The Ohio Journal *of* SCIENCE

OPEN ACCESS • ONLINE • INTERNATIONAL • MULTIDISCIPLINARY

Volume 119 No. 1
April Program
Abstracts

The OHIO JOURNAL *of*
SCIENCE
ISSN 0030-0950
Open Access online

EDITORIAL POLICY

General

The Ohio Journal of Science (OJS) has published peer-reviewed, original contributions to science, education, engineering, and technology since 1900. The OJS encourages submission of manuscripts relevant to Ohio, but readily considers all submissions that advance the mission of The Ohio Academy of Science to foster curiosity, discovery and innovation to benefit society. Annually the Academy produces two issues: peer-reviewed April Program Abstracts and peer-reviewed full papers in December. The Ohio State University Libraries publishes both issues Open Access online on behalf of The Ohio Academy of Science. The Academy distributes a print version of the April Program Abstracts at the annual meeting. **Peer-reviewed articles are published as accepted throughout the year** and compiled at year end into a single, digital volume. Because the OJS is an international multidisciplinary journal, authors should write clearly, concisely, and avoid excessive jargon to assure broad understanding of their work by those whose fields may differ from the authors.

The OJS considers original contributions from members and non-members of the Academy in all fields of science, technology, engineering, mathematics and education. Submission of a manuscript is understood to mean that the work is *original* and *unpublished*, and is not being considered for publication elsewhere. All manuscripts considered for publication will be peer-reviewed. Any opinions expressed by reviewers are their own, and do not represent the views of The Ohio Academy of Science or the OJS.

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FUTURE ACADEMY MEETINGS

2020 April 18 Cleveland State University, Cleveland, Ohio

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Date of Issue—April 2019

Copyediting and design—Philip Winchell,
STEM Education Support Services
Assisted by Mrs. Dorie Gruber

Printing courtesy of:

CAS®
A DIVISION OF THE
AMERICAN CHEMICAL SOCIETY

The Ohio Journal *of* Science

AN OPEN ACCESS, ONLINE, INTERNATIONAL, MULTIDISCIPLINARY JOURNAL

Volume 119 **April 2019** **Number 1**

https://doi.org/10.18061/ojs.v119i1.6832

The Ohio Journal of Science

Dr. Lynn E. Elfner, Editor

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Printed in The United States of America.

Send address changes to:
The Ohio Journal of Science
5930 Wilcox Pl., Suite F
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Hosted by
Columbus State Community College
April 13, 2019

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FRONT COVER PHOTO: Aerial view of the Mallway at the Columbus Campus of the Columbus State Community College. In the foreground are Eibling Hall (left) and Nestor Hall (center) with the Columbus, Ohio, skyline in the distance. -Photo courtesy of Columbus State Community College, https://www.cscc.edu .

The Ohio Academy *of* Science

128th Annual Meeting

Hosted by
Columbus State Community College
Columbus, OH 43215
April 13, 2019

ABOUT THE ANNUAL MEETING

The Ohio Academy of Science's Annual Meeting is for academic, governmental, and industry scientists and engineers, university and pre-college educators, and pre-college, undergraduate, and graduate students, and interested lay citizens in the Ohio region.

WELCOME!

Columbus State Community College, Columbus Campus, welcomes you to the 128th Annual Meeting of The Ohio Academy of Science. We invite you to explore our campus and to share in the excitement and opportunities provided in this program.

REGISTRATION

Registration is required for all meeting attendees and is included in the abstract submission fee. Register online at: **http://www.ohiosci.org/annual-meeting-2019 .** On-site registration will be available.

The Ohio Academy of Science must receive registration by **April 9, 2019**.

Access to sessions is by name tag only. Name tag, information, and receipt will be available at the meeting.

Registration is by credit card on-line at **https://www.memberleap.com/members/evr/regmenu.php?orgcode=OAS .**

For further information, please call 614-389-2182.

Saturday, April 13: Registration at the Conference Center/Center for Workforce Development on the 4th floor.

7:30 AM - 10:00 AM. On-site registration can be paid either by check, VISA, or MasterCard. Cash is discouraged.

MEETING LOCATION

All Ohio Academy of Science events take place on the 4th floor of the Conference Center/Center for Workforce Development (WD), 315 Cleveland Ave., Columbus, Ohio 43215. This is in the northwest quadrant of the campus, just north of the bookstore.

DRIVING INSTRUCTIONS TO CAMPUS

The main address for the Columbus State Community College, Columbus Campus, is 550 East Spring St., Columbus, Ohio 43215.

Video driving instructions are at
https://www.cscc.edu/services/parking/

PARKING ON CAMPUS

Parking permits can be downloaded at **http://www.ohiosci.org/annual-meeting-2019**. Permits must be displayed on dash. Please park in any student lot near the Conference Center/Center for Workforce Development (WD on map). A campus map is on page 31 of this issue and online at
https://www.cscc.edu/services/parking/pdf/map.pdf

MEALS

Saturday, April 13th – Box lunches may be pre-ordered with registration for $10.00 and will be available for pick-up at noon on the 4th floor of the Conference Center/Center for Workforce Development (WD).

Box lunches must be ordered by **March 27, 2019**. **https://www.memberleap.com/members/evr/regmenu.php?orgcode=OAS .**

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Fostering curiosity, discovery and innovation to benefit society.

GENERAL SCHEDULE

Saturday, April 13, 2019

All events take place on the 4th floor of the Conference Center/Center for Workforce Development (WD).

7:30 AM - 10:00 AM	Breakfast (WD Ballroom)
7:30 AM - 10:00 AM	Meeting Registration (table outside WD Ballroom)
8:45 AM	Annual Meeting of the Members (Meeting Room WD 402) (see below)
9:00 AM - 10:00 AM	Poster Session (all presenters) (WD Gallery, 404, and 407)

Note: All posters will be displayed in both morning and afternoon sessions.

10:15 AM - 12:15 PM	Podium Sessions (WD 409E, 409W, 415)
12:15 PM - 1:15 PM	Box lunch pick up (at registration table)
12:15 PM - 1:15 PM	Lunch State of the Academy All-academy Lecture (WD Ballroom)
1:30 PM - 3:00 PM	Poster Session (all presenters) (WD Gallery, 404, and 407)

Note: All posters will be displayed in both morning and afternoon sessions.

Annual Meeting of the Members

The Ohio Academy of Science will hold one annual meeting of the members each calendar year. The annual meeting will take place during the first or second calendar quarter of each year, and will be held at a time and place that the Board designates. The purpose of each annual meeting will be to conclude any old business and conduct any new business that may properly come before the members. The business session of this meeting shall be conducted in accordance with the most recently published edition of "Robert's Rules of Order" or "the Modern Rules of Order."

Our Institutional Host

Columbus State Community College has been meeting the diverse educational needs of the Central Ohio community for more than 50 years. The college is proud to be an important contributor to the growth and progress of the region and to serve as the front door to higher education in Central Ohio.

As a comprehensive community college, Columbus State has a strong commitment to students seeking career and technical education leading to employment and to students who want to pursue an Arts and Sciences curriculum leading to an associate degree and then to an undergraduate degree. Our Career and Technical Division offers certificates and associate degree programs in the areas of business and marketing, computers and interactive media, construction sciences and skilled trades technologies, engineering technologies, health and human services, hospitality, and public services. Columbus State also offers Associate of Arts and Associate of Science degree programs whose coursework fulfills the freshman and sophomore year requirements for bachelor's degree programs offered by four-year colleges and universities throughout the state.

Columbus State now has two campuses serving Central Ohio educational needs. The Columbus Campus is located on 85 acres in downtown Columbus. This campus consists of two dozen buildings housing classrooms, laboratories, student services and college offices. Also, part of this campus is the recently remodeled library in Columbus Hall which provides materials and resources for students. The 108-acre, full-service Delaware Campus is located between Columbus and Delaware along U.S. 23, and has an administration building and Moeller Hall, an 80,000 sq. ft., LEEDS Gold-Certified academic building.

COLUMBUS STATE
COMMUNITY COLLEGE

All-Academy Lecture

A panel discussion will be held during the luncheon at 12:15 PM in the WD ballroom.

Lake Erie: Ohio's Great Lake-Status, Trends, and Threats

The discussion will be led by **Douglas Kane, PhD**. Dr. Kane is a Professor of Biology in the Division of Natural Sciences, Applied Sciences, and Mathematics at Defiance College. His research interests lie in plankton and benthic invertebrate ecology, as well as effects of invasive species on communities and ecosystems, causes and consequences of cultural eutrophication, and ecosystem integrity of Lake Erie. Doug's recent research has focused on effects of the Maumee and Sandusky River systems on the recent re-eutrophication of Lake Erie. Doug has been a Visiting Professor at São Paulo State University in Brazil and a Visiting Researcher at the University of Toledo's Lake Erie Center. Further, Doug has mentored students as a Visiting Scientist in Stone Lab's Research Experience for Undergraduates program for the past decade and a half. Doug has published peer-reviewed papers in *Journal of Great Lakes Research, Ecological Indicators, Inland Waters, Freshwater Biology, Water, Harmful Algae*, and *Ohio Journal of Science*. Doug is current President of the Ohio Lake Management Society, board member of the Water Management Association of Ohio, board member of the Upper Maumee Watershed Partnership, and former board member of the Ohio Academy of Science. He was awarded the Richard W. Stroede Distinguished Faculty Citation at Defiance College in 2017.

Dr. Thomas Bridgeman is a Professor in the Department of Environmental Sciences at the University of Toledo and the director of the UT Lake Erie Center. His research interests center on harmful algal blooms (HABS) and hypoxia in the Laurentian Great Lakes. He has maintained a water quality monitoring program in western Lake Erie since 2002 and he and his students have conducted research on weather-related episodic hypoxia, impacts of turbid river plumes on HAB development, inter-annual variation of HABS, internal loading of phosphorus from lake sediments, and improved bloom monitoring via remote sensing and in-lake sensors. Bridgeman and his graduate students have also studied the effects of hypoxia on fish foraging and the recent spread of the HAB species *Lyngbya wollei* in western Lake Erie. He has published in a variety of peer-reviewed journals, served as a manuscript reviewer and on a national review panel for the NOAA Ecology of Harmful Algal Bloom program. He has received research funding from NSF, NOAA, USEPA-GLNPO, USDA, Ohio Sea Grant, Ohio Dept. of Higher Education, Ohio Great Lakes Protection Fund, US Army, and the Center for Innovative Food Technology.

Dr. Timothy Davis is Associate Professor of Biological Sciences at Bowling Green State University. Dr. Davis has spent the last 13 years studying the ecology of harmful algal blooms. Dr. Davis completed his Bachelor of Science at Southampton College of Long Island University and a PhD from Stony Brook University. Dr. Davis worked as a postdoctoral research fellow at the Australian Rivers Institute in Brisbane Australia and the Canadian Center for Inland Waters in Burlington, Ontario. From 2014-2017, Dr. Davis worked for NOAA Great Lakes Environmental Research Laboratory (GLERL) in Ann Arbor, MI and in August 2017, he joined the faculty of Bowling Green State University. Dr. Davis is the co-Chair of the National HAB Committee and is a member of the US EPA's Board of Scientific Counselors and sits on the Safe and Sustainable Water Resources sub-committee.

Dr. Silvia Newell is an Associate Professor at Wright State University in Dayton, Ohio. She has a PhD in geosciences from Princeton University and did a postdoc at Boston University. She has worked on biogeochemical cycling of nitrogen in low-oxygen marine environments in the Gulf of Mexico, Chesapeake Bay, the Arabian Sea, and Cape Cod. Currently, her work at Wright State focuses on nitrogen as a driver of harmful algal blooms in eutrophic Lake Erie, Lake Okeechobee, Lake Taihu (China), and Estonian lakes, as well as local research on the Great Miami River and Ohio wetlands.
Photo credit: Nate Christopher, Fondriest Environmental.

Brief Schedule of Abstracts

See **Fields of interest index** on page 29
and **First author index** on page 29

Poster Session 9:00 - 10:00 AM
and
Poster Session 1:30 - 3:00 PM

Note: All posters will be displayed in both morning and afternoon sessions.

Located in the Center for Workforce Development (WD) (4th Floor Gallery, 404, and 407)

College and Professional
See page 10

Pre-college Student
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Podium Sessions 10:15 AM - 12:15 PM

Located in the Center for Workforce Development (WD), 4th Floor

Podium Session 1
Medicine and Health
10:15 AM - 12:15 PM
Meeting Room – WD 415
See page 5

Podium Session 2
Materials, Modeling, and Imaging
10:15 - 11:30 AM
Meeting Room – WD 409 East
See page 7

Podium Session 3
Life Science
10:15 - 11:30 AM
Meeting Room – WD 409 West
See page 8

10:15 AM - 12:15 PM
Podium Session 1
Medicine and Health
Meeting Room – WD 415

10:15 - EVALUATION OF TLR-INDUCED SIGNALING AND CYTOKINE PRODUCTION AFTER TREATMENT OF MACROPHAGES WITH HEAT-KILLED *STAPHYLOCOCCUS AUREUS*. Sarah K. Grossman, sgrossman15@students.ndc.edu, Angela C. Johnson, acjohnson@ndc.edu, Notre Dame College, 4545 College Road, South Euclid OH 44121.

Although *Staphylococcus aureus* is commonly found on the surface of the body, it is of significant medical concern with the emergence of methicillin-resistant *Staphylococcus aureus* (MRSA). In an effort to understand the TLR-mediated innate immune against *S. aureus*, heat-killed *S. aureus* was utilized to treat macrophages, which are one of the major classes of innate immune cells. Specifically, this research sought to determine the response, if any, of the macrophage to *S. aureus*. Furthermore, as previous data indicates crosstalk amongst the TLR signaling pathways, the study evaluated the role that TLR3-TRIF signaling may play during the innate immune response to *S. aureus*. Briefly, the macrophage cell line J774 was treated with the following ligands: $Pam_2Cys\text{-}Ser\text{-}(Lys)_4$ (TLR2/TLR6 ligand), $Pam_3Cys\text{-}Ser\text{-}(Lys)_4$ (TLR2/TLR1 ligand), the synthetic dsRNA polyinosinic:polycytidylic acid (TLR3), heat-killed *S. aureus* HKSA (primarily TLR2), and a combination of Poly(I:C) and HKSA. After 24 hours of treatment, supernatants were collected and subjected to ELISA to test for the presence of CXCL2/MIP-2, which is known to be secreted by macrophages following TLR2 triggering, CCL5/RANTES which is known to recruit T-cells into inflammatory sites, and CXCL1/KC, a chemokine known to recruit inflammatory cells. After <2 hours of stimulation, macrophages were analyzed via western blot for MAP kinase activity (phosphorylation of JNK). Preliminary experiments indicate that crosstalk between TLR2 and TLR3 is not occurring at the level of cytokine production; however, cell signaling event remain to be fully evaluated. To this end, signaling via p38, NFκB, and IRF-3 will be determined.

10:30 - THE BIOFILM ADHESION PROTEIN AAP FROM *STAPHYLOCOCCUS EPIDERMIDIS* FORMS ZINC-DEPENDENT AMYLOID FIBERS. Alexander E. Yarawsky[1,2], yarawsar@mail.uc.edu, Stefanie L. Johns[1], sjohns@camargopharma.com, Andrew B. Herr[2,3], Andrew.herr@cchmc.org, [1]University of Cincinnati, Dept. of Molecular Genetics, Biochemistry and Microbiology, Cincinnati OH 45267-0524, [2]Cincinnati Children's Hospital Medical Center, Division of Immunobiology and Center for Systems Immunology and [3]Cincinnati Children's Hospital Medical Center, Division of Infectious Diseases.

The skin-colonizing, commensal bacterium *Staphylococcus epidermidis* has emerged as a leading cause of hospital-acquired and device-related infections. The primary determinant for *S. epidermidis* pathogenesis is its ability to form biofilms, which are multi-layered, surface-adherent bacterial accumulations that show remarkable resistance to chemical and physical stresses. Accumulation-associated protein (Aap) from *S. epidermidis* and its *S. aureus* ortholog SasG have been shown to be essential for biofilm formation. These proteins have a repetitive domain architecture, containing up to 17 tandem B-repeats; the presence of at least 5 tandem repeats in SasG has been shown to be critical for *S. aureus* biofilm formation. Aap B-repeat constructs containing 1-2 B-repeats self-assemble in the presence of zinc to reversibly form anti-parallel dimers. Modeling suggests that the B-repeat region from Aap at the cell surface will form twisted,

rope-like filaments between staphylococcal cells in the biofilm upon exposure to zinc. The present work used a combination of biophysical techniques, fluorescence assays, and electron microscopy to demonstrate longer Aap B-repeat constructs with 3 to 5 intact repeats form functional amyloid fibers in the presence of zinc. Importantly, the presence of Aap-containing amyloid fibers within *S. epidermidis* biofilms was confirmed, and amyloidogenesis was found to occur within the first few hours of biofilm formation. Amyloid fibers are extremely stable, a feature which is likely to confer additional strength and resistance to *S. epidermidis* biofilms. This work provides new insights into *S. epidermidis* biofilm formation and architecture that will potentially lead to new therapeutic treatments for persistent staphylococcal infections.

10:45 - INFLUENCE OF A RAT MODEL OF POST-TRAUMATIC STRESS ON THE GUT-ASSOCIATED BACTERIAL MICROBIOME. Ian F. Smith, i-smith@onu.edu, Phillip R. Zoladz, Katherine Krynak, Ohio Northern University, 305 Imperial Drive, East Liverpool OH 43920.

Recent research has established a relationship between physiological responses to stress and the gut-associated microbiome. Research has also shown that changes in the makeup of the gut-microbiome may lead to anxiety-like symptomatology. However, work concerning how specific anxiety-related illnesses may influence the microbiome is limited. The purpose of the present study is to observe changes in the gut-associated microbiome of Sprague-Dawley rats with induced post-traumatic stress disorder (PTSD)-like symptomatology. The hypothesis is that exposure to stress will lead to a significant change in the composition of the gut-associated bacterial microbiome. Male rats will be exposed to a well-verified 31-day PTSD paradigm consisting of 2 exposures to a cat (each exposure separated by 10 days) and daily social instability, which begins on the day of the first cat exposure. Ten rats will undergo the stress model, and 10 rats will serve as controls. All rats will undergo behavioral testing to assess anxiety-like behavior. Fecal samples will be collected weekly from both stressed and control rats. DNA will be extracted from these fecal samples, polymerase chain reaction (PCR) will be used to amplify the 16S rRNA gene region of bacterial DNA, and terminal fragment length polymorphism (TRFLP) analysis will be used to assess differences in gut-associated bacterial composition across treatments. It is predicted that behavior and the gut-associated bacterial community will be similar across treatments before the PTSD paradigm and will significantly differ following exposure to the stress paradigm.

11:00 - EMOTIONAL AND PHYSIOLOGICAL EFFECTS OF VIRTUAL ENVIRONMENTS. Dennis J. Mohn, d-mohn@onu.edu, Ross M. Kauffman, r-kauffman.2@onu.edu, Ohio Northern University, P.O. Box 1944, 402 W. College Avenue, Ada OH 45810.

Virtual reality (VR), a new and relatively unexplored communication medium, fully immerses users in virtual environments. Analgesic and therapeutic VR applications have shown promise, though work remains to understand physiological mechanisms by which such interventions act. This study tested the hypotheses that (1) VR can elicit emotion, (2) these emotions yield a measurable physiological response, (3) stronger emotions will yield stronger physiological responses, and (4) stronger emotions will make experiences more immersive. Participants ($n=17$) were exposed to 3 virtual environments (in randomized order) designed to elicit fear, awe, and calm, while galvanic skin response (GSR) and heart rate (HR) were monitored. Upon completion of each experience, participants reported their emotional response and sense of presence (sensation of being within the environment). Physiological responses to awe and fear conditions were compared to the calm condition at baseline (T_0) and 4 additional timepoints (T_1 to T_4) during the experience using paired sample t-tests, with a Bonferroni adjustment for multiple comparisons ($\alpha=0.01$). Reported emotions confirmed that each virtual environment most strongly elicited its target emotion. GSR was significantly elevated in the awe condition at T_3 ($p=0.009$) and T_4 ($p=0.009$), and in the fear condition at T_2 ($p=0.001$), T_3 ($p=0.001$), and T_4 ($p<0.0001$). No significant differences in average heart rate were observed. Participants reported higher feelings of presence in the awe and fear conditions compared with the calm condition. These findings support the idea that VR is an effective medium for eliciting strong emotions, and that these emotions, regardless of valence, can increase users' sense of presence.

11:15 - IN VIVO EVIDENCE FOR THE ROLE OF *CG15436* DURING ENDOREPLICATION WITHIN OVARY FOLLICLE CELLS AND SALIVARY GLANDS. Katelyn Karalic, kkaralic15@students.ndc.edu, M. Logan Johnson, mjohnson@ndc.edu, Notre Dame College, South Euclid OH 44121.

Endoreplication is a process where a cell undergoes multiple rounds of replication without cellular or nuclear division. Within *Drosophila* there are 2 classical tissues that undergo endoreplication, the follicle cells of the ovaries, and the salivary glands. One protein previously demonstrated to play a critical role in endocycle replication in follicle cells and salivary glands is SuUR (Suppressor of Under-Replicated). Furthermore, studies have identified similar chromatin localization and protein interactions between SuUR and CG15436. The current study examines *CG15436* in vivo to determine if a phenotypic link can be established between CG15436 and SuUR. Further analysis, both of a null allele and an insertion allele of *CG15436*, demonstrate a reduction of egg production that is exaggerated at a less permissive temperature. Additionally, eggs from *CG15436* mutants, that reach maturity, exhibit slightly smaller appendages on the egg, a phenotype that has been previously demonstrated with *SuUR* mutants. Moreover, analysis of CG15436 expression revealed that the gene is expressed within salivary glands. As a part of this analysis CG15436 was also knocked down using RNAi, which resulted in smaller salivary glands with reduced nuclei. Taken together, this data suggests that the previous molecular associations between SuUR and CG15436 have in vivo relevance during endoreplication within ovary follicle cells, and the salivary glands. This newly assigned role of *CG15436* better defines which molecular members participate in endocycling within the follicle cells, and salivary glands; therefore, elucidating the mechanisms which control differential DNA amplification, not only in *Drosophila*, but other species that undergo endoreplication.

