William Paterson University

Biological and Chemical Sciences

Program and Abstracts

17th Undergraduate Research Symposium

Saturday, April 20th, 2024

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Table of Contents

"FEW WORDS FROM ORGANIZERS"

Few activities are as rewarding as research to the motivated students as well as faculty mentors. In addition to the acquisition of invaluable research skills, students learn how knowledge is created and experience the excitement of the "eureka moment". To celebrate undergraduate achievements, a research symposium has been held since 2007 on the WPUNJ campus for students in biological, chemical and environmental sciences. This symposium provides an opportunity to the students to showcase their talents and share their research achievements with their peers from about 16 universities from the tristate area.

We would like to welcome all of you to an exciting 17th year of the Undergraduate Research Symposium at William Paterson University of New Jersey. This is an example of a budding community of undergraduate researchers. We want to thank all of the students from past and present who participated in the symposium and shared their research with us. We also want to thank all of the research mentors who have made it possible by investing their time, knowledge, resources and energy, so that the undergraduates gain their first-hand research experiences.

We express our gratitude to all of our student volunteers who show great enthusiasm and worked very hard to make this symposium a success.

We are very much obliged to Dr. Ilana Lauren Brito for accepting our invitation as our keynote speaker and investing her valuable time to be with us.

This symposium could not have been successful without the moral and continuous support from our Dean, Dr. Sharma, and Associate Dean, Dr. Zeleke,

who worked very diligently with us so that everything is put together in a professional manner.

We also want to thank Dr. Michael Peek and Dr. Bhanu P. S. Chauhan, (Chairs of the Biology and Chemistry Departments) for their continued support. As well as the Office of Institutional Advancement and the Alumni Association for contributing financially to the event in various capacities.

Finally, we extend our gratitude to Provost Joshua Powers and President Richard Helldobler for their leadership and encouragement to make this symposium a great success.

ORGANIZERS:
Dr. Emily Monroe
Dr. Bhanu P. S. Chauhan

PLENARY ABSTRACT

Unexpected interactions at the host-microbiome interface

Professor Ilana Lauren Brito
Mong Family Sesquicentennial Faculty Fellow in Biomedical Engineering
Meinig School of Biomedical Engineering, Cornell University

Host-microbe interactions are crucial for normal physiological and immune system development and are implicated in a variety of diseases, including inflammatory bowel disease, colorectal cancer, obesity, and type 2 diabetes. Despite large-scale case-control studies aimed at identifying microbial taxa or genes involved in pathogeneses, the mechanisms linking them to disease have thus far remained elusive. We have leveraged publicly available interspecies protein-protein interaction data to find clusters of microbiome-derived proteins with high sequence identity to known human-protein interactors. We observe differential targeting of putative human-interacting bacterial genes in nine independent metagenomic studies, finding evidence that the microbiome broadly targets human proteins involved in immune, oncogenic, apoptotic, and endocrine signaling pathways in relation to IBD, CRC, obesity, and T2D diagnoses. We have also started to use interaction and structural prediction models to better understand interaction mechanisms. These methods have helped us uncover a world of host-microbiome protein-protein interactions that reshape the way we think about interacting with our most intimately associated microbes.

Biography of Professor Brito

Ilana Brito uses systems biology approaches to study the transmission of bacterial and genetic components of the human microbiome. As an undergraduate at Harvard University, she double majored in Biology and Government. Given her long-standing interest in infectious disease, she traveled abroad to perform field and lab research on malaria in Mali. She then earned a Ph.D. at the Massachusetts Institute of Technology in Genetics. She received a postdoctoral fellowship from the Earth Institute at Columbia University where she began studying the transmission of viral pathogens and emerging infectious disease. Ultimately, she shifted her focus to the transmission of the multitude of bacteria inhabiting the human body. To this end, she launched a large field research project in the Fiji Islands. In Eric Alm's lab at MIT, she developed methods to examine signatures of transmission in metagenomic whole genome shotgun sequencing data. She has worked with the Broad Institute and the Cary Institute for Ecosystem Studies.

Prof. Brito's lab pioneers systems-level methods to examine the human microbiome and horizontal gene transfer, the predominant mechanism by which pathogens acquire antibiotic resistance. The Brito Lab studies the transmission of commensal microbes between people and their environments and the health impacts of such transmission events. They employ a combination of microbial engineering, single-cell sequencing approaches, and novel computational algorithms applied to metagenomic data to better understand the relationship between human health and the microbiome.

SYMPOSIUM ORGANIZAING COMMITTEE

ORGANIZERS

Dr. Emily Monroe

Dr. Bhanu P. S. Chauhan

Committee Members

Ms. Karyn Lapadura

Dr. Abdelrahman Elleithy

Dr. Mukesh Sahni

Dr. Nishikant Satam

SCHEDULE OF EVENTS

8:00 am – 9:00 am	Check - In University Commons Ballroom Lobby
9:00 am – 9:30 am	Welcome and Opening Remarks University Commons Ballroom C
9:30 am – 11:30 am	Poster Session A University Commons Ballrooms A & B
11:30 am – 12:45 pm	LUNCH - Wayne Dining Hall University Commons Ballroom
1:00 pm – 2:00 pm	PLENARY TALK – University Commons Ballroom C Professor Ilana Lauren Brito Mong Family Sesquicentennial Faculty Fellow in Biomedical Engineering Meinig School of Biomedical Engineering, Cornell University
2:15 pm – 4:15 pm	Poster Session B University Commons Ballrooms A & B
4:15 pm – 5:00 pm	Refreshments – University Commons Ballroom A
5:00 pm – 5:30 pm	AWARDS CEREMONY- University Commons Ballroom C

Poster Session A: Cell & Molecular Biology (Group A)

JUDGES: Dr. David Slaymaker*
Dr. Michael Hanophy

	of Science, Mathematics and Technology, Kean University, Union, NJ	
CMB 6	**THE LIGAND-BINDING PROMISCUITY OF THE MOLYBDATE BINDING PROTEIN, MODA** ***Angelina Moncrieffe*** and Dr. Jannette Carey; Department of Chemical Engineering , Columbia University, New York, NY Department of Molecular Biology , Princeton University, Princeton, NJ	34
CMB 7	**A COMMON TOOL KIT: DO FLIES AND FISH USE THE SAME RNA BINDING PROTEIN TO REGULATE DORSAL-VENTRAL PATTERNING?** ***Stevia Coralie Nanfack-Tsakem***, Stephen Daramola, and Dr. Marcia L. O'Connell; Department of Biology The College of New Jersey, Ewing, NJ	35
CMB 8	**EFFECTS OF SLC6A6 ATTENUATION ON OVARIAN CANCER PRECURSOR CELLS** ***Teagan Polotaye*[1]**, Dr, Daniel Centeno[1], and Dr, Marcin Iwanicki[1] [1]Department of Chemistry and Chemical Biology Stevens Institute of Technology, Hoboken, NJ	36
CMB 9	**ASSESSING THE ROLE OF THE SIN3-RPD3 HDAC COMPLEX ON ANTIFUNGAL RESISTANCE IN THE FUNGAL PATHOGEN *CANDIDA GLABRATA*** ***Tyler Sanchez***, Zubayeda Uddin, and Dr. Kelley R. Healey Department of Biology; William Paterson University, Wayne NJ	37
CMB 12	**Evaluation of Olipass Reagents Efficacy in Targeting SLC6A6 in Ovarian Cancer Cell Lines** ***Paulina Georgoutsos*[1]**, and Dr. Marcin Iwanicki[1] [1]Department of Chemistry and Chemical Biology Stevens Institute of Technology, Hoboken, NJ	38

