitment to improving STEM education in this country. Mr. Obama is passionate about moving America's students to the "top of the pack" by enabling all students to learn deeply and think critically in STEM fields, and has supported the expansion of STEM education opportunities for students from all backgrounds. CCURI believes that the research experience is the most effective way to promote deep learning and advance critical thinking skills, and with close to 50% of our Nation's undergraduates currently pursuing their education at a community college, the CCURI mission is a critical component of this commitment. We hope that you will enjoy exploring the amazing talent on display at this Regional Conference.

Again, welcome to Nashville, TN and the CCURI conference. I am glad that you are here, and I look forward to your participation.

Sincerely,



James A. Hewlett
Executive Director
CCURI

KEYNOTE ADDRESS
10:00AM – 10:30AM
WEMYSS AUDITORIUM

KENYATTA LOVETT, PH.D.
ASSISTANT VICE CHANCELLOR FOR COMMUNITY COLLEGE INITIATIVES
TENNESSEE BOARD OF REGENTS
OFFICE OF COMMUNITY COLLEGES



Kenyatta Lovett currently serves as the Assistant Vice Chancellor for Community College Initiatives for the Tennessee Board of Regents. He is responsible for managing the administrative implementation of the state's new comprehensive community college system, which includes consolidating major functions across the state's 13 community colleges. Dr. Lovett has led initiatives that have significantly improved the efficiency of the community college system in Tennessee, and is currently leading the effort to establish a shared services operation for the community colleges.

In addition to leading the administrative efficiency strategy for Tennessee's community colleges, Dr. Lovett works with statewide programs focused on improving student access and success. The Tennessean recognized him as one of five key people responsible for the successful launch of the Tennessee Promise, the state's initiative to cover tuition for high school graduates attending a community college. He serves on the advisory board for early high school remediation, as well as other programs designed to improve student performance for adults, foster care students, and underserved populations. Dr. Lovett also serves on local boards in the Nashville area, such as the YMCA, the Technology Access Center, and the Lumina Community Partnership for Attainment.

Dr. Lovett's research focus is in state-level public finance and governance. He recently served as a columnist for the Public Administration Times, and is currently working on his manuscript for an entry in the Global Encyclopedia of Public Administration, Public Policy, and Governance. His dissertation reviewed the diffusion of formal governance in state economic development, using event history analysis. Dr. Lovett is an adjunct professor at Tennessee State University, and teaches graduate courses in public finance, leadership, ethics, and human resource management.

Dr. Lovett has a B.F.A. in graphic design from Howard University, an M.B.A. in supply-chain management from Tennessee State University, and a Ph.D. in public administration from Tennessee State University. Kenyatta and his wife Tracey have two daughters, Kiersten and Kennedy. He enjoys cycling, running, and photography.

LUNCH PRESENTATION
12:45PM-1:15PM
WOODS CAMPUS CENTER – CARPETED DINING ROOM

COURSE-BASED MICROBIOME RESEARCH: SCALABLE UNDERGRADUATE RESEARCH EXPERIENCE IN URBAN MICROBIAL COMMUNITY ANALYSIS

THEODORE R. MUTH, PH.D.
ASSOCIATE PROFESSOR
DEPARTMENT OF BIOLOGY
CUNY BROOKLYN COLLEGE

The increasing accessibility and affordability of next-generation sequencing, in combination with metagenomic strategies, has opened the door to an exciting range of hands-on research projects for undergraduates. We have developed the Authentic Research Experience in Microbiology (AREM) program to take advantage of these technological advances and to broaden the horizons of students by introducing them to another aspect of their environment and how microbiology research relates to their daily activities. AREM started at Brooklyn College of the City University of New York (CUNY) with a novel urban microbiome project in a single undergraduate microbiology lab of 18 students. It has developed into a scalable research module, which is currently incorporated into courses at over 10 campuses across the CUNY system, involving nearly 200 students. Participating students have broad backgrounds: science and non-science majors, taking introductory biology and upper-level capstone courses, attend four-year and community colleges. Our focus on the city is significant - while a great deal of research has investigated microbial diversity from a wide variety of environments around the globe, urban environments, where our students live and study, have largely been overlooked - despite the fact that a majority of the world's population now resides in cities. The AREM program introduces students to a number of important concepts including: human influences on the structure and dynamics of microbial communities, the relationship between the environment and metabolic characteristics required for survival and growth, and the changes that result from the interaction and exchange between the human microbiome and urban microbial communities. The project encourages students to use quantitative reasoning and analysis skills in assessing the microbial diversity data they collect and provides an opportunity to formulate questions and develop hypotheses based on their microbial community investigation. AREM is a successful program in New York City and can be a model for undergraduate microbiome research projects at a wide range of other campuses.

Arizona

Student(s): O. Diaz, I. Gibson, C. Grijalva J. Hall, S. Merk, L. Simmons, L. Taylor, and J. Vasquez

Institution: Cochise College

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Student(s): O. Diaz, I. Gibson, C. Grijalva J. Hall, N. Jacobs, S. Merk, L. Simmons, L. Taylor, and J. Vasquez

Institution: Cochise College

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Student(s): Artemio Chaves, Duane Barbano, and Todd Sandrin

Institution: Glendale Community College

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Student(s): Erica Soboslay, Danielle Brokaw, and Paul Coleman

Institution: Glendale Community College

Display area: 4

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Oral Presentation: Rochelle Center – Thigpin Library – 11:00am

California

Student(s): Sonia Bustos and Wen Huang

Institution: Los Medanos College

Display area: 5

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Student(s): William Forbes and Christopher Romero

Institution: Los Medanos College

Display area: 6

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Student(s): Chase Ballard

Institution: Moreno Valley College

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Oral presentation: Rochelle Center – Thigpin Library – 11:10am

Student(s): James Corbitt

Institution: Moreno Valley College

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Student(s): Maria Gonzalez Bravo
Institution: Moreno Valley College
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Student(s): Hector Lopez, Chase Ballard, and Linda Ean
Institution: Moreno Valley College
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Colorado

Student(s): Sarah Lindquist, Lacy Washington, John Starinieri, and Wyatt Wiening
Institution: Trinidad State Junior College
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Student(s): Naomi Jacquez and Melissa Kleinschmit
Institution: Trinidad State Junior College
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Delaware

Student(s): Mark Shaw¹, Christina Baughan¹, Emily S. Herman², and James R. Pruitt²
Institution: ¹Delaware Technical Community College, ²West Chester University
Display area: 12
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Student(s): William Vanover
Institution: Delaware Technical Community College
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Student(s): Mary C. Williams and John V. McDowell
Institution: Delaware Technical Community College
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Hawaii

Student(s): Joseph Ramos
Institution: Kapiolani Community College
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Student(s): Jason Salseg
Institution: Kapiolani Community College
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Indiana

Student(s): Grace Mansaray, Lionnel Nkurunziza, Iredell Sanders, and Brandon Agnew
Institution: Ivy Tech Community College
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Student(s): Iredell Sanders and Brandon Agnew
Institution: Ivy Tech Community College
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Michigan

Student(s): Alyssa Adamczak
Institution: Muskegon Community College
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Student(s): Gabe Cerchiori
Institution: Muskegon Community College
Display area: 20
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Student(s): Garrett Dixon
Institution: Muskegon Community College
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Student(s): Benancio Rodriguez
Institution: Muskegon Community College
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Oral Presentation: Rochelle Center – Thigpin Library – 11:20am

Student(s): Gary Swain
Institution: Muskegon Community College
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Student(s): Amy Wilson
Institution: Muskegon Community College
Display area: 24
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Oral Presentation: Rochelle Center – Thigpin Library – 11:30am

Student(s): Kang-hyun You
Institution: Muskegon Community College
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Oral Presentation: Rochelle Center – Thigpin Library – 11:40am

Minnesota

Student(s): Cassandra Bauer, Cassandra Keocher, and Maxwell Waite
Institution: Anoka-Ramsey Community College
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Student(s): Tyler LaZerte
Institution: Anoka-Ramsey Community College
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Nevada

Student(s): Tylor Holcomb, Austin Peterson, Cathleen Ritter, Jessica Ponce, and Joshua Beal
Institution: Truckee Meadows Community College
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Oral Presentation: Woods Campus Center – Carpeted Dining Room – 11:00am

Student(s): Sydney Oren, Kristin Sommerfeld, Eric Lundin, Erica Dietlein, Kimberly Penrose, and Connor Brown
Institution: Truckee Meadows Community College
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New Mexico

Student(s): Jenelle Hansen
Institution: Mesalands Community College
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Student(s): Patricia Hansen
Institution: Mesalands Community College
Display area: 31
Page number: 31

Student(s): Garrett LeMons
Institution: Mesalands Community College
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New York

Student(s): Quinton Kolbeck
Institution: Finger Lakes Community College
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North Carolina

Student(s): Ryan Booth
Institution: Gaston College
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Student(s): Ryan Frasure, Esther Adedokun-Babalola, and Chelsey King
Institution: Gaston College
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Page number: 33

Student(s): David Pedraza and Mitchell Brown
Institution: Gaston College
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Page number: 34

Student(s): Lena Ramani
Institution: Gaston College
Display area: 37
Page number: 34

Student(s): Josh Smith
Institution: Gaston College
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Oklahoma

Student(s): B. Acharya, J. Bleichner, J. Cox, B. Curry, S.A. DeLeon, K. Killam, S. B. King, T. Noble, S. Rice, and J. Yang

Institution: Tulsa Community College

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Student(s): Bipina Acharya, Ciara Boatright, Jordan Cox, Brandon Curry, Brian Eccleston, Kameron Killam, Blake King, Samantha Rice, and Jennifer Yang

Institution: Tulsa Community College

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Student(s): Acharya B., Beckham J., Curry B., Darbandi S., Eccleston B., Flippin E., Killam K., King S.B., and Nehmzow K.

Institution: Tulsa Community College

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Oregon

Student(s): Joseph Kincaid and Cali Clements

Institution: Portland Community College

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Student(s): Leslie Villela and Austin Waibel

Institution: Portland Community College

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South Carolina

Student(s): Matthew Brewer

Institution: Piedmont Technical College

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Tennessee

Student(s): Lauren Hunter, Colin Cardwell, and Robert Collins

Institution: Volunteer State Community College

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Student(s): Alexis Seibert and Joshua Taylor
Institution: Volunteer State Community College
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Student(s): Justin Pemerton, Nicholas Rowland, and Kristian Moore
Institution: Volunteer State Community College
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Student(s): Kristian Moore, Nicholas Rowland, Justin Pemerton, and Philip Clifford
Institution: Volunteer State Community College
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Texas

Student(s): Lorie Leyva
Institution: Del Mar College
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Student(s): Kenneth McGraw
Institution: Del Mar College
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Student(s): Bianca Mendonca and Erin Pena
Institution: Del Mar College
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Student(s): Vasupradha Vasudevan
Institution: Lone Star College
Display area: 52
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Oral Presentation: Woods Campus Center – Carpeted Dining Room – 11:10am

Student(s): Nichole Gonzales
Institution: Lone Star College
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Student(s): Justin McKenzie
Institution: Lone Star College
Display area: 54
Page number: 46

Student(s): Candace Piccola
Institution: Lone Star College
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Student(s): Irma Garcia-Villarreal¹ and Ricky Johnson², M.S
Institution: Lone Star College¹, and University of Houston²
Page number: 6
Oral presentation: Woods Campus Center – Carpeted Dining Room – 11:20am

Student(s): Kennedy Chudej, Jonathan Briscoe, and Jennifer Leard
Institution: McLennan Community College
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Student(s): Gabby Garcia
Institution: McLennan Community College
Display area: 57
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Student(s): Mariana Juarez, Erin Castillo, and Joanna Flores
Institution: McLennan Community College
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Student(s): Kara Schmidt
Institution: McLennan Community College and Texas Tech University
Display area: 59
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Oral presentation: Woods Campus Center – Carpeted Dining Room – 11:30am

Washington

Student(s): Bassam Halabiya
Institution: Edmonds Community College
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Student(s): Alicia Kelly
Institution: Edmonds Community
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Student(s): Lanessa Cerrillo
Institution: Everett Community College
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Student(s): Sophia Maggio

Institution: Everett Community College

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Oral presentation: Woods Campus Center – Carpeted Dining Room – 11:40am

Student(s): Selena Perez

Institution: Everett Community College

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Oral presentation: Woods Campus Center – Carpeted Dining Room – 11:50am

Student(s): Madeline Sayed

Institution: Everett Community College

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Student(s): Rachel Nies, Mathew Ridgway, and Emad Shirazi,

Institution: Lake Washington Institute of Technology

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STUDENT ORAL PRESENTATIONS
MONDAY APRIL 11, 2016
11:00AM-12:00PM
ROCHELLE CENTER – THIGPIN LIBRARY
AND
WOODS CAMPUS CENTER – CARPETED DINING ROOM

Arizona

DIFFERENTIAL DNA METHYLATION IN THE ALZHEIMER'S DISEASE BRAIN

Erica Soboslay, Danielle Brokaw, and Paul Coleman

Glendale Community College

James Tuohy (*Faculty Advisor*)

Location: Rochelle Center – Thigpin Library

11:00am

DNA methylation is an epigenetic modification that can alter gene expression without changing the underlying nucleotide sequence. 5-methylcytosine is formed by the binding of a methyl group to the cytosine base of CpG dinucleotides. These modifications may inhibit gene transcription, particularly when present at transcription start sites. Differential DNA methylation has been associated with many human diseases including Alzheimer's disease (AD; Bradley-Whitman & Lovell, 2013; Coppieters et al., 2013; De Jager et al., 2014; Lunnon et al., 2014; Mastroeni et al., 2010; Van den Hove et al., 2013) although the exact role of epigenetic modifications in the pathology of these diseases has yet to be elucidated. In this study DNA methylation was assayed with an Illumina 450K microarray containing samples from the middle temporal gyrus (MTG) and cerebellum (CBL) of human post-mortem brain. 121 female and 99 male participants with AD neuropathology (n= 220) and 75 female and 98 male participants without AD neuropathology (n= 173), were represented on the microarray, with each subject contributing a MTG and a CBL sample. Raw data was preprocessed and normalized in the R programming platform employing the Minfi package from Bioconductor (Aryee et al., 2014). Local (DMP) and regional (DMR) methylation was detected using the Minfi peak analysis and bumphunter algorithms, respectively. Significant DMPs were determined by false discovery rate q-value cutoff 0.05 and significant DMRs by family wise error rate cutoff of 0.05. Significant DMRs and DMPs were determined statistically in terms of brain region, disease state, and gender. The biological relevance of each significant DMP and DMR was determined using the UCSC Genome Brower. DMR analysis revealed 137 CpGs to be significantly associated with disease state, 75 of which were specific to the CBL, and 62 to the MTG. Of the 137 CpGs, 42 were found to be significantly correlated with disease in both the CBL and MTG. Statistical analysis of DMRs determined 93 CpG sites were affected by gender state, 53 of which were specific to the MTG and 40 to the CBL. 20 CpGs were significantly correlated with gender in both the CBL and MTG. Five DMRs were found to be significantly correlated with disease, an additional 15 DMRs were significant with respect to gender and disease, and seven additional DMRs were significantly associated with brain region, gender, and disease. Genes found to correspond to disease-associated DMRs include the previously reported AD gene, HLA-DRB5 (Yu et al., 2015), as well as CCDC140, TLX3, HLA-DQA1, ZFP57, ZNF596, RPH3AL and OTX2. This study has described changes in the DNA methylation state of CBL and MTG of participants with AD, determined statistical significance with respect to brain region, disease, and gender, and utilized this information to make novel contributions to the growing list of AD epigenetic signatures.