11:30 - THE HUMAN HOMOLOGUE JAZF-1/CG12054 INTERACTS DIRECTLY WITH PROTEINS IN THE TIP60 AND SAGA COMPLEXES. Starr Minor, sminor13@students.ndc.edu, Alisha Noon, anoon16@students.ndc.edu, M. Logan Johnson, mjohnson@ndc.edu, Notre Dame College, South Euclid OH 44121.

Jazf-1 has been shown to be associated with cancer formations in humans. While this association occurs in a fusion gene, the basic molecular function of Jazf-1 has yet to be characterized. Jazf-1 has been isolated in several high-throughput studies across different species with proteins associated with the TIP60 and SAGA complexes. The TIP60 and SAGA complexes are known to regulate gene expression with acetylation modifications of histones. Therefore, this study sets out to determine if Jazf-1/CG12054 is part of the TIP60 and/or SAGA complex using the *Drosophila melanogaster* model system. A yeast two hybrid system was utilized to determine direct protein-protein associations with a panel of selected genes. The results were that 2 proteins, MrgBP, and

Atxn7 directly interacted with Jazf-1. For the first time this demonstrates a direct protein interaction to other proteins in the TIP60 and SAGA complexes. Genetic interactions investigating whether Jazf-1 plays a role in the regulation of Notch, a known target of the TIP60 and SAGA complexes, have been conducted. Although the results are preliminary, this suggest that Jazf-1 may help in Notch regulation. Taken together this study confirms that Jazf-1 is involved in gene regulation, most likely through the TIP60 and SAGA complexes. Additionally, given that members of the TIP60 and SAGA complexes, and Notch have all been associated with different forms of cancer, this study serves to further understand how mutations in Jazf-1 may play a role in the development of cancer.

11:45 - EFFECT OF NANO-DYSFERLIN ON MEMBRANE REPAIR IN A/J MOUSE MUSCLE. Bhageerathi Ganesan, bhageerathi.ganesan@osumc.edu, Thomas Kwiatkowski, Thomas.Bodnar@osumc.edu, Sayak Bhattacharya, sayak.bhattacharya@osumc.edu, Eric X Beck, eric.beck@osumc.edu, Roger B. Sutton, Roger.B.Sutton@ttuhsc.edu, Matthew Hirsch, mhirsch@email.unc.edu, Noah Weisleder, noah.weisleder@osumc.edu, The Ohio State University, Department of Physiology and Cell Biology, Dorothy M. Davis Heart and Lung Research Institute, 473 W. 12th Ave, Columbus OH 43210.

Dysferlin (DYSF) is a gene whose protein product is highly expressed in skeletal muscle and is well-known to play a critical role in the regulation of plasma membrane repair by concentrating at transverse tubules in adult skeletal muscle cells. Mutations in the dysferlin gene can lead to the pathologies associated with several different types of myopathies, particularly limb-girdle muscular dystrophy type 2B. As there is currently no treatment for dysferlin deficiency, there is interest in using gene therapy to replace mutant DYSF; this is complicated, however, by the large size of the gene. The efficacy of nano-dysferlins (engineered shortened dysferlin cDNAs) in replacing full-length DYSF and rescuing plasma membrane repair was tested. This was tested by electroporating four nano-dysferlins or normal DYSF (as a positive control) into the muscles of A/J mice that do not normally express DYSF. Membrane repair capacity was assessed by dye influx analysis following laser injury induction. Additionally, co-immunoprecipitation following overexpression in HEK cell lines was used to evaluate the extent of the interaction between nanodysferlin with another membrane repair protein MG53/TRIM72. Multiple nano-dysferlins rescue membrane repair to levels comparable to that seen in wild type cells, however the efficacy of particular nano-dysferlins vary across different constructs are reported. Additionally, all tested nano-dysferlins associate with MG53/TRIM72, suggesting that the interaction of DYSF with MG53/TRIM72 is critical to maintaining membrane repair capacity.

12:00 - POTENTIAL LEAD AND CADMIUM EXPOSURE IN DECORATED GLASSWARE. Chelsea R. Myers, cmyers14@ashland.edu, Kaitlin M. Snider, ksnider2@ashland.edu, Ashland University, Dept. of Chemistry, Ashland OH 44805.

Ingestion of, or skin contact with, heavy metals—particularly lead and cadmium—can cause detrimental health effects. Lead causes damage to the developing brain at extremely low concentrations. No safe level of exposure has been identified. Toxic effects of cadmium exposure include bone and kidney damage. The objective of this study was to assess potential metal exposures from decorated glassware. Lead and cadmium are commonly used in pigments for glassware decorations. Decorations on 50 glassware items were screened for heavy metals using a portable x-ray fluorescence spectrometer. Of 178 analyses performed on 13 different colors on the glassware, lead ranged from no-detect to 290,000 ppm (median 68,000 ppm); 154 analyses were greater than no-detect. Cadmium ranged from no-detect to 26,000 ppm (median 1,800 ppm); 152 analyses were greater than no detect. Wipe tests were digested, then analyzed by inductively coupled plasma spectrometry (ICP) for 107 glassware items to estimate how much lead and cadmium could be picked up through handling. Forty-one items yielded more than 10 micrograms of lead, and 15 items released more than 50 micrograms. Twelve glassware items yielded more than 5 micrograms of cadmium. Glassware decorated in the lip contact area (less than 20 millimeters from the rim) were extracted by placing the glass upside down in 4% acetic acid. Three of 10 samples tested by ICP released concentrations of lead that exceeded 10 milligrams per liter. These results show that decorated glassware is a potentially significant source of heavy metal exposure which should be thoroughly evaluated.

10:15 - 11:30 AM
Podium Session 2
Materials, Modeling, and Imaging
Meeting Room – WD 409 East

10:15 - VALIDATION OF A NEW TEST METHOD CREATED TO EVALUATE NOVEL INSULATING MATERIALS FOR HYPERSONIC AEROSPACE APPLICATIONS. Evan Kolodey[1], evan.kolodey@gmail.com, Miranda Ghrist[1], mghrist@lorainccc.edu, Eleana Cintron[1,2], ecintron2119@gmail.com, Paul Warkentien[1,2], pwarkentien@lorainccc.edu, Steve Miller[3], smiller@sdmatech.com, Regan Silvestri[1], rsilvestri@lorainccc.edu, [1]Lorain County Community College, Department of Chemistry, Elyria OH 44035, [2]NASA Glenn Research Center, Cleveland OH, and [3]S. D. Miller and Associates, Flagstaff AZ.

A novel insulating material has been developed which is anticipated for use in hypersonic aerospace applications. The flexible fibrous alumina is novel in that it has an exceptionally high-porosity, which results in high-temperature insulating properties suitable for hypersonic applications. As this insulating material is unprecedented in its thermal properties, it was necessary to develop a new test method for characterization of the material. The newly developed test method, coined THERMIC for THERMal Insulation Characterization, is an adaptation of the ISO 9151 standard and comprises measuring the temperature gradient through layers of insulating material as heat is applied to one side. Subsequent solution of a 1-dimensional heat transfer model allows calculation of both the thermal conductivity and specific heat of the insulating material. Presented herein are repeatability and reproducibility data for the newly developed THERMIC test, which has been collected for a standard sample of APA-2 paper insulation with known thermal properties as a means of validating this new test method. Repeatability and reproducibility of the raw temperature data, between operators and between labs, is less than or equal to 4% to 2% depending on the location measured and magnitude of the temperature. Validation of this new test method substantiates application of the test for comparison of thermal properties of future prototype insulations.

10:30 - NUMERICAL SOLUTIONS OF HEAT TRANSFER MODELS TO DETERMINE THERMAL PROPERTIES OF NOVEL INSULATING MATERIALS FOR HYPERSONIC AEROSPACE APPLICATIONS. Miranda Ghrist[1], mghrist@lorainccc.edu, Evan Kolodey[1], evan.kolodey@gmail.com, Eleana Cintron[1,2], ecintron2119@gmail.com, Paul Warkentien[1,2], pwarkentien@lorainccc.edu, Steve Miller[3], smiller@sdmatech.com, Regan Silvestri[1], rsilvestri@lorainccc.edu, [1]Lorain County Community College, Department of

Chemistry, Elyria OH 44035, [2]NASA Glenn Research Center, Cleveland OH, and [3]S. D. Miller and Associates, Flagstaff AZ.

An alumina based insulating material, developed for use in aerospace applications, has been evaluated using a test method that effectively mimics the thermal loads experienced during hypersonic flight applications. Coined THERMIC for THERMal Insulation Characterization, the test method comprises of measuring the temperature gradient through layers of insulation as heat is applied to one side (in room temperature conditions) until a maximum temperature load of 250 °C to 300 °C is reached. In combination with a 1-dimensional heat transfer model of the test method, this yields calculated values for thermal conductivity and specific heat of a known standard insulation with an accuracy of 80%, demonstrating the validity of this new test method. Presented herein are numerical solutions to the 1-dimensional heat transfer model of the developed test method when applied in Python™.

10:45 - TESTING OF A FOOD COMPUTER CONCEPT CONSTRUCTED USING RECYCLED APPLIANCES. Aaron Washington, aaronwashington1999@gmail.com, Marcus Nagle, mnagle@centralstate.edu, Cadance Lowell, clowell@centralstate.edu, Central State University, Wilberforce OH 45384.

The EPA estimates that around 9 million refrigerators/freezers are disposed of in the United States annually. This research presents an innovative approach to food production via fusion of the MIT food computer and the NYU food refrigerator. A functioning prototype of a controlled-environment farm (CEF) within a repurposed refrigerator was constructed using a hydroponic tray system under LED lights. A Raspberry Pi® computing unit and an Arduino® microcontroller were outfitted for automation and regulation of the system, engaging machine learning through artificial neural network programming and MIT software. Tests were run to train and validate the constructed CEF system regarding regulation of air temperature and CO_2 concentration as well as dissolved oxygen and nutrient content of the hydroponic solution. Fine tuning of the system was able to realize self-regulation with variations of <5%. The system was interfaced with the OpenPhenome Project to provide feedback data for phenotypic responses of plants, which can be used to encourage certain traits. The CEF design created in this project represents a home gardening system that can be made and used by almost anyone. The results can help to solve the problem of food security, especially within urban areas commonly defined as food deserts. This is true since this system is made from readily-available, affordable, and even recycled materials. People can easily source supplies and construct their own CEFs. This system indicates potential to increase self-sufficiency in food desert communities.

11:00 - DRONE MAPPING OF AGRICULTURAL SUBSURFACE DRAINAGE LINES IN OHIO. Barry J. Allred, allred@ars.usda.gov, USDA/ARS – Soil Drainage Research Unit, 590 Woody Hayes Drive, Room 234, Columbus OH 43210.

To improve the soil water removal efficiency of drained farmland, and thereby increase crop yields, new drain lines are often installed between pre-existing drain lines. To better evaluate the overall environmental risks of nitrate and phosphate release into the environment from farm fields, the intensity of subsurface drainage practices within an agricultural landscape need to be estimated. Consequently, there are both economic and environmental benefits to finding effective and efficient methods for mapping agricultural subsurface drainage systems. Aerial imagery obtained with drones may provide a solution. A fixed-wing drone mounted with visible, multispectral, and thermal infrared cameras was evaluated for drainage-pipe mapping at field sites in Defiance, Fulton, Hancock, Madison, Morrow, Pickaway, Ross, and Seneca Counties, Ohio. Drone thermal infrared imagery detected drainage pipes at most of the sites. Normalized difference vegetation index (NDVI) and normalized difference red edge (NDRE) orthomosaics generated from drone multispectral imagery also proved useful for mapping subsurface drainage systems. Although results are preliminary, drone imagery appears to have substantial potential for use in mapping agricultural drainage. Future research will focus on developing guidelines regarding field conditions (soil type, crop residue, tillage practice, wetness level, etc.) in which drone imagery can be employed to map agricultural subsurface drainage systems.

11:15 - APPROACHES TO INTEGRATE BUILDING INFORMATION MODELLING (BIM) AND LIFE CYCLE ASSESSMENT (LCA). Muhammad M. Mereb, mmereb@cscc.edu, Columbus State Community College, Biological and Physical Sciences Department, Room NH 432, 550 E. Spring St., Columbus OH 43215.

LCA is a tool for systematically analyzing environmental performance of products, processes, or buildings over their entire life cycle. Interest is increasing in incorporating LCA methods into building construction decision making. BMI is defined as a set of interacting policies, processes, and technologies generating a methodology to manage the essential building design and project data in digital format. BIM is a promising tool to implement LCA in the building field; recent interest has focused on integration of BIM and LCA. BIM can aid in different aspects of sustainability including building massing, daylight analysis, water harvesting, energy modeling, sustainable material, and site management. This study examined the literature related to the different approaches used to integrate BIM and LCA that were published between 2008 and 2018. Four approaches have been identified. One approach is to export data from BIM to external LCA software. A second approach is to link the quantities generated by BIM with LCA databases via file exchange. A third approach is to add LCA functionality to existing BIM in a form of extensions or plug-ins. The final approach is to include LCA parameters in the BIM objects. The advantages and limitations of these approaches are discussed. Further studies are required on the integration of BIM and LCA.

10:15 - 11:30 AM
Podium Session 3
Life Science
Meeting Room – WD 409 West

10:15 - CITIZEN SCIENCE AND THE CONSERVATION OF BIOLOGICAL DIVERSITY: TAXONOMIC BIAS AND THREATENED & ENDANGERED SPECIES. Kevin R. Ruegg, kruegg1@kent.edu, Rebecca A. Ohm, rcrabb@kent.edu, (Gregory A. Smith, gsmith62@kent.edu), Kent State University at Stark, Department of Biological Sciences, 6000 Frank Avenue NW, North Canton OH 44720.

Citizen science has rapidly become a common way to increase data collection for scientific research. Within conservation biology, such projects have stated goals of (1) expanding the knowledge base for biological diversity, and (2) connecting users with nature. This research investigates the first item by quantifying data collected within the state of Ohio using the iNaturalist® platform. This application allows the untrained community member to make biological observations and share them

with others in a large database. This study examines 270,000 observations in the state of Ohio between 2012 and September 2018. The data represent over 6,000 species in all 88 of Ohio's counties. Given that these observations were documented by the public rather than disciplined or trained scientists, a level of taxonomic bias was expected to be present in the data. In other words, data collected by the public was not expected to represent the actual biodiversity present in nature. The secondary goal was to measure the conservation value of the project, by identifying the observations in the database representing Ohio's threatened and endangered species. One of iNaturalist's intentions is to create quality data for scientists to use in protecting biodiversity. Assessment of this goal is useful as citizen science becomes an established part of conservation education. It is important to evaluate and understand citizen science projects so that future projects can leverage citizen engagement into the best possible science.

10:30 - POPULATION TRENDS OF GRASSLAND BIRDS IN AN EXOTIC, COOL-SEASON LANDSCAPE ACROSS FIELD SEASONS. Colton Wilson, cwilson@muskingum.edu, Taya Titchenell, tayat@muskingum.edu, Jim Dooley, jdooley@muskingum.edu, Danny Ingold, ingold@muskingum.edu, Muskingum University, Biology Dept., 163 Stormont St., New Concord OH 43762.

Although it has long been known that reclaimed surface mines provide suitable nesting habitat for numerous grassland bird species, several studies during the past decade suggest that woody vegetation encroachment has adverse effects on obligate grassland birds during the breeding season. However, few long-term studies examining population trends of grassland birds on reclaimed mines have been undertaken. To this end, the presence/absence of 4 grassland bird species (Henslow's Sparrows, *Ammodramus henslowii*; Grasshopper Sparrows, *A. savannarum*; Bobolinks, *Dolichonyx oryzivorus*; and Eastern Meadowlarks, *Sturnella magna*) were monitored using 40 point count stations during May, June, and July of 2013, 2014, 2015, 2016, and 2018. Colonization and extinction probabilities between each sampling year for each species were estimated using program PRESENCE. Colonization rates across our study site declined, while extinction probabilities increased for all 4 grassland bird species. These results mirror declines suggested by count data (unadjusted for capture probability) over the same time period. Habitat analyses conducted during the same period provided strong evidence that shrub species including Common Yellowthroats (*Geothlypis trichas*) and Song Sparrows (*Melospiza melodia*) were encroaching across the grassland habitats. Future investigations will be designed to determine whether shrub encroachment is the cause for the declines observed in colonization probability and increases in local extinction probability.

10:45 - THE DIFFERING QUALITY OF 2 WETLAND PLANT COMMUNITIES AND THE POSSIBLE IMPACT ON THREATENED RAILS. Emily R. Nicholls[1], enicholl@ashland.edu, Patricia Saunders, psaunder@ashland.edu, Merrill Tawse, mtawse@ashland.edu, (Dolly Crawford, dcrawfo9@ashland.edu), [1]6678 Beckholt Road, Mount Vernon OH 43050.

This study focused on observing differences in the quality of the plant communities of 2 marshes for the purpose of monitoring potential changes due to invasive reed canary grass (*Phalaris arundinacea*). Threatened *Rallus limicola* and *Porzana carolina* rails have been repeatedly observed at a native plant marsh but only for one short period at a *P. arundinacea*-dominated marsh. It is speculated that this is due to differences in the plant communities present. Quality was assessed at each marsh using the Floristic Quality Assessment Index (FQAI). Transects were established at both marshes and divided into 5 sections spanning from the tree line to the open water and sub-sampled by section for species abundance. Biomass data were collected for *Sparganium androcladum*, *Carex camosa*, *Typhus angustifolia*, and *P. arundinacea*. Aerial photographs were also collected so that GIS techniques could supplement manual sampling in identifying community structures. It was expected that the *P. arundinacea* marsh would have less diversity due to its monotypic tendencies and be lower quality than the native vegetation marsh. Both transects fluctuated in the amount and types of vegetation present across the marshes but the *P. arundinacea* marsh had less species richness. *Phalaris arundinacea* accounted for over 90% of the plants sampled in most sections at its marsh while *S. androcladum* at the native marsh was typically only between 20 to 70%. These differences may highlight how invasive plants change wetlands and the ability for native species to thrive.

11:00 - FORCE GENERATION AND ENCAPSULATION OF FLUOROPHORES IN SWELLABLE ORGANICALLY MODIFIED SILICA. Ryan A. Reffner[1,2], ryanreffner@hotmail.com, Paul A. Bonvallet[2], pbonvallet@wooster.edu, Regan L. Silvestri[1], rsilvestri@lorainccc.edu, [1]Lorain County Community College, Department of Chemistry, Elyria OH 44035, [2]The College of Wooster, Departments of Physics and Chemistry, Wooster OH 44691.

Swellable organically modified silica (SOMS) is a solid, sol-gel material, that absorbs organic solvent and expands while retaining its rigid structure. When SOMS becomes swollen with organic solvent, mechanical energy stored in its polymer matrix is released causing a measurable force. Expansion force was measured for various sample masses between 10 mg and 600 mg, in addition to the measurement of discrete grain sizes of SOMS. A mathematically predictable relationship between the mass of SOMS and the force exerted upon swelling was derived in the form $F = F_0/(1+(m_0/m))$ where F is force generated, m is SOMS mass, and F_0 and m_0 are constants related to force and SOMS mass respectively. Optical microscopy was used to examine the encapsulation of organic solvent and fluorescent compounds inside SOMS. Upon swelling, distinct color changes were observed when the organic solvent leaves the interior of SOMS before returning to its original state. When fluorophores were encapsulated inside SOMS, visual changes in the emission color were also observed during various stages of the swelling-drying cycle.

11:15 - ASSESSMENT OF THE CORAL MICROBIOME AND THE UNDERLYING CORAL PHYSIOLOGY ACROSS A NATURAL RANGE OF TEMPERATURE AND pCO_2 ENVIRONMENTS IN HAWAII. James T. Price[1], price.1118@osu.edu, Rowan H. McLachlan[1], mclachlan.8@osu.edu, Christopher P. Jury[2], jurycp@hawaii.edu, Robert J. Toonen[2], toonen@hawaii.edu, Michael J. Wilkins[3], mike.wilkins@colostate.edu, (Andréa G. Grottoli[1], grottoli.1@osu.edu), [1]The Ohio State University, School of Earth Sciences, Columbus OH 43210, [2]Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Kāne'ohe HI, and [3]Colorado State University, Soil and Crop Sciences, Fort Collins CO.

Increasing sea surface temperatures and ocean acidification are threatening the long-term survival of corals and the persistence of coral reef ecosystems. The coral microbiome has been identified as a potential factor in the resilience of corals to these changing environmental conditions. Improving our understanding of the relationships between the coral host and their microbial associates under changing ocean conditions could produce innovative approaches to coral reef restoration. Coral reefs surrounding Oahu, Hawai'i, USA, exist among a natural gradient of environmental conditions, with some sites experiencing summertime temperature and pCO_2

levels not expected to occur in most tropical waters until mid-century. It has been suggested that local variability in seawater temperatures and pCO_2 may drive coral-associated bacterial community composition, and that those differences are likely species-specific. To test this, the bacterial communities of 5 coral species were characterized from 6 sites around Oahu. Preliminary results suggest that the bacterial community composition differs between *Porites* and *Pocillopora* corals, primarily due to higher relative abundances of *Endozoicomonas* sp. in the *Porites* corals. However, the structure of these communities was unrelated to several parameters of coral physiology. Additional analyses are underway to determine if differences in the temperature and pCO_2 properties among sites further influences the bacterial community composition. Overall, characterizing the coral microbiome across a range of environmental conditions can help restoration and protection efforts to target corals better adapted for predicted future ocean conditions.

College Student and Professional Poster Sessions 9:00 – 10:00 AM and 1:30 – 3:00 PM WD 4th Floor Gallery, 404, and 407

Note: All posters will be displayed in both morning and afternoon sessions.

Poster Board No. 01 - THE EFFECTS OF O I CONTAMINATION ON *SUZAKU* DATA. Cassady Croy, ccroy@student.cscc.edu, (Anjali Gupta, agupta1@cscc.edu, Smita Mathur, The Ohio State University), Columbus State Community College, 550 E. Spring St., Columbus OH 43215.