***Coordinator**

Poster Session A: Ecology, Evolution and Environmental Sciences

JUDGES: Dr. Meriam Bendaoud*
Dr. Joseph Agugliaro

Poster#	Title, Author(s), Affiliation(s)	Page#
EEE 1	**WHY THE TACOMA NARROWS BRIDGE COLLAPESED: AN ENGINEERING ANALYSIS** ***Luis Flores*[1]**, and Dr. Debananda Chakraborty, Ph. D.[1]; Department of Physics, New Jersey City University, Jersey City, NJ	3

	Dept. of Mathematics, New Jersey City University, Jersey City, NJ	
EEE 2	**THE TROPHIC ECOLOGY OF BLACKNOSE DACE IN THE BRONX RIVER;** ***Juliet Hernandez***, and Dr. Matthew Lundquist; Department of Biology, Marymount Manhattan College, New York, NY	40
EEE 3	**USING MICROBIAL SOURCE TRACKING (MST) TO IDENTIFY WASTEWATER POLLUTANTS IN THE SAW MILL RIVER** ***Katrina Isidore, Samantha Lungren***, Zabe Waguespack, Kathalene Lamboy, and Dr. Michelle Hersh; Department of Biology, Sarah Lawrence College, Bronxville, NY	41
EEE 4	**NONINVASIVE ACOUSTIC MONITORING OF BATS IN NEW JERSEY;** ***Kamil Kozlowski***[1], and Dr. Angelo Soto-Centeno[1,21]Department of Earth and Environmental Sciences, Rutgers University – Newark, Newark, NJ; [2]Department of Mammalogy, American Museum of Natural History, New York, NY	42
EEE 5	**MOLECULAR DIET ANALYSES OF PROBOSCIS BATS (*RHYNCHONYCTERIS NASO*) FROM BELIZE;** [1]***Najat Majid***, [1]Sarah Dougherty, and [1,2] Dr. Melissa Ingala; [1]Department of Biological Sciences, Fairleigh Dickinson University, Madison, NJ; [1]Department of Mammalogy, American Museum of Natural History, New York, NY	43
EEE 6	**HONEY BEE COLONY POLLEN FORAGING PREFERENCES AND FOOD PLANT AVAILABILITY THROUGHOUT THE 2023 SEASON IN NORTHERN NEW JERSEY** ***Cole Moran-Bariso*** and Dr. David Gilley; Department of Biology; William Paterson University of New Jersey, Wayne, NJ	44
EEE 7	**EFFECTS OF WASTWATER TREATMENT PLANT EFFLUENT AND ROAD SALT ON FRESHWATER ALGAE, SELENASTRUM CAPRICORNUTUM, POPULATION GROWTH;** ***Mina Rizkalla*** and Dr. James Salierno, Department of Biological Sciences; Fairleigh Dickinson University, Florham, NJ	45
EEE 8	**UBC PRIMER 846 AS A TOOL FOR DETERMINING GENOTYPIC DIVERSITY OF *AMMOPHILA BREVILIGULATA* (AMERICAN**	46

	BEACHGRASS) IN NEW JERSEY COASTAL DUNES; ***Asad Saleh***, Katherine O'Donnell, Michael Carlos, Luke Luzzi, Michael Piraino, Dr. Michael Peek, and Dr. David Slaymaker; Department of Biology, William Paterson University of New Jersey, Wayne NJ	
EEE 9	**A DECADE OF FEEDERWATCH: FOSTERING A DIVERSE AVIAN COMMUNITY ONE SEED AT A TIME;** ***Anthony Santonastaso, Darlyn Breton, Catherine Saldana, Danilo Rocenovic, Suleimy Gomez Colon,*** Helberth Quisbert, Katherine Rodriguez, and Dr. Katherine Wydner; Department of Biology, St. Peter's University, Jersey City, NJ	47
EEE 10	**GLACIAL BOULDERS FROM THE SHAWANGUNK FORMATION AS EYEWITNESSES TO CLIMATE CHANGE: EVIDENCE FROM THE WILLIAM PATERSON CAMPUS REGION AND SURROUNDING COUNTIES;** ***Jenna Black, Jeannette Hewitt,*** Sean Jakubiak, Evelyn Pena, Connor Shillcock, Sinaiah Spivey, Jacob Vander Pyl, and Dr. Martin A. Becker; Department of Environmental Science; William Paterson University of New Jersey, Wayne, NJ	48

***Coordinator**

Poster Session A: Microbiology

JUDGES: Dr. Allyson Salisbury*
Dr. Melissa Ingala

Poster#	Title, Author(s), Affiliation(s)	Page#
MB 1	**ANTIMICROBIAL AND ANTIBIOFILM PROPERTIES OF L-ASCORBIC ACID AND BITTER MELON FRUIT EXTRACT;** ***Jerry Louis*****,** Adriana Pinheiro Machado, Mark Sadek, and Dr. Meriem Bendaoud; Department of Biology, New Jersey City University, Jersey City, NJ	49
MB 2	**EXPLORING ANTIMICROBIAL NANOPARTICULATES FOR ENHANCED SUNSCREEN PROTECTION;** ***Vincent Notabartolo*****,** Divya Chapati, and Dr. A. Benzecry; Department of Biological Sciences, Fairleigh Dickinson University, Teaneck, NJ	50

***Coordinator**

Poster Session A: Physiology, Behavior and Toxicology

JUDGES: Dr. James Moran*
Dr. Marcia O'Connell

	CAUDAL FIN REGENERATION; ***Tasnia R. Hossain;*** ***Arpita Das***; Dr. Kyle A. Murphy; Dr. Lori A. White Department of Biochemistry and Microbiology Rutgers University, New Brunswick, NJ	
PBT 8	**ANALYSIS OF SHOOT CIRCUMNUTATION DEVELOPMENTAL PROFILE IN *ARABIDOPSIS THALIANA;*** ***Wenkai(Kevin) Huang***, and Dr. Eric Brenner Department of Biology, Pace University, Ny, NY	64
PBT 9	**THE TOXICITY OF NANOPLASTICS IN THE OVARY;** ***Maira Nadeem*****, Hanin Alahmadi** and Dr. Genoa Warner; Department of Chemistry and Environmental Science New Jersey Institute of Technology, Newark, NJ	65
PBT 10	**EFFECTS OF VARIOUS SUGAR ALTERNATIVES ON THE WEIGHT OF ZEBRAFISH;** ***Gabriela Rivera Pira*** and Dr. Gaby Fahmy Department of Biology, Felician University, Lodi, NJ	66