California

DEVELOPMENTAL GENETICS OF ARABIDOPSIS THALIANA

Chase Ballard

Moreno Valley College

Joanna Werner-Fraczek PhD (*Faculty Advisor*)

Location: Rochelle Center – Thigpin Library

11:10am

Flower development in a flowering plant is a complex process controlled by many genes that is not well understood. In order to determine gene functions in the model plant, Arabidopsis thaliana, GUS staining was used across various seed lines across several weeks of development from seedling to 8-week maturation in standardized artificial lighting and watering conditions. Results were varied based on seedling lines displaying dispersed, weak, and strong staining observed in different developmental stages based on the specific gene targeted by GUS. After a detailed comparison of the seedling lines, specifically gene line A and gene line B, it was determined that line B was the known gene, NPY1, and line A contained an unknown gene, which needs further study due to different observed results.

Michigan

ANAEROBIC DIGESTION BACTERIA

Benacio Rodriguez

Muskegon Community College

Dr. Darren C Mattone (*Faculty Advisor*)

Location: Rochelle Center – Thigpin Library

11:20am

Biofuels are an alternative source of energy, and are more environment friendly when compared to the use of fossil fuels for energy. A biofuel process known as anaerobic digestion breaks down organic waste products using anaerobic bacteria: it produces methane, carbon dioxide, and hydrogen sulfide in addition to other trace gases. The determination of the quantity of each of these gases produce can often involve rather expensive instrumentation. In this applied research, a practical approach using readily accessible materials and chemicals was performed in order to design an affordable anaerobic digestion gas monitoring process. Cow manure was collected and incubated at 35°C for 21 days with two different substrates. The use of carbon dioxide, water, and hydrogen sulfide gas traps were then used in order to determine how much methane was actually being produced by difference from total gas volume. An anaerobic respirometer was used to track the volume of each gas after the gas trap. Results indicated an unexpected amount of carbon dioxide was being produced and that little methane was being produced. In previous experiments and literature, gas production in anaerobic digestion has been assumed to be a mixture of 20-40% CO₂ and 50-80% methane. These results indicate that such assumptions may lead to inaccurate conclusions where the gas traps are not used to identify the percentage of carbon dioxide present.

USING A MINI DNA BARCODING TECHNIQUE TO TEST FOR ADULTERATION IN COOKED MEAT PRODUCTS

Amy Wilson

Muskegon Community College

Dr. Darren C Mattone (*Faulty Advisor*)

Location: Rochelle Center – Thigpin Library

11:30am

With an emphasis on eating healthy and being informed regarding all aspects of our food, there is a large discrepancy between what is grown locally and what is purchased from other manufacturers. In fact, a recent study found that nearly 21% of sampled domestic ground meat products were found to be combined with an unlike product due to cross contamination, or were mislabeled entirely. Using DNA barcoding techniques, cooked meats from three different national pizza chains were tested to determine if the meat was pure, unadulterated meat product. Uni-Mini-bar and RonPing primers were utilized because of their ability to isolate and amplify mammalian DNA that has been exceptionally degraded. Amplicons were sequenced and a BLAST search was used to identify the organism. Those samples that yielded expected results were considered unadulterated. Samples with indecipherable sequencing data were assumed to be adulterated and subject to cloning of the amplicon into plasmid, followed by the transformation of competent *E. coli*. Plasmids were extracted from the cultured bacteria and subjected to restriction enzyme digestion to remove the amplicon. Sequencing of the cloned amplicons was conducted to determine the mammalian organisms in the food sample. The intent of analysis was to determine the purity of said samples and identify contamination or adulteration if present.

THE EFFECT OF PH ON THE GROWTH OF CELLULOSE PRODUCING BACTERIA

Kang-hyun You

Muskegon Community College

Dr. Darren C Mattone (*Faulty Advisor*)

Location: Rochelle Center – Thigpin Library

11:40am

Cellulose degrading bacteria grow optimally in soils with a pH of 5.5 to 8. Soil pH changed by acid rain or other conditions affects the mineral structures of the soil and decomposing organic materials. Due to reduced cation exchange rate, and also hydrogen ions reacting with organic materials, reduced the decomposition of cellulose by the soil microorganisms. The purpose of this experiment was to determine if different species of cellulose degrading bacteria will grow under various pH ranges, and what genus and species these bacteria are from. Agar plates were prepared with carboxymethyl cellulose powder and HCl or NaOH to create the desired pH. Plates ranged from pH 3.5 to 10.5. Soil obtained from the Muskegon Community College campus was mixed with water and centrifuged. Various volumes of the supernatant were pipetted onto the surface of agar plates and the liquid distributed with sterile beads. Plates were cultured at 37C for up to 96 hours. Individual bacterial colonies were isolated and DNA extracted from the colonies for PCR and subsequent sequencing. A BLAST search was conducted with the sequence data to determine the specific organisms present on the cellulose-containing plates

Nevada

ISOLATION, PURIFICATION, AND CHARACTERIZATION OF BACTERIOPHAGE COOKIES

Tylor Holcomb, Austin Peterson, Cathleen Ritter, Jessica Ponce, Joshua Beal, and Tina Slowan-Pomeroy

Truckee Meadows Community College

Laura A. Briggs, PhD (*Faculty Advisor*)

Location: Woods Campus Center – Carpeted Dining Room

11:00am

The goal of this study was to isolate, purify, and characterize bacteriophages found in the soils of Northern Nevada. In conjunction with the Howard Hughes Medical Institute Science Education Alliances PHAGES program, this research expands our understanding of the diversity of bacteriophages in this region. Specifically, this study aims at sequencing and annotating the DNA of Cookies, a bacteriophage found in Northern Nevada soil along the Truckee River during the summer of 2014. Unveiling the relationship between how bacteriophages interact with organisms and their environment allows for further insight into their ability to evolve under selective pressure. *Mycobacterium smegmatis* mc2155 was used as the host for this project. After soil collection, samples were enriched with *M. smegmatis* and screened for possible plaque formation. Through serial dilution purification protocols, bacteriophages were isolated until a uniform phage was found. A High Titer Lysate (HTL) was prepared from pure culture and DNA was isolated for analysis. The bacteriophage was imaged by transmission electron microscopy at the University of Nevada, Reno. Cookies DNA was then sent to Pittsburg State University (PSU) for sequencing followed by annotation using DNA Master Software.

Texas

CHLAMYDOMONAS REINHARDTII USED AS A MODEL ORGANISM FOR THE EXPRESSION OF A PROKARYOTIC HOUSEKEEPING GENE

Vasupradha Vasudevan

Lone Star College

Janeu R Houston, Ph.D (*Faculty Advisor*)

Location: Woods Campus Center – Carpeted Dining Room

11:10am

Bacteria have been used as model organisms to study genetic sequences by many researchers. They can be easily transformed and possess the ability to produce proteins in high concentrations. However bacteria have inherent limitations as model organisms when used to investigate eukaryotic phenomena. For example, prokaryotic genes are arranged and expressed differently than their eukaryotic counterparts. In addition, Gram-negative bacteria, which are most often used in genetic studies, contain lipopolysaccharides, that interfere with many downstream applications such as protein expression, purification and assay.

Chlamydomonas reinhardtii conversely, is a unicellular haploid green alga that has been used as a eukaryotic model organism to investigate numerous life processes including photosynthesis and cellular motility. C. reinhardtii holds the advantages of having a relatively small genome, both autotrophic and heterotrophic capabilities, fast growth rate, ease of transformation and an ability to reproduce sexually and asexually. C. reinhardtii is an attractive organism to use since algal surfaces lack LPS and algae can be easily manipulated. A prokaryotic housekeeping gene sequence will be PCR amplified, restriction digested and ligated into a plasmid. C. reinhardtii will be transformed with this recombinant plasmid, the culture will be expanded in liquid culture and the plasmids will be isolated. Finally, the housekeeping gene sequence will be verified using PCR and gel electrophoresis analysis.

A COMPARATIVE STUDY AND A PHYLOGENETIC EXPLORATION OF THE
COMPOSITIONAL ARCHITECTURES OF PROKARYOTIC AND FUNGI GENOMES

Irma Garcia-Villarreal¹, and Ricky Johnson², M.S

Lone Star College¹, and University of Houston²

Daniel Kainer, Ph.D., and Dan Graur, PhD (*Faculty Advisors*)

Location: Woods Campus Center – Carpeted Dining Room

11:20am

The scientific published paper “A Comparative Study and a Phylogenetic Exploration of the Compositional Architectures of Mammalian Nuclear Genomes” by Dan Graur and Eran Elhaik in November 2014 is the base for this research. The idea is to explain the compositional organization of the genome of prokaryotic and fungi genomes from an evolutionary perspective using the sequenced genome from the National Center for Biotechnology Information (NCBI) database for all prokaryotes and fungi organisms. For the past four decades, most of the explanations were adhered to the “isochore theory,” which has long been rebutted because it considers that genomes are depicted as mosaics of fairly long isochores (of 300kb or more). Analyzing genomes using IsoPlotter –a recursive segmentation algorithm that employs a dynamic threshold, which takes into account the composition and length of each segment, the compositional domains identified by IsoPlotter are contiguous genomic segments, each with a characteristic GC content that differs significantly from the GC content of its adjacent upstream and downstream compositional domains. By comparing the GC content variance of compositional domains with that of the chromosomes on which they reside, compositional domains can be further classified and analyzed.

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

Kara Schmidt^{1,2}, Traesha Robertson¹, Stephanie Lockwood², and Donna Hamilton³

McLennan Community College¹, Texas Tech University², University of North Texas³

Stephanie Randell (*Faculty Advisor*)

Location: Woods Campus Center – Carpeted Dining Room

11:30am

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

Washington

A COMPARISON OF HEAVY METAL UPTAKE IN ELEGRASS (ZOSTERA MARINA) AND PHYTOPLANKTON IN POSSESSION SOUND

Sophia Maggio

Everett Community College

Robin Araniva (*Faculty Advisor*)

Location: Woods Campus Center – Carpeted Dining Room

11:40am

Possession Sound, an estuary located in Everett, WA, is influenced by the interaction of seawater from Puget Sound and freshwater from the Snohomish River. Students at the Ocean Research College Academy (ORCA) study eelgrass (*Zostera marina*) in the estuary, specifically near Mukilteo, Whidbey Island, and Snohomish River. In previous studies, *Z. marina* exhibited a high uptake capacity for metals concentrated in sediment; however, low pH levels can desorb heavy metals from sediment, causing bioaccumulation in phytoplankton and limiting primary production. While *Z. marina* photosynthesizes, it is hypothesized to possess the ability to biodegrade heavy metals in sediment, and thus is expected to exhibit lower concentrations than phytoplankton. Heavy metal concentrations in root, shoot, and blade, sediment, and phytoplankton samples were analyzed in an Inductively Coupled Mass Spectrometer (ICP-MS) by Everett Environmental Lab. At Mukilteo and Whidbey, copper and zinc concentrations in *Z. marina* consistently exceeded detection limits, with the highest zinc concentration of 78.9 mg/kg in shoot samples and the highest copper concentration of 10.8 mg/kg in root samples at Whidbey. Cadmium was highest in blade and shoot samples at both sites, but undetected in phytoplankton. However, arsenic was highly concentrated in phytoplankton (30.7 mg/kg at Mukilteo, relative to detection limit of 8.478 mg/kg), as was zinc, with a mean concentration of 4700 mg/kg. Preliminary data reveal a more complex pattern dependent on metal type and biological tissue; therefore, additional data are being collected to ascertain the necessity of certain metals for specific parts of *Z. marina* and phytoplankton.

MICROPLASTIC TYPE AND ABUNDANCE IN RIVER OTTER SCAT AND SEDIMENT

Selena Perez

Everett Community College

Josh Searle (*Faculty Advisor*)

Location: Woods Campus Center – Carpeted Dining Room

11:50am

Microplastics are a type of marine debris and pollutant comprised of synthetic polymers and is often broken down from larger plastics entering the marine environment by natural processes. Ingestion of microplastics has been observed in a variety of organisms and may be a factor in the transfer of chemical additives or hydrophobic pollutants to marine biota. This study is focused on the distribution of types of microplastics found in the river otter (*Lutra Canadensis*) population and sediment located throughout the Possession Sound estuary within the Salish Sea.