Suzaku observations are commonly used to examine the characteristics of the circumgalactic medium (CGM) of the Milky Way and the nuclear components of Fermi Bubbles. However, the sun omitted solar X-rays that interacted with the oxygen in Earth's atmosphere and generated a fluorescent omission line (O I) that may have contaminated any *Suzaku* data that was taken after 2011. To accurately determine the structure of the CGM and the components of the Fermi Bubbles, data from *Suzaku* will be analyzed with the contamination taken into account. If the O I contamination is not analyzed, the O VII line could be overestimated, which could affect results significantly. The problem of this contamination can be mitigated through spectral modeling. The X-ray diffuse emission will be monitored through this process to be able to identify various components. The ultimate goal is to analyze the contaminated data in order to give an overview of the Milky Way CGM in its entirety.

Poster Board No. 02 - MISSING BARYONS AND THE WARM-HOT CIRCUMGALACTIC MEDIUM OF LATE TYPE GALAXY NGC3221. Cody P. Null, null.cody1@gmail.com, (Anjali Gupta), The Ohio State University, Dept. of Astronomy, Columbus OH 43210.

Late-type galaxies are missing a large fraction of their baryonic mass, some of which is expected to be in the hot gaseous halo. However, searches of such a circumgalactic medium (CGM) have given mixed results throughout. Theoretical models suggest that CGM properties depend on galaxy properties such as gravitational mass, stellar mass, and specific star formation rate (sSFR). Observations so far have focused on galaxies with high mass and low sSFR. NGC3221 has smaller stellar mass and higher sSFRs, probing an unexplored range of parameter space. Suzaku and Chandra observations look deeper into the CGM of NGC3221 in emission. Results on the detection and characterization of the warm-hot CGM in NGC3221 are reported.

Poster Board No. 03 - A DEGLACIAL POLLEN RECORD FROM THE SEDIMENTS OF SILVER LAKE, SUMMIT COUNTY, OHIO. Sierra E. Swisher, ses167@zips.uakron.edu, (John A. Peck, jpeck@uakron.edu), University of Akron, Department of Geosciences, Akron OH 44325.

Lake sediment pollen records can provide a better understanding of past vegetation changes. Silver Lake in Summit County, northeastern Ohio, was formed as a kettle lake following deglaciation of the Laurentide Ice Sheet. The complete lake sediment record was recovered in a 13.5-meter core in May 2015. A 1-meter-long core segment, spanning the deepest horizon where organic

matter increased, was selected for this pollen study. Pollen was isolated from 28-subsamples using standard chemical acetolysis extraction methods. The pollen was then identified and counted under a light microscope at 400× magnification. The deepest samples (1,109 to 1,069 cm) contain predominately *Picea* indicating moist soils and cold conditions. Above this, *Pinus* predominates (1,069 to 1,008 cm), indicating a change to drier soils and cool conditions. The change from *Picea* to *Pinus* shows climate change varied with an increase in temperature and a decrease in precipitation. These late Pleistocene conditions are vastly different from the northeastern Ohio forests that were present prior to modern land clearance. These more recent forests were dominated by *Fagus*, *Acer*, *Quercus*, and other deciduous trees that favor moist soils and warm conditions.

Poster Board No. 04 - THE SUGAR TEST: ANALYSIS OF THE RELATIONSHIP BETWEEN NUTRITIONAL GRAPHICS AND SUGAR CONTENT JUDGMENTS. Kathryn E. Kemp, kk308414@ohio.edu, Randall Harbour, rh341414@ohio.edu, (Claudia Gonzalez-Vallejo, gonzalez@ohio.edu), Ohio University, Dept. of Psychology, 1 Ohio University Drive, Athens OH 45701.

Added sugars are a component in a great majority of all food and drink products available to consumers. In the United States, sugar is one of the leading causes of major, non-communicable health issues including tooth decay, heart disease, diabetes, and obesity. In fact, the obesity epidemic within the United States is well documented—showing obesity rates as high as 25% in 41 states and above 20% in all states. *The Sugar Test: Understanding the Relationship between Nutritional Graphics and Sugar Consumption* investigates the relationship between labeling techniques of sugar amounts and the accuracy of judgements about sugar content in various bottled drink products—including milk, smoothies, and juice. The study also examines consumption intentions as a function of the product label. The primary investigative question in this research is: will informational graphics concerning sugar content reduce estimation errors with regards to amount of sugar/proportion of sugar in drinks? Three iconographic conditions were tested in a between-subjects design (2 new enhanced labels and a control label containing the current nutritional information of the drink). Participants were university students (n = 105) who completed an online survey indicating estimates of sugar content using different measurements. They also provided their intentions to consume the products, and a choice of a real sugary or non-sugary drink to take with them at the end of the study. Results at the group level suggest greater judgment accuracy when judging sugar content in the presence of well-designed infographics relative to the control condition. Individual level analyses are currently being conducted to more clearly understand the pattern of accuracy at the level of each individual. The significance of this research is to advance a simple decision aid that can help consumers judge the amount of sugar in food products. The labels tested are small enough that they could be added to current product labels and promote healthier eating habits.

Poster Board No. 05 - CAN ACCOUSTIC CHARACTERISTICS OF VOICE PREDICT HELPING SKILLS. Glynnis A. Hixson[1,3], gh402216@ohio.edu, Ashleigh M. Johnson[1], aj516215@ohio.edu, Timothy Anderson[1], andersot@ohio.edu, Chao-Yang Lee[1,2], leec1@ohio.edu, Clara E. Hill[2], cehill@umd.edu, [1]Ohio University, Department of Psychology, Athens OH 45701, [1,2]Department of Communication Sciences and Disorders and [2]University of Maryland, Department of Psychology, College Park MD 20742, [3]745 Mary Street, Belpre OH 45714.

The role of voice in psychotherapy rarely has been studied. The Facilitative Interpersonal Skills (FIS) experimental procedure was developed for collecting a prospective helper's (e.g., therapist, counselor, mental health technician) verbal responses to standardized client video presentations. Because FIS was designed to create challenging, critical psychotherapy incidents, it was predicted that physical characteristics of voice such as pitch, loudness, or quality would provide objective, non-observer measures that would be correlated with independent measures of helping skills. The on-going study includes 33 females in helping skills training. FIS responses were collected at the beginning of training using the clinical experimental procedure of recording helper vocal responses to the client stimulus video clips. Three general types of helping skills were rated (included exploratory, insight, and active forms) during practice interactions. Other self-report measures of helping skills, FIS ratings (i.e., ratings of facilitative therapist skills such as empathy, alliance building capacity, warmth, and building hope), and other helper measures were also collected. Acoustic analyses of the helpers' voice recordings were conducted using the Praat software on several acoustic measures that have been previously associated with emotional responsivity, including mean fundamental frequency (F0, indicating voice pitch), F0 standard deviation (StdF0, indicating voice pitch variation), and spectral slope (SS, indicating voice breathiness/loudness). Correlational trends of SS, F0, and StdF0 with Exploratory Helping Skills and FIS were in the predicted negative direction but mixed in terms of statistical significance. Notable is the preliminary result that SS and exploratory skills used in the practice session were negatively correlated with F0 and StdF0, whereas active skills uses were positively correlated. Vocal characteristics associated with more exploratory helping skills were associated with a more breathy and lower-pitched voice quality, whereas more active-oriented helping skills were associated with a less breathy and higher-pitched voice quality.

Poster Board No. 06 - AN ANALYSIS OF VARYING METHODS OF FUNGICIDE APPLICATION ON THE YIELD AND PROFITABILITY OF CORN. Abigail R. Hissong, ahissong21@gmail.com, Wilmington College, 4146 Nashville Road, Troy OH 45373.

The economic merits of fungicide application are often debated. An experiment was conducted to determine if fungicide application can increase yields, and if it is profitable. The fungicide used for this experiment was Stratego® Yield Pro by Bayer® because it was compatible with the seed variety used which was Channel STX 207-19. Two fields were prepared to test differing methods of applying fungicide. These fields were broken up into 4 sections each: no application (control), ground application with 3 oz/ac of Stratego, aerial application with 4 oz/ac of Stratego, and both ground and aerial application with a combined 7 oz/ac of Stratego. The total acreage was 95.66 acres. A stand count and leaf samples were collected to assess fungus damage compared between plots. Northern Leaf Blight and Gray Leaf Spot were looked for, as they cause the most damage to corn in the Ohio region. The results showed that on the no application section, the average yield was 220.95 bushels per acre, ground application was 232.89 bushels per acre, aerial application was 227.04 bushels per acre, and for both aerial and ground it was 247.56 bushels per acre. These results suggest that aerial and ground application combined to produce the highest yields, while no application produced the lowest yields. The economic advantage using standard grain prices for corn and standard rates for fungicide prices were computed. The aerial and ground application had an average profit of $829.49 per acre compared to no application at a profit of $773.31 per acre, ground application at $801.26 per acre, and aerial application at $771.53 per acre. These results can be used to help farmers make educated decisions pertaining to fungicide. By knowing that aerial and ground application combine to form higher yields and greater profits, farmers can generate profits for their business while still raising larger amounts of corn.

Poster Board No. 07 - THE UTILIZATION OF CITIZEN SCIENCE AS A MEANS TO MONITOR INVASIVE SPECIES POPULATIONS IN OHIO. Rebecca A. Ohm, rcrabb@kent.edu, Kevin Ruegg, kruegg1@kent.edu, (Gregory Smith, gsmith62@kent.edu), Kent State University at Stark, Department of Biological Sciences, 6000 Frank Avenue NW, North Canton OH 44720.

Invasive species are one of the most globally pervasive threats to the conservation of biological diversity. As citizen science has expanded its utility by engaging more non-scientists, the potential exists for a popular citizen science platform (iNaturalist®) to aid in invasive species management. This study quantified the reliability and accuracy of collecting data on invasive species through citizen science programs. It was hypothesized that the use of citizen science data would be an effective means of monitoring invasive species populations within Ohio. Data were collected using the iNaturalist platform within the state from 2012 to 2018. Records for 22 invasive species were examined for location of the species and number of organisms in the population. Of the 22 focal species, 2,310 research-grade observations were recorded. The location and quantity of observations were correlated with human population of the county in which the species were observed. The results thus far show that there is little correlation between the number of species observations and the human population of the county in which the observation took place. Citizen science is an important tool that can be used to locate areas of concern for high levels of invasive species and to help in the persistence of native species that have been negatively affected by the invasive species in those areas.

Poster Board No. 08 - PILOT STUDY: EFFECT OF PULSED AVAILABILITY OF HIGH AND LOW DENSITIES OF PREY ON PIT CONSTRUCTION OF ANTLIONS, *MYRMELEON IMMACULATUS*. Julia R. Langan, jlangan@muskingum.edu, Jamie L. Rafter, jrafter@muskingum.edu, Muskingum University, 163 Stormont St., New Concord OH 43762.

Antlions build pits that capture prey and alter their pit construction in response to prey density. The aim of the project is to determine if there are any differences in pit construction of antlions, *Myrmeleon immaculatus* (n=24), in response to pulsed availability of high (4 fruit flies per week) and low (1 fruit fly per week) densities of prey. Three antlions from each of 4 collection sites were randomly assigned into treatment groups. Individuals were weighed at the beginning and end of the 5-week experimental period. Measurements of pit ratio (diameter/depth) were taken daily. Data on antlion percent weight change were analyzed using a 2-way ANOVA. Data on pit ratios were analyzed using a 3-factor (treatment, location, and time) mixed model with repeated measures design with 'antlion' nested within treatment as a random effect. There were differences in percent weight loss ($F=5.04$, $p=0.004$). All antlions lost weight, with antlions in the low-density treatment losing more weight than those in the high-density treatment ($F=6.26$, $p=0.024$). Location also had an effect on percent weight change ($F=6.02$, $p=0.006$) and there was an interaction between these 2 factors ($F=3.65$, $p=0.035$). With respect to pit diameter, there were no differences between or within treatment groups. All individuals lost weight suggesting not enough food was provided. Thus, pit ratios are similar among all individuals. Differences due to location suggest there may be genetic/physiological differences between individuals from each site and/or differences in environmental factors. These hypotheses require further investigation.

Poster Board No. 09 - HABITAT ASSOCIATIONS OF GRASSLAND BIRDS IN AN EXOTIC, COOL-SEASON LANDSCAPE. Madison Sikorski, madisons@muskingum.edu, Faith Swartz, fswartz@muskingum.edu, Danny Ingold, ingold@muskingum.edu, Jim Dooley, jdooley@muskingum.edu, Muskingum University, Biology Dept., 163 Stormont St., New Concord OH 43762.

The ecological succession of reclaimed surface mines from cool-season grasses to autumn olive (*Elaeagnus umbellata*) dominated landscapes likely has a negative influence on the abundance of obligate grassland bird species. Point-count surveys of obligate grassland bird species on exotic, cool-season habitat patches were conducted during May and June of the 2018 breeding season. In addition, several habitat measures were obtained at the sites of actual bird observations, as well as randomly chosen sites, in order to determine whether birds demonstrated habitat preferences that differed from random sites. A discriminate function analysis (DFA) was used to look for potential differences in the habitat birds were observed in versus random sites. DFA revealed that each of the 4 focal species (Henslow's Sparrows, *Ammodramus henslowii*; Grasshopper Sparrows, *A. savannarum*; Bobolinks, *Dolichonyx oryzivorus*; and Eastern Meadowlarks, *Sturnella magna*) were observed in habitats that differed significantly ($P<0.01$) from random locations. Contrary to what was predicted however, all 4 species were observed in areas with a higher percentage of shrubs compared to random locations. In addition, all 4 species were observed in areas with a shorter mean plant height and a lower percentage of bare ground versus random locations. These findings suggest that the focal species tolerated a certain level of woody shrub encroachment. In a broader sense these species were observed in habitat types that likely reflected their preference to a larger habitat mosaic rather than to any single habitat variable.

Poster Board No. 10 - CHANGING HABITAT PREFERENCES OF SOUTHEASTERN BUTTERFLIES. Ashley N. Ramsey, adowler@muskingum.edu, (James L. Dooley Jr., jdooley@muskingum.edu), Muskingum University, 163 Stormont St., New Concord OH 43762.

Conversion of landscapes has occurred for centuries. These conversions can take many forms and result in a wide array of impacts on the land. The Appalachian region is amongst the numerous regions that have suffered from conversions. Specifically, the Appalachian region has drastically been altered from its original state due to the process of surface mining. Surface mining in southeastern Ohio has changed the quality of landscapes, which has altered the ecology of populations that inhabit them. Butterflies are amongst the populations suffering from surface mining in this region. This is occurring because butterflies are niche specialists that utilize particular host plants and nectar species. Through surface mining, host plants and nectar species are lost to butterfly populations—which is causing population declines. Therefore, the objective of this experiment was to monitor the abundance of butterflies and their diversity across a landscape with a history of surface mining. This experiment focused on several species which included Black Swallowtail, Monarch, Eastern Tiger Swallowtail, Eastern Tailed Blue, and Meadow Fritillary butterflies. Data were collected from the Wilds property in Cumberland, Ohio, by utilizing line transects. This geographical site allowed for comparison of multiple areas to determine if the abundance and diversity of these species varied from each area observed in this previously surface-mined location. Data were collected from 17 line transects, however, it was not limited to line transect and encompassed observations from the Jeffrey Birding Station and the Wetlands at the Wilds faculty. Through observations, 448 individuals were observed across 16 species.

Poster Board No. 11 - THE COMMON PHEASANT'S (*PHASIANUS COLCHICUS*) GROWTH RATE IN CAPTIVITY. Jordan A. Risner, jrisner@muskingum.edu, (James L. Dooley Jr., jdooley@muskingum.edu), Muskingum University, 199 Stormont St., New Concord OH 43762.

Captive breeding is the process of breeding animals in controlled environments, such as wildlife reserves, zoos, and other facilities. This process can include the release of individuals back into their natural habitat, if their habitat can support such release. Captive breeding is important for the conservation of species because it may save a species from complete extinction, or help to increase populations in the wild. With increasingly more species being raised in captivity, it leads to the question as to whether these animals are being affected from captive breeding. The objective of this research is to examine growth of the common pheasant in captivity and compare the findings to research of wild pheasant growth. Captive pheasant eggs were weighed and then incubated for approximately 24 days. Once hatched, the pheasants were weighed and then banded. Analysis will compare weights of captive pheasants at 3, 8, 12, and 16 weeks to growth rates of other research on wild pheasants, also at 3, 8, 12, and 16 weeks. It is hypothesized that the pheasants born and raised in captivity will be heavier and grow faster than pheasants who were born and raised in the wild. The reasoning is because captive pheasants will have more readily available food compared to wild pheasants.

Poster Board No. 12 - A CHEMICAL AND BIOLOGICAL ASSESSMENT OF ROADSIDE FRESHWATER STREAMS IMPACTED BY ROAD SALT IN NORTH CANTON, OHIO. Ellie Miller[1], emiller0607@starkstate.net, Colin McCauley[1], xmccauly0709@starkstate.net, (Curtis Clevinger[1], cclevinger@starkstate.edu, Jennifer Clevinger[2], jclevinger@walsh.edu), [1]Stark State College, 6200 Frank Avenue NW, North Canton OH 44720, [2]Walsh University, 2020 East Maple Street, North Canton OH 44720.

In many northern climates with snowfall, the application of salts is the only practical solution that will enable safe driving conditions. These salts then enter the local freshwater systems where they could disrupt biogeochemical processes and affect the organisms that live in these systems. During the winter of 2015-2016 an initial assessment of these impacts on streams in North Canton, Ohio, was performed as a service-learning project at Walsh University. The results were presented to the North Canton City Council. Sites (n=6) were sampled upstream and downstream from main road arteries and followed a downstream progression through the watershed. Chemical analysis of macronutrients and commonly measured chemical indicators was performed in addition to macroinvertebrate sampling and biological oxygen demand calculations. Additional studies were performed at these sites in the fall and spring of subsequent years to address a variety of hypotheses utilizing similar methodologies. During the winter of 2015-2016 North Canton used a below-average amount of road salt, and the initial study thus led to mostly baseline data relating to the effect of road salt on freshwater streams. Because of raising chloride levels in local water sources, the effect of road salt is still a local concern. This study will assess the effect of road salt on freshwater streams during the winter of 2018-2019 using similar sites and methodology as the initial study.

Poster Board No. 13 - THE EFFECTS OF CONSTRUCTION ON STREAM ECOLOGY OF HOOVER DITCH, IN THE NIMISHILLEN CREEK (NORTH CANTON, OHIO). Meghan E. Skrypka[1], mskrypka1@walsh.edu, Jennifer A. Clevinger[1], jclevinger@walsh.edu, Curtis C. Clevinger[2], cclevinger@starkstate.edu, [1]Walsh University, Division of Mathematics and Sciences, 2020 E. Maple St., North Canton OH 44720, and [2]Stark State College, Dept. of Biology.

Hoover Ditch is classified as a first order stream, and a tributary of the West Branch of the Nimishillen Creek, in Stark County, Ohio. In 2012, a baseline biogeochemical study of Hoover Ditch was conducted by Walsh University. Since then, the area has undergone extensive nearby road construction and commercial development. It is hypothesized that non-point pollution from nearby road construction has negatively impacted the biogeochemistry of Hoover Ditch. In 2018-2019, Hoover Ditch was resampled for stream macroinvertebrates as a proxy to assess overall stream health. Ohio EPA's rapid bioassessment protocols, or Macroinvertebrate Aggregated Index for Streams (MAIS), were utilized to collect stream macroinvertebrate samples for comparison of number of sensitive species. Qualitative Habitat Evaluation Index (QHEI) scores were recalculated to reflect current riparian health. Additionally, chemical analysis was conducted, measuring nitrate, phosphate, ammonium nitrate, alkalinity, pH, and conductivity of water samples. Preliminary data suggests a decline in overall macroinvertebrate diversity of Hoover Ditch, significant changes in riparian cover, and elevated nutrient inputs near road construction. A single cause of the decline in overall stream health is indeterminate, and likely the result of multiple adverse environmental factors. The data establishes an adjusted baseline for the biogeochemistry of Hoover Ditch, therefore enabling future researchers to better analyze the long-term impacts of urban/suburban development on riparian ecosystems.

Poster Board No. 14 - ASSESSING HOST-SYMBIONT RELATIONSHIPS TO INFORM RESTORATION EFFORTS OF EASTERN OYSTERS (*CRASSOSTREA VIRGINICA*) IN THE GULF OF MEXICO. Alyson K. Milks[1], a-milks.4@onu.edu, Kelli L. Hill, k-hill.5@onu.edu, Bailey M. Logsdon, b-logsdon@onu.edu, Katie Konchar, Katie.Konchar@myfwc.com, Sandra D. Brooke, sbrooke@fsu.edu, Katherine L. Kryna[2], k-krynak@onu.edu, [1]402 W. College Ave, Unit 1962, Ada OH 45810, [2]corresponding author.

Eastern oyster (*Crassostrea virginica*) reefs provide valuable ecosystem services such as water filtration and prevention of coastal erosion. Oyster reefs have dramatically declined in recent years due to deteriorating estuarine environments along the Gulf Coast. Reef restoration is imperative and therefore studies assessing differing methodologies need to be tested to improve restoration success. Adjunct to a study conducted by the Florida Wildlife Commission (FWC) and the Florida State University Coastal and Marine Laboratory (FSUCML) examining oyster density and growth across differing artificial reef substrates, Ohio Northern University students assessed the health of the oysters by means of comparing symbiotic bacterial communities of the oysters across these artificial reef substrates. It was hypothesized that substrate type influences bacterial composition. It was predicted that bacterial community variation is associated with nutrient availability from the artificial reef substrates. Bacterial communities of oysters (n=25) were compared across 5 substrates using terminal restriction fragment length polymorphism (TRFLP) analysis of polymerase chain reaction (PCR) product amplifying the 16s rRNA gene region of bacterial DNA from emulsified oysters. Nonmetric multidimensional scaling ordination and permutation-based analysis of variance indicated no significant effects of restoration substrate on oyster bacterial community composition (PREMANOVA $F_{(4,20)}=1.4$, $P=0.134$). Despite potential importance of symbiotic bacterial communities to oyster health, as well as potential concern in regards to food-borne illnesses as a result of oyster consumption, knowledge of these symbiotic bacterial communities is lacking. The finding that substrate type did not influence bacterial community composition of the oysters was a desired result in that substrate choice need not be a limiting factor to restoration efforts, but substrate considerations can instead be focused on rapid oyster recruitment.