***Coordinator**

Poster Session A: Organic Chemistry

JUDGES: Dr. Suresh Sahni*****
Dr. Jonathan Ouellet
Dr. Ish Kumar

Poster#	Title, Author(s), Affiliation(s)	Page#
OC 1	**DE NOVO SYNTHESIS OF THIOPHENE NATURAL PRODUCTS VIA [3+2] CYCLOADDITION OF SULFUR YLIDE AND NITROALKENE;** ***Preethi Devarapalli***, Busola Owolabi, Nurzat Ristovski, and Dr. Nishikant Satam; Department of Chemistry, William Paterson University of New Jersey, Wayne, NJ	67
OC 2	**PHOTOACID GENERATOR CATALYSIS FOR CONJUGATE ADDITION REACTIONS** ***Sahil D'Souza*** and Dr. Joseph Badillo; Department of Chemistry & Biochemistry, Seton Hall University, South Orange, NJ	68

OC 3	**PHOTOPHYSICAL PROPERTIES OF ANCHORING GROUPS BINDING TO TiO_2 FILMS;** ***Jenny Gavazi, Lola Frey***, Marzieh Heidari, Elena Galoppini*; Department of Chemistry, Rutgers University-Newark, Newark, NJ	69
OC 4	**COMPUTATIONAL INVESTIGATION OF SULFONAMIDE-ALDEHYDE DERIVATIVES** ***Gerard Loras*** and Dr. Haoari; Department of Chemistry New Jersey City University, Jersey City, NJ	70
OC 5	**A GREENER ROUTE TO THE SYNTHESIS OF ANTIDEPRESSANT (*S*)-DULOXETINE (CYMBALTA);** ***Alyssa Negron[1*]*,*** **Mariam Haroun[2]**, and Dr. Xiaolei Gao[1]; [1]Department of Natural Sciences, Caldwell University, Caldwell, NJ	71
OC 6	**NICKEL-CATALYZED OXIDATIVE ESTERIFICATION;** ***Jakia Uddin, Rafiatou Bikienga*** and Dr. Parminder Kaur; Department of Chemistry, William Paterson University of New Jersey, Wayne, NJ	72
OC 7	**GOLD NANOPARTICLE INDUCED STEREOSPECIFIC BENZYLIC OXIDATION TO SYNTHESIS δ-HYDROXYALKYNONES: TOTAL SYNTHESIS OF CATECHOL PYRAN ISOLATED FROM PLECTRANTHUS SLYVESTRIS;** ***Julia Zandomenega***, Juan Rodrigues and Dr. Nishikant Satam, Department of Chemistry, William Paterson University of New Jersey, Wayne, NJ	73

*Coordinator

Poster Session A: Nanochemistry

JUDGES: Dr. Mihaela Jitianu*
Dr. Natalya Volashchuk
Dr. Supratik Kar

Poster#	Title, Author(s), Affiliation(s)	Page#
NC 1	**PRUSSIAN BLUE, FROM ARTISTS' PALETTE TO A PROMISING SOLUTION TO RECOVERY OF PRECIOUS METALS FROM ELECTRONIC WASTE;** ***Ishaq Ansari***, and Dr. Xiaolei Gao; School of Natural Sciences, Caldwell University, Caldwell, NJ	74

***Coordinator**

Poster Session A: Theoretical and Analytical Chemistry

JUDGES: Dr. Nishikant Satam*
Dr. Mihaela Leonida
Dr. Kyle Murphy

	LEARNING; ***Jordania Urquizo***, Dr. Natalia Nemeria, and Dr. Colin Kinz-Thompson; Department of Chemistry Rutgers University-Newark, Newark, NJ	
TAC 8	**SYNTHESIS AND CHARACTERIZATION OF PYRROLE-BASED PNP MOLYBDENUM COMPLEXES FOR NITROGEN FIXATION** ***Jane G. Wang[1],*** Souvik Mandal[1], and Dr. Alan S. Goldman[1] [1]Department of Chemistry and Chemical Biology Rutgers, The State University of New Jersey, Piscataway, NJ	88
TAC 9	**COMPREHENSIVE COMPUTATIONAL ANALYSIS TO IDENTIFY DUAL-TARGET INHIBITORS FOR THE NIPAH VIRUS THROUGH THE REPURPOSING OF APPROVED DRUGBANK SMALL MOLECULES** ***Siyun Yang,*** and Dr. Supratik Kar*; Chemometrics and Molecular Modeling Laboratory,Department of Chemistry and Physics, Kean University, Union, NJ	89

***Coordinator**

Poster Session B: Cell & Molecular Biology (Group B)

JUDGES: Dr. Katsuhiro Kita*****
Dr. Matthew Lundquist

Poster#	Title, Author(s), Affiliation(s)	Page#
CMB 10	**CHARACTERIZATION OF THE 5' ENDS OF POLYKETIDE SYNTHASE TRANSCRIPTS IN THE HARMFUL ALGAL BLOOM SPECIES, *KARENIA BREVIS;*** ***Rafi Espinoza Vernier*** and Dr. Emily A. Monroe; Department of Biology, William Paterson University of New Jersey, Wayne, NJ	90
CMB 11	**EXPLORING THE EFFECTS OF AUTOPHAGY ON GABA RECEPTOR EXPRESSION IN HEK 293 CELLS;** ***Britanny Figueroa[1*]***, **Seif Youssef[2]**, **Valerie Egharevba[3]**, and Dr. Reed Carroll[1]; Department of Biology New Jersey City University, Jersey City, NJ	91
CMB 12	**Moved to Morning Session**	---
CMB 13	**THE INFLUENCE OF HPV+ CANCER ON GENOMIC STABILITY AND HUMAN NUCLEI**	92

***Coordinator**

Poster Session B: Cell & Molecular Biology (Group C)