Microplastics are found through river otter scat dissections sampled since 2012 and performed by students attending Ocean Research College Academy in Everett, WA. Further sampling consists of collecting beach sediment near river otter latrine sites. From a small sample size of 30 scat samples; preliminary results suggest a 30% presence of polystyrene, a low-density plastic often used in packaging, disposable plastic cutlery and dineware, and floating docks. Other polymers observed consist of polypropylene, a versatile and widely used plastic often found in a fiber-like form and zinc stearate, an insoluble powder-like polymer often used in cosmetic products. This study hypothesizes a strong correlation between types of plastics found in sediment and river otter scat samples and suggests the primary plastic pollutant to be polystyrene

STUDENT POSTER PRESENTATIONS
APRIL 11, 2016
2:00PM-4:00PM
PICKEL FIELD HOUSE

Arizona

WILDLIFE CORRIDORS ON THE SAN PEDRO RIVER

O. Diaz, I. Gibson, C. Grijalva J. Hall, N. Jacobs, S. Merk, L. Simmons, L. Taylor, J. Vasquez,
H. Jones, and E. Priddis
Cochise College
Kari Durham (Faculty Advisor)
Display area: 1

The San Pedro River, located in Southeastern Arizona, is the last free-flowing river in the Southwest, and flows north from Mexico into Arizona. It is an important migration route for birds, a year round source of water for over 80 mammalian species, and home to two endangered plant species. This study looks at the San Pedro River and washes radiating from it as possible corridors for the movement of wildlife. The ecological importance of the region is examined through observed trends of species abundance relating to seasonality, species pairings, and water availability. To achieve this, camera traps were deployed at the Gray Hawk Nature Center situated on the San Pedro River, and were positioned at locations where potential corridors converged. The Reconyx cameras used were equipped with infrared motion sensors, and featured time-stamp and moon phase technology. Photos were then cataloged and analyzed using a camera trap data analysis program. Statistical analysis of data collected revealed correlations between puma and skunk sightings, and overall movement of species to higher elevation during the months of heavy rainfall. Competitive predator relationships were also identified between pumas, bobcats, and coyotes. Future studies will involve shared camera trap data between Cochise College and other research teams in the region that use identical cameras and data analysis programs. The larger sample of data resulting from these partnerships with Bureau of Land Management, United States Fish and Wildlife Service, and University of Arizona will help all parties pinpoint regional trends more effectively. In addition, the number of camera traps and range of placement will be expanded to areas south of Grey Hawk Nature Center. In these areas, a neighborhood internet database will be developed, where local citizens can report animal sightings. Employing a social media-type interface, this application will empower the community to become an active part of the research that's being done in Cochise County. Ultimately, the data gathered through the identification of corridors and the understanding of river use by wildlife will inform conservation efforts and aid in the protection of these wildlife routes.

A COMPARISON OF PROTEIN EXTRACTION PROTOCOLS FOR BEAN BEETLE PROTEIN ANALYSIS

O. Diaz, I. Gibson, C. Grijalva J. Hall, S. Merk, L. Simmons, L. Taylor, J. Vasquez, H. Jones,
and E. Priddis

Cochise College

Kari Durham (*Faculty Advisor*)

Display area: 2

Proteins are one of the fundamental types of macromolecules essential to the workings of a cell. Thus identifying proteins present in cells and their functions has garnered much interest as seen in the rise of proteomics. In order to identify proteins using various electrophoresis techniques, the proteins must be extracted. In this study we developed the superlative protein extraction protocol for protein extraction from Bean Beetles (*Callosobruchus maculatus*). To accomplish this task, various methods of protein extraction were developed and tested to determine which would produce the highest concentration of protein in the sample. The methods were tested on both male and female adult beetles. The three methods used for extraction were: simple homogenization, acetone precipitation, and homogenization using Laemmli buffer and reducing agent, BME. The extracted protein samples were compared with the protein standards (2, 4, 6, 8, and 10 mg Bovine Serum Albumin (BSA)/ml) in a spot test. Using the spectrophotometer at 590 nm the absorption was determined for each of the standards and bean beetles samples. The protein standards were graphed against the absorptions and the best fit line was determined. Using the slope intercept, the protein concentration was calculated in each of the samples of bean beetle and standards. The calculations obtained will be used to load an equal amount of protein for the Vertical Gel SDS Page Electrophoresis for identifying the proteins. Old data showed simple homogenization was the best extraction method, however, learned that the best method is using homogenization with Laemmli buffer and reducing agent, BME. Using the best method, we separated the proteins from adult male and female beetles, eggs, and the larval stage using the Vertical Gel SDS Page Electrophoresis, in order to compare and contrast the types of proteins of the three main Bean Beetle life stages. Our results show there are similar and different weighted proteins from each life stage. We hope to expand on our results using a 2D gel electrophoresis with the aim of more significant separation the proteins.

Key Words: *Callosobruchus maculatus*, superlative protein extraction, protein concentration, Protocol.

THE USE OF PROTEIN EXTRACTION MASS SPECTROPHOTOMETRY FOR RAPIDLY
ESTABLISHING PHYLOGENETIC RELATIONSHIPS WITHIN THE GENUS
DEINOCOCCUS

Artemio Chaves, Duane Barbano, and Todd Sandrin

Glendale Community College

James Tuohy (*Faculty Advisor*)

Display area: 3

The approximately 50 species of the genus Deinococcus are typically characterized as radiation-resistant mesophiles although there is much functional and morphological variation within the group. The relationship of Deinococcus to other microbial groups has also been difficult to establish. For instance, Deinococcus was originally placed in the Micrococcus genus (Brookes and Murray 1981). Deinococcus is known to share a number of genes with the Archaebacteria but unlike the Archaebacteria has peptidoglycan in its cell wall. Furthermore, they stain positive with gram stain but have a second membrane, characteristic of gram negative bacteria. In short, a systematic phylogenetic analysis of the genus is necessary. To establish phylogenetic relationships it is typical to rely on a comparison of the sequence of the small subunit ribosomal RNA (16S) gene. However, it has been pointed out that a phylogenetic tree inferred using the 16S rRNA gene may differ significantly from a tree based on other marker genes (Eisen 1995). Matrix-assisted laser desorption/ionization – Time of Flight (MALDI-TOF) mass spectrophotometry of whole cell protein extracts has recently been developed to produce a summary spectra and a characteristic fingerprint for a given organism. While MALDI-TOF spectra has been used to rapidly identify many species of bacteria in a clinical setting, the technique has not been used to phylogenetically fingerprint Deinococcus. This study develops a protocol for whole cell protein extraction and MALDI-TOF analysis to establish phylogenetic relationships between *D. radiodurans*, *D. gobiensis*, *D. deserti* and *D. hopiensis*.

UNDERSTANDING THE ROLE OF LEA GENES IN DEINOCOCCUS

Erica Soboslay and Danielle Brokaw

Glendale Community College

James Tuohy (*Faculty Advisor*)

Display area: 4

The bacterial genus Deinococcus is replete with stress-tolerant species. For example, *Deinococcus radiodurans*, the best known species in the genus, can tolerate 1000-fold more ionizing radiation than humans and can repair hundreds of double stranded breaks per cell without loss of viability (Battista, 1997). Similarly, it can survive both severe oxidation and desiccation. *Deinococcus hopiensis* is a more recently discovered species of Deinococci isolated from the Sonoran desert. Relatively little is known about the ruggedness of this species. Late Embryogenesis Abundant (Lea) proteins are widely found in plants and desiccation resistant bacteria. In plants, the proteins accumulate late in seed development as well as during conditions of environmental stress. Lea proteins are thought to contribute to the desiccation resistance of the Deinococci (Goyal, Walton, Tunnacliffe, 2005), and previous studies have shown that Lea proteins from soybeans confer desiccation resistance and salt tolerance upon *E. coli* (Liu & Zheng, 2005). In this study, lea genes from *D. radiodurans* (DR1172 and DR1372) and *D. hopiensis* (Deiho_01242 and Deiho_01840) were PCR amplified and inserted into an expression vector, which was then used to transform *E. coli*. DNA plasmid isolation and DNA sequencing confirmed the successful insertion of his-tagged lea genes into *E. coli*. Subsequent expression studies were used to further characterize Lea proteins from *D. radiodurans*, determine the function of these proteins in *D. hopiensis*, and clarify the class of Lea proteins found in Deinococci.

California

EXPLORING THE IMPACT OF WATER QUALITY ON AQUATIC PLANT GROWTH

Sonia Bustos and Wen Huang

Los Medanos College

Danielle Liubicich (*Faculty Advisor*)

Display area: 5

California's agriculture industry is currently threatened by a shortage of water supplies due to an ongoing drought. How will our growing population cope with diminished access to water? In order to explore alternative agricultural water sources, our research team conducted an experiment in order to determine the effects of water quality on plant growth. The plant used in the experiment was Elodea canadensis, a freshwater plant that can continue its growth even while uprooted by absorbing nutrients within the water supply. Our team collected water samples from nine sites within Contra Costa County district, ranging from freshwater to brackish to household tap water to distilled water. We exposed the Elodea plants to different water treatments and collected qualitative and quantitative data, such as plant morphology and growth, for six weeks. Alterations in physical characters such as color, deterioration, and new growth were used as indicators of growth. Samples were categorized according to the general quality of water, and the final conditions of the plants were compared to each other. Our experiment revealed that Elodea plants show the least deterioration when exposed to freshwater. Our data also revealed that tap water and drinking water had a significant contribution to changes in stem length and amount of chloroplasts present in the cells. Results of this experiment may aid in the search for a sustainable water supply for agricultural use. The data collected during this experiment will also give us insight into the effects of water quality on ecosystem health, and agricultural success.

CHEMICAL KINETICS USING BISULFITE AND IODINE

William Forbes and Christopher Romero

Los Medanos College

Melinda Capes (*Faculty Advisor*)

Display area: 6

When a solution of starch and iodine is pushed to completion, it creates a specific color pigment of dark brown-black. In order for this to happen, however, we had to strategically introduce the corrections so that the reaction would be pushed to said completion. The concentrations of Sodium bisulfite and Potassium Iodate were varied in separate experiments to determine the effects of each on the rate law for the reaction: $3\text{HSO}_3^- + \text{IO}_3^- \rightarrow \text{I}^- + 3\text{HSO}_4^-$. This reaction forms the color we are looking for, which is to signify the presence of the I^- ion. In order to form the proper ions to obtain the desired color, we had to add a few different things, all while keeping an eye on our timer. We also then used a catalyst to decrease the activation energy in our experiment which took the longest time after performing the experiment many times and identified the limiting reagent. This helped us to see the effect of a catalyst first hand, allowing us to witness how much the reaction would be sped up. We then graphed our data to figure out what order our reaction followed, finding that KIO_3 (aq) and NaHSO_3 (aq) were in fact both first order. This allowed us to conclude what order our reaction was, with respect to each reagent, which we obtained from the line of best fit of our respective graphs.

EXAMINATION OF CLIFF SWALLOWS NEST'S AND NESTING ALTERNATIVE

James Corbitt

Moreno Valley College

Joanna Werner-Fraczek PhD (*Faculty Advisor*)

Display area: 7

Every year, Moreno Valley College (MVC) experiences the migration of cliff swallows (*Petrochelidon pyrrhonota*) coming from Central or South America to breed. They build multiple nests around campus utilizing the nearby lake as a water source, and the surrounding hills as a mud source for their nests. The abundance of these birds has inspired the development of the Flying With Swallows (FWS) undergraduate research project with many avenues of scientific investigations. The studies being conducted are a thorough analysis of the cliff swallows nest, which include measurements, component break down, environmental factors and influences, and location. The studies regarding measurements of the nests are; nest thickness, height, width, and mud pellets size. The research concerning component break down include; mud to vegetation ratio, insect inhabiting nests identification, concentration and diversity, and foreign chemical concentrations. The other topic for investigation is environmental factors. The studies conducted in this field are; locality of specific insects in the Cliff Swallows trophic cascade, weather affecting nearby water source, and diversity of numerous species. Currently, the location of nests have been monitored by video recording for two years and presented on the college map using ArcGIS. In addition, the college started collaboration with James Kulbeth, biologist from Colorado, to build alternative nesting structures at MVC. The overall objective is to create a mutualistic interspecific interaction with the Cliff Swallows by utilizing the alternative nesting structures as their new homing area.

MORENO VALLEY COLLEGE FAUNA AS REVEALED BY CAMERA TRAPPING

Maria Gonzalez-Bravo

Moreno Valley College

Joanna Werner-Fraczek PhD (*Faculty Advisor*)

Display area: 8

The location of Moreno Valley College next to recreational hills adjacent to San Jacinto Wildlife Area in Southern California promotes studies of wildlife around the campus. Observations of fauna involving camera trapping have been incorporated into the Organismal and Population Biology course for the last two years (2013-2015). The presence of animals is recorded on a map using Esri's ArcGIS and their Snap2Map photo application. Bobcats, coyotes, deer, rabbits, foxes, raccoons, opposes, mice, owls, roadrunners, hawks, garden snakes, and rattle snakes have been observed in the surroundings of the college. In addition to the map, students prepare flyers about the identified species living in the area; these flyers are distributed around the campus to build wildlife awareness in our community.

USING DNA BARCODING AND METABARCODING TO IDENTIFY POTENTIAL BENEFITS AND RISKS ASSOCIATED WITH THE PRESENCE OF CLIFF SWALLOWS

Hector Lopez, Chase Ballard, and Linda Ean

Moreno Valley College

Joanna Werner-Fraczek PhD (*Faculty Advisor*)

Display area: 9

Moreno Valley College (MVC) is a breeding site to cliff swallows, migratory, and colonial birds that nest on a number of buildings around the campus from February till June. The Cliff swallows most likely feed on flying insects such as flies, beetles and mosquitoes. The presence of Cliff swallows also brings about the presence of other insects such as swallow bugs, ticks and fleas since they are ectoparasitic and reside in both the nests and the surrounding areas. The elimination of mosquitoes or flying termites can benefit humans, while the presence of bird bugs related to bed bugs or bird fleas can present a human hazard. This project is designed to identify both groups of insects using DNA barcoding and metabarcoding methods in order to understand the effects of the presence of these birds on campus.

Colorado

REPRODUCTIVE TRAITS OF THE HOUSE FLY, MUSCA DOMESTICA (L.)

Sarah Lindquist, Lacy Washington, John Starinieri, and Wyatt Wiening

Trinidad State Junior College

Clifford Wiening (*Faculty Advisor*)

Display area: 10

Reproductive traits of the House Fly *Musca domestica* (L.) were examined in relation to a protein food source. It was hypothesized that egg production and hatching will be higher as the protein concentration increases. Four identical fly colonies were established in cages. Two colony was feed a constant diet of half strength protein solution while the other two colonies were feed a full strength solution. Eggs were collected, counted and allowed to hatch, the hatching rate was observed and recorded. Results are still pending at current time.

ANNOTATION OF D. ELEGANS CHROMOSOME 3L CONTIG 3

Naomi Jacquez and Melissa Kleinschmit

Trinidad State Junior College

Melissa Kleinschmit (*Faculty Advisor*)

Display area: 11

The first complete sequence of the *Drosophila melanogaster* genome was published a little over a decade ago, and since that time its genome has continued to be studied and used as a reference to investigate other genomes. In this project we were annotating genes on contig3 of the 3L chromosome of *D. elegans* using *D. melanogaster* as a reference species, to identify conserved regions of DNA and to better understand the evolutionary history of the *Drosophila* genus. In the annotation process we used the Genomics Education Partnership's (GEP) gene record finder and UCSC Genome Browser mirror accessed from the GEP website to investigate the genes on this contig. The GEP website provided information such as gene predictors, RNA-Seq Alignments, and *D. melanogaster* protein alignment tracks. Three genes have been annotated within contig3 including the genes slif, CG11131, and CG12768 using evidence collected through genome browser tracks as well as de novo comparative genomic techniques. There were also five other genes; CG5535, CG7255, CG13248, CG12531, and CG7565, that were shown by the genome browser to be present in contig3, based on BLASTX alignment, but other evidence places these genes in other areas of the 3L chromosome or another chromosome.