Poster Board No. 15 - ANTIGENOTOXIC EFFECT OF EPIGALLOCATECHIN-3-GALLATE (EGCG) ON BLEOMYCIN IN VITRO INDUCED DNA DAMAGE IN HUMAN LYMPHOCYTES. Paige Hoffman, hoffmanp@findlay.edu, Elizabeth Claus, clause@findlay.edu, Vivian Lee, leev@findlay.edu, Richard Dudley, dudley@findlay.edu, Jordan Ringenberg, ringenberg@findlay.edu, Alexander Vaglenov, vaglenov@findlay.edu, University of Findlay, College of Pharmacy, Findlay OH 45840.

Epigallocatechin-3-gallate (CAS 989-51-5) is the main polyphenol present in green tea (*Camellia sinensis*). It has been reported that EGCG has antibacterial, antiviral, antioxidative, antimutagenic, and anticarcinogenic effects. However, reports on the antigenotoxic effects of EGCG are scarce. The aim of this study was to evaluate the in vitro antigenotoxic (protective) effect of EGCG through cytokinesis-block micronucleus method in human peripheral lymphocytes in presence of the DNA damaging agent bleomycin. To determine the existence of protective effect as a consequence of EGCG treatment, peripheral human lymphocytes from 4 donors were treated with different concentrations of bleomycin as follows: 2, 4, and 8 μg/mL. A comparison has been done with bleomycin plus 5 μg/mL, 10 μg/mL, 20 μg/mL, and 40 μg/mL EGCG. A statistically significant decrease in binucleated cells with micronuclei treated with bleomycin + EGCG, compared to the group treated with bleomycin, was established. The results obtained suggest a statistically significant protective effect, which increased with doses of EGCG ($p < 0.001$). The scale of in vitro protective effect of EGCG in μg/mL measured by binucleated cells with micronuclei is as follows: $5 < 10 < 20 > 40$. The highest dose of EGCG (40 μg/mL) together with all investigated bleomycin doses revealed not only lower protection, but also a toxic effect on lymphocytes.

Poster Board No. 16 - CELL DIFFERENTIATION AND PROLIFERATION DURING DEVELOPMENT OF THE OLFACTORY BULB. Sarah L. Maxson, sarah.maxson@otterbein.edu, David C. Sheridan, dsheridan@otterbein.edu, Otterbein University, Department of Biology & Earth Science, 1 South Grove Street, Westerville OH 43081.

During brain development, cells can proliferate and differentiate into either neuronal or glial cells. Neuronal cells are capable of sending signals, while glial cells function to provide nutrients and structural support. The objective of this study is to determine at what point proliferation and differentiation occur, specifically with respect to the olfactory bulb. The olfactory bulb is unique because olfaction is the only sense that is directly connected and does not need to travel through the thalamus. We hypothesize that a larger volume of the cells will develop into neuronal cells because this part of the brain must be capable of quickly sending a large amount of signals, especially during the first 2-weeks of life when the eyes are closed. In order to complete this project in neuroscience, a new technique called the isotropic fractionator will be utilized to estimate neuronal cell count. Nuclei from the rodent brains day 1 to 28 will be isolated and stained for analysis. A total cell count is achieved through the use of 4′,6-diamidino-2- phenylindole (DAPI), a DNA specific blue fluorescent dye. In order to estimate the number of neuronal cells specifically, nuclei will be incubated with the antibody NeuN, which recognizes a neuron-specific nuclear protein. The addition of a secondary antibody (Cy3) allows the nuclei to be seen at a different wavelength in the red spectrum. Results will be analyzed with a *t*-test and can give insight into olfactory bulb structure and function in comparative studies among species and in studies of phylogenesis and pathology.

Poster Board No. 17 - INFLUENCE OF LIPID BILAYER COMPOSITION ON PLASMA MEMBRANE REPAIR CAPACITY. Diana Hallak, hallak.1@osu.edu, Kevin McElhanon, Kevin.Mcelhanon@osumc.edu, Brian Paleo, paleo.1@buckeyemail.osu.edu, Thomas Kwiatkowski, bodnar.51@buckeyemail.osu.edu, Eric X Beck, Eric.Beck@osumc.edu, Noah Weisleder, Noah.Weisleder@osumc.edu, The Ohio State University, Department of Physiology and Cell Biology, Dorothy M. Davis Heart and Lung Research Institute, Columbus OH 43210.

Lipids are a major constituent of the plasma membrane where they are found in great diversity of structure and proportions. Modifying dietary fat intake has been shown to be an effective method for changing the fatty acids (FA) composition of the plasma membrane. Membrane FA composition influences the fluidity and diffusion process of the membrane. In addition, various protein activities may be influenced by affecting the recruitment of lipid-binding proteins and protein homeostasis. Thus, became the hypothesis that altering the plasma membrane's FA composition will have an effect on the resealing process of the plasma membrane. To test this hypothesis, laser damage assay was used on flexor digitorum brevis (FDB) muscle cells from sedentary dysferlin knockout mice fed diets high in oleic acid or palmitic acid for a period of 5 to 6 weeks. A multiphoton laser was used to injure the muscle cells in presence of a lipophilic dye. The resealing capacity was measured through observing the change in dye fluorescence over time. The laser injury assay was a measure of the repair capacity of the plasma membrane. IgG staining was done using 488 goat anti mouse antibody on histological sections of the extensor digitorum longus (EDL) muscle from the dysferlin knockout mice that were fed the different diets to measure membrane integrity. The results did not show a significant difference in repair capacity or integrity of the membrane in mice that were fed diets high in oleic acid versus those that were fed diets high in palmitic acid. An enhanced membrane resealing process can be a step forward in treating various muscular dystrophies.

Poster Board No. 18 - MULTIPLE POLOXAMERS IMPROVE MEMBRANE REPAIR IN A CELL-TYPE DEPENDENT MANNER. Aubrey L. Rose, rose.1279@buckeyemail.osu.edu, Thomas A. Bodnar, bodnar.51@buckeyemail.osu.edu, Ana Capati, anacapati@yahoo.com, Kevin McElhanon, kevin.mcelhanon@osumc.edu, Brian J. Paleo, paleo.1@buckeyemail.osu.edu, Eric X Beck, eric.beck@osumc.edu, Noah Weisleder, noah.weisleder@osumc.edu, The Ohio State University, Department of Physiology and Cell Biology, Dorothy M. Davis Heart and Lung Research Institute, 473 W. 12th Ave., Columbus OH 43210.

Sarcolemmal membrane fragility is a major contributor to the pathology of various muscular dystrophies. Muscle fibers with fragile membranes are more likely to be damaged and as a result exhibit increased necrosis. One potential therapeutic approach is to increase membrane repair by exposing muscle fibers to poloxamer 188 (P188), a polymer that has an affinity to intercalate between the phospholipids of the cell membrane. P188 is one of many poloxamers, all of which are co-block polymers that contain a hydrophobic region of polyoxypropylene flanked by 2 hydrophilic chains of polyoxyethylene. These chains vary in length between different poloxamers. Although P188 has shown promise in increasing membrane repair, few other poloxamers have been tested for their effects on membrane repair. We hypothesize that other poloxamers in the P188 family will reseal damaged membranes as effectively as P188. To investigate this hypothesis, a novel rotation damage assay was used where cells were damaged through impact with small glass beads (106 μm diameter) while exposed to poloxamers. The lactate dehydrogenase (LDH) released from the cell into the supernatant is measured to determine how effectively the membrane is repaired. An independent multiphoton laser injury assay using entry of a lipophilic dye as a readout was used to confirm these results in HEK cells and ex vivo muscle fibers. Entry of this fluorescent dye was measured over time to determine the membrane repair capacity. Multiple poloxamers reduced dye influx

and LDH release indicating that these poloxamers improved membrane repair capacity in the examined cell types.

Poster Board No. 19 - ESTABLISHMENT AND SCREENING OF 2 STABLY TRANSFECTED EPITHELIAL CELL LINES EXPRESSING HUMAN SOX18 VARIANTS. **Cassandra Barone[1], cbarone1@walsh.edu, Jeremy Prokop[2], prokop54@gmail.com, Dinah Qutob[1], dqutob@walsh.edu, Adam Underwood[1], aunderwood@walsh.edu, [1]Walsh University, 2020 East Maple Street NE, North Canton OH 44720 and [2]Michigan State University Grand Rapids Research Center, Grand Rapids MI.**

The SOX18 gene encodes a transcription factor that is a member of the HMG-box (High Mobility Group box) family of DNA binding proteins. SOX18 plays an important role in both blood and lymphatic vessel development. Our laboratory has identified a unique mutation at amino acid 137 in human SOX18 that changes a glutamic acid (E) to a lysine (K) residue. The objective of this project was to stably transfect HeLa and A375 cells with protein expression constructs carrying native SOX18 or SOX18-E137K using ViaFect™ transfection reagent. Transfected cells were maintained in DMEM medium supplemented with 10% FBS and 450 µg/ml G418 and cells from all lines were separated into 96 well plates. After 2 cell passages, the most robust cells from 24 wells (6 colonies per cell line) were selected and cultured in 100 mm plates. After 30 days, one 100 mm plate derived from each colony from each cell line was collected for expression analysis. Protein was extracted, fractionated onto SDS PAGE gels and immobilized onto PDVF membrane for immunoblotting and probing with an antibody that hybridizes to a C-terminal fusion tag (HaloTag®; Promega Corporation) linked to both the native and mutant form of SOX18. All 24 colony-forming units expressed the desired protein, allowing the conclusion that both HeLa and A375 cells be used for in vivo expression of both native and mutant forms of SOX18.

Poster Board No. 20 - RAT SCL39A9 LUCIFERASE REPORTER IS TRANSCRIPTIONALLY REGULATED BY THE TESTIS DETERMINING FACTOR SRY. **Jill Blacksten, jblackst1@walsh.edu, Dinah Qutob, dqutob@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Walsh University, 2020 East Maple Street NE, North Canton OH 44720.**

The solute carrier family 39a9 (slc39a9) gene encodes the transmembrane transport protein, ZIP-9 (zinc ion transporter isotype 9), which is associated with coordinating zinc ion mediated apoptosis in target cells. In addition to functioning as a zinc ion transporter, ZIP-9 also has been shown to function as a membrane bound androgen receptor (mAR) for testosterone. This protein can stimulate a rapid G protein mediated non-genomic signaling response to testosterone. SRY (sex-determining region of the Y chromosome) is a male specific transcription factor shown to directly modulate expression and intracellular activity of cytoplasmic androgen receptors. The objective of this project was to determine if SRY can bind to and upregulate transcription of a luciferase reporter construct encoding -665 base pairs of the rat slc39a9 promoter sequence (pGL3/rat39a9). This project began by seeding 1.5×10^4 Chinese hamster ovary (CHO) cells into individual chambers of a 96-well cassette. Cells were incubated for 24 hr in a humidified environment at 37°C and 5% CO_2. CHO cells were then transiently cotransfected with the pGL3/rat39a9 reporter, either pEF1/Sry or pEF1/MT (pEF1/Myc-His vector lacking an insert) effector, and control vector pHRL/Null. All runs were completed in triplicate and repeated 4 times and statistical significance was determined using Student's t-test. Analysis was performed in SigmaPlot®13 software (Systat Software Inc.) with significance assumed at $p<0.05$. Results show a 2-fold increase in luminescence in CHO cells cotransfected with the Sry relative to MT. These results indicate that Sry can potentially regulate testosterones' genomic and non-genomic impact on target cell activity.

Poster Board No. 21 - PREPARATION OF SOX18/pTYB4 BACTERIAL EXPRESSION CONSTRUCTS AND RECOMBINANT PROTEIN EXPRESSION. **Mary Rose Bruno[1], mbruno1@walsh.edu, Dinah Qutob[1], dqutob@walsh.edu, Jeremy Prokop[2], jprokop54@gmail.com, Adam Underwood[1], aunderwood@walsh.edu, [1]Walsh University, 2020 East Maple Street NE, North Canton OH 44720 and [2]Michigan State University Grand Rapids Research Center, Grand Rapids MI.**

SOX18 is a gene on the chromosome 20 that is linked to endothelial and vascular development. The SOX18 protein contains a High Mobility Group (HMG) box DNA binding domain that allows this protein to function as a transcription factor. Sequence analysis of the SOX18 gene identified a novel mutation within the human SOX18 HMG-box that replaces glutamic acid (E) for lysine (K) at amino acid 137 (rs201931544). The objective of this project was to insert the native and variant SOX18-E137K gene into the pTYB4 (New England Biolabs®) prokaryotic expression plasmid and collect the recombinant protein for use in future SOX18 research. A C-terminal chitin binding tag encoded by pTYPB4 allows for one-step purification of the SOX18 protein by using chitin beads (New England Biolabs®). All SOX18 genes were successfully cloned into pTYB4. All constructs were transformed into Lucigen® BL21(DE3) *E. coli* and induced for 2 hours with 0.75 mM IPTG at a cell density of 0.8 at OD600. Collection and subsequent analysis of recombinant protein by SDS-PAGE confirmed expression from both SOX18 variants.

Poster Board No. 22 - AN INVESTIGATION INTO THE BINDING OF METAL IONS TO RIBOFLAVIN BINDING PROTEIN IN EGGS. **Ariana E. Shannon, ashannon2@capital.edu, Michael J. Bibyk, mbibyk@capital.edu, Tracey Arnold-Murray, tmurray2@capital.edu, Capital University, 1 College Ave. and Main, Bexley OH 43209.**

Riboflavin binding protein (RBP) is a small protein found in the eggs of many birds and reptiles. RBP binds both riboflavin and copper (II) ions in a 1:1:1 ratio. It has been hypothesized that RBP is used to store riboflavin and copper ions in the egg for release to the developing embryo. Other metal ions of similar size and charge, such as zinc (II), chromium (II), manganese (II), and nickel (II) are found in these kinds of eggs, and we have discovered that RBP also binds to these ions, although not in the 1:1 ratio seen for copper (II). In order to better understand the role of RBP in chicken eggs, we explored preferential binding of these metals to RBP and if they were competing for the same binding site. In a series of tests, RBP was dialyzed against all combinations of pairs of metal ions both in equal ratios and in physiological ratios. Ultra-violet visible spectroscopy and atomic absorption spectroscopy were used to measure RBP and metal ion concentrations respectively. Preliminary data suggest that zinc (II) "outcompeted" copper (II) for the binding site on RBP at both equal and physiological concentrations. The other metal ions tested did not affect copper (II) binding on RBP.

Poster Board No. 23 - HOMOLOGY MODELING OF HUMAN SOX6 PROTEIN, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. **Brynne Africa, bafrica1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.**

The human SOX6 protein is part of the High Mobility Group (HMG) Box protein family and functions in the nucleus of the cell as a DNA transcriptional activator. It

plays an important role in many developmental processes, including neurogenesis and skeleton formation. Homology modeling with the YASARA program determined the 3-dimensional structure of the human SOX6 protein. Molecular dynamics verified that this is a stable and realistic model of this structure. The use of online ConSurf software determined the sequence regions of high and low amino acid conservation. The highly conserved regions are likely to be important for either the structure or function of the protein. The gnomAD database of human genome variants allows the identification of variants that will cause a change in the amino acid sequence of the protein. Human variants that create missense, loss of function, or frameshift mutations were mapped onto the 3-dimensional structure of the protein, allowing assessment of the phenotypic consequences of amino acid substitutions. Amino acid substitutions found at highly conserved positions include Glu104Lys, Arg109Cys, Arg122Cys, Gly125Trp, among others. The Catalog of Somatic Mutations in Cancer (COSMIC) shows that mutated versions of the SOX6 gene appear in a small percentage of cancers tested, notably, in breast tissue, stomach tissue, large intestine tissue, and haematopoietic and lymphoid tissue. It is hoped that this sequence-to-structure-to-function-to-phenotype approach will contribute to the future of genomic medicine.

Poster Board No. 24 - USING BIOINFORMATICS IN PHARMACOGENOMICS; PREDICTING HUMAN VARIANTS THAT WOULD INTERFERE WITH STATIN DRUG INHIBITION OF HMG-COA REDUCTASE. Kathryn Bisaha, kbisaha1@walsh.edu, Austin Coulter, acoulter1@walsh.edu, Philip Dougherty, pdougher1@walsh.edu, Garret Galentine, ggalenti1@walsh.edu, Angela Kruk, akruk1@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

Hydroxymethylglutaryl-CoA Reductase (HMGCR) is the rate limiting enzyme in cholesterol synthesis. HMGCR is the target of statin drugs that bind competitively at the HMG-CoA (substrate) binding site. A homology model of human HMGCR was created using the YASARA program. One of the templates used to generate the YASARA homology model of HMGCR, based on sequence similarity to experimentally determined structures, contained a bound ligand, the experimental statin drug PF-3052334 (RIE). Using PyMOL, the Python™-based molecular visualization program, polar contacts between RIE and HMGCR's active site were identified. Most of these are also binding sites of the substrate HMG-CoA, except for the contact made at Arginine 590. A database of human variants, the gnomAD database, showed no human variants at the substrate binding sites, which are all highly conserved amino acid positions, but did show a variant at the drug binding site: Arg590His. The statin drugs that interact with the Arginine 590 binding site include Simvastatin, Rosuvastatin, and RIE. Because they bind to Arginine 590, the Arg590His variant has the potential to decrease the efficacy of these drugs in inhibiting cholesterol synthesis. Docking simulations between the drug molecule RIE and the target protein correctly identified the drug binding site. This work is the start of a new research direction involving bioinformatics, genomics, and pharmacology, wherein student researchers identify molecular targets for drug treatment, determine 3-dimensional structures of the targets and their drug-binding sites, then identify and model the common human variants that are likely to alter the efficacy of drug treatments. This sequence-to-structure-to-function-to-phenotype approach will enhance the practice of genomic medicine.

Poster Board No. 25 - HOMOLOGY MODELING OF HUMAN TAF1 PROTEIN, ITS VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Kathryn Bisaha, kbisaha1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The human protein TAF1 is part of the High Mobility Group (HMG) Box protein family. It functions as part of the DNA-binding general transcription factor complex TFIID. A 3-dimensional structure of TAF1 was obtained via YASARA-based homology modeling. Molecular dynamics was used to verify that this structure was stable and realistic. ConSurf, an online software program, allowed regions of high and low conservation to be identified through the comparison of orthologous TAF1 proteins. Some regions of high conservation that were identified include amino acids: 561-571, 820-865, and 985-1047. Regions of high conservation traditionally tend to be important to structural and functional aspect of proteins. Human variants of the protein were identified by the use of the gnomAD database and a focus placed on those that caused missense, loss of function, and frameshift mutations. Mutations in areas of high conservation included: Asn569Ser, Asp820Ala, and Ser1039Phe. These mutations can be mapped to the 3-dimensional structure of the protein to assess the phenotypic consequences of the mutations. The presence of TAF1 in all human tissues was determined through the use of the Human Protein Atlas. The Catalogue of Somatic Mutations in Cancer (COSMIC) was used to identify cancer related mutations of TAF1, namely, that TAF1 mutations are present in 26% of malignant melanoma cancers. It is hoped that this sequence-to-structure-to-function-to-phenotype approach will enhance the practice of genomic medicine.

Poster Board No. 26 - HOMOLOGY MODELING OF HUMAN HMGX3 PROTEIN, VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Michelle Cugino, mcugino1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The human HMGX3 protein is part of the High Mobility Group (HMG) Box protein family and functions as an architectural transcription factor that brings distant regulatory elements into close proximity to RNA-polymerase II, thus modulating transcriptional activity. Homology modeling with the YASARA program predicted the 3-dimensional structure of the HMGX3 protein. Molecular dynamics verified that this is a stable and realistic model of this structure, also quantifying the mobility of each amino acid of the protein. Evolutionary analysis using the online ConSurf software determined the sequence regions of high and low amino acid conservation by comparing orthologous proteins from many species. The highly conserved regions are most important for either the structure or the function of the protein. The gnomAD database of human genome variants allowed the identification of common germ-line variants in the HMGX3 gene that would cause a change in the amino acid sequence of the protein leading to phenotypic and functional changes. Amino acid substitutions found at highly conserved positions include Pro290Ser, Trp344Arg, and Glu576Gly, among others. The COSMIC database contains cancer cell line mutants at highly conserved positions in the HMGX3 gene including Ile322Asn, Ile1182Thr, Pro1341Ser, among others. These mutants with a high conservation score are worth investigating. All human variants that create missense, loss of function, or frameshift mutations were mapped onto the 3-dimensional structure of the protein, allowing assessment of the phenotypic consequences of mutations. The Human Protein Atlas (HPA) shows that mutated versions or altered expression of the HMGX3 gene appear in a small percentage of cancers tested, notably in endocrine tissue. It is hoped that this sequence-to-structure-to-function-to-phenotype approach will contribute to a future database for the practice of genomic medicine.

Poster Board No. 27 - THE FIRST FULL-LENGTH HOMOLOGY MODEL OF HUMAN CAPICUA PROTEIN, ITS VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Philip Dougherty, pdougher1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The HMG-box protein Capicua (CIC) is a transcriptional repressor with 2 isoforms produced from alternative splicing, CIC-S and CIC-L, which each have a C1 domain required for DNA binding in addition to the HMG-box domain. CIC is important for development of the central nervous system, and its malfunction results in some cancers. With the YASARA program, multiple models containing various regions of CIC were combined to create the most complete structure of human CIC to date. Evolutionary analysis using the online ConSurf server determined the amino acid positions of high evolutionary conservation. The amino acid sequence was compared to the gnomAD database of common human genomic variants, identifying CIC gene variants at highly conserved amino acid positions, most likely to have phenotypic, medically relevant consequences. This method of determining phenotypic relevance was confirmed in existing research literature, in which the highly conserved C1 domain was determined to be necessary for DNA binding. The C1 domain spans 40-45 amino acids with a highly invariable core of 11 residues. Twelve common human variants are found within this domain: Gln1476His, Gln1479Glu, and a duplication of the code for amino acids Phe1484—Ser1486 to name a few. The C1 domain is necessary for DNA binding and transcription repression, and mutations within this region such as Phe1501Val or Cys1506Tyr have been found in cancer cells, according to the COSMIC database. Using this sequence-to-structure-to-function-to-phenotype (SSFP) method, a database for future genomic medicine may be created, allowing medical professionals to predict phenotypic consequences from genomic information.