JUDGES: Dr. Carey Waldburger*
Dr. Katherine Wydner

Poster#	Title, Author(s), Affiliation(s)	Page#
CMB 20	**OPTIMIZING *IN VITRO* TRANSCRIPTION TO STUDY PQ CHANNEL MUTATIONS IMPLICATED IN EPILEPSY;** ***Zoubeida Fliesen*** and Dr. Zafir Buraei; Department of Biology, Pace University, New York, NY	99
CMB 21	**INVESTIGATING THE EFFECTS OF GABARAP ON INDUCED AUTOPHAGY IN HEK 293 CELLS;** ***Mary Granados*****[1]**, Kudret Selin Ozkaya[2], Israa Sbateen[2], and Dr. Reed Carroll, Ph. D.[1] Department of Biology, New Jersey City University, Jersey City, NJ	100
CMB 22	**MODELLING INTRACELLULAR CONCENTRATIONS OF FREE AMINO ACIDS IN CULTURED OVARIAN CANCER PRECURSOR CELLS;** ***Michael Greenberg*****[1]** , Dr. Marcin Iwanicki[1] , and Daniel Centeno[1]; [1]Department of Chemistry and Chemical Biology, Stevens Institute of Technology, Hoboken, NJ	101
CMB 23	**CREATING A COST EFFICENT METHOD TO DETERMINE THEOPHYLLINE RIBOSWITCH ACTIVATION;** ***Thomas Hintelmann*****,** Olivia Enny, Mika Schievelbein, James Tilton, and Dr. Jonathan Ouellet [1] Department of Chemistry & Physics, Monmouth University, Long Branch, NJ	102
CMB 24	**AN RNAI SCREEN IDENTIFIED THE *P38 MAP KINASE*, PMK-1, AS A POTENTIAL REGULATOR OF CELL MIGRATION DURING *C. ELEGANS* EMBRYOGENESIS.** ***Avery LaRusso, Nicholas Salierno***, and Dr. Andre Wallace; Department of Biological Sciences, Fairleigh Dickinson University, Teaneck, NJ	103
CMB 25	**MOLECULAR BIOPHYSICS: CLBS DYNAMIC DOCKING WITH AMINO ACIDS;** ***Rubi Larancuent*****[1]** and Dr. Jannette Carey2; 1Mathematics Department, Princeton	104

	University, Princeton, NJ; [2]Chemistry Department, Princeton University, Princeton, NJ	
CMB 26	**CHARACTERIZATION OF THE 5´ ENDS OF HYBRID NONRIBOSOMAL PEPTIDE SYNTHETASE/POLYKETIDE SYNTHASE TRANSCRIPTS IN THE HARMFUL ALGAL BLOOM SPECIES, *KARENIA BREVIS*** ***Bryan Menendez*** and Dr. Emily A. Monroe; Department of Biology, William Paterson University of New Jersey, Wayne, NJ.	105
CMB 27	**THE ROLE OF TAURINE IN AGE-RELATED MACULAR DEGENERATION (AMD)** ***Maria Mihalatos[1]***, Dr. Marcin Iwanicki[1], Tonja Pavlović[1] [1]Department of Chemistry and Chemical Biology (CCB) Stevens Institute of Technology, Hoboken, NJ	106
CMB 28	**INVESTIGATION OF GABARAP AND GABA RECEPTORS DURING AUTOPHAGY** ***Israa Sbateen[1]***, ***Mary Granados[2]***, and Dr. Reed Carroll, Ph. D[1] Department of Biology, New Jersey City University, Jersey City, NJ	107
CMB 29	**THE CELL WALL INTEGRITY PATHWAY IS REQUIRED FOR *FKS2*-MEDIATED ECHINOCANDIN DRUG RESISTANCE IN *CANDIDA GLABRATA;*** ***Zubayeda Uddin***, Saira Tahsin, Gabrielle Popencuk, and Dr. Kelley R. Healey; Department of Biology, William Paterson University of New Jersey, Wayne, NJ	108

***Coordinator**

Poster Session B: Ecology, Evolution and Environmental Sciences

JUDGES: Dr. Karen Swanson*****
Dr. Kathleen Nolan

Poser#	Title, Author(s), Affiliation(s)	Page#
EEE 11	**ASSESSMENT OF DIVERSITY OF SAPROXYLIC FUNGAL COMMUNITIES IN BOREAL FOREST USING THE MYCOPINS METHOD;** ***Sarah Apgar, Joel Lim***, Madhumitha Sadhasivan Gayathri, Laura Vengine, Breanne Hoyte, Mariela Nunez, and Dr. Maria Shumskaya; Biology Department Kean University, Union, NJ	109

EEE 12	**DEVELOPING TREE RING RECORDS FROM HIGH MOUNTAIN NEW JERSEY** ***Jenna Black, Jason Peralta*** & Dr. Nicole Davi Department of Environmental Science; William Paterson University of New Jersey, Wayne, NJ	110
EEE 13	**INVESTIGATING WATER QUALITY IN INTERCONNECTED BODIES OF WATER IN NORTHERN NEW JERSEY;** ***Ashley Buchman, Thomas Morris***, Dr. Mourad Frites; The School of Natural, Health, Social, and Behavioral Sciences; Centenary University, Hackettstown, NJ	111
EEE 14	**BUG ROADS: MODELING THE POTENTIAL DISPERSAL ROUTES OF HYMENOPTERAN POLLINATORS IN NEW YORK CITY** ***Brianna Fay*** and Dr. Matthew J. Lundquist; Department of Natural Sciences; Marymount Manhattan College, NY, NY	112
EEE 15	**THE BACTERIAL SYMBIONTS OF THE PARASITIC PLANT *RAFFLESIA*— MICROSCOPIC PARTNERS FOR CONSERVING THE WORLD'S LARGEST FLOWERS? ;** ***Wenkai (Kevin) Huang,*** Sara Musovic, and Dr. Jeanmaire Molina; Department of Biology, Pace University, NY, NY	113
EEE 16	**BEEING TOGETHER: INVESTIGATING HONEYBEE FORAGING DYNAMICS AND POLLEN DIVERSITY;** ***Ali Kone*** and Dr. David Gilley Department of Biology, William Paterson University of New Jersey, Wayne, NJ	114
EEE 17	**EFFECTS OF TEMPERATURE ON MANGANESE DEMAND IN A MARINE DIATOM, *THALASSIOSIRA PSEUDONANA*** ***Seoane Oaxaca***, ***Fabrizio Candiani,*** Anthony R Himes, andn Dr. Adam Kustka; Department of Earth and Environmental Science, Rutgers University – Newark, Newark, NJ	115
EEE 18	**UBC PRIMER 810 AS A TOOL FOR DETERMINING GENOTYPIC DIVERSITY OF *AMMOPHILA BREVILIGULATA* (AMERICAN BEACHGRASS) IN NEW JERSEY COASTAL DUNES;** ***Katherine O'Donnell, Michael Carlos,*** Asad Saleh, Luke Luzzi, Michael Piraino, Dr. Michael Peek, and Dr. David Slaymaker; Department of Biology, William Paterson University, Wayne NJ	116

EEE 19	**VARIABILITY IN COMMON YELLOWTHROAT SONGS AND THE IMPACT OF ANTHROPOGENIC NOISE;** ***Danilo Rocenovic*** and Dr. Katherine S. Wydner; Department of Biology Saint Peter's University, Jersey City, NJ	117
EEE 20	**THE EFFECTS OF CLIMATE ON THE GROWTH OF EASTERN COTTONWOOD IN AN URBAN PARK;** ***Gianna Tavormina*** and Dr. Allyson Salisbury; Department of Ecology, Evolution and Natural Resources, Rutgers University, New Brunswick, NJ	118