Delaware

DIFFERENTIAL DNA METHYLATION IN THE ALZHEIMER'S DISEASE BRAIN

Mark Shaw¹, Christina Baughan¹, Emily S. Herman², and James R. Pruitt²

¹Delaware Technical Community College, ²West Chester University

Dr. Virginia Balke (*Faculty Advisor*)

Display area: 12

Streptomyces are soil dwelling bacteria that naturally produce antibiotics and release them to their immediate surroundings. The genus is responsible for producing over half of the antibiotics used today to treat bacterial infections in humans. Pathogenic bacteria rapidly develop resistance to commonly used antibiotics, underscoring the need for the discovery of new antibiotic compounds with different mechanisms of action. In this study, we are investigating the structures of antibiotics from Streptomyces cultured from various soils. The Streptomyces isolates were classified using 16S rRNA gene sequences. Antibiotic production was demonstrated by co-culturing the Streptomyces isolates with representative Gram-positive and Gram-negative bacteria and observing growth inhibition. Antibiotic compounds were extracted from solid growth media and separated by thin layer chromatography (TLC). TLC stains were utilized to identify the general structure of antibiotic compounds found in the extract. Further structure determination will be done using LC-MS and NMR.

DELAWARE GREEN BUILDING GROWTH VS GREEN BUILDING GROWTH OF SURROUNDING STATES

William Vanover

Delaware Technical Community College

Dr. Virginia Balke (*Faculty Advisor*)

Display area: 13

With climate change becoming a more concerning issue, it is important for us to know what we are doing to reduce our Co2 emissions. Green buildings play an important role in our Co2 reduction since buildings account for such an immense amount of energy consumption. By reducing the amount of energy a building uses, you reduce environmentally damaging Co2 emissions. As of 2015, the state of Delaware has a total amount of Energy Star labeled buildings that is comparable to surrounding states but is lacking in LEED certified buildings. The American Council for an Energy Efficient Economy (ACEEE) ranked Delaware 24th of all states on their 2015 state efficiency scorecard. This rank is below the rank of all states bordering Delaware. The Clean Power Plan goals for Delaware are lower than most surrounding states, other than New Jersey, and Delaware is the only state on track to surpass those goals by 2020. The Renewable Portfolio Standard for Delaware requires 25% of electricity to be generated by renewable resources by 2025. This is 5% more than the closest surrounding state. Delaware energy efficiency programs have also afforded millions in energy savings and have reduced significant amounts of harmful emissions. Delaware is best in some of the categories mentioned above but also falls short in others. The state of green building in Delaware is good overall and it will continue to improve with the goals and regulations that have been set in place.

**CHARACTERIZATION OF THE PSEUDOMONAS FLUORESCENS BW6L FRUR
TRANSCRIPTIONAL REGULATOR**
Mary C. Williams and John V. McDowell
Delaware Technical Community College
Dr. Virginia Balke (*Faculty Advisor*)
Display area: 14

FruR (cra) is a well-characterized fructose utilization regulator in Gram-negative bacteria E. coli and Pseudomonas putida. Studies indicate that the regulation of fructose utilization genes differs extensively between the two species reflecting their differing natural niches. With the genome sequencing of P. fluorescens BW6L, a comparison of P. fluorescens FruR function with E. coli and P. putida can be studied using genome annotation and cloning techniques. To accomplish this, the P. fluorescens FruR gene was cloned into pET expression vector, protein expressed, and purified. An upstream region containing the putative binding sequence was PCR amplified. Studies investigating the binding of the P. fluorescens FruR will be conducted to confirm the function of this protein in P. fluorescens. These results will be compared to published studies on the function of FruR in P. putida and E. coli.

Hawaii

KNOW YOUR SURROUNDINGS
Joseph Ramos
Kapiolani Community College
Keolani Noa (*Faculty Advisor*)
Display area: 15

In this day and age, it is more common to use synthetic products and chemicals as opposed to using the natural counterparts like our Native Hawaiian ancestors had many years ago. These synthetic products often come with a long list of negative side effects and are widely misused because of their potential for extreme outcomes. Native Hawaiian ancestors relayed oral legends about plants because they were important to our culture, like the legend of the naupaka plant (Scaevola taccada and Scaevola gaudichaudii) and its strange half flowers. The naupaka legend led me to look into the traditional medicinal and functional uses of naupaka and why Native Hawaiians felt it held importance. There are two varieties of naupaka, Naupaka kahakai, which lines many of the beaches in Hawai`i, and Naupaka kuahiwi, which can also be found widely in the mountains. Therefore relaying the plant's accessibility from mountain to sea. The naupaka found by the ocean has multiple medical properties including it's use to treat wounds, skin disease, sooth inflamed eyes, and jellyfish stings. Both Naupaka varieties (ocean and mountain) were also used as a food source in times of famine, or to refresh while traveling (I found that the fruit and leaves hold quite a bit of water in them). The returning to traditional plants for everyday uses brings an awareness to what surrounds us.

MICRO-ZONE MANAGEMENT MODIFICATION IN COMMERCIAL HEATING,
VENTILATION AND AIR CONDITIONING SYSTEMS

Jason Salseg

Kapiolani Community College

Aaron Hanai (*Faculty Advisor*)

Display area: 16

From my experience working in the commercial HVAC industry in Hawaii over the last 10 years, I have witnessed little change in the development and implementation of climate control technology in the Hawaii commercial sector. Commercial clients have expressed genuine concern and need for the reduction of their electrical operating costs, the largest of which is the cost of air conditioning. Thermostat controls for these systems can be a socially complicated and a managerial and financial nightmare when many varying occupants take control of the system settings. This has been seen to be a common ongoing struggle within operations throughout the industry. My design, SAM (Smart Air Management), hopes to fill a market need by providing a scalable solution for medium to large commercial facilities. The purpose of initiating a prototype is to improve upon both the standard commercial forced air and VAV (Variable Air Volume) systems. This new design, SAM, will address energy costs concerns with a modern, economical, personal and scalable way to control how rooms are cooled, heated and ventilated by controlling air supplied to and from the HVAC unit. By monitoring static pressure data, controlling air flow to unoccupied rooms and condenser fan speed as a function of system pressure will allow occupants to personalize the temperature and air flow in their respective micro zone via the SAM registers. This precise control of air balance hopes to allow the user, administrator or owner to bypass global thermostat settings while improving the overall system efficiency and maintaining an unchanged and ideal climate.

Indiana

EFFECTS OF THE PREPARATION OF SOY ON THE PROLIFERATION OF BREAST-CANCER CELLS IN VITRO

Grace Mansaray, Lionnel Nkurunziza, Iredell Sanders, and Brandon Agnew

Ivy Tech Community College

Professor George Twaddle (*Faculty Advisor*)

Display area: 17

The reduced incidence of breast cancer in Asia has been partially attributed to a diet rich in soy. However, there must be other contributing to this apparent protective effect since the soy is a major part of the American diet. One variable might be in difference in methods that are used to process soy-based foods for consumption. In the East it is common to boil soy (100C) to make a curd, like "tofu" or to use the curd to make a fermentable product, like "nori." In contrast, in the West, soy based food are often baked in the US in temperatures exceeding 200C. We hypothesize that protective effect of soy might be due to constituents that are heat labile or are produced in the process of fermentation. Using the MCF-7 breast cancer cells, we have initial evidence to suggest that a soy-based medium induces sub-optimal proliferation of MCF-7 cells in vitro and that the addition of estrogen further reduces the level of proliferation suggesting that estrogen might synergize with some constituent(s) of soy to provide a protective effect. We are in the process of optimizing our MCF-7 to measure proliferation and potential cytopathic effects, like necrosis and apoptosis, induced by the constituents of soy in the presence of estrogen. We plan to test soy processed into curd, fermented curd, or baked into a bread to test our hypothesis that the method of preparation of soy for consumption may contribute to the preservation of its beneficial effects in regards to cancer.

A BIOASSAY FOR THE SAFETY AND EFFICACY OF THE ELIMINATION OF
ESTROGEN ACTIVITY IN WASTEWATER BY GAMMA IRRADIATION

Iredell Sanders and Brandon Agnew

Ivy Tech Community College

Professor George Twaddle (*Faculty Advisor*)

Display area: 18

Chemical pollution of American streams and rivers is of great concern for the health of flora and fauna, the security of potable water supplies and recreational safety. One set of chemical pollutants that is having a profound negative effect on aquatic ecosystem biota are estrogenic compounds. A major source of compounds with estrogenic activity is human sewage and our present methods of sewage treatment before environmental release do not eliminate this activity. One proposed approach to reclamation of water is the treatment of wastewater with ionizing radiation with the intention of widespread production of oxygen radicals and the destruction of the hormone. In cooperation with Dr. Steven Mezyk and colleagues at California State University – Long Beach, who is pioneering this method, we are developing an assay for the presence of estrogenic activity by assessing the effect of gamma-irradiated solutions of 17-beta estradiol on the proliferation of the estrogen-sensitive breast cancer cell line, MCF-7 expressing Green fluorescent protein. Specifically we are seeking to optimize the fluorescence signal-to-noise ratio of sub-confluent cells growing in log-phase. In addition we are also screening for radiation-induced cytotoxicity in samples of irradiated 17 beta-estradiol by assessing the proliferation of MCF-7 in the presence of added, non-irradiated 17-beta estradiol. We are also assessing cytotoxicity by using a non-estrogen sensitive mammalian cell line BHK-21. Our goal is to establish both the efficacy and safety of this approach to chemical remediation of estrogen or estrogen mimics.

Michigan

HOW DOES THE MICROBIAL COMMUNITY OF THE HUMAN AXILLARY REGION CHANGE AFTER WASHING WITH A STANDARD ANTIBACTERIAL SOAP?

Alyssa Adamczak

Muskegon Community College

Dr. Darren C Mattone (*Faulty Advisor*)

Display area: 19

With an average surface area of 1.8m², the skin is one of the largest and most important organs of the human body. While some of the skin's major functions include protection and temperature control, the skin also serves as a host for a diverse ecosystem of microorganisms, including bacteria. Collectively, these microorganisms make up what is known as the skin microbiome. Because the surface of the human skin is so topographically disparate, the types of microorganisms that can be identified largely depend on where they are found. In the human axillary (armpit) region – classified as a “moist” region – bacterial species such as *Corynebacterium* have been found to be dominant. Bacterial samples were collected from the axillary regions of research subjects, both before and after the introduction of an antibacterial agent, in order to observe the changes in the bacterial community. DNA was extracted from the bacteria and the 16S rRNA gene was amplified through PCR. The amplicons were cloned into plasmids and competent *E. coli* was transformed with the cloned plasmids. After incubation, colonies were selected and the plasmids removed from the *E. coli*. The amplicon was removed from the plasmid with restriction enzyme digestion and the DNA subsequently sequenced. From these results, the types of bacteria most and least resistant to an antibacterial agent were determined.

THE FRESHWATER SPONGE EPHYDATIA FLUVIATILIS AS A BIO-INDICATOR
SPECIES FOR LEAD CONTAMINATION

Gabe Cerchiori
Muskegon Community College
Dr. Darren C Mattone (*Faulty Advisor*)
Display area: 20

Freshwater sponges are known as bio-indicators because of their role as filter feeders on the bacteria and organisms within the surrounding water. Despite knowing this, there is still gaps in the research on freshwater sponge species in general. With the recent spotlight of lead in the municipal water in Flint, Michigan, the question was posed concerning the role of sponges as an early warning system for detecting lead in the water supply. Could freshwater sponges potentially warn us of water toxicity, or even help to remove the lead from waterways? Sponge gemmules from *Ephydatia fluviatilis* were placed in spring water and allowed to grow into sponges. The sponges were exposed to different concentrations of lead II nitrate. Observations on the color, size, and morphology of the sponges were made daily for five days. Following the five-day observation period the different sponge samples were analyzed by x-ray fluorescence to determine if lead was absorbed by the sponges. In addition, the water in which the sponges were grown was tested to determine the concentration of residual lead. This study will help establish the known lead threshold for *E. fluviatilis* and help to develop further experiments on the usage of freshwater sponges to monitor our lakes, streams and rivers. While introducing mass amounts of sponges into a body of water may not be a viable solution to cleaning them up, they should be appreciated for their ability to filter out some of the contaminations that might be present in the water.

DNA BARCODE AUTHENTICATION OF GINKGO BILOBA HERBAL DIETARY
SUPPLEMENTS
Garrett Dixon
Muskegon Community College
Dr. Darren C Mattone (*Faulty Advisor*)
Display area: 21

Since the 2004, the United States has seen a rise in the use of the herbal supplements for dietary and alternative medical purpose. The growth percentages of U.S. herbal sales have risen for 10 years straight and continue to rise. With this increase in consumption of natural alternatives, there has been an increase in the frequency of mislabeled supplements. Whether this is due to increased consumption or unscrupulous business practices has yet to be determined. In addition, loosening of regulations on herbal supplement producers by the passing of DSHEA in 1994, has allowed producers to market their products without FDA approval. The only way in which an herbal supplement can be removed from the market is to be proven unsafe by the FDA.

Regardless, consumers should be concerned with mislabeled herbal supplements or products containing unlabeled fillers. DNA barcoding was used to validate the authenticity of the popular herbal supplement Ginkgo biloba. Ginkgo biloba, which is consumed to improve cognitive capacity by boosting blood perfusion and mitochondrial function, is one of the top five herbal supplements in the United States and therefore is a good candidate for this study. DNA was extracted from multiple brands of Ginkgo biloba capsules. DNA amplicons for the matK and rbcL regions of the chloroplasts were produced by PCR. DNA amplicons were sequenced and subjected to a BLAST search to verify authenticity of the product. DNA barcoding could be a simple way for manufacturers, distributors, and government and regulatory agencies to authenticate the purity of herbal supplements. In addition, other than authenticating purity, DNA barcoding could eliminate herbal products containing poisonous plants as fillers. Falsifying herbal supplement composition is fraud, and brings to light the health concerns that come with substitution without proper labeling.