Poster Board No. 28 - HOMOLOGY MODELING OF HUMAN WDHD1 PROTEIN, ITS VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Julianna Franzino, jfranzin1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The human WDHD1 protein is a member of the High Mobility Group (HMG) Box protein family and functions in the nucleus of the cell as a DNA replication initiation factor that brings together the helicase and DNA polymerase complex. This protein is highly expressed in actively replicating cells, therefore any human variants that cause a change in the structure or function of WDHD1 are likely to affect these cell types. Homology modeling with the YASARA program predicted the 3-dimensional structure of the human WDHD1 protein. Molecular dynamics verified that the predicted structure is a stable and realistic model of WDHD1 and also predicted the mobility of the individual residues of the protein. The use of the online ConSurf software determined the sequence regions of high and low amino acid conservation. The highly conserved regions are suspected to be important to either the structure or function of the protein. The gnomAD database of human genome variants allowed the identification of WDHD1 gene variants that code for altered amino acids. Missense variants have been found at several highly conserved positions including Gln434His, Pro439Thr, and Thr549Ala. There are human variants causing frameshifts at Phe470 and His476. Variants that create missense or frameshift mutations were mapped onto the 3-dimensional structure of the protein, allowing prediction of the phenotypic consequences of the amino acid substitutions. The Catalog of Somatic Mutations in Cancer (COSMIC) shows that mutated versions of the WDHD1 gene appear in a small but significant percentage of cancers tested, notably in breast tissue, soft tissue, and urinary tract tissue. Such a sequence-to-structure-to-function-to-phenotype database could enhance the practice of genomic medicine.

POSTER 29 - HOMOLOGY MODELING OF HUMAN PBRM1 PROTEIN, ITS VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Kesley Putman, kputman1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The human PBRM1 protein is part of the High Mobility Group (HMG) Box protein family and functions in the nucleus of the cell, binding acetylated lysine's in histone proteins and facilitating chromatin remodeling. This process must work properly for gene activation, and its failure has the potential to contribute to cancer progression. PBRM1 is thought to act as a tumor suppressor gene. Homology modeling by use of YASARA program predicted the 3-dimensional structures of the PBRM1 protein. Molecular dynamics verified that this is a stable and realistic model of its structure, while also determining the mobility of the various domains of the protein. Evolutionary analysis with the online ConSurf software determined the sequence regions of high and low amino acid conservation comparing orthologous PBRM1 proteins from more than 100 species. The highly conserved amino acids are suspected to be important to the structure or function of the protein. The gnomAD database of human genome variants allowed for the identification of common variants that cause a change in the amino acid sequence of the protein. Variants found in highly conserved amino acid positions include Arg 836 to Gln, Tyr 834 to Cys, and Phe 845 to Ser or Cys among others. All human variants that create missense, loss of function, or frameshift mutations can be mapped onto the 3-dimensional structure of the protein, allowing predictions of the phenotypic consequences of the mutations. Significantly, no variants were found corresponding to the acetylated lysine binding pocket surrounding Asn 263. The Catalog of Somatic Mutations in Cancer (COSMIC) shows that mutated versions of the PBRM1 gene appear in a small percentage of cancers tested, notably, in the kidney and male/female reproductive organs. It is hoped that this sequence-to-structure-to-function-to-phenotype approach will enhance the practice of genomic medicine.

Poster Board No. 30 - HOMOLOGY MODELING OF HUMAN TOX3 PROTEIN, ITS VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Xavier Soehnlen, xsoehnle1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The human TOX3 protein is part of the High Mobility Group (HMG) Box protein family and functions in the nucleus of the cell, preventing cell death by inducing anti-apoptotic transcripts and repressing pro-apoptotic transcripts. This makes TOX3 a potential target for new anti-cancer drugs that inhibit apoptosis inhibitors. It has been suspected that variants in the TOX3 gene are associated with breast cancer susceptibility. Homology modeling by use of the YASARA program predicted the 3-dimentional structure of the human TOX3 protein. Molecular dynamics verified that this structure is likely to be a stable and realistic model of this protein and predicted the mobility of individual residues of the protein. Evolutionary analy-

sis using the online ConSurf software determined the sequence regions of high and low amino acid conservation by comparing orthologous TOX3 proteins of 200 species. The highly conserved regions are suspected to be important to either the structure or function of the protein. The gnomAD database of human genome variants allowed for the identification of variants that cause changes in the amino acid sequence of the protein. Rare variants that were found at positions conserved by evolution include Phe 576 to Ser, His 489 to Gln, and a 509-512 deletion, among others. Variants that create missense, loss of function, or frameshift mutations were mapped onto the 3D structure of the protein, allowing prediction of the structural and potential phenotypic consequences of the mutations. The Catalog of Somatic Mutations in Cancer (COSMIC) shows that altered expression of the TOX3 gene appears in a small percentage of cancers tested, notably, in the breast and adrenal tissues. This sequence-to-structure-to-function-to-phenotype approach could be an enhancement of the practice of genomic medicine.

Poster Board No. 31 - THE FIRST FULL-LENGTH HOMOLOGY MODEL OF HUMAN MAELSTROM PROTEIN, ITS VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Madison J. Wobser, mwobser1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The human male testes protein Maelstrom (MAEL) is characterized as a High Mobility Group (HMG) Box protein. MAEL is important for preservation of male fertility, as it works along the RNA interference (RNAi) pathway, potentially shuttling proteins to and from the nucleus and thus aiding in the process of transposon silencing. Homology modeling with the YASARA program was used to create a predicted structure of the MAEL protein. Only part of the protein was modeled through YASARA, so RaptorX was used to generate the remaining protein structures. Once the protein segments were joined, a molecular dynamics simulation verified that the predicted structure was stable enough to be realistic. ConSurf, an online software program that determines evolutionary conservation among amino acids in protein structures, was then used to determine the conservation of MAEL amino acids. These results were aligned with gnomAD data regarding the human genome variants of the protein to determine the relationship between amino acid conservation, such as Pro37Leu, Pro136LeufsTer23, and Leu146Pro in the nine conservation region, and significant human genome variants in the form of frameshift and loss of function mutations. This research program of starting with genome sequences and using evolutionary conservation as a pointer for which genome variants will be consequential for human health, is part of the establishment of a database for the future of genomic medicine.

Poster Board No. 32 - HOMOLOGY MODELING OF HUMAN PMS1 PROTEIN, VALIDATION BY MOLECULAR DYNAMICS, AND IDENTIFICATION OF COMMON GENOME VARIANTS THAT ARE LIKELY TO HAVE PHENOTYPIC CONSEQUENCES. Sydney Film, sfilm1@walsh.edu, Adam Underwood, aunderwood@walsh.edu, Thomas M. Freeland, tfreeland@walsh.edu, Walsh University, Department of Biology, North Canton OH 44720.

The human protein PMS1 is a protein that functions in DNA mismatch repair. PMS1 is part of the High Mobility Group (HMG) Box protein family. Using homology modeling in the YASARA program, a 3-dimensional structure of the PMS1 protein was produced and the structure was verified as realistic using molecular dynamics. Evolutionary analysis using the online ConSurf software identified the amino acid positions of the PMS1 protein with high and low evolutionary conservation. Sequences with high conservation scores indicate important structural and functional domains of the proteins. Screening the gnomAD database, composed of nearly 14,000 human sequences, common human variants of PMS1 were identified. During this screening, focus was placed on variants that result in missense, loss of function, and frameshift mutations. These amino acid substitutions were mapped onto the 3-dimensional structure of PMS1 protein. These are the variants expected to result in phenotypic consequences. Using the online Human Protein Atlas, PMS1 was found to be expressed in all tissues. However, it is most abundant in cells with a high mitotic turnover rate, like cells in the digestive tract. Malfunctioning of PMS1 leads to genome instability and more frequent mutations, which can cause genetic defects or cancers. The Catalogue of Somatic Mutation in Cancer (COSMIC) was used to identify cancer related mutations of PMS1, and colorectal cancer is the most likely cancer to have mutated versions of PMS1. Using the sequence-to-structure-to-function-to-phenotype approach, it is hoped that a database can be created that will contribute to the development of genomic medicine for treatment and prevention of disease.

Poster Board No. 33 - REPRODUCTIVE POPULATIONS OF *C. REMANEI* IN ROTTING WALNUTS. Scott E. Baird, scott.baird@wright.edu, Sean P. Webb, webb.158@wright.edu, Wright State University, Dept. of Biological Sciences, Dayton OH 45435-0001.

Caenorhabditis remanei is a free-living rhabditid nematode. Non-feeding dauer larvae (a dispersal stage) of *C. remanei* have been found in Wright State University woods as associates of isopods, snails and beetle larvae. The goal of this study was to identify the reproductive microenvironments of *C. remanei*. It was expected that, like other species of *Caenorhabditis*, reproductive populations of *C. remanei* would be found in rotting vegetation. Surveys were conducted in which a variety of rotting vegetation was collected, placed on agar plates, and scored for the presence of nematodes. From these collections, multiple strains of nematodes were established from gravid females. Individuals from these strains were scored by microscopic observations to identify *Caenorhabditis* species. Species identifications were made from reciprocal crosses of *Caenorhabditis* strains to reference strains of *C. remanei*, *C. briggsae* and *C. nigoni*. Viable F1 and F2 progeny were obtained only from crosses to *C. remanei*. Reproductive populations of *C. remanei* only were found in rotting eastern black walnut drupes (*Juglans nigra*). In rotting walnuts, *C. remanei* populations were found at 6 of 8 collection sites. Only one other nematode species was found in walnuts, a single hermaphrodite from an as yet unidentified species of *Rhabditis*. Thus, rotting black walnuts are a preferred microenvironment for reproductive populations of *C. remanei* and few, if any, other nematodes utilize this habitat.

Pre-college Student Poster Sessions
9:00 – 10:00 AM
and
1:30 – 3:00 PM
WD 4th Floor Gallery, 404, and 407

Note: All posters will be displayed in both morning and afternoon sessions.

Poster Board No. 34 - ELECTRAE - AN INNOVATIVE, MODULAR DEVICE TO GENERATE ENERGY FROM 3 SOURCES. Laalitya Acharya, laalityaacharya@gmail.com, 4517 Woodside Place, Mason OH 45040, (William Mason High School).

Energy poverty is a global crisis with over 3 billion people without access to electricity. Those who do have access, mostly rely on energy from fossil fuels. In the United States < 10% is from renewable sources. This generates 5,271 million metric tons of CO_2. The world needs a cost-effective, adaptable and renewable energy source. Electrae is a modular prototype to generate electricity from 3 sources. It used the following components: (1) Piezo ceramic to generate energy from vehicle traffic. Piezo ceramic has an unique property—electricity is generated from mechanical stress. The device is installed on a road and when vehicles pass over it, the piezo mechanism generates electricity. Based on multiple trials conducted, polyvinylidene fluoride (PVDF) with mass was selected for flexibility, durability, and electrical output. Readings were taken based on a wooden road with a simulated "vehicle" created from Lego® MindStorms®. (2) Homemade, flow-channel tested, multiple 3D printed, custom designed turbines. Flow was regulated through a manifold garden hose. Turbines were tested at different flow rates for electricity output. Direct belt, gear train designs were tested for transmission to generator. Finally 4.8:1 gears were used. (3) Photovoltaic panels were selected based on trials conducted under cloudy and sunny conditions. Readings were taken at different times of the day at 10 to 15 minute intervals. A setup with dome shaped structure was finalized as it produced maximum electricity under most conditions. A final prototype combined all components and generated 5 to 11 watts.

Poster Board No. 35 - LIGHT WAVELENGTH'S EFFECT ON EARLY STAGE GARDEN BEAN (*PHASEOLUS VULGARIS*) DEVELOPMENT. AARON C. ZIEGLER, aaronziegler21@gmail.com, 9541 Bluewing Terrace, Cincinnati OH 45241, (Seven Hills High School).

The energy efficiency of light-emitting diodes (LEDs) make them attractive for indoor plant lighting. However, LEDs do not create broad-spectrum lighting efficiently. Additionally, LEDs' effect on garden beans (*Phaseolus vulgaris*) is not well known. The purpose of this study is to find light colors of specific wavelengths to grow plants under indoor conditions. The hypothesis was that each of the chosen light colors (purple, red, and green) would promote early bean growth better than natural sunlight as measured by both qualitative and quantitative data. Four garden-bean plants grew under each of the red, green, and purple LED lights (Philips®, 8 watt), and natural sunlight, for 16 days after planting the seeds in soil. Average plant height after 16 days under purple, red, green, and natural light were 354 mm, 298 mm, 311 mm, and 359 mm, respectively. The average leaf width for plants under purple, red, green, and natural lights were 41 mm, 47 mm, 57 mm, and 36 mm, respectively. Bonferroni adjusted T-tests found statistical differences for height and leaf width between the plants under the green light and the plants under the purple and natural lights ($p = 0.004$, 0.006, 0.001 and 0.000). Qualitative observations based upon visual inspections of leaf health, maturity, and root development revealed the plants under red light were the healthiest, nearest to fruition, and had the healthiest roots, followed by those under green light. The findings of this study suggest certain narrow-spectrum light can perform better than broad-spectrum light on early garden bean growth.

Poster Board No. 36 - IDENTIFYING PHRENIC MOTOR NEURON ENRICHED GENES. Aambar Agarwal[1], (aagarwal21@hb.edu), Polyxeni Philippidou[2] (pxp282@case.edu), [1]3940 Waterford Ct., Beachwood OH 44122, [2]Case Western Reserve University, Department of Neuroscience, Cleveland OH, (Hathaway Brown School).

Phrenic motor neurons (PMNs), located in the cervical spinal cord, play a critical role in breathing as they provide motor innervation to the diaphragm muscle to control its contractions. The purpose of this project was to identify PMN-enriched transcripts in the *Mus musculus* spinal cord, to determine if the corresponding proteins play a role in PMNs. To identify initial candidates, we surveyed the Allen Spinal Cord Atlas for transcripts expressed in the stereotypical position occupied by PMNs in the cervical ventral spinal cord. This approach identified *Chn1,* Cplx1, *Hspb8, Lrsam1, Sncg, Cpeb1, Lgals1,* and *Timp3*, which were validated by in-situ hybridization in mouse embryonic spinal cord. In order to detect RNA transcribed from these genes, oligos were designed to amplify cDNA corresponding to a region of these genes and used reverse transcription to make RNA probes. Probe concentration was determined by gel electrophoresis. All but Timp3 were enriched in PMNs as shown by in-situ hybridization and immunofluorescence, and Cplx1 and Sncg were highly enriched in the ventral spinal cord in every image of the 4 embryos. These results suggests that Cplx1 and Sncg may play a more critical role in PMNs and breathing as opposed to the other genes. To determine if the proteins synthesized by these RNA transcripts are essential for breathing, they could be targeted for mouse knockouts. If these mice develop respiratory problems, it would suggest that these proteins are essential for respiratory function and they could be targeted in future treatments for breathing disorders.

Poster Board No. 37 - ARE HAND SANITIZERS AND WIPES REALLY ADEQUATE SUBSTITUTES FOR HAND WASHING WITH SOAP AND WATER? Annie WT Xia, axpinkie@yahoo.com, 2317 West Clifton Ave, Cincinnati OH 45219, (Walnut Hills High School).

The purpose of this study was to determine if hand sanitizers and wipes really are adequate substitutes to washing hands with soap and water. It is commonly advised to use these substitutes when soap and water are not available, but the Centers for Disease Control and Prevention (CDC) guidelines for hand washing does not state any compromising nature in using sanitizers. The hypothesis was that the use of soap and water is equivalent to the use of sanitizers and wipes, but it was predicted that soap and water would be more effective than hand sanitizers. To test this hypothesis, the efficiency of each cleanser was studied. Dial® Liquid, Softsoap® Liquid, Safeguard™ Bar, Zest Bar, Wet Ones® Wipes, Germ-X® Wipes, Purell® Sanitizer, and Germ-X® Sanitizer were used. Five volunteers made handprints on petri dishes before and after cleansing their hands. After 3 days of culture, the efficiency of each cleanser was calculated with the percent decrease formula. There was an average bacterial reduction of 44.64% for water, 90.90% for Dial, 88.98% for Softsoap, 88.79% for Safeguard, 90.84% for Zest, 84.70% for Wet Ones, 85.59% for Germ-X Wipes, 81.96% for Purell, and 83.60% for Germ-X Sanitizer. The T-test statistical analysis indicated that most of the soap-

to-substitute tests exhibited significant differences. The hypothesis was not supported statistically, but the prediction was confirmed since statistics clearly showed that soap outperformed sanitizers and wipes. However, when soap and water are not available, it is recommended to use the substitutes rather than plain water, as they all exhibited at least an 80% efficiency.

Poster Board No. 38 - COMPARING 3 METHODS FOR THE BEST ASSESSMENT OF WATER QUALITY AND MACROINVERTEBRATE DIVERSITY. Noor Amir, nooramir903@gmail.com, 4325 MacKenzie Ct., Mason OH 45040, Dr. Jessica B. Sakash Replogle, replogle_j@summitcds.org, (Summit Country Day School).

One of the most essential ecosystems are fresh water systems because they replenish and purify water used by human beings. Therefore, there is a strong need to assist in the preservation and monitoring of freshwater ecosystems. Grand Valley Preserve, located in Camp Dennison, Ohio, was selected as the study site to monitor the water quality and determine diversity of macroinvertebrates 15 years into the conservation efforts of this reclaimed area. The Water Quality Index and macroinvertebrate biomonitoring were used to survey the diversity of macroinvertebrates and determine the water quality of the lake during winter, summer, and fall of 2018. Additionally, DNA barcoding was compared to traditional methods to evaluate macroinvertebrate diversity and water quality in this reclaimed body of water. The Water Quality Index assessment ranked the water quality as fair/good in both the winter and fall, and good in the summer. The biotic index of water quality rated the water as excellent in both the winter and summer and fair in the fall. DNA sequencing results of the CO1 barcoding region yielded identification to the genus level on 27% of the specimens collected (n=11). Poor quality sequencing results limited DNA barcoding identification and did not reveal a greater species diversity compared to the visual identification methods. DNA barcoding did not provide an accurate or cost-effective method of water quality analysis. A combination of the Water Quality Index and macroinvertebrate bioindicators proved a more consistent and accessible method for the citizen scientist.

Poster Board No. 39 - ACCURACY OF A CUSTOM-BUILT ELECTROGONIOMETER FOR MEASURING FINGER-JOINT ANGLES. Lina I. Zein[1], lzein20@hb.edu, Jayme S. Knutson, jsk12@case.edu, [1]2820 Broxton Road, Shaker Heights OH 44120, (Hathaway Brown School).

Measurement of finger-joint angles is valuable in evaluating treatment effectiveness in patients with hand paralysis. The goal of this study was to evaluate the accuracy and precision of measuring finger-joint angles with a new, custom-built electrogoniometer compared to a standard goniometer. A hinged wooden dowel was set at a fixed angle, and the 3 sensors of the electrogoniometer were used to measure the angle 10 times, with removal and repositioning between measurements. The 3 sensors measured the angles of the metacarpophalangeal (MCP), proximal interphalangeal (PIP), and distal interphalangeal (DIP) joints. The mean of the measured angles was within 0.2%, 4.3%, and 2.1% of the true angle value at which the dowel was initially set for the MCP, PIP, and DIP sensors, respectively—each less than the 5% typically considered the threshold for acceptance. The range of angles measured with the electrogoniometer was 3.7° (MCP), 3.6° (PIP), and 1.2° (DIP). These values are lower than those reported for the standard goniometer. The coefficients of variation of 2.3% (MCP), 2.1% (PIP), and 1.0% (DIP) were also less than the 2.4% (MCP), 2.9% (PIP), and 6.2% (DIP) measured with the standard goniometer. These data suggest that the custom-built electrogoniometer has greater accuracy and precision than standard goniometry. In addition, unlike standard goniometers, the electrogoniometer can measure angles in motion. Widespread availability of this device could improve assessment of active range of motion of fingers in patients receiving treatment for hand paralysis. Human studies comparing the 2 goniometers will be a next step.

Poster Board No. 40 - THE CO-CULTURE OF PROBIOTICS AND FIBER TO PRODUCE SHORT-CHAIN FATTY ACIDS WITH IMPLICATIONS TO TREAT DIVERSION COLITIS (AN IN VITRO STUDY). Jing-Jing Shen, jshen@beachwoodstudents.org, 24661 Tunbridge Ln., Beachwood OH 44122, (Beachwood High School).

This project evaluated the potential use of fiber and probiotics to increase short-chain fatty acid (SCFA) production by colonic bacteria in patients with diversion colitis (DC). DC is the inflammatory condition of the colon, resultant of the surgical rerouting of the colon from the digestive pathway. Patients with DC have little prospect for normal digestion and thus a normal lifestyle. A rare but detrimental disease, it has not attracted sufficient scientific attention. The speculated disease mechanism is that fecal diversion leads to a lack of bacteria and subsequent deficiency in SCFAs, culminating in pain and difficult digestion. It is suspected, but not yet confirmed, that patients with DC have a lack of SCFAs in their bowels. Current treatments, like compounded SCFA enemas, are limited and costly ($60 per dose). The hypothesis was that patients with DC have an SCFA deficiency, and over-the-counter probiotic bacteria and fiber supplements could be co-cultured to produce SCFAs to counteract DC. The aims are to investigate if: (1) SCFA amounts are lower in DC, and (2) probiotic-fiber co-culture can produce SCFAs. Fecal samples were collected from patients with DC (n=5; the diverted colon is not exposed to the fecal stream, thus no bowel prep is needed; samples were collected from secretions from the colonic mucosa) and without DC (n=11; samples were aspirated during colonoscopy) and underwent gas chromatography mass-spectrometry (GC-MS) to confirm different levels of SCFAs present in populations of patients with and without DC. Separate in vitro experiments were performed to test the effects of 3 different variables: 1 or 2 tablespoons of Benefiber®; 1, 2, 3, 4, or 5 Probiotic 10™ capsules; and different fermentation settings and temperatures (including aerobic culture at room temperature, aerobic culture incubated at 37°C, and anaerobic culture at room temperature) on SCFA production. Samples were centrifuged and supernatants were extracted and quantified for SCFA with GC-MS. Results suggest patients with DC have significantly lower concentrations of SCFAs than those without diversion and that as the concentration of probiotics and/or fiber increased, amounts of SCFAs produced increased, in aerobic and anaerobic environments. Overall, a combined regimen of probiotics and fibers, which yields quantifiable SCFAs, may provide a viable, cost-effective treatment option for DC.