***Coordinator**

Poster Session B: Physiology, Behavior and Toxicology

JUDGES: Dr. Emmanuel Onaivi*****
Dr. Jeffery Erickson

Poster#	Title, Author(s), Affiliation(s)	Page#
PBT 11	**EFFECT OF INCREASED WINTER TEMPERATURE ON METABOLISM AND OXIDATIVE DAMAGE IN OVERWINTERING LUNA MOTHS (*ACTIAS LUNA*);** ***Julia Aid[1]***, and Dr. Joeseph Agugliaro[1]; [1]Department of Biological Sciences Fairleigh Dickinson University, Madison, NJ	119
PBT 12	**FLOPPING MOVEMENT AND DEVELOPMENT IN *MICROSTEGIUM VIMINEUM* RECORDED USING TIMELASE;** ***Alessandra Arnoldi[1]***, and Dr. Eric Brenner[1]; [1]Department of Biology, Dyson College Pace University, NY, NY	120
PBT 13	**THE PHYSIOLOGICAL AND BEHAVIORAL SUBLETHAL EFFECTS OF HEAVY METAL ZINC ON ADULT *AMERICAMYSIS BAHIA*** ***Danielle Bouchard***, and Dr. Kestrel Perez Department of Biology, St Joseph's University, Brooklyn, NY	121
PBT 14	**THE EFFECT OF MELATONIN ON HERB PLANT;** ***Gloria Cobian*** and Dr. Gaby Fahmy Natural Sciences, Felician University, Lodi, NJ	122
PBT 15	***IN SILICO* MODELING OF AQUATIC TOXICITY OF ORGANIC CHEMICALS TO THREE TROUTS' SPECIES: AN**	123

	ENVIRONMENTAL TOXICITY DATA GAP FILLING STUDY; ***Andrea Gallagher***, and Dr. Supratik Kar; Chemometrics and Molecular Modeling Laboratory,Department of Chemistry and Physics, Kean University, Union, NJ	
PBT 16	**MUD PUDDLING BAHAVIOR IN BUTTERFLIES;** ***Emily Lamie***, Dr. Elise R. Morton and Dr. Harald F. Parzer, Department of Biological Sciences, Fairleigh Dickinson University, Madison, NJ	124
PBT 17	**THE ROLE OF THE MAIN OLFACTORY EPITHELIUM DURING MOTHERHOOD** ***Racheal (Eun Li) Lee[1],*** Valentine Andreu[2], Nour Mimouni[3], Bianca J. Marlin[2,3,4,5] 1. Barnard College of Columbia University 2. Department of Neuroscience, Columbia University, New York, NY,10032. 3. Mortimer B. Zuckerman Mind Brain and Behavior Institute, Department of Neuroscience, Columbia University, New York, NY, 10027 USA. 4. Department of Psychology, Columbia University, New York, NY, 10032 USA 5. Howard Hughes Medical Institute	125
PBT 18	**UNRAVELING THE IMPACT OF MICROPLASTICS ON REGENERATION OF *DUGESIA TIGRINA* (PLANARIA);** ***Barbara Munoz*** and Dr. Laura H. Twersky; Department of Biology Saint Peter's University, Jersey City, NJ	126
PBT 19	**HARD METALS LINKED TO AUTISM?: A STUDY IN NORTHERN NEW JERSEY COUNTIES;** ***Ka'Chané Russell*** and Dr. Gaby Fahmy; Department of Biology, Felician University, Lodi, NJ	127
PBT 20	**EVALUATING THE IMMUNE AND INFLAMMATORY RESPONSES IN MICEFOLLOWING EXPOSURE TO THE ARTIFICIAL OXYGEN CARRIER OXYVITA®** ***Mackenzie Zupko, Alina Mendelowski*** and Dr. James Moran Department of Natural Science; Mount Saint Mary College, Newburgh, NY	128

***Coordinator**

Poster Session B: Biochemistry

JUDGES: Dr. Nishikant Satam*
Dr. Kyle Murphy

Poster#	Title, Author(s), Affiliation(s)	Page#
BC 1	**DESIGNING GFP PURIFICATION PROTOCOL FOR TEACHING LAB;** ***Vani Bhagat, Alyssa Allijan***, and Dr. Natalya Voloshchuk; Department of Biochemistry and Microbiology, Rutgers University SEBS, New Brunswick, NJ	129
BC 2	**ISOLATION OF AN APTAMER SELECTIVE TO GLUCOSE ;** ***Deirdre Campbell***, and Dr. Jonathan Ouellet Department of Chemistry and Physics, Monmouth University West Long Branch, NJ	130
BC 3	**INVESTIGATING THE ROLE OF THE BIR2 DOMAIN AS A CASPASE INHIBITOR** ***Rebecca Delp[1],*** and Dr. Mathew Junker[2] [1]Department of Physical Sciences, Kutztown University of Pennsylvania, Kutztown, PA [2]Department of Physical Sciences, Kutztown University of Pennsylvania, Kutztown, PA	131
BC 4	**REEVALUATION OF CATECHOL DERIVATIVES TOWARDS CATALYTIC DOMAINS OF MMPS;** ***Manoj Kumar Depuru, Priyanka Meda***, Dr. Ish Kumar; Department of Chemistry, Biochemistry & Physics, Fairleigh Dickinson University, Teaneck, NJ	132
BC 5	**INVESTIGATION OF THE KINETICS AND INHIBITION OF TM1785, AN ACETYLORNOTHINE AMINOTRANSFERASE FROM *THERMOTOGA MARITIMA*** ***Gabriela Garcia, Drishti Agrawal***, and Dr. Jennifer Martin Department of Chemistry, Stockton University, Galloway, NJ	133
BC 6	**RANDOM PROTEINS BIND RANDOM LIGANDS;** ***Eric Harbinson****, and Dr. Jannette Carey† *Electrical Engineering, Rutgers University †Chemistry, Princeton University; NSF REU Training Site in Biophysics, Nové Hrady, Czech Republic, Summer 2023	134
BC 7	**INVESTIGATING AN ALTERNATIVE METHOD FOR ENDOGLUCANASE CELB2 PRODUCTION IN *E. COLI;*** ***Jyoti Kandel, Yongjian Qin,*** and Dr. Natalya Voloshchuk; Department of Biochemistry and Microbiology, Rutgers University, New Brunswick, NJ	135

BC 8	**I-R3 DNA ENZYME CATALYTIC CHEMISTRY THROUGH ION PROMOTED CLEAVAGE** ***Madison Pellerito*** and Dr. Jonathan Ouellet Department of Chemistry and Physics, Monmouth University, Edison Hall, West Long Branch, NJ	136
BC 9	**SYNTHESIS AND UV-VIS/HPLC SPECTRA ANALYSIS OF NOVEL BENZIMIDAZOLE ANALOGUE HAVING SUGAR MOETY AS CHEMOTHERAPEUTIC AGENT;** ***Ronelle Robinson*** and Dr. Abu Gafar Hossion; College of Science and Society, Chemistry Department, University of Bridgeport, Bridgeport, CT	137
BC 10	**BIOPHYSICAL CHEMISTRY OF AGING** ***Helen Yousaf*[1]**, and Dr. David A. Snyder[1] [1]Department of Chemistry, William Paterson University of New Jersey, Wayne, NJ	138
BC 11	**FUNCTIONAL INVESTIGATIONS OF TM1347: AN ESSENTIAL PROTEIN FOR CELL GROWTH AND PROLIFERATION FROM THERMOTAGA MARITIMA;** ***Neelam Zala*** and Dr. Jennifer Martin; Department of Biochemistry; Stockton University, Galloway, NJ	139