ANAEROBIC DIGESTION BACTERIA

Benancio Rodriguez

Muskegon Community College

Dr. Darren C Mattone (*Faculty Advisor*)

Display area: 22

Biofuels are an alternative source of energy, and are more environment friendly when compared to the use of fossil fuels for energy. A biofuel process known as anaerobic digestion breaks down organic waste products using anaerobic bacteria: it produces methane, carbon dioxide, and hydrogen sulfide in addition to other trace gases. The determination of the quantity of each of these gases produce can often involve rather expensive instrumentation. In this applied research, a practical approach using readily accessible materials and chemicals was performed in order to design an affordable anaerobic digestion gas monitoring process. Cow manure was collected and incubated at 35°C for 21 days with two different substrates. The use of carbon dioxide, water, and hydrogen sulfide gas traps were then used in order to determine how much methane was actually being produced by difference from total gas volume. An anaerobic respirometer was used to track the volume of each gas after the gas trap. Results indicated an unexpected amount of carbon dioxide was being produced and that little methane was being produced. In previous experiments and literature, gas production in anaerobic digestion has been assumed to be a mixture of 20-40% CO₂ and 50-80% methane. These results indicate that such assumptions may lead to inaccurate conclusions where the gas traps are not used to identify the percentage of carbon dioxide present.

COMPARISON BETWEEN EXOTIC PHRAGMITES AND NATIVE PHRAGMITES

Gary Swain

Muskegon Community College

Dr. Darren C Mattone (*Faulty Advisor*)

Display area: 23

The common reed, known as Phragmite australis, line the wetlands of the Eastern coast of the United States and filter water pollutants. The invasive European subspecies of Phragmite australis affects plant biodiversity in wetlands by choking out other plant species. This European subspecies cause more problems for the environment than they correct. To learn more about Phragmite australis and its relationship with nitrogen fixing bacteria, soil from the root tips of the invasive and noninvasive form of P. australis was collected. DNA was extracted from the soil and amplified by PCR. The DNA amplicons were cloned into plasmids, followed by the transformation of competent E. coli with the cloned plasmids. After incubation, colonies were selected and the plasmids extracted. The amplicons were removed from the plasmids with restriction enzymes and sent out for sequencing. A comparison of the bacteria from the different subspecies will likely show that many of the bacteria are similar between the two plant species. However, if invasive P. australis is shown to have a higher diversity of nitrogen fixing bacteria as compared to noninvasive P. australis, this information may be useful in developing further research projects examining methods to eradicate invasive P. australis.

USING A MINI DNA BARCODING TECHNIQUE TO TEST FOR ADULTERATION IN COOKED MEAT PRODUCTS

Amy Wilson

Muskegon Community College

Dr. Darren C Mattone (*Faulty Advisor*)

Display area: 24

With an emphasis on eating healthy and being informed regarding all aspects of our food, there is a large discrepancy between what is grown locally and what is purchased from other manufacturers. In fact, a recent study found that nearly 21% of sampled domestic ground meat products were found to be combined with an unlike product due to cross contamination, or were mislabeled entirely. Using DNA barcoding techniques, cooked meats from three different national pizza chains were tested to determine if the meat was pure, unadulterated meat product. Uni-Mini-bar and RonPing primers were utilized because of their ability to isolate and amplify mammalian DNA that has been exceptionally degraded. Amplicons were sequenced and a BLAST search was used to identify the organism. Those samples that yielded expected results were considered unadulterated. Samples with indecipherable sequencing data were assumed to be adulterated and subject to cloning of the amplicon into plasmid, followed by the transformation of competent *E. coli*. Plasmids were extracted from the cultured bacteria and subjected to restriction enzyme digestion to remove the amplicon. Sequencing of the cloned amplicons was conducted to determine the mammalian organisms in the food sample. The intent of analysis was to determine the purity of said samples and identify contamination or adulteration if present.

THE EFFECT OF PH ON THE GROWTH OF CELLULOSE PRODUCING BACTERIA

Kang-hyun You

Muskegon Community College

Dr. Darren C Mattone (*Faulty Advisor*)

Display area: 25

Cellulose degrading bacteria grow optimally in soils with a pH of 5.5 to 8. Soil pH changed by acid rain or other conditions affects the mineral structures of the soil and decomposing organic materials. Due to reduced cation exchange rate, and also hydrogen ions reacting with organic materials, reduced the decomposition of cellulose by the soil microorganisms. The purpose of this experiment was to determine if different species of cellulose degrading bacteria will grow under various pH ranges, and what genus and species these bacteria are from. Agar plates were prepared with carboxymethyl cellulose powder and HCl or NaOH to create the desired pH. Plates ranged from pH 3.5 to 10.5. Soil obtained from the Muskegon Community College campus was mixed with water and centrifuged. Various volumes of the supernatant were pipetted onto the surface of agar plates and the liquid distributed with sterile beads. Plates were cultured at 37C for up to 96 hours. Individual bacterial colonies were isolated and DNA extracted from the colonies for PCR and subsequent sequencing. A BLAST search was conducted with the sequence data to determine the specific organisms present on the cellulose-containing plates.

Minnesota

BENEFICIAL POLLINATING INSECT STUDY ON VARIOUS FLOWERING FIELDS: WILDFLOWERS, RESTORED PRAIRIE, AND AN ENERGY CROP OF CANOLA

Cassandra Bauer, Cassandra Keucher, and Maxwell Waite

Anoka-Ramsey Community College

Melanie Waite-Altringer (*Faculty Advisor*)

Display area: 26

There has been much concern across the U.S. recently regarding the rapid decline of beneficial pollinating insect populations. Increasing natural habitats for pollinating insects is crucial for these insects to increase in population numbers. The purpose of this study was to compare the positive effect of various flowering environments on the population numbers and diversity of beneficial pollinating insects. The main question to be answered was: Does varying the field environments (restored prairie, canola, and wildflowers) have an effect upon beneficial insect counts? The prediction prior to the study was: If varying field environments have an effect upon beneficial insect counts, then the canola field will have the greatest number of beneficial insects, and the restored prairie and wildflower fields will have the greatest diversity of pollinating insects. Beneficial insect counts were performed on each field twice a week throughout the flowering season of 2015. The plots were set up in various locations throughout each field. The insect counts consisted of the observers walking each plot for two minutes counting all insects. Data analysis showed that the canola field averaged the greatest density of pollinating insects. The wild flower field averaged the highest effective group richness (eH'), which suggests this field had the most diversity. The eH' of the restored prairie for the most part stayed consistent, even though the density declined throughout the season. The results suggest that having many diverse environments in an area will positively affect the beneficial insect population over the greatest amount of time.

EFFECTS OF CAPTIVE PREDATORY SPECIES ON THE BEHAVIOR OF WILD
ANIMALS EXPOSED USING CAMERA TRAPS

Tyler LaZerte

Anoka-Ramsey Community College

Jennifer Braido (*Faculty Advisor*)

Display area: 27

The purpose of this investigation was to determine the effect of the presence of captive predatory species on the behavior of wild animals. Our study location was the Wildlife Science Center in Linwood, Minnesota. We hypothesized wild predatory species would be attracted to or inquisitive of captive predator species due to their natural relationships in common territory whereas wild prey species would avoid captive fauna due to their innate fear of predators. We deployed two camera traps in two distinct areas of our study location; one set at the entrance to the grounds along a driveway and a second set approximately one hundred feet from a predatory species enclosure in a wooded area. Data was collected for five weeks and included organisms detected, proximity of each captured animal to the nearest enclosure, and activity of each species. Prey animals such as squirrels, rabbits, and opossums were predominantly detected by the camera closest to the enclosures while predatory species such as coyote and grey fox were mainly detected by the camera placed farther from the enclosures. Our findings indicate the presence of captive predatory animals has no significant effect on the behavior of wild animals, instead it is possible prey species feel safer in a wooded area with more cover availability whereas larger predatory species prefer the convenience of the trail provided by the driveway for movement along the grounds. Additional studies are needed to discern the effects of the presence of captive predatory animals on the behavior of wild animals.

Nevada

ISOLATION, PURIFICATION, AND CHARACTERIZATION OF BACTERIOPHAGE COOKIES

Taylor Holcomb, Austin Peterson, Cathleen Ritter, Jessica Ponce, and Joshua Beal

Truckee Meadows Community College

Laura A. Briggs, PhD (*Faculty Advisor*)

Display area: 28

The goal of this study was to isolate, purify, and characterize bacteriophages found in the soils of Northern Nevada. In conjunction with the Howard Hughes Medical Institute Science Education Alliances PHAGES program, this research expands our understanding of the diversity of bacteriophages in this region. Specifically, this study aims at sequencing and annotating the DNA of Cookies, a bacteriophage found in Northern Nevada soil along the Truckee River during the summer of 2014. Unveiling the relationship between how bacteriophages interact with organisms and their environment allows for further insight into their ability to evolve under selective pressure. *Mycobacterium smegmatis mc2155* was used as the host for this project. After soil collection, samples were enriched with *M. smegmatis* and screened for possible plaque formation. Through serial dilution purification protocols, bacteriophages were isolated until a uniform phage was found. A High Titer Lysate (HTL) was prepared from pure culture and DNA was isolated for analysis. The bacteriophage was imaged by transmission electron microscopy at the University of Nevada, Reno. Cookies DNA was then sent to Pittsburg State University (PSU) for sequencing followed by annotation using DNA Master Software.

PROFILE OF BACTERIA AND BACTERIOPHAGES FROM THE MASON VALLEY FISH HATCHERY

Sydney Oren, Kristin Sommerfeld, Eric Lundin, Erica Dietlein, Kimberly Penrose, and Connor

Brown

Truckee Meadows Community College

Laura A. Briggs, PhD (*Faculty Advisor*)

Display area: 29

The goal of our research project is to isolate and identify bacteria and bacteriophages found at the Mason Valley Fish Hatchery in Yerington, Nevada. Bacteriophages are an important treatment alternative for pathogenic bacterial infections that are resistant to antibiotics. Through our collaboration with the fish hatchery we hope to eventually use isolated bacteriophage to assist them with their fight against cold water disease caused by *F. psychrophilum*. On October 17th, 2015 we collected sick fish from the hatchery as well as took bacterial samples of the raceways the fish are kept in. We dissected and swabbed the organs and lesions of the trout back at the lab and homogenized the organs for enrichments. Over 50 types of bacteria from the samples were isolated and we are working on performing biochemical assays and identifying them. Phages were found on the ulcer and kidneys of two fish and a high titer lysate (HTL) is being prepared in order to be ready for imaging via transmission electron microscopy at the University of Nevada-Reno.

New Mexico

PETRIFIED WOOD OF THE UPPER TRIASSIC TRUJILLO FORMATION IN EASTERN NEW MEXICO

Jenelle Hansen

Mesalands Community College

Axel Hungerbuehler (*Faculty Advisor*)

Display area: 30

Several specimens of petrified wood have been collected/excavated from the Upper Triassic Trujillo Formation of eastern New Mexico. Both the preservation and the physical characteristics of these specimens have uniquely local traits that seem to be limited to specific horizons within the Trujillo Formation. These three specimen groups were collected from three different locations and are preserved by replacement with calcite. Specimens from the first set appear to have incurred a fungal growth before preservation. The possible fungal growth is all that is preserved. Specimens from the second set appear to have come from a long, slender tree, bearing four symmetrical branch-growth knots located on the same tier. Specimens from the third set contain many fragmented specimens that are flat in appearance, suggesting that either they were subjected to great pressure while being preserved or they grew in a natural flat state. While most of the original cells of the organic material have been obliterated by calcification, a detailed, physical description of each specimen group and the mineralization characteristics will be presented.

THE SACRUM OF A NEW SHUVOSAURID ARCHOSAUR FROM THE LATE TRIASSIC OF NEW MEXICO

Patricia Hansen

Mesalands Community College

Axel Hungerbuehler (*Faculty Advisor*)

Display area: 31

A sacrum from the Upper Triassic Redonda Formation in eastern New Mexico has three crescent-shaped fused vertebrae that are approximately the same size. Fused vertebrae and the crescent-shaped centra are two characteristics of shuvosaurid archosaurs. Shuvosaurids, which include the taxa *Effigia* and *Shuvosaurus*, are gracile, bipedal reptiles that belong to the crocodilian lineage of archosaurs. These two genera have sacra described as having at least four fused vertebrae, of which the last one is the largest. The Redonda Formation sacrum has perfect articulation surfaces on the anterior end of sacral one and the posterior end of sacral three with no breaks or obvious signs that another sacral vertebra had begun to fuse. By comparison with *Effigia* and *Shuvosaurus*, it is confirmed that this sacrum is from a shuvosaurid. The absence of evidence for a fourth sacral vertebra indicates that this sacrum represents a different shuvosaurid taxon.

POSSIBLE NEW SHUVOSAURID OF THE LATE TRIASSIC IN NEW MEXICO

Garrett LeMons

Mesalands Community College

Axel Hungerbuehler (*Faculty Advisor*)

Display area: 32

Shuvosaurid pseudosuchians are a distinct group of archosaurs in the Late Triassic, which are found in West Texas and eastern New Mexico. Shuvosaurids are about 9 feet long (head to tail), standing bipedal with a gracile build, and a toothless beak. Students attending Mesalands Community College's Natural Science program in field research have uncovered 1 tibia in the Redonda Formation of eastern New Mexico, quite similar to that of the shuvosaurid Effigia and Shuvosaurus. By visually comparing differences in characteristics of each, I'll demonstrate that our specimen is in fact a shuvosaurid, then determine if it is Shuvosaurus, Effigia, or a new taxon altogether.

New York

SPECIES RICHNESS OVER TIME

Quinton Kolbeck

Finger Lakes Community College

John VanNiel (*Faculty Advisor*)

Display area: 33

We analyzed camera trap data taken from the same location each fall over a four year period. Multiple cameras were set each October for about a two week period. Sites were not randomly selected but rather were chosen because of the presence of wildlife sign. Analysis includes creation of species richness curves for each season and a comparison among seasons of both species captured and latency to detection.