Poster Board No. 41 - HONEYCOMB STRUCTURES AS A HELMET LINER MATERIAL. Garrett Blum, gblum20@us.edu, 7325 Stump Hollow Lane, Russell OH 44022, (University School).

Despite advancements in helmet technology, traumatic brain injury is still a grave threat to health and safety. Polymer foams, including expanded polystyrene (EPS), are today's common energy absorbers. Honeycomb structures also appear to have the desired properties such as absorbing large sums of energy while achieving high strain rates. This research intended to determine whether aluminum honeycombs (ALHC) could be an effective helmet liner material and, if so, quantify the relationship between impact velocity (v), thickness (h), density, and pertinent safety criteria (Peak Linear Acceleration (PLA), Head Injury Criterion (HIC), Gadd Severity Index (GSI), strain, and energy absorbed) for both materi-

als separately and in layered hybrids. First, 25 PSI EPS was compared with ALHC and 48 PSI EPS was compared with 45 PSI ALHC using quasi-static compression and dynamic drop tests. In quasi-static testing, 45 PSI ALHC was able to absorb more energy than the 48 PSI EPS (t-test, $p = 0.047$) while the 25 PSI ALHC absorbed less energy (t-test, $p < 0.001$) than the 25 PSI EPS. In dynamic drop tests, the ALHC broadly performed better than its EPS counterpart across all 5 safety criteria (t-test, $p < 0.05$) with the exception of the 45/8 PSI comparison at low impact velocities. Since the ALHC showed promising results, data were collected to create regression models. Preliminary results show that PLA, HIC, and GSA are exponentially related to the independent variables. Since ALHC were able to maintain better safety criteria, while absorbing more energy at higher strain rates, it is reasonable to conclude that honeycombs could contribute to an improved helmet liner.

Poster Board No. 42 - STABILIZATION OF OIL-IN-WATER EMULSIONS WITH GRAPHENE OXIDE AND COBALT OXIDE NANOSHEETS. Louisa R. Wang[1], lwang21@hb.edu, Katelynn Edgehouse[2], kje17@case.edu, Dr. Emily Pentzer[2], ebp24@case.edu, [1]8915 Crystal Ct., Streetsboro OH 44241, [2]Case Western Reserve University, Department of Chemistry, Cleveland OH, (Hathaway Brown School).

Pickering emulsions consist of oil droplets dispersed into a continuous water phase stabilized by solid particles. Such particle surfactants can affect the properties of the emulsions, providing access to many applications such as electrode materials for energy harvesting and management. Recent attention has been given to the use of 2D particle surfactants such as graphene oxide (GO) and cobalt oxide (CO) nanosheets. Pickering emulsions stabilized by combinations of GO and CO nanosheets were prepared. The impact of GO:CO ratio, oil type, and concentrations of flocculating agents (i.e., ionic/organic salts) on the formation and stability of the emulsions were tested for facilitating oil-in-water emulsions with composite particle surfactants. When no flocculating agent was added, emulsions with a higher content of CO led to the aggregation of nanosheets, while the GO:CO ratios of 2:1, 1:1, and 1:2 were still successful in forming droplets in the absence of a flocculating agent. However, these emulsions did not form as well as the GO emulsion, suggesting that the interaction between the particles interfered with the formation of the emulsion. Both GO and CO nanosheets contain a negative charge, which causes them to repel each other. The addition of salts dramatically improved the quality of the emulsions, due to their ability to balance the negative charge. The best emulsion found used toluene in 1:1 GO:CO with 0.20 M [Emim] [PF_6]. This new-found method can be used to create GO-CO capsules, substituting ionic liquid for oil to create a highly conductive and efficient electrode material for supercapacitors.

Poster Board No. 43 - DETERMINATION OF CRUDE (4-METHYLCYCLOHEXYL) METHANOL (MCHM) CONSTITUENTS IN ENVIRONMENTAL SAMPLES BY THIN-FILM MICROEXTRACTION. Rachel M. Avina, 628972@sylvaniastudents.org, 5622 Parkwood Blvd., Sylvania OH 43560, (Sylvania Northview High School).

In 2014, gallons of crude 4-methylcyclohexyl methanol (MCHM) leaked from a coal plant, contaminating West Virginia's Elk River. The goal of this experiment was to optimize thin-film microextraction (TFME) for testing of MCHM in water. TFME utilizes absorbent properties of solid phase microextraction, but with a membrane to maximize surface area for extraction of analytes. Optimization of the environmentally sustainable TFME for MCHM analysis, which uses less solution in testing, included conditions of desorption, agitation, ionic strength, extraction temperature, and extraction time. Analyte carryover on the thin-film after running the thermal desorption unit measured desorption; other conditions were analyzed by GC-MS. Average, standard deviation, and relative standard deviation were taken from the peak areas. Results below 20% for relative standard deviation were considered quality values. Optimized conditions were observed at 270 °C for 2.5 minutes for desorption, 900 rpm for agitation, ionic strength of 20%, and temperature at 55 °C. Extraction time reached equilibrium at 60 minutes, but sufficient resolutions appeared at 15 minutes, and therefore used for the method. After analysis, optimized conditions were tested at concentrations ranging from 0.1 ppb to 500 ppb. Calibration curves were created based on toluene D_8 and methyl benzoate D_8 with evaluation using 3.5, 35, and 350 ppb as standard concentrations. The new method of TFME was tested using Elk River water. After no contamination was identified, the method was tested using ultra-pure water spiked with various concentrations of MCHM; the results compared to the calibration curve confirmed validation of this method.

Poster Board No. 44 - CYTOTOXICITY OF MICROWAVES ON PROBIOTIC BACTERIA. Sohum S. Kapadia, skapadia21@us.edu, 210 East Orange Hill Circle, Orange OH 44022, (University School).

Microwaves, gas stoves, and convection ovens are used daily to prepare food. This project attempted to determine the harmful effects of these heating methods by evaluating the growth of probiotic bacteria, organisms that are crucial in keeping the digestive system healthy. Bacterial growth was measured by using the effectiveness of the bacteria to turn milk into yogurt. The hypothesis was that there were no differences among the instruments used to heat food. It was predicted, however, that the microwave oven would be the most harmful to probiotic bacteria, while the convection oven and gas stove would be the least harmful. To test this, 18 culture cups were prepared, each with yogurt (15 mL) and milk (118.3 mL). For each heating method, 6 random cups were heated to 45 °C. For the control, no bacteria were exposed to direct heating. All cultures were placed at room temperature for 32 hours. The conversion of milk into yogurt was measured by the amount of liquid left and the pH of the culture. Heating in the convection oven led to the greatest growth in probiotic bacteria (37 ± 2.0 mL), while the control showed the least growth (58 ± 1.1 mL). The microwave (46 ± 2.3 mL) and gas stove (54 ± 2.2 mL) were each more harmful to probiotic bacteria compared to the convection-oven. An ANOVA was performed ($F_{(3,20)} = 133.09$, $p < 0.00001$), indicating that although differences exist between treatments, the harmfulness of each heating method was not what was expected. The pH was consistent at 6.0 across all trials. While it was expected that the microwaves would be the safest for probiotic bacteria, the gas stove appeared to be the most harmful to probiotic bacteria.

Poster Board No. 45 - SITE-SPECIFIC DELIVERY OF IMMUNE ADJUVANTS FOR ANTI-TUMORAL RESPONSE OF THE TUMOR MICROENVIRONMENT. Shruthi Ravichandran[1], sravichandran21@hb.edu, Peter Bielecki[2], pab88@case.edu, Efsthathios Karathanasis[2], exk210@case.edu, [1]26905 Morgan Run, Westlake OH 44145, [2] Case Western Reserve University, Department of Biomedical Engineering, (Hathaway Brown School).

Tumor mediated immunosuppression allows tumors to hide from the immune system and avoid recognition. One way of reversing this suppressive microenvironment is to activate antigen-presenting cells (APCs) within the tumor that recruit other immune cells to the area. Cyclic diguanylate monophosphate (c-di-GMP), a drug that works within the cytosol of APCs like macrophages, is used to release inflammatory cytokines like IFN-ß to recruit immune cells and initiate an anti-tumor response. However, therapy using freely injected c-di-GMP is limited because c-di-GMP cannot easily cross cell membranes

and is quickly cleared from the body. It is hypothesized that c-di-GMP loaded into a nanoparticle will more effectively deliver drug into the cytosol of APCs, which are widespread within the tumor. An quantity of 30 µg of c-di-GMP was loaded into mesoporous silica nanoparticles, a versatile nanoparticle platform that is biocompatible and easily modified. In vitro studies showed c-di-GMP-loaded silica nanoparticles boosted the secretion of cytokine IFN-ß from murine macrophages by 6-fold compared to free c-di-GMP. Meanwhile, unloaded silica nanoparticles induced low levels of IFN-ß secretion comparable to untreated macrophages, verifying the particle has low immunogenicity. This preliminary work demonstrates a potential new treatment that safely increases the efficacy of c-di-GMP. Ongoing and future work includes in vivo studies optimizing the delivery of nanoparticles to tumor-associated macrophages and evaluating the therapeutic effects on tumor burden and overall survival.

Poster Board No. 46 - A NOVEL-HOT-MELT-PRESSURE-SENSITIVE-ADHESIVE FOR REUSABLE MAIL ENVELOPES AND PACKAGES. Edward D. Dan, edw656@gmail.com, 6955 Woodlands Ln., Solon OH 44139, (Solon High School).

The United States Postal Service reported 154.2 billion pieces of mail delivered in 2015. Currently, twice-reusable envelopes utilizing 2 gum lines are on the market. There is a gap in the knowledge base how to improve upon the current model. A multi-use envelope can save billions of dollars and billions of envelopes. This would reduce the CO_2 in the atmosphere. In this research, a novel hot-melt pressure-sensitive adhesive was created based on a styrene ethylene butylene styrene (SEBS) polymer (high molecular weight) with tackifiers (low molecular weight) to allow damageless reopening of envelopes with heat. This allowed the envelopes to be reusable multiple times. In 7 trials of shear and peel tests at room temperature, 48.0 × 25.4 mm envelope strips with adhesive on a steel plate either exceeded the max weight of the scale (13 kg) or tore the manila envelope paper. This far exceeds the USPS 301 Physical Standards. Twenty trials of opening tests show that envelopes sealed with the adhesion can be opened using a hair dryer and iron at an average of 68.2 °C in 66 seconds and 20 seconds, respectively. A dynamic mechanical analysis (DMA) temperature sweep test from 0 to 175 °C confirmed the glass transition temperature of 36 °C and the storage modulus of 104 to 105 Pa from 0 to 36.6 °C. Storage modulus dropped below 1000 Pa at 68.2 °C. Twenty repeated envelope openings showed no signs of degrading the adhesive bonding. If each envelope is used 4 times with this adhesive, an estimated $5.78 billion and 115.65 billion envelopes (equivalent to 780,638 tons of paper and 4.4 billion pounds of CO_2) will be saved. The next step is to commercialize and design a mass production process for this product. Further experimentation will expand adhesive applications to cardboard boxes and larger shipment packages.

Poster Board No. 47 - CREATING A CARBON FIBER REINFORCED POLYMER MATRIX COMPOSITE (PMC) WITH IMPROVED ELASTIC PROPERTIES. Ryan D. Devine, rdevine20@us.edu, 28220 Red Raven Road, Pepper Pike OH 44124, (University School and NASA Glenn Research Center).

Lighter, stronger, and safer: carbon fiber reinforced polymer matrix composites (PMCs) could completely change the field of aerospace engineering. Beginning with the first aircraft, construction materials have been essential to an aircraft's safety and performance. Modern aircraft require materials with high strength to withstand the stresses of high-speed flight. PMCs are attractive to engineers because of their high durability, strength, and low weight. By varying the method of fabrication, the PMCs can be altered to specialize their mechanical properties. The purpose of this project was to create a PMC with higher flexural strength, elongation at failure, and elasticity modulus than standard resin-matrix composites without a significant (>5%) decrease in ultimate strength. To test different matrices, the PMCs were impregnated by vacuum infusion and cured at room temperature. By testing ultimate tensile strength and 4-point flexural strength, as well as visible resistance to impacts, the mechanical properties of each PMC matrix can be compared. The average ultimate tensile strength of 6 inch × 1 inch resin matrix composites is 3,620 kg ± 298 kg with 2.1% elongation at failure. In previous testing, silicone matrix composites showed a lower ultimate tensile strength than resin-matrix composites (x = −4.6%) and higher elongation (x = +17%) and flexural strength (x = +6.8%) and an improved resistance to damage from impacts. Future testing will vary the compound of silicone used as the matrix. Data from this lab can be used to correlate the mechanical properties of the virgin matrix against those of the final composite.

Poster Board No. 48 - A DIAGNOSTIC CLASSIFIER DIFFERENTIATING MIA/AIS FROM FRANK-INVASIVE ADENOCARCINOMA. Jessica H. Chang[1], jchang21@hb.edu, Pranjal Vaidya[2], pranjal.vaidya@case.edu, Kaustav Bera[2], kaustav.bera@case.edu, Kevin Hsieh[3], kevinh9396@tmu.edu.tw, Gong-Yau Lan[3], langongyau@yahoo.com.tw, Pradnya Patil[4], patilp@ccf.org, Robert Gilkeson[5], Robert.Gilkeson@uhhospitals.org, Frank Jacono[2], frank.jacono@case.edu, Vamsidhar Velcheti[6], Vamsidhar.Velcheti@nyulangone.org, Philip Linden[5], Philip.Linden@uhhospitals.org, Anant Madabhushi[2], anant.madabhushi@case.edu, [1]6532 West Point Dr., Hudson OH 44236, [2]Case Western University, Dept. of Biomedical Engineering, [3]Taipei Medical University, Dept. of Radiology, [4]Cleveland Clinic Foundation, Dept. of Hospital Medicine, [5]University Hospitals, Dept. of Radiology, [6]NYU Langone, Dept. of Oncology, (Hathaway Brown School).

AIS (adenocarcinoma-in-situ) and MIA (minimally-invasive-adenocarcinoma) in lung have nearly-identical 5-year survival rates of around 97%. Early stage invasive adenocarcinoma (IA) has a 5-year survival rate of 50 to 90%, depending on time of diagnosis and early treatment. This experiment explored the possibility of using computer extracted (radiomic) texture features to differentiate MIA/AIS from IA invasive adenocarcinomas. Selected (n = 101) cases with non-contrast CT scans were obtained from 3 sources, consisting of 50 invasive cases (Cleveland Clinic Foundation), 6 AIS cases (Taipei Medical University), and 46 MIA cases (Memorial Sloan Kettering Cancer Center). The cases were divided into a training cohort (n = 50) and a testing cohort (n = 51). Each lung nodule was manually segmented by a radiologist, then used to extract a total of 4,464 intratumoral (IT) and peritumoral (PT) features. The mRMR (minimum redundancy maximum relevance) algorithm was used to select the top 5 features. Gabor and haralick-class IT and PT less than 3 mm from the nodule were found to be the most predictive features. Six classifiers were trained to distinguish between the 2 classes. All 6 were able to differentiate invasive adenocarcinoma from MIA/AIS with high accuracy and precision, with the most predictive being the KNN (k-nearest neighbor) and RBF (radial basis function) classifiers with AUCs of 0.9954. The other AUCs were as follows: 0.9938 (SVM), 0.9908 (RF), 0.9400 (LDA), and 0.9177 (QDA). These results suggest radiomics can be used to successfully differentiate invasive lung cancer variants from MIA/AIS, providing a non-invasive tool for diagnosis and treatment selection.

Poster Board No. 49 - FUNCTIONAL HETEROGENEITY OF STEM CELLS. Neha Devireddy[1], 20ndevireddy@beaumnotschool.org, David Wald[2], David.Wald@case.edu, [1]6665 Ayleshire Drive, Solon OH 44139, [2]Case Western Reserve University, Dept. of Pathology, (Beaumont school).

Stem cells are widely used to repair, replace or regenerate damaged cells and tissues. However, reports of successful

clinical effectiveness are variable. Although often referred to and treated as a uniform cell population, stem cells are actually a heterogeneous cell mixture, which differ in size. It is not known whether changes in size affect stem cell function; therefore, it is hypothesized that "the function of a stem cell depends on size." The functions of stem cells that vary in size will be examined. Using a spiral microfluidic channel, operating on the principle that a larger object migrates slowly compared to a smaller object, stem cells were separated into distinct groups based on their size (ranging from large to small cells). Size-separated stem cells were further studied for their ability to grow and to form specialized cells. Using spiral microfluidics, stem cells were separated and grouped into large and small cells. Large size stem cells appeared to grow slowly compared to small stem cells. In addition, large stem cells were observed to form fat cells, whereas small stem cells were inclined to form bone cells upon stimulation with appropriate chemicals. The propensity of stem cells to differentiate into various specialized cells depends on their size. Traditional therapies using a mixture of stem cells yielded variable outcomes due to random distribution of large and small cells. However, by using a specific subset of stem cells, (i.e., small cells to treat bone defects), consistency in clinical outcomes may be improved. Therefore, this and associated studies have implications for designing appropriate stem cell-based therapies.

Poster Board No. 50 - OPTIMAL MEAL SELECTION AT POPULAR FAST FOOD AND FAST CASUAL RESTAURANTS. Tiffany Huang, tiffany.huang14@gmail.com, 2593 Thomas Jefferson Drive, Beavercreek OH 45434, (Beavercreek High School).

The rise of both fast food and fast casual restaurants in the nation has raised numerous health concerns. The objective of the study was to identify all possible ways, if any, to order a meal (defined as any combination of the 10 popular McDonald's® items chosen for consideration) in accordance with specific nutritional guidelines and at minimal cost. These nutritional guidelines were based on the daily nutritional requirements released by the United States Food and Drug Administration (FDA) and included the following: the meal must be at least 30% (600 calories) and at most 50% (1,000 calories) of the daily number of calories, at most 60% (39 g) of total fat, at most 60% (1,440 mg) of sodium, and at least 50% (25 g) of protein. A mathematical model was established consisting of a cost function and a complex system of inequalities involving 10 variables corresponding to the above nutritional guidelines. This model was solved through carefully observing and using special structures of the inequalities; 7 possible ways to order a meal satisfying the guidelines were identified. This mathematical model was also extended to other fast food and fast casual restaurants such as Wendy's® and Panera Bread®, yielding similar results. This optimal meal selection implies that meals can be ordered from the restaurants mentioned in a manner that is both nutritious and cost-efficient.

Poster Board No. 51 - HYPOXIA SENSING OF CELLS MODULATED BY BETA BLOCKERS. Prajwal Guruprasad[1], pguruprasad20@us.edu, Yu Sun[2], suny4@ccf.org, Sathyamangla Prasad[2], prasads2@ccf.org, [1]29350 Miles Road, Solon OH 44139, [2]Cleveland Clinic Lerner Research Institute, (University School).

Hypoxia is reduced oxygen supply which results in cell stress. Loss of oxygen supply to the heart or the brain is a primary cause of heart failure or stroke, but little is known about the underlying mechanisms. Recent work shows that the beta2-adrenergic receptor (ß2AR) responds to adrenaline rush, which is regulated by oxygen levels. To test this premise, cell lines expressing ß2AR were developed. These were incubated either in normoxia or hypoxia (2% O_2) for 3 and 6 hours to assess functional changes. Western immunoblotting was performed to assess receptor phosphorylation with anti-phospho ß2AR as increased phosphorylation indicates dysfunction. Hypoxia treatment resulted in an ≈2.0-fold increase in ß2AR phosphorylation compared to normoxia. To test whether ß-blockers change ß2AR response to hypoxia, cells were treated with a ß-blocker (propranolol) and hypoxia. ß-blocker treatment increased ß2AR phosphorylation (≈2.3-fold over control) in normoxia and reduced phosphorylation in hypoxia (≈0.5-fold over control). To test whether ß2AR function is altered in hypoxia, the downstream secondary messenger cAMP was quantified in the cells. Consistently, normoxia cells generated 154.41 pmol/mg protein compared to 30.26 pmol/mg protein for those in normoxia reversed by ß-blocker treatment. These studies show that hypoxia results in ß2AR dysfunction and ß-blocker reverses it—these observations have significant clinical implications. ß-blockers can potentially be used for acute treatment of stroke patients.

Poster Board No. 52 - EFFECT OF TRANSCRIPTOME REGULATION ON GLIOBLASTOMA PATIENT SURVIVAL. Michelle Dong[1], mdong20@hb.edu, Lindsay C. Stetson[2], lxs442@case.edu, Jill S. Barnholtz-Sloan[2], jsb42@case.edu, [1]5113 Lansdowne Dr., Solon OH 44139, [2]Case Western Reserve University, Case Comprehensive Cancer Center, (Hathaway Brown School).

Glioblastoma is the most common primary brain tumor in adults. Patients have a poor outcome with a median survival time of 12 months; the disease is always fatal. Long non-coding RNAs have been shown to play an important role in regulating gene expression, but their significance in glioblastomas is unclear. This study aimed to identify long non-coding RNA associated with the survival time of glioblastoma patients. The R package DESeq2 quantified the relative differential expression of aligned long non-coding RNA. The package was used to normalize glioblastoma data from The Cancer Genome Atlas to determine the long non-coding RNAs differentially expressed (q-value < 0.01) between short-term survivors (n=46, overall survival <9 months) and long-term survivors (n=30, overall survival >18 months). We identified 11 long non-coding RNAs differentially expressed in glioblastoma patients. LOXL1-2 and LOXL1-AS1 were highly expressed among short-term survivors. Understanding the role of transcriptomics in gene expression is critical for gaining insight into improved targeted drug treatment. Further directions include statistically analyzing long non-coding RNA in other independent data sets and biologically validating the impact of long non-coding RNA on gene expression and protein abundance.