***Coordinator**

Poster Session B: Material Chemistry

JUDGES: Dr. Suresh Sahni*****
Dr. Jonathan Ouellet

Poster#	Title, Author(s), Affiliation(s)	Page#
MC 1	**Immobilization of Bis(2-Pyridylmethyl)amine Frameworks onto Solid Supports;** ***Ava DeFino***, Sarah Dougherty, and Dr. Justin Bogart; Department of Chemistry, Biochemistry, and Physics Fairleigh Dickinson University, Madison, NJ	140
MC 2	**SYNTHESIS OF SILICA-METAL COMPOSITE NANOPARTICLES DECORATED WITH POLY-RHODANINE;** ***Nathfelli I. Garcia, Christopher Trochez***, Dante Gilberti, and Bhanu P. Chauhan* Engineered Nanomaterial Laboratory, Department of Chemistry William Paterson University of New Jersey, Wayne NJ	141

MC 3	**GREEN RECOVERY OF SILVER FROM X-RAY FILMS AND PHOTOGRAPHIC/X-RAY FIXER WASTE;** **Jayden Heron[1*], Chidimma Chima[2]** and Dr. Xiaolei Gao; School of Natural Sciences, Caldwell University, Caldwell, NJ	142
MC 4	**THE IMPACT OF 3D PRINTING ON THE GROWTH OF BIOFILMS ON 316L STAINLESS STEEL;** ***Ashley Igbokwe*** and Dr. Gary Halada; Department of Biology; New Jersey City University, Jersey City, NJ Materials Science/Chemical Engineering, Stony Brook University, Stony Brook, NY	143
MC 5	**RHEOLOGY – A METHOD OF MATERIALS CHARACTERIZATION;** ***Fernando Rojas[1]***, Dr. Andrei Jitianu[2], and Dr. Mihaela Jitianu[1] [1]William Paterson University of New Jersey, Department of Chemistry, Wayne, NJ [2]Lehman College, CUNY, Department of Chemistry, Bronx, NY	144
MC 6	**SILVER NANOPRISMS WITH VINYL FUNCTIONALITIES;** ***Mark Tabor,*** Dwayne Brown, Elijah Cook, and Dr. Bhanu P. S. Chauhan Engineered Nanomaterials Laboratory, Department of Chemistry William Paterson University of New Jersey, Wayne NJ	145
MC 7	**CONTROLLED MESOPOROUS SILICA GEL** ***Arianna Yom[1]***, Qiaxian R. Johnson[2], Clairissa Yom[2], and Dr. Bhanu P. S. Chauhan[2]* [1]Northern Valley Old Tappan High School, Old Tappan, NJ [2]Engineered Nanomaterials Laboratory, Department of Chemistry William Paterson University of New Jersey, Wayne, NJ	146
MC 8	**COCHINEAL RED AS A PH-RESPONSIVE FOOD FRESHNESS INDICATOR, A NEW DESTINY FOR THE BUGS TO DYE FOR;** ***Pamela Nolasco***, Gabriela Moran, and Dr. Xiaolei Gao; School of Natural Sciences Caldwell University, Caldwell, NJ	147

***Coordinator**

RME-8'S OLIGOMERIZATION CAPABILITY AFFECTS ITS LIMITING FUNCTION ON THE DEGRADATIVE MICRODOMAIN IN *C. ELEGANS*

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Endocytosis is a process by which a cell takes in extracellular material from the surrounding environment by engulfing the cargo with the cell membrane. After endocytosis, the transmembrane cargo reaches endosomes, which include the early endosome. The early endosome contains microdomains that consist of protein coats that direct some transmembrane cargo to be recycled or degraded. One of the proteins that is part of the recycling microdomain is called RME-8, which is physically different from the degradative microdomain. It even limits the degradative microdomain from localizing around the endosome. RME-8's function is essential for many physiological processes like nutrient uptake, cell polarity, Alzheimer's, and Parkinson's disease. This research aims to understand how RME-8 limits the degradative microdomain.

The Grant Lab has identified an allele of RME-8 that is hyperactive, and the hypothesis is that this allele alters the oligomerization status of RME-8. We are also collaborating with structural modelers who have used the AlphaFold program to predict that RME-8 can form monomers, dimers, and tetramers. Furthermore, using native gel electrophoresis, we can see RME-8 migrates on the gel in several different bands, which are consistent with a monomer, dimer, and tetramer. The structural models identified four high-fidelity domains that make up RME-8, and I have cloned each of these domains for protein expression and GST-pull-down binding experiments. If indeed RME-8 forms an oligomer and our hyperactive allele of RME-8 disrupts this oligomerization, we would predict that the wild-type RME-8 domains would dimerize in the presence of another wild-type RME-8, but in the presence of allele-mutated RME-8, the wild-type RME-8 wouldn't bind to the mutated RME-8. If this allele mutation does disrupt the oligomerization of RME-8, we can hypothesize that a lack of oligomerization leads RME-8 to be in a hyperactive conformation that limits the degradative microdomain more than wild-type RME-8.

OPTIMIZING BIODEGRADABLE GELATIN ELASTIN CRYOGEL SCAFFOLDS FOR ADVANCING REGENERATIVE MEDICINE APPLICATIONS

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A fundamental aspect of regenerative medicine is the development of scaffolds that facilitate cell growth. While there are numerous studies exploring scaffold development for supporting cell growth, there is an increasing need for novel biomaterials that are simple to manufacture, biodegradable, and possess mechanically strong biophysical properties. Cryogel scaffolds, a form of hydrogels, can absorb fluids and provide continuous hydration to wound sites, stimulating cell migration and differentiation. Cryogels has recently grown as promising substitute to standard wound dressings, however one challenge with cryogel biomaterials is their relatively low mechanical strength compared to chemically manufactured materials.