North Carolina

ANTIBIOTIC RESISTANCE WITHIN HUMAN WASTEWATER

Ryan Booth

Gaston College

Susan Whittemore and Cliff Grimsley (*Faculty Advisor*)

Display area: 34

Antimicrobial compounds do not completely metabolize in humans, causing large amounts of them to enter wastewater treatment plants. The wastewater treatment facilities in Gaston County, North Carolina currently do not test for, or practice the removal of any known antibiotic compounds in wastewater effluent. This study focused on an area wastewater treatment plant found in North Carolina. We hypothesized the following: If antibiotic compounds are not treated within WWTPs, the result will be a proliferation of antibiotic resistant bacteria between levels of treatment. We compared the level of antibiotic bacteria between the primary and secondary levels of treatment inside the treatment plant. Water samples were taken from each level and were plated on agar plates. After a series of culturing and inoculation all samples were streaked onto plates containing the following antibacterial discs: Streptomycin, Erythromycin, Tetracycline, and Ampicillin. Zones of inhibition were measured and noted for each antibiotic. Statistical comparisons were made between both sites to determine any significant difference.

EXTRACTION OF TERPENE HYDROCARBONS FROM HUMULUS LUPULUS

Ryan Frasure, Esther Adedokun-Babalola, and Chelsey King

Gaston College

Dr. Virginie Maggiotti (*Faculty Advisor*)

Display area: 35

H. lupulus, commonly known as hops, has been used in beer brewing since the 9th century. It is highly valued not only for its bitter flavor and distinct aroma, but also its anti-microbial properties, making beer brewed using hops much less prone to contamination by bacteria. Researchers used a Soxhlet extractor to extract the various organic compounds in three varieties of hops: Cascade, Nugget and Fuggles. The terpenes were then separated and subjected to identification by NMR spectroscopy and other analytical methods. In order to test the antimicrobial properties of the terpenes, researchers selected three species of bacteria known to commonly cause spoilage during the fermentation process: *Acetobacter aceti*, *Lactobacillus brevis* and *Pediococcus cerevisiae*. Colonies of these selected bacteria were then exposed to the purified terpenes isolated from each of the three hops varieties. The resulting data gives insight into the organic compounds in *H. lupulus* that lend it the antimicrobial properties it is renowned for and potential commercial uses for those compounds.

ANALYSIS OF SOIL ISOLATES FROM ANTIBIOTIC PRODUCING BACTERIA

David Pedraza and Mitchell Brown

Gaston College

Cliff Grimsley (*Faculty Advisor*)

Display area: 36

The Small World Initiative (SWI) incorporates the search for antibiotic producing microbes from soil in the undergraduate biology curriculum. Gaston College has integrated the SWI in introductory Microbiology (BIO 275). Antibiotics are commonly used in the farming industry on different kinds of food animals, including chickens, cows, and pigs. The purpose of this antibiotic use is to promote growth in these animals, and to preserve their health. However, excessive use of these antibiotics in farm animals can lead to naturally occurring bacterial strains becoming antibiotic resistant (Zuraw, 2013). These bacterial strains can then be passed to humans upon consumption of these food animals. The “ESKAPE” pathogens cause serious and life-threatening infections, and are also currently the cause of the majority of U.S. hospital infections and effectively “escape” the effects of available drugs (Relman, 2012). Gramicidin and pumulin are examples of secondary metabolites yielding antibiotic activity (Abdulkadir). For this project, soil samples from various chicken farms located within a 30-mile radius from Gaston College were plated. Techniques used included spread/patch against safe relative and a combination of biochemical and genetic techniques. Various chemical testing, including solubility, separation, and extraction of organic solvents was also used. Separation techniques are used to enhance the desirable outcome. The media used was LB agar with cycloheximide to decrease fungal growth and MacConkey agar for enteric classification.

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COMPARISON OF THE CONCENTRATIONS AND ANTIBACTERIAL EFFECTS OF TREE TEA OIL ON STAPHYLOCOCCUS EPIDERmidis

Lena Ramani

Gaston College

Dr. Anat Lev (*Faculty Advisor*)

Display area: 37

This study investigates the anti-bacterial properties of Tree Tea Oil against the common microorganism *Staphylococcus epidermidis* isolated from skin surface. The anti-bacterial effectiveness of tree tea oil (TTO) is determined by using different concentrations of water soluble tree tea oil formula and showing its inhibitory capabilities against the bacteria. The bacteria was obtained by using sterile swabs by swabbing around the umbilical area and applied to a Petri dish containing agar, and liquid broth, then tested with different concentrations TTO. Results concluded that higher concentrations of TTO provided more inhibitory properties than lower concentrations. Additional experiments test the antibacterial properties of the active ingredients in TTO.

**ANTIBIOTIC RESISTANCE IN PRIMARY AND SECONDARY EFFLUENT IN
WASTEWATER**

Josh Smith

Gaston College

Susan Whittemore (*Faculty Advisor*)

Display area: 38

The hypothesis, Secondary wastewater effluent will be significantly more resistant to antibiotics than Primary wastewater effluent, was tested. Primary (raw sewage) and Secondary (treated sewage) effluent from a local wastewater treatment plant was obtained and tested for antibiotic resistance. Several serial dilution trials were performed on both the Primary and Secondary effluent samples. Each dilution trial was plated and incubated. Individual colonies from the serial dilutions were aseptically transferred and quadrant streaked onto a second set of plates to isolate pure colonies. Isolated pure colonies were then transferred and cultured in slant agar tubes and labeled. Each colony was then tested for resistance against the following antibiotics: Ampicillin, Erythromycin, Streptomycin, and Tetracycline. Results were recorded. A statistical analysis was performed between the Primary effluent and Secondary effluent results to see if a significant difference in resistance were detected between the two samples. All samples were then analyzed using PCR and RFLP to isolate the 16S rRNA gene sequence of the wastewater microbes. The PCR product was then tested for pure DNA product using Agarose Gel Electrophoresis. All samples that showed good bands were prepared and sent to Yale University for DNA sequencing and identification.

Oklahoma

**NOVICE TAXONOMISTS ASSESS BIODIVERSITY IN HYPERDIVERSE ARTHROPODS
USING DNA BARCODING**

B. Acharya, J. Bleichner, J. Cox, B. Curry, S.A. DeLeon, K. Killam, S. B. King, T. Noble, S. Rice, and J. Yang

Tulsa Community College

Dr. Diana Spencer (*Faculty Advisor*)

Display area: 39

With an estimated 10-15 million species on Earth, it has become increasingly difficult for taxonomists to effectively identify species. Some morphological keys are only effective at certain stages in an animal's life, so classification of these organisms is problematic. With only 0.01% of species being identifiable by taxonomists, much improvement is needed, particularly with cryptic and hyperdiverse taxa. DNA barcoding has emerged, with broad acceptance, as an adequate method to sort through the biodiversity of our planet. Barcoding has successfully aided in species identification across many taxa since its inception in 2003. The COI gene, classified as a mitochondrial housekeeping gene, exhibits a strong phylogenetic signal due to its universal primers being very robust. COI has a lack of introns, limited recombination, and haploid inheritance. This generates a higher rate of molecular evolution that is swift enough to distinguish between closely related species. Ants, being a hyperdiverse and cryptic taxa, are difficult to identify morphologically. Integration of both methods is rapid and accurate, accelerating the global taxonomic effort.

WHAT CHO CELLS SAY ABOUT THE SUPPLEMENTS, CELLUCOR C4 AND ASTAXANTHIN

Bipina Acharya, Ciara Boatright, Jordan Cox, Brandon Curry, Brian Eccleston, Kameron Killam, Blake King, Samantha Rice, and Jennifer Yang

Tulsa Community College

Dusti Sloan (*Faculty Advisor*)

Display area: 40

More than one half of the people living in the United States take dietary supplements. However, the Dietary Supplement Health and Education Act of 1994 mandated that dietary supplements were to be regulated as food rather than drugs, leading to less testing overall of dietary supplements. Hence, the present study aims to determine the toxicity of two dietary supplements, Cellucor C4 and Astaxanthin. Toxicity was determined by performing an MTT viability assay on CHO cells. An ANOVA showed that there was a statistically significant decrease in the viability of the cells grown in media containing 1.25% and 2.5% Astaxanthin. The results for the C4 compound were inconclusive. Overall, Astaxanthin has very little toxic effect on CHO cells and the MTT assay is not effective using the Cellulcor C4 dietary supplement.

ANALYSIS OF GAPC GENES IN MULTIPLE PLANT FAMILIES FOUND IN OKLAHOMA GRASSLANDS

Acharya B., Beckham J., Curry B., Darbandi S., Eccleston B., Flippin E., Killam K., King S.B., and Nehmzow K.

Tulsa Community College

Dr. Diana Spencer (*Faculty Advisor*)

Display area: 41

The aim of our project was to clone the GAPC gene from the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene from plants in Oklahoma grasslands, insert the fragments into plasmid vectors, and analyze the sequences of the resultant clones using current bioinformatics tools. These genes are considered housekeeping genes because they catalyze glycolysis in respiration. Plants were gathered and the DNA extracted with subsequent capture of the GAPC gene through nested PCR. The purified amplicons were ligated into cloning vectors and transformed with HB101 E. coli cells through heat shock methods. The recombinant products were screened on agar plates, multiplied through growth in selective broth, and finally assessed through mini-prep restriction digests. Bioinformatics tools used were FinchTV, CAP3, NCBI Vector Masking, BLASTn, BLASTx and MEGA Muscle Alignment and Phylogenetic Analysis. Our hypothesis stated that the phylogenetic analysis would yield relationships with yarrow indicating most similar sequences and similar to other asters while the winged sumac and Sabatia compestris (meadow pink) would yield greater genetic distance.

Oregon

EFFICACY OF DILUTE GARLIC JUICE CONCENTRATIONS IN THE INHIBITION OF BACILLUS SUBTILIS

Joseph Kincaid and Cali Clements

Portland Community College

Ksenia Everton (*Faulty Advisor*)

Display area: 42

Common garlic (*Allium sativum*) has been used for centuries in medicine to treat bacterial and fungal infections, and recent research has identified several sulfur-containing compounds in garlic that demonstrate significant antibacterial and antifungal properties. We sought to determine whether the concentrations of garlic commonly found in food would be sufficient to harness its antibacterial properties. Juice from a bulb of garlic was pressed and added to three agar plates containing *Bacillus subtilis*. The remaining juice was then diluted to 0.407% in sterile water, relating to the concentrations of garlic commonly found in food items; this was then added to three separate agar plates that also contained *B. subtilis*. Prior studies suggest *B. subtilis* is more sensitive to the antibacterial components of garlic than most other bacterial species. Therefore, if the dilute solution of garlic juice was unable to inhibit *B. subtilis*, it is reasonable to deduce that other bacterial strains would not be inhibited either. After a 24 hour incubation period, the agar plates containing pure garlic juice showed average zones of inhibition 15mm in radius. The dishes containing dilute garlic juice did not exhibit any inhibition. We concluded that, while concentrated garlic juice exhibited moderate antibacterial properties, the concentrations of the active compounds therein were below their respective minimum inhibitory concentrations in the solution that was diluted to common food levels, and was thus ineffective as an antibacterial agent.

BIOCHEMICAL CHARACTERIZATIONS OF ASPERGILLUS ORYZAE AMYLASE AND
BACILLUS SUBTILUS

Leslie Villela and Austin Waibel
Portland Community College
Josephine Pino (*Faculty Advisor*)
Display area: 43

Enzymes have a wide use in industry which have catapulted the efficiency in bio-chemical reactions and decreased the cost of production. Of particular interest to us was to compare the enzymatic activity between Aspergillus oryzae (A. oryzae) amylase and Bacillus subtilus (B. subtilus) amylase for their potential to increase efficacy in disinfectants within the medical industry. Medical establishments are environments where microbes exhibit both antibiotic and antimicrobial resistance to these chemicals and research indicates that part of this resistance comes from the bacteria's ability to build colonies that create polysaccharide biofilms for protection against outside chemical changes. We chose to focus on alkaline based disinfectants as these are preferred for medical devices due to their efficiency at dissolving proteins and fat residues. Amylase converts potato starch into maltose, its biochemical activity could be extrapolated to be used against similarly composed polysaccharides. We used a concentration of 1% for both amylase enzymes and each were separated into three test tubes after being diluted to 0.125%, with 2ml of buffer pH 8, 1% potato starch, and 2ml of deionized H₂O. Our results gave us an average reaction time for A. oryzae of 287 seconds while B. subtilus had an average reaction time of 227 seconds, giving an increase of 26% of activity. Indicating that B. subtilus amylase would be more effective as an additive to disinfectants given its increased enzymatic activity. The lack of wide ranging disinfectants that can target microbial colonies with evolved biofilms makes this field of research ever more relevant.

South Carolina

WATER QUALITY STUDY

Matthew Brewer

Piedmont Technical College

Melissa Hayes, PhD (*Faculty Advisor*)

Display area: 44

Water quality is important to monitor and control to provide a safe aquatic and surrounding environment for all life. Water quality is essential to monitor to sustain adequate life for aquatic life and humans. During July 2015 water quality was monitored for Rocky Creek, Rock Creek Pond, Turner Branch Creek, and Lake Greenwood. The two creeks feed into Lake Greenwood, which is a water source for residents and power for Greenwood County. It is important to monitor the two creeks that run into Lake Greenwood because if pollutants are high in the lake then it can be used to locate where the problem began. It is especially important to monitor the Rock Creek Pond and Lake Greenwood because residents consume fish within them. Tests and samples were conducted and collected in the water sources. The tests were used to calculate summation of T and Q values. The samples were compared the water quality index chart. The water quality index (WQI) has a scale of 0-100 in an increasing trend, with 0 being very poor, and 100 being a perfect water source. For this study, the recorded values tested included: temperature, pH, nitrogen in the form of nitrates, phosphorus in the form of phosphates, dissolved oxygen (DO), biological demand of oxygen (BOD), turbidity, total dissolved solids, coliform plate count, total aerobic plate count, and Salmonella plate count.

Tennessee

ANALYSIS OF HYPOTHETICAL ORFS IN THE ACIDIANUS HOSPITALIS GENOME

Lauren Hunter, Colin Cardwell, and Robert Collins

Volunteer State Community College

Dr. Billy Dye (*Faculty Advisor*)

Display area: 45

Using the online bioinformatics platform GENI-ACT, we have analyzed hypothetical open reading frames (ORFs) from the genome of an archaean, Acidianus hospitals. Our goals are to verify the predicted start codons of these ORFs and to annotate the A. hospitalis genome database with more explicit functional or structural information for these genes. We find that sequence similarity searches (BLAST) often yield little information as most homologs are also of unknown function, whereas searches for conserved domains, predicted transmembrane helices, and other structural motifs are more fruitful. Mispredictions of start codons appear to be rare.