Poster Board No. 53 - THE EFFECT OF REFLECTIVE GLASS MEDIA SIZE ON RETROREFLECTIVITY PERFORMANCE OF PAVEMENT MARKINGS. Grace A. Elhindi, gelhindi@roadrunner.com, 377 Kirkshire Ct., Highland Heights OH 44143, (Beaumont School).

The experiment was designed to study the retroreflectivity performance of glass beads in providing night visibility under simulated road conditions. The simulation included evaluation of retroreflectivity with newly installed and weathered pavement markings under wet, dry, plowed, and unplowed pavement conditions. The experiment included using Powder Reflective Beads (Type 1, Mesh 100-200), Standard DOT Reflective Beads (Type 1, 45-850 microns), Airport Quality Reflective Beads (Type 4, Mesh 12-30) and Large Deco Molded Reflective Beads (Type 4, 3 mm). The glass beads were broadcasted to saturation over 12 panels with white coating and 12 panels with yellow coating to simulate the most commonly used pavement markings. The glass beads were applied using a single drop method when using a single bead type, and a double drop method when using 2 bead types. The experimental data supported the hypothesis as the Large

Molded Deco Beads had the highest retroreflectivity measurements of 95.3 mcd/lux/m^2 on the yellow-coated samples that have been exposed to weathering and plowing conditions. However, the experimental data did not support the hypothesis as the double drop combination of Large Molded Deco beads and Standard DOT beads exhibited the highest retroreflectivity measurements of 221.5 mcd/lux/m^2 on the white-coated panels exposed to plowing and weathering conditions. The experimental results further showed that white panels with all glass beads configurations exhibited higher retroreflectivity measurements than any yellow panels. The results also showed that wet conditions, plowing, and weathering reduced retroreflectivity readings by 6.3% to 58.5% for yellow samples and by 42.3% to 69.4% for white samples. Other factors such as the color of the coating, reflective bead embedding, and the roundness and clarity of the reflective beads had an impact on the retroreflectivity readings.

Poster Board No. 54 - RESCUING EAR FUNCTION IN AN USHER SYNDROME MOUSE MODEL USING GENE THERAPY. Quinn M. McDermott[1,2], qxm59@case.edu, Weinan Du[2], wxd28@case.edu, Qing Zheng[2], qyz@case.edu, [1]15911 Aldersyde Drive, Shaker Heights OH 44120, [2]Case Western Reserve University, Department of Otolaryngology–Head and Neck Surgery, (Shaker Heights High School).

Usher syndrome is a rare but devastating genetic disorder that results in deafness, blindness, and a lack of balance. These defects stem from flaws in hair cells of the ear and photoreceptors of the eye. There is no cure for this disease in humans. Recently, a genetic model mouse for Usher syndrome was made by knocking out the gene in the mouse. These mice are deaf and lack balance, so they emulate Usher syndrome defects that occur in humans. Using a synthetic adeno-associated viral vector that carries a wild-type copy of the Usher gene, ear function of the mutant mouse was rescued. This indicates that this form of gene therapy is effective for treating Usher syndrome.

Poster Board No. 55 - THE EFFECTS OF DRUGS IN TARGETING GLIOBLASTOMA. Sophia E. Laye[1], slaye21@hb.edu, Eli E. Bar[2], eli.bar@case.edu, Raffaella Spina[2], rxs644@case.edu, [1]7070 Bramshill Cir., Chagrin Falls OH 44023, [2]Case Western Reserve University, Department of Neurosurgery, (Hathaway Brown School).

Glioblastoma (GBM) is the most common and most lethal primary malignant brain tumor in adults, causing about 14,000 deaths each year in the United States alone. Median survival following diagnosis is less than 15 months with maximal surgical resection, radiation, and temozolomide chemotherapy. These tumors are notoriously difficult to treat due to chemotherapy resistance, immune evasion, and rapid infiltration throughout the brain; making GBM an unmet medical need requiring novel, more effective treatment approaches. Several small-molecule drug libraries were screened in an effort to identify agents that effectively and specifically target GBM patient derived neurospheres. Collectively, these efforts yielded 3 drugs: AGSC9, AGSC11, and AGSC12—all capable of inhibiting GBM cells but showing no effect against normal neural stem cells (NSC). These drugs were then tested on astrocytes at concentrations of 10 μM, 1 μM, 0.1 μM, 0.01 μM, and 0.001 μM, using dimethyl sulfoxide, DMSO, at a concentration of 0.1% as the control as it was used as the drug vehicle for this experiment. Astrocytes were chosen to determine the effects of the drugs on typical, noncancerous cells of the brain. Cell proliferation was observed using the alamarBlue® assay to remain consistent with the previous drug screening. The data shows that the drugs did not kill the astrocytes with the exception of drug AGSC9 at a high dose. Future preclinical experimentations will be done in vivo to determine the drugs' effects on tumors implanted in mice.

Poster Board No. 56 - PLANTNET: A CONVOLUTIONAL NEURAL NETWORK BASED APPROACH TO PLANT DISEASE DIAGNOSIS. Maanasa Mendu, Maanasa2@gmail.com, 8398 Ashmont Way, Mason OH 45040, (William Mason High School).

Over 75% of the world's crop output comes from 12 plant species. The homogeneity of the agricultural system, along with climate change, has increased plant disease damage. The key to reducing this damage is through early, accurate detection. Current plant disease diagnostic methods rely on visual inspection by plant pathologists and/or expensive and time-consuming lab-based methods like ELISA and PCR. The goal of this research was to (1) develop a machine learning algorithm that identifies plant disease with an 80% (or greater) overall accuracy and (2) apply the algorithm to a mobile app and server application to directly utilize smartphone images for disease detection. Convolutional Neural Networks (CNNs) have developed into a powerful tool in the field of machine learning to address the challenge of classifying images of different angles, resolutions, and lighting without intensive feature extraction. In phase 1, the optimal CNN configuration was determined by considering the network architecture, dataset type (RGB/grayscale/segmented), and training method (transfer learning/scratch) in 9 CNNs implemented in MATLAB®. The CNN application, PlantNet, trained using transfer learning and 50,000 RGB images from the PlantVillage dataset classifies 38 classes of plant disease with an overall accuracy of 95.40%, supporting the hypothesis. In phase 2, the PlantNet algorithm was integrated with a mobile application and web server through Python™ Flask. There are more than 3.4 billion smartphone subscriptions worldwide; whether integrated onto smartphones or drones for continuous monitoring, machine learning based plant disease diagnosis has great potential for application.

Poster Board No. 57 - DISRUPTION OF HEARING MEMBRANE PROTEIN (HMP) 1 USING CRISPR IN A ZEBRAFISH MODEL. John S. Pape[1], jpape21@us.edu, Michael Dercoli[2], mrd124@case.edu, Shaoyuan Zhu[2], xz305@case.edu, Brian McDermot[2], bmm30@case.edu, [1]197 W. Market, Warren OH 44481, [2]Case Western Reserve University School of Medicine, Department of Otolaryngology–Head and Neck Surgery, (University School).

Deafness is a common sensory disorder in the United States. It affects as many as 1 in 1000 newborns. Traditionally, hearing research has used mice as a model, but zebrafish are an important and useful organism for modeling this system as well. Sensory hair cells are responsible for hearing and vestibular function in humans and mice. There is evidence showing that hearing membrane protein (HMP)1 is a central component of the hair cell stereocilia. In zebrafish, stereocilia are responsible for translating sound waves and water motion into electrical signals. Defects in HMP1 are predicted to lead to deafness through structural disruption of the stereocilia. Clustered regularly interspaced short palindromic repeats (CRISPR)/associated nuclease 9 (Cas9) technology was used to interrupt the function of HMP1. The goal was to lesion HMP1 by CRISPR/Cas9 to determine if this gene is required for hearing in zebra fish—in hopes of helping human hearing in the future. To do this, the F1 generation of injected zebrafish were genotyped (through fin clipping) followed by PCR cleanup to amplify and purify the DNA. Of the 50 zebrafish injected, a 90% success rate was achieved. Gel electrophoresis confirmed the presence of amplified HMP1. Samples were then sent to be

sequenced and analyzed. After reviewing the sequence data, a successful lesion of HMP1 by CRISPR/Cas9 had been achieved. Sequencing results show a successful disruption of the HMP1 gene, allowing future testing of the fish to see if the damaged HMP1 had any effect on the hair-cell protein.

Poster Board No. 58 - HEALTH IMPLICATIONS OF A CLIMATE CHANGE DIET. Carmen P. Pape[1], carmenppape@gmail.com, Amanda P. Waller[2], amanda.waller@nationwidechildrens.org, [1]1289 Euclid Ave, Delaware OH 43015, [2]The Research Institute at Nationwide Children's Hospital, Columbus OH (Rutherford B. Hayes High School).

Climate change models predict vast changes to worldwide food production and availability within the next 50 years. Much of the population will face less access to fresh produce and animal protein sources, with a concomitant increase in consumption of processed foods higher in simple carbohydrates (CHO) and sodium but with lower protein content expected. Thus, the aim of this study was to investigate potential health implications of a climate change diet (CCD). It was hypothesized that consuming a CCD would result in weight gain and higher blood pressure. Using n=5 female Fischer-344 rats we compared a CCD (12% protein, 58% CHO, 0.4% sodium) with an isocaloric control (C) diet (16% protein, 48% CHO, 0.2% sodium), in 3-week phases (C1, CCD, & C2). Blood pressure was measured by a noninvasive tail cuff method in conscious, lightly restrained rats. Differences ($P<0.5$) between diet phases were assessed by 1-way ANOVA with repeated measures. Blood pressure ($P=0.029$) and water intake ($P<0.001$) were significantly increased during CCD while, interestingly, body weight was decreased ($P = 0.008$). Behavioral observation scores for unprovoked vocalizing, food guarding, and negative social interaction ("quarreling") were also significantly increased during CCD. Except for a mild transient chromodacryorrhea during the CCD, there were no differences in any clinical observation scores. In conclusion, short-term consumption of a low protein/high CHO/ high sodium CCD resulted in increased blood pressure, water intake, and frequency of negative social behaviors. This study provides important evidence implicating a CCD with possible detrimental effects to physical, psychological, and environmental health.

Poster Board No. 59 - AFFINITY BETWEEN SORAFENIB AND CYCLODEXTRIN. Zuha A. Jaffar[1], zuhajaffar@gmail.com, Kathleen Young[2], Horst von Recum[2], [1]3380 Concord Circle, Avon OH 44011, [2]Case Western Reserve University, (Hathaway Brown School).

Cyclodextrin (CD) is a family of compounds consisting of several glucose subunits and has an affinity for small molecule drugs. In the pharmaceutical industry, CD has mainly been used as complexing agents to increase aqueous solubility of poorly soluble drugs and to increase their stability. Multiple drugs are used during cancer treatment, hence the term "broad spectrum chemotherapy," which is prescribed because it targets different types of cancer cells. Tumors can develop a tolerance for a single drug if it's used for a long period of time. Combinations of cancer drugs have a synergistic effect. Since sorafenib is currently being used in combination therapy to treat hepatocellular carcinoma, it raised the question: Does sorafenib have affinity for CD? Docking simulations were performed using PyRx to model the docking of sorafenib with alpha, beta, and gamma CD. The results showed variation in the docking affinity of the 3 cyclodextrins. With a docking affinity of 30.7 kcal/mol, alpha CD showed little affinity for sorafenib (a larger number indicates a lower docking affinity). The other 2 cyclodextrins tested showed much greater affinities for sorafenib. Gamma CD had an affinity with -5.8 kcal/mol, and beta CD had an affinity of -6.4 kcal/mol. Because the affinity of sorafenib with the beta CD was the strongest, future work will involve using an SPR to find the physical binding affinity and kinetics, drug refilling assays, drug release from polymers (in the form of disks), cancer-cell killing capacity, and using other drugs with sorafenib for the synergistic effect.

Poster Board No. 60 - NOVEL 3D PRINTED PHOTOCURING POLYMER COMPOSITE SCAFFOLDS FOR BONE TISSUE REGENERATION. Nipun U. Jayatissa, nipunj980@gmail.com, 6053 Sunny Lake Ct., Sylvania OH 43560, (Maumee Valley Country Day School).

The regeneration of bone defects caused by trauma, fracture, and disease is a significant clinical challenge for patients in the United States and around the world. Annually, the cost for bone fracture repair exceeds $19 billion and costs are projected to increase by 50% in 2025. The ideal scaffold for bone repair should provide biocompatibility, pore architecture, biodegradability, mechanical support, and cell attachment sites. Conventionally fabricated polymer scaffolds are still unable to make ideal scaffolds for bone repair. In this study, new 3D printing technology was used to print porous scaffolds using poly(ethylene glycol) methacrylate (PEGMA), methyl cellulose, and nano-hydroxyapatite (nHA) as the main components. The objective of this study is to engineer 3D bioprinted porous scaffolds that can mimic the porosity, pore morphology, mechanical properties, biocompatibility, and cell attachment and growth similar to human bone. Polymer scaffolds with a pore size of 1,000 µm were designed using computer software. These scaffolds were printed and cured using UV-visible light energy in the 3D printer. These scaffolds were characterized for structural analysis and pore morphology using Fourier Transform Infra Red (FTIR) Spectroscopy and Scanning Electron Microscope (SEM), respectively. Scaffolds were also evaluated for cell viability, and cell proliferation with murine osteoblasts. The scaffolds show biocompatibility and cell proliferation as determined by in vitro Live/Dead cell assay. These scaffolds also showed mechanical properties similar to human bone. Potentially, 3D printed porous scaffolds could be used for bone tissue regeneration applications.

Poster Board No. 61 - THROMBUS-DIRECTED DRUG DELIVERY SYSTEMS FOR TARGETED FIBRINOLYSIS. Tejal Pendekanti[1], tpendekanti20@hb.edu, Michael Sun[2], mbs109@case.edu, Anirban Sen Gupta[2], axs162@case.edu, [1]2344 Carousel Court, Westlake OH 44145, [2]Case Western Reserve University, Dept. of Biomedical Engineering, (Hathaway Brown School).

The primary cause of cardiovascular disease, like myocardial infarction and ischemic stroke, is the blockage of blood vessels by blood clots. Treatment requires fibrinolytic agents, like tissue plasminogen activator (tPA), to rapidly remove clots and restore blood flow. Although effective, fibrinolytic drugs pose unwanted side effects like intracranial hemorrhage due to off-target action. Such side effects can be avoided by specifically targeting clots and releasing the drug at the target site through packaging fibrinolytic agents within drug delivery systems (DDS). In this framework, previous studies have shown the benefit of modifying the surface of liposomal nanoparticle-based DDS with ligand motifs that bind to active platelets or fibrin, allowing for clot-relevant binding. Building on this, it was hypothesized that DDS which simultaneously bind to active platelets and fibrin will significantly enhance targeting of clots compared to DDS which bind to platelets or fibrin only. To test this, liposomal DDS surfaces were decorated with peptide GSSGRGDSPA (lRGD) which binds to active platelet integrin GPIIb-IIIa or with peptide cyclo-AC-Y(DGI) C(HPr)YGLCYIQGK-Am (FBP) which binds to fibrin (homomultivalent decoration) or with a combination of

both (heteromultivalent decoration). Liposomes bearing various ligand densities and ratios were flowed over human blood clots in microfluidic channels, and liposome binding was analyzed by fluorescence microscopy. Studies showed that hetermomultivalent decorations had enhanced binding and reached peak binding with lower ligand density compared to homomultivalent decorations. Future studies will focus on adapting this heteromultivalent targeting strategy on unique DDS that, upon binding to clots, will release fibrinolytic agents via local stimuli.

Poster Board No. 62 - EFFECTIVENESS OF CELASTROL IN PREVENTING GLUCOCORTICOID RESISTANCE IN ACUTE LYMPHOBLASTIC LEUKEMIA CELLS. William E. Spencer, wspencer19@us.edu, 35070 Jackson Rd., Moreland Hills OH 44022, (University School).

Administration of glucocorticoids is the universal treatment for acute lymphoblastic leukemia (ALL). Glucocorticoids require the presence of the glucocorticoid receptor NR3C1 to translocate to the nucleus. Within the nucleus they make transcriptional changes that lead to apoptosis of ALL cells. While glucocorticoids are typically an effective treatment, an issue arises when ALL cells become resistant to glucocorticoids. Resistant ALL cells contain an unusually high quantity of caspase-1 (CASP 1) and its activator NLRP3. Caspase-1 proteolytically cleaves the glucocorticoid receptor NR3C1, preventing glucocorticoids from triggering apoptosis. The incorporation of celastrol could have potential in alleviating this issue. The triterpinoid celastrol is a natural product with potent anti-inflammatory and anti-cancer properties. One of these properties is the inhibition of NLRP3 inflammasome activation. It was hypothesized that celastrol will increase the effectiveness of prednisolone, a glucocorticoid commonly used for the treatment of ALL. In this experiment, ALL cells were exposed to varying concentrations of prednisolone and celastrol. A combination of lipopolysaccharide and adenosine triphosphate was added to simulate NLRP3 overexpression. The experiment was then repeated with half the concentration of cells. After incubating overnight, MTT assays displayed an increase in ALL cell death while prednisolone and celastrol are together. This helps to reveal celastrol's usefulness in the treatment of ALL.

Poster Board No. 63 - EFFECTS OF AUDIO AND VISUAL DISTRACTIONS ON RUNNING. Faith C. Myers, myersfc10@gmail.com, 4251 N. County Line Rd., Sunbury OH 43074, (Big Walnut High School).

This experiment determined if running with no distraction, audio (upbeat music), or visual (action movie) distraction affect pulse, blood pressure, and completion times. Hypotheses: (1) listening to music through headphones while running will lead to faster completion times, uneven pacing, and a higher pulse and blood pressure compared to the control; (2) watching a movie with subtitles while running will lead to slower completion times, even pacing, and a lower pulse and blood pressure compared to both listening to music and the control. Twenty students individually ran 2 miles for each randomly ordered case. Times were recorded, and pulse and blood pressure were recorded before and after running. The first and second mile mean running times were 8.3, 8.3, and 9.2 minutes and 8.9, 8.9, and 9.4 minutes, for the control, audio, and visual distraction cases respectively. The mean percent increase in pulse after running was 72.7%, 86.7%, and 93.4% for the 3 cases. The mean percent increase in systolic blood pressure at run completion was 11.8%, 19.6%, and 13.7% for the 3 cases. The first hypothesis was partially supported, as for the audio case heart rates increased (14%) as did systolic blood pressure (7.8%), while completion times and pacing remained unchanged. The second hypothesis was partially supported compared to the control. There were slower completion times and even pacing, but heart rates were not reduced and blood pressure results were mixed. When comparing the visual to audio cases, completion times were slower, pacing even, and blood pressures reduced, but heart rates increased.

Poster Board No. 64 - CHIRALITY IN LIQUID CRYSTALS: MECHANICAL VS. ELECTROMECHANICAL EFFECTS. Helen Sun, hsun20@hb.edu, 34378 Claythorne Rd., Solon OH 44139, (Hathaway Brown School).

Liquid crystals (LCs)—substances that exhibit properties intermediate between solid and liquid—possess molecular chirality (i.e., the absence of mirror symmetry). The molecules of these "chiral liquid crystals" twist around an axis, which also can be induced by using chiral dopants and a nonchiral LC. The chiral dopant can be categorized as left-handed and right-handed, meaning they twist clockwise or counterclockwise. The goal of this project is to compare a purely mechanical and an electromechanical chiral response. In the experiments both left-handed and right-handed chiral dopants (CB15 and ZLI-811) were added at different ratios to a nonchiral LC (MBBA). For one set of concentrations the helical pitch (a purely mechanical response) becomes infinite. For a different set of concentrations the electroclinic response (an electromechanical effect in which an electric field causes the molecules to tilt) vanishes. Electroclinic effect (ECE) measurements and wedge-cell experiments were performed to determine the mechanical pitch and electromechanical response of the doped LCs, and then compared with one another. Polarized microscopy measurements show that 2% dopant in LC having ratios of 0.533, 0.566, 0.600, and 0.700 ZLI-811 to CB15 chiral dopant still display characteristics of finite pitch (with multiple twist domains) and therefore non-vanishing mechanical chirality. The ECE measurements also indicate that electromechanical chirality has not been eliminated. Results suggest that these ratios of chiral dopants have not eliminated chiral behavior and the appropriate ratios that do have not been found yet.

Poster Board No. 65 - IS YOUR WATER SAFE TO DRINK: DEVELOPMENT OF A NOVEL HOME TEST METHOD TO QUANTITATIVELY DETERMINE THE CONCENTRATION OF LEAD IN WATER - PHASE II. Mukund A. Seshadri, mukie2002@gmail.com, 7104 Timberview Dr., Dublin OH 43017, (Dublin Coffman High School).

The purpose of this research is to develop a novel home test method for lead in water. Lead contamination in drinking water is a significant public health concern, with cities throughout the country still having drinking water with lead levels higher than 15 ppb: the EPA safe standard. There is currently no inexpensive, quantitative test for lead in water. Sodium rhodizonate is a chemical compound which generates a red color when it reacts with lead. Colorimetric analysis can determine the concentration of a chemical contaminant in a solution. The hypothesis of this research is that colorimetric analysis of water, using sodium rhodizonate as the reagent, will be a quick, accurate, affordable, and quantitative method to test for lead in water. A concentration-absorbance calibration curve was created by colorimetrically analyzing 5 solutions of water with varying concentrations of lead: 15 to 95 ppb. These solutions were analyzed using a free mobile color analyzer application. A value for green light being transmitted was found (G value). This value was used to calculate the absorbance of red light: "Absorbance = $-\log(G_{Unknown}/G_0)$." Cincinnati EPA water samples with unknown concentrations of lead were tested with the calibration curve. The range in differences between calculated and actual concentrations was 1 to 13 ppb. All samples with a level of lead >15 ppb were also calculated to have this concentration. The cost of the test was calculated to be $36 per 12 tests—approximately $3 per test. These results show this novel test to be quick, accurate, affordable, and quantitative.