We aimed to develop gelatin-based cryogels that can withstand the magnitude of mechanical forces generated within our bodies. We incorporated elastin, an extracellular matrix protein, into our cryogels due to their elastic and protective nature in connective tissues and other organs in the body. Our experiments revealed an optimal elastin concentration for maximal elastic modulus and tensile strength, consistently observed across multiple tests. Elastin concentration up to 0.5%, increased elasticity, while the tensile strength/ force reached a breakpoint at 0.15-0.2N. Our results suggest that elastin can increase the elasticity and tensile strength of gelatin-elastin cryogels. We also tested the feasibility of gelatin-based cryogels for microscopic imagining to ensure their potential as effective imaging substrates. We discovered that gelatin-based cryogels can be stained with pyronin Y (and 561 nm laser). We observed the Pyronin Y stained cryogels using the far-red channel (Alexa Fluor 633/647) allowing for specific visualization. Clear visualization achieved through staining and imaging methods allows for accurate observations of dual color imaging with mesenchymal stem cells (MSCs) with no crosstalk, which may increase the applicability of gelatin elastin cryogels for biomedical applications. These findings suggest elastin's potential as a valuable component in biodegradable cryogels for regenerative medicine.

CLONING AND EXPRESSION OF A CASPASE-3 CANDIDATE FROM THE HARMFUL ALGAL BLOOM SPECIES, *KARENIA BREVIS*

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Karenia brevis is a dinoflagellate responsible for harmful algal blooms off the coast of Florida, which produces toxins that impact marine life and human health. The molecular mechanisms involved in bloom termination remain poorly understood, but programmed cell death (PCD) has been suggested to be involved. Caspases are enzymes involved in PCD, and a caspase 3 candidate (KB-cas) was identified in a 2014 *K. brevis* transcriptome. This gene was overexpressed in *E. coli* and showed caspase activity. However, overexpression was not strong, and *E. coli* stopped growing once the gene was induced, suggesting the product was harmful *to E. coli*. A new *K. brevis* transcriptome revealed additional sequence on the 5´ end of the original KB-cas 3 candidate sequence which included additional sequence in the open reading frame. The objectives of this study were to first make a new KB-cas construct using the entire open reading frame in a new vector that may improve expression and then to overexpress the KB-cas 3 candidate in *E. coli* to measure caspase activity of the caspase candidate. The KB-cas 3 gene from the new transcriptome was PCR amplified from *K. brevis* cDNA, cloned into a pET46 EK/LIC vector, and transformed into BL21 pLysS *E. coli* competent cells. Transformed *E. coli* were grown at 37°C to mid-log phase in LB broth containing ampicillin (150 µg/mL) and chloramphenicol (25 µg/mL), and protein expression was induced using 0.5 and 1.0 mM IPTG. Induced *E. coli* cultures were grown overnight at 20°C with shaking. Samples were taken pre-IPTG induction, 3 hours post induction, and overnight after induction, and samples were stored at -80°C until analyzed. For preliminary SDS-PAGE analysis, cell pellets were resuspended in BioRad protein sample buffer, heated for 5 min at 95 °C, and run on a 4-20% BioRad Mini-PROTEAN TGX stain-free gel at 200 V for 30 minutes. Gels were imaged using BioRad ImageLab software. Preliminary analysis suggested an induced protein around 70 kDa consistent with the caspase protein size. To confirm the results, transformed *E. coli* were grown at a larger volume in the same manner as described above. An untransformed control was also run in parallel in LB without antibiotics during this experiment. From this experiment, SDS-PAGE analysis did not show protein products unique to the transformed sample based on the total protein imaging. To determine if a His-tagged protein was overexpressed in the transformed sample, Western blots were performed using an anti-His antibody on uninduced and induced protein lysates from both transformed and untransformed samples. All protein lysates contained a protein of the same size that cross-reacted with the anti-His antibody suggesting the transformed cells were not overexpressing our KB-cas 3 candidate. Future work will focus on troubleshooting the overexpression of KB-cas in *E. coli* and determining caspase activity of this caspase candidate. Characterization of a caspase protein in a dinoflagellate will increase our understanding of PCD processes in single-celled eukaryotes and may be useful in mitigation of *K. brevis* bloom events.

INVESTIGATING GABARAP AND GABA RECEPTORS DURING AUTOPHAGY

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Autophagy is a natural cellular process that plays a crucial role in maintaining homeostasis by eliminating damaged or unnecessary components. It involves the degradation and recycling of cellular material, such as organelles and proteins, through the formation of specialized structures called autophagosomes. Autophagy is tightly regulated and can be triggered by various cellular stressors, including nutrient deprivation, oxidative stress, and infection. Malfunction of autophagy has been linked to neurodegenerative diseases such as Alzheimer's and Parkinsons disease.

An important protein involved in this process is the GABA Receptor Associated Protein (GABARAP). GABARAP has been suggested to target cargos to the autophagosomes and the binding of lysosomes to autophagosomes. GABARAP is also known to bind to GABA neurotransmitter receptors and appears to be involved in the trafficking of the receptors. As GABARAP plays a role in both of these processes, a question arises as to whether GABA receptors are regulated by autophagy and if GABARAP plays a role in this process. This study addresses these questions by investigating the effects of autophagy on GABARs and GABARAP in HEK cells.

THE HEALTH EFFECTS OF GREEN COFFEE OIL IN *Caenorhabditis elegans*

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Green coffee oil (GCO) is a triglyceride mixture derived from green coffee beans used in the cosmetics industry as an antioxidant. GCO contains fatty acids (e.g. linoleic and palmitic acid) and other minor components, such as diterpenes (e.g. cafestol and kahweol), polyphenols and phenolic acids. Due to its composition, there are potential new usages of GCO for human health and wellness, as the antioxidant nature of GCO may support cell functions by reducing oxidative stress.

Caenorhabditis elegans is a nematode (roundworm) used as a biological model due to its short life cycle, short lifespan, and molecular similarities with humans. The transparent *C. elegans* body and its small size make it easier to observe their morphology and identify different life cycle stages. The goal is to evaluate the health effects of GCO on growth, oxidative stress resistance, and lifespan of *C. elegans*.

Worms were treated with 0.1% and 0.5% GCO, and 0.5% dimethyl sulfoxide as the vehicle control. After 48 hours of incubation, the growth rate assay was performed by observing the stages and size of *C. elegans* under the microscope. The effects of GCO in growth are helpful to determine its beneficial doses in *C. elegans*. Next, we will study the effects of GCO on oxidative stress resistance and lifespan assay. This research will give us insights on the benefits of GCO as a potential dietary supplement or food for humans. Further experiments using GCO in *C. elegans* may be used to evaluate the molecular pathways against oxidative stress and aging.

THE LIGAND-BINDING PROMISCUITY OF THE MOLYBDATE BINDING PROTEIN, MODA

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Ligand-Binding promiscuity of many proteins is overlooked due to their low binding potential when viewed under static frames. These proteins have not been given the opportunity to be further studied under dynamic simulations in order to determine their true promiscuous nature. The focal point of this research is to utilize computational molecular dynamics in order to study the binding behavior pattern of the Molybdate Binding Protein, ModA. This protein was chosen under loose criteria, such as size, resolution, and orientation, and was computationally docked with all 20 amino acids, as well as additional tetrahedral shaped ligands such as Phosphate, Sulphate, Adenosine Monophosphate, and S-Adenosylmethionine. Results revealed unknown binding sites with predicted energies comparable to those promising for pharma lead compounds. Addition of other functional groups to some amino acids doubled the predicted binding energy. Thus, readily accessible computational tools for dynamic evaluation enable the identification and quantification of the ligand-binding protein promiscuity for various protein structures.