GENOMIC ANNOTATION OF ACIDIANUS HOSPITALIS

Alexis Seibert and Joshua Taylor
Volunteer State Community College
Dr. Billy Dye (*Faculty Advisor*)
Display area: 46

Gene annotation is the process of identifying the locations of genes in a genome and determining the function of the encoded protein. Gene annotation is necessary for comparing like gene sequences among different organisms to determine function and classification.

We have looked at hypothetical genes of the archaean Acidianus hospitalis, which has a minimally sized chromosome of about 2.13 Mbp. The genes we are studying are annotated as “hypothetical ORF” because there is no biochemical evidence of their expression, and the functions of the proteins they are predicted to encode are unknown. We analyzed the sequences of these genes using several online databases and bioinformatics tools through the GENI-ACT platform. Once similar genes were identified, we compared their sequences to our hypothetical gene to determine its function.

GREEN AND MICROSCALE METHODS IN THE SYNTHESIS OF SEVERAL FLAVONES WITH UV-VIS FLUORESCENCE STUDIES

Justin Pemerton, Nicholas Rowland, and Kristian Moore
Volunteer State Community College
Parris Powers (*Faculty Advisor*)
Display area: 47

Building on previous research, several flavones were synthesized using green and microscale techniques. Flavones are secondary plant metabolites with notable medicinal properties. The use of green solvents minimizes risk exposure and reduces the generation of hazardous waste products. Microscale synthesis allows for a cost effective/high impact laboratory experiments for students of second semester organic chemistry. A three step synthesis involving (1) esterification, (2) the Baker-Venkataraman Rearrangement and (3) an acid-catalyzed dehydration prepared the flavones. UV- Vis fluorescence spectroscopy techniques were used at various pH levels to measure samples from this study, as well as samples from prior syntheses. Melting points were determined for all intermediates and products throughout the three-step synthesis.

ANALYSIS AND DETERMINATION OF RISK FACTORS BASED ON WATTAGE OF E-CIGARETTES

Kristian Moore, Nicholas Rowland, Justin Pemerton, and Philip Clifford

Volunteer State Community College

Parris Powers (*Faculty Advisor*)

Display area: 48

E-cigarettes have been found to contain a multitude of toxins with a broad range of toxic effects. Several toxins have been identified as carcinogens and may pose a greater health risk than traditional cigarettes. In order to determine the risk factors associated with e-cigarettes, data from previous experiments were collected in order to extrapolate mathematical values that could propose descriptive risk factors. The collected data and extrapolated values were organized into graphs representing a risk factor per wattage of vaping for 11 different e-cigarette liquids. This mathematical model provides a graphical assessment of risk factors associated with toxin production at varying wattages of e-cigarettes.

Texas

ISOLATION AND CHARACTERIZATION OF THE NOVEL ACTINOBACTERIOPHAGE “DRACO” AND ANNOTATION OF THE PHAGE ‘OOGWAY’

Lorie Leyva

Del Mar College

J. Robert Hatherill (*Faculty Advisor*)

Display area: 49

Bacterial resistance to antibiotics has become a global epidemic that is steadily increasing. Research on what causes resistance and ways to stop it are in high demand. Bacteriophages are viruses that are being studied to help combat antibiotic resistant bacteria because they are target-specific, can lyse the bacteria, and can be used to produce treatments for bacterial infections. The ability to find a bacteriophage that is able to infect and then destroy target bacteria that are nonpathogenic for humans would be of great importance in the biomedical field. We studied the genes of the Actinobacteriophage ‘Oogway’ using bioinformatics software. We were able to discover a novel Actinobacteriophage isolated from the host bacteria *Mycobacterium smegmatis*, mc²155, ‘Draco.’ By comparing the novel phage ‘Draco’ with other novel phages isolated from the same host, such as ‘Oogway,’ we may be able to find genes that have similar functions. By comparing phage genomes, we are able to probe the function of the individual genes that have been studied, sequenced, and tested. Of particular interest was gene 32 in the novel phage ‘Oogway,’ which codes for a putative D-ala-D-ala-carboxypeptidase that may have originated from lateral gene transfer from its host. Carboxypeptidase enzymes are known for penicillin-binding proteins and may serve as possible binding sites to lyse bacterial strains that have become antibiotic resistant. We hypothesize that with future research it may be possible to show similar antimicrobial gene products in the novel phage ‘Draco.’

EFFECT OF GNTR AND IMMUNITY REPRESSOR PROTEINS IN
ACTINOBACTERIOPHAGE INFECTION CAPABILITY

Kenneth McGraw

Del Mar College

J. Robert Hatherill (*Faculty Advisor*)

Display area: 50

Due to increasing cost for treating medical conditions, preventative medicine is quickly overtaking more traditional, invasive methods of treatment. The result of this new research direction is an increasing demand for scientists to understand some of the regulatory mechanisms of organisms responsible for conditions effecting humans. Regulatory mechanisms can operate in various pathways within the cell of an organism such as gene transcription. Our research project included the in vitro isolation and characterization of the Actinobacteriophage ‘SeaMonayy’ followed by the in silico annotation of phage ‘Oogway’. In the course of our research, we have putatively identified two genes within ‘Oogway’ that appear to influence gene regulation. These genes encode for GntR family transcriptional regulator and the immunity repressor proteins. The GntR family transcriptional regulator contains a N-terminal DNA-binding domain consisting of a 3-helical bundle core with a small beta-sheet. Immunity repressor proteins assist in repressing the immune response of target bacterial hosts. With additional research, it may be possible to generalize our findings to the mechanisms of human pathogen actions. We hypothesize that the presence of these genes can contribute to the ability for a bacteriophage to successfully infect host bacterial cells.

EFFECTS OF LATERAL GENE TRANSFER FROM HOST TO BACTERIOPHAGE IN THE
ACTINOBACTERIOPHAGE ‘OOGWAY’

Bianca Mendonca and Erin Pena

Del Mar College

J. Robert Hatherill (*Faculty Advisor*)

Display area: 51

Mycobacteriophage are some of the most diverse life forms on earth, based not on morphology but on genomic architecture. This diversity presents itself once the genomes of the phage are compared to each other. Phage genomes are highly mosaic yet contain highly conserved genes that mediate the phage life cycle. We isolated Actinobacteriophage ‘Paralelepidio’ from a soil sample. Additionally the bioinformatic programs DNA Master, Phamerator, and Starterator were used to annotate the genome of Actinobacteriophage ‘Oogway.’ The genome of ‘Oogway’ is 61,626 base pairs in length with 88 putatively identified genes. The gene products of ‘Oogway’ were predicted by homology detection and structure via HMM-HMM comparison (HHpred). In the process of annotating ‘Oogway,’ it was identified that gene 32 shared high homology with genes that produce beta lactamase. Research surrounding this gene suggests that it allows bacteria to resist certain types of antibiotics. Additional research into the annotation of ‘Oogway’ yielded that gene 73 appears to code for a superinfection immunity protein-coding region. This coding region has functionality similar to that of the CRISPR-Cas system of bacterial adaptive immunity. The co-evolution of bacteriophage and their hosts has resulted in a diverse range of defensive and offensive strategies that we must investigate. We hypothesize that the source of both of gene 32 and 73, found within the ‘Oogway’ genome, is through lateral gene transfer with the host bacteria. Currently studies are being conducted to determine the functionality of specific gene products.

CHLAMYDOMONAS REINHARDTII USED AS A MODEL ORGANISM FOR THE
EXPRESSION OF A PROKARYOTIC HOUSEKEEPING GENE

Vasupradha Vasudevan

Lone Star College

Janeu R Houston, Ph.D. (*Faculty Advisor*)

Display area: 52

Bacteria have been used as model organisms to study genetic sequences by many researchers. They can be easily transformed and possess the ability to produce proteins in high concentrations. However bacteria have inherent limitations as model organisms when used to investigate eukaryotic phenomena. For example, prokaryotic genes are arranged and expressed differently than their eukaryotic counterparts. In addition, Gram-negative bacteria, which are most often used in genetic studies, contain lipopolysaccharides, that interfere with many downstream applications such as protein expression, purification and assay.

Chlamydomonas reinhardtii conversely, is a unicellular haploid green alga that has been used as a eukaryotic model organism to investigate numerous life processes including photosynthesis and cellular motility. C. reinhardtii holds the advantages of having a relatively small genome, both autotrophic and heterotrophic capabilities, fast growth rate, ease of transformation and an ability to reproduce sexually and asexually. C. reinhardtii is an attractive organism to use since algal surfaces lack LPS and algae can be easily manipulated. A prokaryotic housekeeping gene sequence will be PCR amplified, restriction digested and ligated into a plasmid. C. reinhardtii will be transformed with this recombinant plasmid, the culture will be expanded in liquid culture and the plasmids will be isolated. Finally, the housekeeping gene sequence will be verified using PCR and gel electrophoresis analysis.

ALGAL BIOFUEL PRODUCTION: COMPARISONS OF PROCESSING EFFICACIES

Nichole Gonzales

Lone Star College

Daniel B. Kainer Ph.D (*Faculty Advisor*)

Display area: 53

Using advancements in biodiesel production technology in tandem with sustainable feedstocks such as algae, researchers can provide industry with alternatives to crude oil and the associated fluctuations in cost and availability. The conventional production cycle of algae biodiesel necessitates a multi-step approach that renders the technology impractical when applied to an industrial scale of production. One-pot biodiesel eliminates the multi-step requirements by using a supercritical CO₂ extraction module to conduct selective extraction with the inclusion of supercritical methanol to drive the transesterification of triglycerides into fatty acid methyl esters (FAME). Factors such as temperature, pressure, acidic/basic heterogeneous catalysts as well as the ratios of co-solvents CO₂ and methanol seek to increase the solubility of FAME and effective yield from the original algae biomass. This process holds the potential to streamline the algal biodiesel production process by combining the steps of lipid extraction and conversion to biodiesel in a method that will increase the feasibility of large-scale applications such as algaebiorefineries that can readily provide biodiesel alternatives in the wake of volatile oil markets. We propose a study comparing the efficacy of conventional algal biofuel production methods with their supercritical fluid-mediated counterparts, including: 1) supercritical CO₂ extraction of biocrude compared to the more conventional Soxhlet method and 2) transesterification of whole algal biomass-derived triglycerides via supercritical methanol compared to the subcritical reaction of waste vegetable oil (WVO) triglycerides with subcritical methanol.

MICROBIAL FUEL CELLS AND CHROOCOCCIDIOPSIS: A NOVEL COMBINATION
FOR HUMAN LIFE SUPPORT ON MARS

Justin McKenzie

Lone Star College

Dr. Daniel Kainer (*Faculty Advisor*)

Display area: 54

Microbial fuel cells (MFCs) comprise a technology that exploits the exoelectrogenic capabilities of particular classes of anaerobic microorganisms (e.g., Geobacter and Shewanella spp) that feed on organic material in soil or wastewater and convert that chemical energy into electricity. Because such organisms hold the potential to be utilized *in situ* as an off-grid electricity producer, they hold great promise as an energy-producing resource for NASA missions, potentially including missions to Mars. One obstacle to developing Martian MFCs is the lack of organic material in Martian regolith capable of supporting anaerobic bacterial growth. Certain cyanobacteria, including Chroococcidiopsis, thrive in extreme conditions (severe cold and dryness, high UV intensity, etc.) reminiscent of Mars-like conditions, making them good candidates as a primary source of organic material derived from the largely inorganic Martian surface. The Texas Space Grant Consortium (TSGC) recently provided funding to support undergraduate research at Lone Star College-Montgomery centered on different ways to utilize cyanobacteria as a resource enhancing the life support systems of future Martian astronauts. We propose a series of experiments in which Martian regolith simulant is combined with cyanobacterial lysate and then evaluated as a food source for exoelectrogenic bacteria in MFCs. This “proof of concept” study will provide insight into the feasibility of using cyanobacterial photosynthesis as a mechanism for converting inorganic Martian resources into organic matter and Geobacter exoelectrogenesis as a mechanism for generating electricity.

LONE STAR'S BIOTECHNOLOGY CLUB AS A RESEARCH OUTREACH TO
UNDERGRADUATE STUDENTS

Candace Piccola

Lone Star College

Daniel B. Kainer, Ph. D (*Faculty Advisor*)

Display area: 55

Lone Star College's Biotechnology Club is an extracurricular student organization that encourages undergraduate students to partake in research of their own. Each semester, club members vote on a project theme which is then divided into multiple individual experiments. Club members form teams based on the experiment of their choice. Each group is responsible for researching their topic, writing and updating their experimental procedure, determining their budget, keeping detailed records for their projects, and communicating with the club officers and/or sponsor. A project head is elected to act as the go between for the club sponsor and the groups, taking responsibility for the project. In the 2015 Fall Semester, the club took advantage of Texas Space Grant Consortium funding supporting undergraduate research centered on evaluating the role of cyanobacteria as life support resources for future Martian astronauts. Specifically, club members chose to grow cyanobacteria under specific conditions similar to those found on the Martian surface. The sub-experiments were as follows: growing cyanobacteria in a predominantly CO₂ atmosphere, low pressure, varying temperature, UV light, and regolith. Each of these experiments are meant to scan various strains of cyanobacteria for growth output. Growing plants on cyanobacteria lysate and using cyanobacteria as an oxygen source for a fuel cell are two additional projects were added to use cyanobacteria in ways that could sustain human life on Mars. Undergraduate support is scarce. Often undergraduates don't get the opportunity to do their own research. This club solves this problem by not only creating opportunities but providing direction and support along the way.

BEHAVIOR OF THE CLEANER FISH ELACATINUS SPP. AND THEIR CLIENTS IN
ROATAN, HONDURAS

Kennedy Chudej, Jonathan Briscoe, and Jennifer Leard
McLennan Community College
Stephanie Randell (*Faculty Advisor*)
Display area: 56

Gobiidae is the largest family of marine fish. The four most common species and primary cleaner fish in Roatan, Honduras are the Elacatinus luisae, E. lori, E. colini and E. lobeli. Elacatinus use coral and sponges for cleaning stations and protection. At cleaning stations, cleaner fish remove ectoparasites and client fish benefit through reduction of ectoparasite loads. This study was conducted to determine the behaviors and ratios of Elacatinus and client fish at individual cleaning stations in Roatan, Honduras. Research dives were conducted from May 17-22 at 5 established dive sites within the Sandy Bay Marine Park. Each site was surveyed twice and on different days. Water conditions, cleaning substrate, species frequency, and behavior were recorded. Corals, primarily Orbicella annularis, were most frequently used as cleaning station substrates. The most frequent cleaning behaviors were nibbling and chasing. Zig/Zag swimming and cleaning inside operculum and gills were the least frequently observed behaviors. The most frequently observed client behaviors were: pectoral fin display, tilting right, tail stand, and opening mouth. Fanning operculum, quivering fins, and freezing were the least frequently observed client behaviors. The most frequently observed client fish were Chromis cyanea (Blue Chromis), Sparisoma viride (Stoplight Parrotfish), and Acanthurus couruleus (Blue Tang). In the future, cameras with viewing screens should be used to better capture fish behaviors underwater.