Poster Board No. 66 - ROLE OF MICRORNA-223 IN CHOLESTEROL METABOLISM IN MACROPHAGES. Sejal N. Sangani[1], Paul Haddad[2], Christopher A. Nmai[3], Jeffrey A. Deiuliis[2], [1]28700 Settlers Lane, Pepper Pike OH 44124, [2]Case Western Reserve University, Cardiovascular Research Institute, Cleveland OH, [3]Harvard University, Cambridge MA, (Hathaway Brown School).

Previous studies have concluded that microRNA-223 (miR-223) is a regulator of macrophage activation, which plays an important role in causing cardiovascular disease. The risk of cardiovascular disease increases with elevated cholesterol levels. This project aims to determine if miR-223 regulates cholesterol metabolism in mouse macrophages. Bone marrow was isolated from wild type (WT) and miR-233 knockout (miR-223 KO) mice and differentiated to macrophages in cell culture. The macrophage cells were then treated with human low-density lipoprotein (LDL), which is the transporter of cholesterol in blood. The LDL had been damaged previously by an acetylation reaction, as macrophages ingest acetylated LDL (acLDL). Macrophages take up acLDL through receptors on their surfaces, known as scavenger receptors (SR). A particular SR, SR-B3, does the majority of this uptake and was present in very low levels in miR-223 KO cells compared to control cells. As expected, it was found that miR-223 KO macrophages had reduced uptake of acLDL compared to WT cells as measured by fluorescent microscopy and Oil Red O (ORO) staining. These results suggest that miR-223 is involved in the regulation of macrophage uptake of damaged LDL via SR-B3. Confirmation of these findings in human macrophages may yield significant data in combating cardiovascular disease.

Poster Board No. 67 - DEFENSE BEHAVIOR OF ROLLIE POLLIES (FAMILY ARMADILLIDIIDAE) COMPARED WITH TRILOBITA SPECIMENS. Lorena E. Jevnikar, lorenjevnikar2001@icloud.com, 4253 Parklawn Dr., Willoughby OH 44094, (Willoughby South High School).

Throughout the Paleozoic Era, from 542 to 251 million years ago, Trilobita—a class of extinct marine fossil arthropods commonly known as trilobites—populated the seas with more than 20,000 species. These marine creatures are thought to be the oldest known organisms to develop a defense behavior. Trilobites tucked their legs and antennae under their exoskeleton, creating a ball that protected their vulnerable underside. In the United States, an excellent location to collect trilobites is Penn Dixie Fossil Park & Nature Reserve, located near Buffalo, New York. In May 2018, *Phacops rana* specimens were collected from the site. The majority of the specimens were in the defense position. Why were they typically preserved coiled rather than outstretched? To test this question, an experiment was conducted using 20 specimens of the arthropod family Armadillidiidae, commonly known as pill bugs or rollie pollies. The reaction of pill bugs was recorded when they faced different conditions. Over half of the pill bugs in all 3 trials rolled into a ball when threatened from touch or a sudden environmental change. It is presumed that trilobites reacted similarly when in contact with a predator. Results from this experiment show Trilobita and Armadillidiidae may have had similar defense mechanisms.

Poster Board No. 68 - IMPACT OF HALTERE REMOVAL ON GRAVIPERCEPTION. Anya N. Razmi[1] arazmi20@hb.edu, Jessica Fox[2], jlf88@case.edu, [1]4020 Hemlock Circle, Orange Village OH 44122, [2]Case Western Reserve University, College of Arts and Sciences, Cleveland OH, (Hathaway Brown School).

Found on dipteran insects, halteres are mechanosensory organs known to aid flies in detecting shifts in gravity. Certain flies oscillate halteres during walking, such as Sarcophagidae, while in others, including Dolichopodidae, halteres do not oscillate. In *Sarcophaga bullata* subjected to a free fall while stationary, halteres are necessary to respond to the sudden gravitational shifts. However, the utility of these organs in flies that do not oscillate halteres during walking, or in flies responding to sudden changes in gravity while walking, have yet to be explored. In this study, wild-caught, stationary Dolichopodidae (various species) and walking *Sarcophaga bullata* were observed. Each intact or haltereless (removal via forceps) fly was placed in a clear, plastic container hung 2 cm above a surface and filmed (using a high-speed video camera) as the container fell. It was hypothesized that there would be no difference in median velocity during the fall between intact and haltereless Dolichopodidae. This was proven correct ($n=9$; 5 trials intact, 5 trials ablated per fly; $p>0.05$), suggesting that flies that oscillate halteres while walking are more adept at reacting to shifts in gravity. Secondly, it was hypothesized that haltereless (as opposed to intact) *Sarcophaga bullata* would have a lower mean velocity during the fall; however, the difference in mean velocity of intact and haltereless *Sarcophaga bullata* ($n=10$) was not significantly different ($p>0.05$). A possible explanation for these results is that flies are inherently unstable while walking, and this instability overrides the benefits of halteres when subjected to shifts in gravity.

Poster Board No. 69 - OPTIMIZATION OF SULFUR CONTENT IN HIGH-PERFORMANCE LI-S BATTERIES. Aniv Ray[1], anivray10@gmail.com, Kevin Tran[2], tran.473@buckeyemail.osu.edu, Drew Noble[2], drewnoble@gmail.com, Vicky Doan-Nguyen[2], doan-nguyen.1@osu.edu, [1]831 Clayton Drive, Worthington OH 43085, [2]The Ohio State University, Department of Chemical and Biomolecular Engineering, Department of Materials Science and Engineering, (Columbus Academy).

Energy storage has become a vital area of research because sustainable energy sources are needed to meet the world's increasing energy demands, while reducing use of carbon-emitting energy sources such as coal. Lithium-ion batteries (LIB), with a maximum energy density of 272 mAh/g ($LiCoO_2$), can be improved to increase capacity and to allow renewable energy sources to satisfy today's needs. The lithium-sulfur (Li-S) battery has a theoretical capacity of 1,672 mAh/g and is one of the most promising alternatives. However, the challenge of using Li-S batteries is the formation of lithium polysulfides that degrade the battery's capacity over multiple charge/discharge cycles. To address this, high-performance Li-S batteries were developed by varying the sulfur concentration (50% to 70%) of the cathode to find the optimal value. Additionally, the composition of different electrolytes were optimized by testing the salts LiFSI and LiTFSI (0.5 M to 1.0 M) to find the balance between maximizing energy density and mitigating polysulfide formation. The modified Li-S batteries show an improvement in energy density over lithium-ion batteries, reaching an actual energy density of approximately 630 mAh/g, as measured by cyclic voltammetry (CV) and galvanostatic cycling with potential limitation (GCPL) tests. They also reduce the formation of lithium polysulfides by the incorporation of additives such as dimethoxyethane (DME) and triethylene glycol (TEG) into the electrolyte solution. Because elemental sulfur is non-toxic, abundant, and inexpensive, these batteries can be produced at a large scale. The results suggest that new generation Li-S batteries could provide a higher energy density at a lower cost and become the future of energy storage.

Poster Board No. 70 - SODIUM-ION BATTERIES AS LOW-COST ALTERNATIVE FOR RECHARGEABLE LITHIUM-ION BATTERIES. Pravin S. Jayatissa, pravinj2003@gmail.com, 6053 Sunny Lake Ct., Sylvania OH 43560, (Sylvania Northview High School).

Batteries are an effective way to store and release energy. As the market demand increases, so do the basic raw materials for battery manufacturing. The need for lithium has subsequently increased with the popularity of lithium-ion batteries. Because supplies of lithium are limited, the use of an alternative raw material to make batteries was investigated. Sodium, more abundant than lithium, was selected as a good substitute. In metal-ion based rechargeable batteries, cathode and anode materials are the most important components. It was hypothesized that the use of a stable sodium-ion compound would enhance the durability and performance of sodium-ion batteries. To test this hypothesis, 2 sodium-containing metallic compounds, sodium titanate and sodium tungstate, that have identical basic characteristics but different material stability and natural occurrence, were used. In this investigation, an attempt was made to fabricate a cathode material using a novel sodium-containing chemical which can store more sodium ions than other cathode materials. The battery assembly was carried out using polymer-based electrolyte and a carbon anode. Research was conducted in the direction of material fabrication, material testing, and electrochemical characterization of coin cell battery structure using a swage lock split batter battery arrangement. This battery performed to the level of a typical sodium-ion battery, which has an energy density near 280 mAh/g. These results indicate that the sodium-ion battery capacity can be increased by appropriate selection of cathode material based on sodium derivatives as the cathode material.

Poster Board No. 71 - EFFECT OF UPF PROTEIN OVEREXPRESSION ON NMD EFFICIENCY. Ella N. Kazazic[1], ekazazic20@hb.edu, Savannah F. Mills[2], sfm60@case.edu, Kristian E. Baker[2], keb22@case.edu., [1]3870 W. 134th St., Cleveland OH 44111, and [2]Case Western Reserve University, Department of Genetics and Genome Sciences, Cleveland OH, (Hathaway Brown School).

Nonsense-mediated mRNA decay (NMD) is a quality control process in the gene expression pathway that rapidly degrades messenger RNA (mRNA) with a nonsense mutation, which is when a stop signal for protein synthesis exists upstream of the actual termination site on the mRNA. The workings of NMD are attributed to the proteins Upf1, Upf2, and Upf3, the absence of which would render the NMD process dysfunctional. One of the leading models for NMD, the 3' untranslated region (UTR) sensing model, suggests that Upf1 randomly binds mRNA, and the selection of NMD substrates is determined by the probability of Upf1 binding the mRNA past the termination codon. Thus, the probability of a substrate being selected for NMD is affected by the abundance of Upf1 protein and the length of mRNA downstream of the stop codon. In order to test the former hypothesis, this project was designed to generate an overabundance of the 3 Upf proteins in different combinations. Preliminary data displays a decrease in mRNA abundance when Upf proteins are overexpressed with a high copy number plasmid, but NMD efficiency will be driven further by cloning in the *TDH3* promoter using the Gibson assembly® process. The effects of overexpression can be determined using northern blot analysis, and transcriptional shut-off analysis will verify the destabilization of the mRNA half-life that would indicate a direct effect of Upf protein overexpression on NMD. NMD selection processes require further investigation, which would greatly benefit the treatment of diseases caused by nonsense mutations.

Poster Board No. 72 - CYBER SECURITY VULNERABILITIES IN CONNECTED MEDICAL DEVICES. Arya K. Sambandan, aryakamalam@gmail.com, 35650 Sedge Circle, Solon OH 44139, (Solon High School).

This research is about testing cyber security vulnerabilities of connected medical devices. Each year, roughly 2 million patients are readmitted, costing Medicare $27 billion, of which $17 billion are spent on readmissions that could be classified as potentially avoidable. To address this expensive, episodic care, health care systems are moving toward continuous care through remote patient monitoring (RPM) using connected medical devices. Today more than 500 million connected medical devices with sensors collect patient information. These devices communicate to the RPM using Bluetooth® technology and RPMs transmit data to the doctor's office through protocols (e.g., TCP®, HL7® and XNET®). The data are vulnerable at the point of data collection, in-transit, and at rest. HL7, or Health Level Seven®, is a widely used protocol in the medical device industry; HL7 transmits data in clear text and is extremely vulnerable. This project used a Merlin® RPM and implanted cardioverter defibrillator (ICD), EntraCare® connected medical devices (blood pressure monitor, oximeter, Fitbit®, weighing scale, Kardia By AliveCor®, glucometer, Samsung® Tablet), Raspberry Pi®, and Wireshark® penetration testing tools. Point-to-point tests with Merlin's RPM and ICD passed the security vulnerabilities. Three trials were conducted on the ICD and 7 trials on the EntraCare kit. But, EntraCare's RPM failed application vulnerability in MobiControl® and Kardia's (EKG sensor) interface. EntraCare acknowledged the denial of service (DoS), issued a product recall, and provided remote bug fixes for MobiControl.

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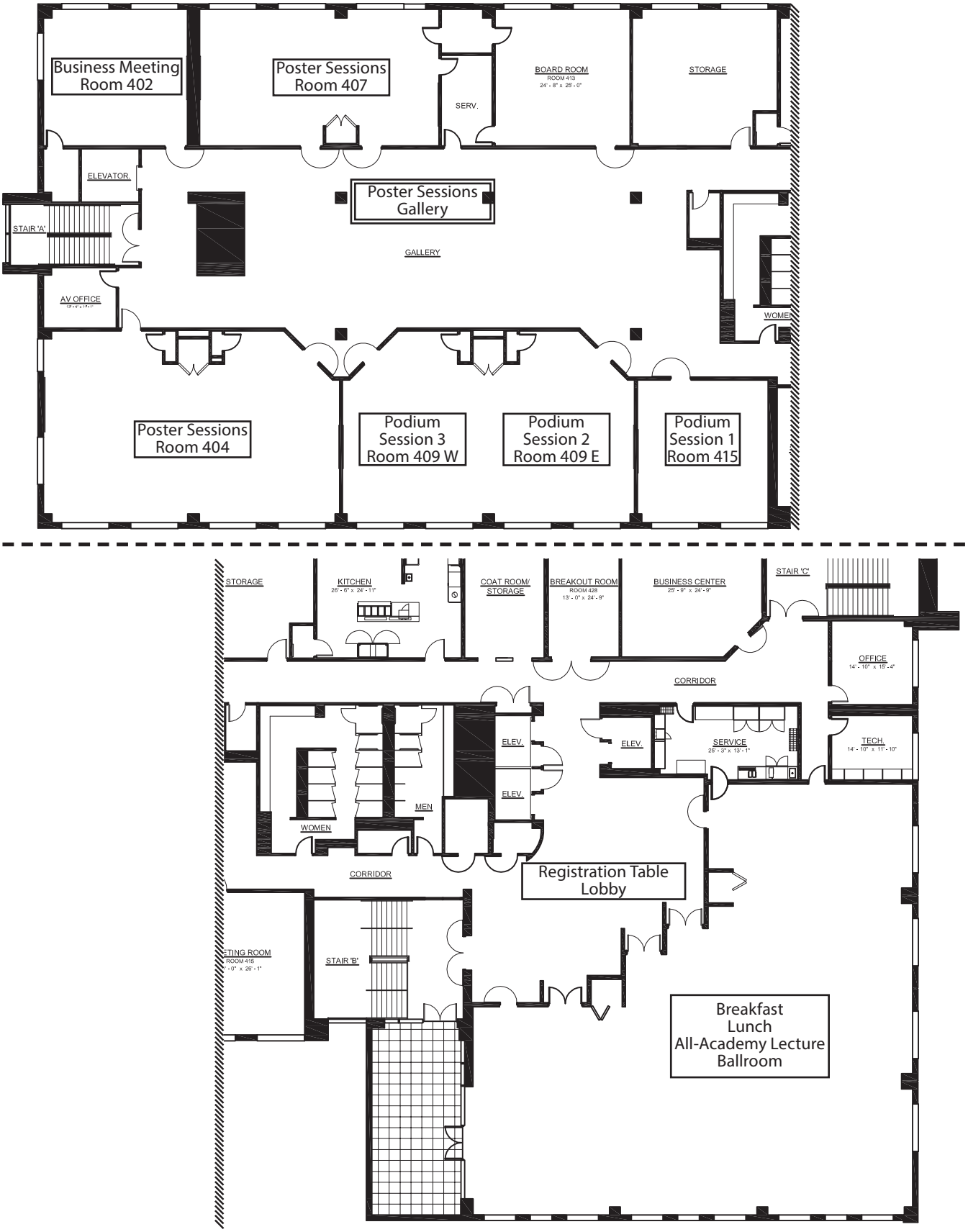
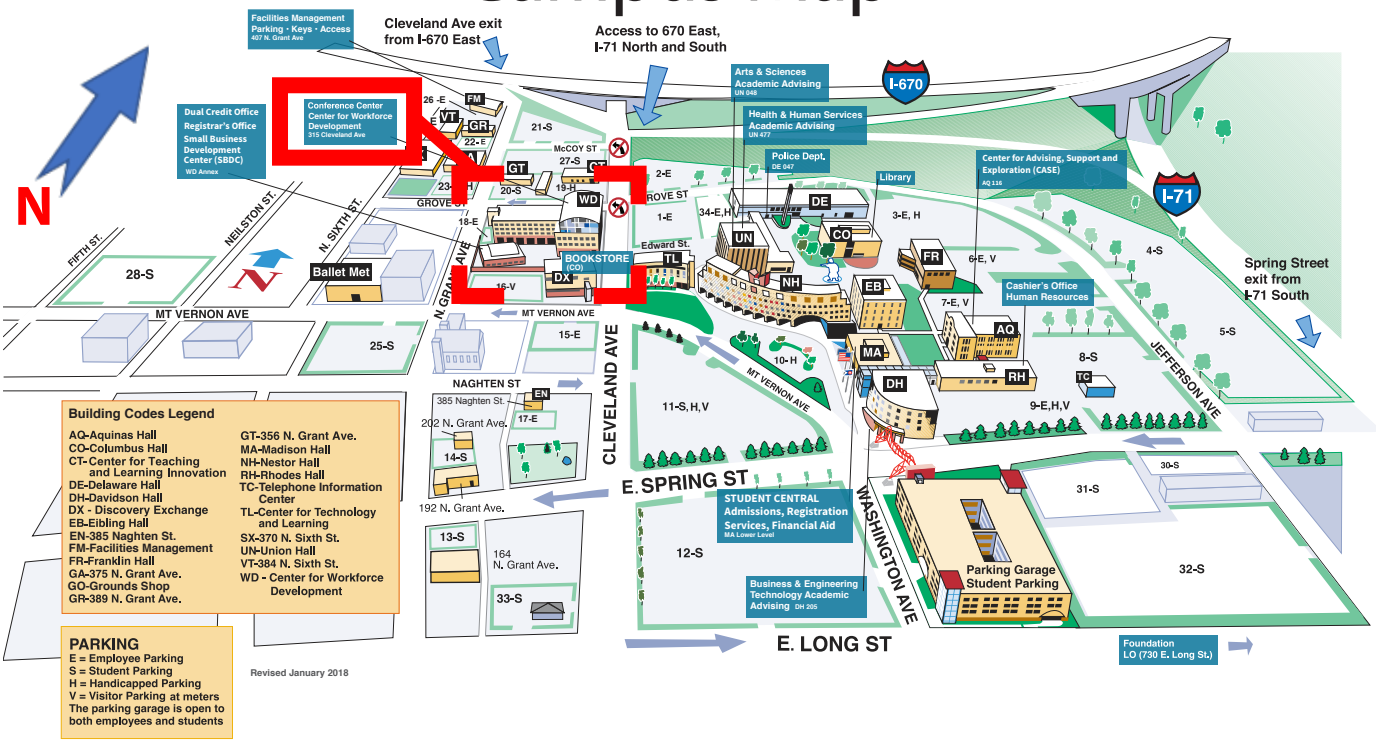


Columbus State Community College Campus Map



Building Codes Legend

AQ-Aquinas Hall
CO-Columbus Hall
CT-Center for Teaching and Learning Innovation
DE-Delaware Hall
DH-Davidson Hall
DX - Discovery Exchange
EB-Eibling Hall
EN-385 Naghten St.
FM-Facilities Management
FR-Franklin Hall
GA-375 N. Grant Ave.
GO-Grounds Shop
GR-389 N. Grant Ave.
GT-356 N. Grant Ave.
MA-Madison Hall
NH-Nestor Hall
RH-Rhodes Hall
TC-Telephone Information Center
TL-Center for Technology and Learning
SX-370 N. Sixth St.
UN-Union Hall
VT-384 N. Sixth St.
WD - Center for Workforce Development

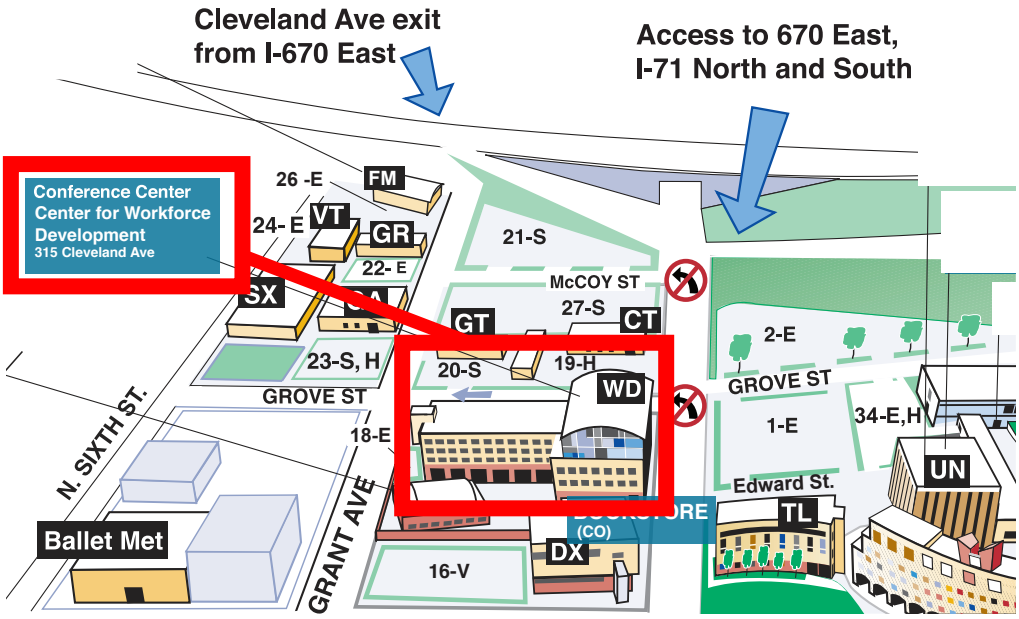
PARKING

E = Employee Parking
S = Student Parking
H = Handicapped Parking
V = Visitor Parking at meters
The parking garage is open to both employees and students

Parking permits can be downloaded at *http://www.ohiosci.org/annual-meeting-2019*.
Permits must be displayed on dash.
Please park in any student lot near the Conference Center/Center for Workforce Development (WD).
Student lots are marked with an "S" on the inset below.

Inset

Conference Center
Center For Workforce Development - (WD)



See you next year!

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