FREQUENCIES FOR DARK SPOT SYNDROME ON THREE CORAL SPECIES IN
ROATAN, HONDURAS

Gabby Garcia

McLennan Community College

Stephanie Randell (*Faculty Advisor*)

Display area: 57

Dark Spot Syndrome is prevalent in the Caribbean and appears as discolored spots that can range from brown, purple, blue or black. Though the affected tissue has been linked to physical and microbiological causes, the causative agent is still unknown. DSS rarely causes whole colony mortality. There is no documentation on prevalence of DSS its growth rate, or its coral preference in Roatan, Honduras. The study was conducted to determine the coral species affected by DSS and area coverage of DSS on the Mesoamerican Reef in Roatan, Honduras. Sampling occurred from May 17 - 22, 2015 at five established dive sites within the Sandy Bay Marine Park. Each dive site was visited twice, on different days. Randell-Robertson Marine Survey Technique (RRMST) was adapted for optimal *Siderastrea siderea*, *Siderastrea radians*, and *Stephanocoenia intersepta* observations. For each coral species observed, the date, dive site, water condition, coral species, volume, depth, temperature, and coral health were recorded. A 0.5x 0.5 meter quadrant was placed on corals affected with DSS for area calculation. Of the sampled corals, 33% were affected with DSS. *Siderastrea siderea* and *Stephanocoenia intersepta* were the only corals observed, with DSS only found on *S. siderea*. The northernmost dive site, Barry's Reef, had the highest percentage (69%) of corals affected by DSS. There was weak but statistically significant correlation (Pearson's correlation $r=0.66258$; $d=24$) between the average area of DSS and the volume of the affected corals across all dive sites.

FISH BITE PREVALENCE ON THREE CORAL SPECIES WITH DARK SPOT SYNDROME
IN ROATAN, HONDURAS

Mariana Juarez, Erin Castillo, and Joanna Flores

McLennan Community College¹

Stephanie Randell (*Faculty Advisor*)

Display area: 58

Dark Spot Syndrome (DSS) is prevalent on corals in the Caribbean; however, no studies of DSS have been conducted in Roatan, Honduras. Goreau suggested that fish bites could provide an entryway for pathogens that are carried through water currents or fish fecal matter and may be contributing to transmission of DSS. This study was conducted to determine number of fish bites and total area of coral tissue affected with Dark Spot Syndrome on three coral species: Siderastrea siderea, S. radians, and Stephanocoenia intersepta in Roatan Honduras. Surveys were conducted at five dive sites within the Sandy Bay Marine Park from May 18-22, 2015. Each site was visited twice, on different days, with a bottom time of 45 minutes. The Randell-Robertson Marine Survey Technique was used, starting at the deepest depth of the coral species range (10.5 - 14m) and ended at the shallowest depth (3- 4.5m). For each coral species observed, these data were collected: frequency, volume, and disease status. There was no correlation between fish bites and DSS. A significantly higher percentage of DSS was recorded at Barry's Reef and Bear's Den, both located near the northwestern side of the island. Barry's Reef was nearest to a municipal dump and a golf course. The higher percentage of DSS at the northwestern sites may be associated with pollution pulses or nutrient run off. Future studies should investigate these and other ecological factors that could be instrumental in the cause of DSS.

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

Kara Schmidt^{1,2}

McLennan Community¹, and Texas Tech University²

Stephanie Randell (*Faculty Advisor*)

Display area: 59

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

Washington

ANALYZING THE PERIOD OF A COMPLEX PENDULUM

Bassam Halabiya

Edmonds Community

Rachel Wade (*Faculty Advisor*)

Display area: 60

In this experiment, the period of a complex pendulum was examined. The pendulum consisted of a long thin rod (physical pendulum) suspended from a pivot with a simple pendulum (a string of negligible mass holding a pendulum bob) suspended from the bottom of the physical pendulum. After release, the motion of the double pendulum is irregular and chaotic for a period of time until which the two pendula synchronize and behave as a single pendulum. It was hypothesized that the synchronization period of the complex pendulum would be longer than the natural period of the individual physical pendulum, due to the increased length. Initial findings indicate that when the length of the string of the simple pendulum and the angular displacement of the physical pendulum remain constant, the synchronization period of the system can be modeled as a simple pendulum and the synchronization time is constant. Further analysis of the complex pendulum will be conducted to examine how varying the simple pendulum length and the initial displacement impact the synchronization time and synchronization period to verify the synchronized simple pendulum model and further explore the complex nature of the system. Understanding the synchronization of chaotic systems can lead to the engineering of more complex systems.

MAPPING SUSTAINABILITY

Alicia Kelly

Edmonds Community

Gem Baldwin (*Faculty Advisor*)

Display area: 61

"Mapping Sustainability" is an ongoing interdisciplinary undergraduate research project run by the Anthropology, Diversity Studies, English, and Pre-College Departments at Edmonds Community College. The project increases community awareness of local businesses utilizing environmentally sustainable practices - composting, recycling, use of organic and/or local ingredients, fair trade, and "green" building techniques and materials, etc.. Students choose a site, design and complete an ethnographic study, prepare a published report of their findings, which is then disseminated to the public via the "Mapping Sustainability" website. We define sustainability based on what we value. This project satisfies the larger goals of community-based research by linking EdCC students with the local community to contribute to a sustainability knowledge base while contributing to student educational success by developing research and analysis skills and linking the classroom to the real world. This poster outlines the project and provides an assessment of the educational outcomes for the students. We find that participants in this project report greater levels of academic confidence and competence and increases in the ability to see the linkages between the classroom and the Real World. This translates into greater persistence towards intended degrees.

UND AND EL NIÑO SOUTHERN OSCILLATION TEMPORAL PATTERNS

Lanessa Cerrillo

Everett Community College

Robin Araniva (*Faculty Advisor*)

Display area: 62

The El Niño Southern Oscillation pattern has been linked to dramatic changes in the marine environment, such as unusually warm surface waters, a flattened thermocline, and reduced upwelling within an estuary system. Data collected by students in the Ocean Research College Academy (ORCA), an early college program through Everett Community College, suggests that the fluctuation of surface temperature had a significant impact on phytoplankton abundance and primary productivity within the Snohomish River Estuary. Monthly State of Possession Sound (SOPS) cruises were utilized to gather phytoplankton data from multiple sites near the mouth of the Snohomish River from 2010-2016. The Snohomish River estuary is influenced by freshwater from the Snohomish River as well as high saline waters from the Pacific Ocean. Mount Baker Terminal, a site south of the mouth of the river, was equipped with a Seabird CTD probe. The probe collected temperature data every fifteen minutes. Data collected was analyzed with respect to the cyclical temporal patterns created by the El Niño Southern Oscillation pattern and its correlation to phytoplankton abundance. It is hypothesized that with higher surface temperatures and an increase in atmospheric temperatures, phytoplankton abundance will increase.

THE UPTAKE OF HEAVY METALS BY EELGRASS (*ZOSTERA MARINA*) AND
PHYTOPLANKTON IN POSSESSION SOUND

Sophia Maggio
Everett Community College
Robin Araniva (*Faculty Advisor*)
Display area: 63

Possession Sound, an estuary located in Everett, WA, is influenced by the interaction of seawater from Puget Sound and freshwater from the Snohomish River. Students at the Ocean Research College Academy (ORCA) study eelgrass (*Zostera marina*) in the estuary, specifically near Mukilteo, Whidbey Island, and Snohomish River. In previous studies, *Z. marina* exhibited a high uptake capacity for metals concentrated in sediment; however, low pH levels can desorb heavy metals from sediment, causing bioaccumulation in phytoplankton and limiting primary production. While *Z. marina* photosynthesizes, it is hypothesized to possess the ability to biodegrade heavy metals in sediment, and thus is expected to exhibit lower concentrations than phytoplankton. Heavy metal concentrations in root, shoot, and blade, sediment, and phytoplankton samples were analyzed in an Inductively Coupled Mass Spectrometer (ICP-MS) by Everett Environmental Lab. At Mukilteo and Whidbey, copper and zinc concentrations in *Z. marina* consistently exceeded detection limits, with the highest zinc concentration of 78.9 mg/kg in shoot samples and the highest copper concentration of 10.8 mg/kg in root samples at Whidbey. Cadmium was highest in blade and shoot samples at both sites, but undetected in phytoplankton. However, arsenic was highly concentrated in phytoplankton (30.7 mg/kg at Mukilteo, relative to detection limit of 8.478 mg/kg), as was zinc, with a mean concentration of 4700 mg/kg. Preliminary data reveal a more complex pattern dependent on metal type and biological tissue; therefore, additional data are being collected to ascertain the necessity of certain metals for specific parts of *Z. marina* and phytoplankton.

MICROPLASTIC TYPE AND ABUNDANCE IN RIVER OTTER SCAT AND SEDIMENT

Selena Perez

Everett Community College

Josh Searle (*Faculty Advisor*)

Display area: 64

Microplastics are a type of marine debris and pollutant comprised of synthetic polymers and is often broken down from larger plastics entering the marine environment by natural processes. Ingestion of microplastics has been observed in a variety of organisms and may be a factor in the transfer of chemical additives or hydrophobic pollutants to marine biota. This study is focused on the distribution of types of microplastics found in the river otter (*Lutra Canadensis*) population and sediment located throughout the Possession Sound estuary within the Salish Sea.

Microplastics are found through river otter scat dissections sampled since 2012 and performed by students attending Ocean Research College Academy in Everett, WA. Further sampling consists of collecting beach sediment near river otter latrine sites. From a small sample size of 30 scat samples; preliminary results suggest a 30% presence of polystyrene, a low-density plastic often used in packaging, disposable plastic cutlery and dine ware, and floating docks. Other polymers observed consist of polypropylene, a versatile and widely used plastic often found in a fiber-like form and zinc stearate, an insoluble powder-like polymer often used in cosmetic products. This study hypothesizes a strong correlation between types of plastics found in sediment and river otter scat samples and suggests the primary plastic pollutant to be polystyrene.

THE EFFECT OF TEMPERATURE ON THE GENETIC DIVERSITY OF EELGRASS IN
POSSESSION SOUND
Madeline Sayed
Everett Community College
Robin Araniva (*Faculty Advisor*)
Display area: 65

Zostera marina, or eelgrass, is a marine flowering plant species native to the estuarine coastlines of North America and Eurasia. The plants thrive in the cool, saline waters of Possession Sound and provide critical habitat for numerous species. Global declines in eelgrass populations and rising water temperatures threaten a crucial building block of a healthy marine environment. The decline in eelgrass abundance has been linked to anthropogenic influences and global climate change. The reproduction of eelgrass is sensitive to surrounding conditions; it is able to reproduce sexually and asexually. Students in the Ocean Research College Academy (ORCA), a dual credit program though Everett Community College, collect eelgrass samples from three locations in Possession Sound. Temperature data collected by a CTD deployed near one location demonstrates an increasing temperature average over the last five years. In 2010, the average yearly temperature was measured at 10.32°C, while 2011, 2012, 2013 and 2014 measured 9.88°C, 9.89°C, 10.41°C, and 10.52°C, respectively. In 2015, the average temperature increased by 1.12°C, averaging 11.64°C. To determine if temperature changes have an effect on genetic diversity, eelgrass DNA will be extracted using Sigma-Aldrich procedures specific to plant material and target genes will be amplified through PCR. Samples will be sequenced and analyzed. It is hypothesized that higher temperatures in the water column will increase the occurrence of sexual reproduction, increasing the genetic diversity of the population.

MITOCHONDRIAL CYTOCHROME -C- OXIDASE 1 GENE (MT-CO1 GENE)
EXPRESSION IN PACIFIC NORTHWEST SALMON SPECIES

Rachel Nies, Mathew Ridgway, and Emad Shirazi

Lake Washington Institute of Technology

Sahba Fatherazi (*Faculty Advisor*)

Display area: 66

This research project focused on the study of the mitochondrial Cytochrome -c- Oxidase 1 gene (mt-CO1), in close salmon species of the Pacific Northwest. The mt-CO1 gene encodes for a protein located in most eukaryotic cells called Cytochrome-c-Oxidase 1. More specifically, this protein is located in mitochondria and plays an extremely important role in cellular metabolism. The mt-CO1 gene has become the standard sequence for a technique called DNA Barcoding. The idea of this technique is to compile mt-CO1 gene sequences in a database in which researchers can use computer software to accurately identify a species and analyze the subtle differences between them from a small tissue sample. This allows taxonomists to accurately identify new species, and track changes in a given population of organisms. The laboratory techniques used in this research project included DNA extraction, polymerase chain reaction (PCR), gel electrophoresis, DNA imaging, gene sequencing and analysis. Our results indicated expression of the identical mt-CO1 gene within northwest salmon species. The Department of Science at Lake Washington Institute of Technology (LWIT) is currently in the process of reforming the existing Cellular Biology 211 course by implementing the CURE model (Course Undergraduate Research Experience), of CCURI. With this implementation, biology students have the opportunity to get exposure to innovative and advanced research methodologies and techniques. In this project we collaborated with Dr. Erica Cline from the Department of Environmental Science and Studies, University of Washington, Tacoma, WA.



Supported by NSF Awards #1118679 and #1524353

CCURI is funded through the National Science Foundation Transforming Undergraduate Education in STEM (TUES) Type III and Improving Undergraduate STEM Education (IUSE) grants awarded to Finger Lakes Community College in Canandaigua, NY.

The CCURI model of incorporating undergraduate research (UR) into community college curricula, engages students from the moment they enter the classroom. The model employs active learning methods of instruction in the first year coursework, which teaches basic scientific concepts within the context of an ongoing research project. Students are then given an opportunity to explore those projects as either a CURE (Course Undergraduate Research Experience), a SURE (Summer Undergraduate Research Experience) or a PURE (Program Undergraduate Research Experience). The growing CCURI network has become a rich source of collaboration on both the curricular and research sides of the CCURI model. With over 50 community colleges implementing the CCURI undergraduate research model; thousands of students are connected to research and opportunities that are vital to the successful pursuit of a STEM career.

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