A COMMON TOOL KIT: DO FLIES AND FISH USE THE SAME RNA BINDING PROTEIN TO REGULATE DORSAL-VENTRAL PATTERNING?

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The translucent embryos of zebrafish (*Danio rerio*) make them ideal organisms for studying dorsal-ventral patterning of the embryo in vertebrates. Much of the regulation of this patterning occurs during early embryogenesis, when the fertilized zygote is relying on maternally provided gene products, and before the transition has occurred to zygotic gene expression (the MBT, or mid-blastula transition). In zebrafish, this activation of the zygotic genome does not occur until several hours after fertilization, during the 1K-high stages. Therefore, as is true for all vertebrates, much of the regulation of early embryogenesis is dependent on the translational control of maternal mRNAs. We have pursued an analysis of the role of a specific mechanism of translational control, called cytoplasmic polyadenylation, in dorsal-ventral patterning, by taking the candidate gene approach. We have identified a family of four genes in zebrafish, called the *zsquid* family (A-D) that are homologous to the single dorsoventral patterning gene in *Drosophila melanogaster*, called *squid*. Within the family of zebrafish genes, we have demonstrated that the protein products of the four *zsquid* genes are closely related to one another, and form a single clade. In addition, all four *zsquid* mRNAs are maternally provided. Furthermore, in the case of *zsquidA* - which is most closely related to *Drosophila squid* - its mRNA is polyadenylated at a key time during embryogenesis, with all transcripts fully polyadenylated by the 1K cell stage. Therefore, we are currently testing a model whereby the translation of the *zsquidA* maternal mRNA is regulated by cytoplasmic polyadenylation, and at precisely the correct time for the zsquidA protein to participate in dorsal-ventral patterning. Here, we present experiments aimed at determining whether the *zsquidA* mRNA a) can restore a normal phenotype to *zsquidA* morphants via microinjection, and b) is bound to a CPEB protein involved in cytoplasmic polyadenylation, via co-IP experiments.

EFFECTS OF SLC616 ATTENUATION ON OVARIAN CANCER PRECURSOR CELLS

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Non-ciliated fallopian tube epithelial (FNE) cells are precursor cells for the most frequently occurring type of ovarian cancer, high-grade serous ovarian cancer (HGSOC). Tumor protein p53 (TP53) is nearly ubiquitously mutated in ovarian cancers, and it is frequently associated with FNE cell transformation. How mutant p53 contributes to HGSOC development and progression is not well understood. Thus, we wanted to determine the consequences of mutant p53 expression in FNE cells. Previously conducted mass spectrometry of cell surface proteomics from our lab suggests that mutant p53 FNE induces expression of SLC6A6 taurine transporter, indicating the possibility that taurine transport mechanisms are involved in FNE-m-p53-dependent transformation. To investigate this possibility we used shRNA to attenuate SLC6A6 expression levels. Various phenotypical changes such as decreased proliferation and morphology changes were observed. Furthermore, we have demonstrated that lower SLC6A6 expression increases sensitivity to genotoxic stress evoked by cisplatin, a commonly used chemotherapy agent for HGSOC. With these findings, we plan to further validate these phenotypical changes in multiple ovarian cancer cell lines and move on to a mechanistic study.

ASSESSING THE ROLE OF THE SIN3-RPD3 HDAC COMPLEX ON ANTIFUNGAL RESISTANCE IN THE FUNGAL PATHOGEN *CANDIDA GLABRATA*

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Invasive fungal infections caused by *Candida glabrata* yeast exhibit elevated rates of antifungal drug resistance. Resistance to echinocandin antifungals is characterized by mutations within genes (*FKS1* or *FKS2*) that encode for the echinocandin target enzyme, beta-1,3-glucan synthase. Research has shown the importance of gene regulation through histone acetylation and deacetylation in antifungal susceptibility and resistance development. Here, we aimed to determine the role of the Sin3-Rpd3 histone deacetylase (HDAC) complex in *C. glabrata* drug resistance. Previous studies identified both *SIN3* and *RPD3* knockout strains in screens for increased echinocandin drug susceptibility; however, their role in resistance has not been described. We first determined frequencies of drug-resistant colonies through selection of wild type and *SIN3* and *RPD3* knockout strains on echinocandin (micafungin and caspofungin) drug plates. Results showed that the knockout strains yielded decreased frequencies of colonies compared to wild type indicating the importance of the Sin3-Rpd3 HDAC complex in echinocandin resistance development. Another aim was to disrupt *SIN3* and *RPD3* in drug resistant mutants to determine if these genes are essential in echinocandin resistance stability. We transformed competent cells of *FKS1* and *FKS2* resistant mutants with a PCR-amplified deletion marker targeted to either the *SIN3* or *RPD3* locus. Colonies grown up on selective medium were PCR-screened and sequenced to confirm successful gene deletion. Drug susceptibility assays showed no significant differences in micafungin or caspofungin minimum inhibitory concentrations (MICs) in echinocandin resistant strains disrupted for *SIN3* compared to the resistant controls; however, moderate decreases (4-fold) in MICs were observed upon disruption of *RPD3*. Overall, our work suggests that the Sin3-Rpd3 HDAC complex is involved in echinocandin tolerance, resistance development, and to some extent, resistance stability.

Evaluation of Olipass Reagents Efficacy in Targeting SLC6A6 in Ovarian Cancer Cell Lines

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Non-ciliated fallopian tube epithelial (FNE) cells are precursor cells for the most common ovarian cancer, high-grade serous ovarian cancer (HGSOC). Solute carrier 6A6 (SLC6A6) mediates cellular taurine uptake. Our findings demonstrate that taurine confers cisplatin resistance in ovarian cancer cell lines and that SLC6A6 is expressed in cisplatin-resistant cells. This highlights SLC6A6 as a potential therapeutic target to enhance cisplatin sensitivity in ovarian cancer. Collaborating with OLIPASS Inc., we are developing strategies to target SLC6A6 in cell culture. Their Olipass Peptide Nucleic Acid (OPNA) technology modulates mRNA splicing to alter protein expression. Through western blot we have successfully knocked down SLC6A6 at a concentration of 1 uM OPNA in FNE cells. We are currently evaluating the efficacy of multiple SLC6A6-targeting OPNAs on several OC cell lines in targeting SLC6A6 downregulation.

WHY THE TACOMA NARROWS BRIDGE COLLAPESED: AN ENGINEERING ANALYSIS

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The Tacoma Narrows Bridge is the historical name given to the twin suspension bridge—originally built in 1940—that spanned the Tacoma Narrows strait. It collapsed just four months later due to aeroelastic flutter. The Tacoma Narrows Bridge collapsed primarily due to the aeroelastic flutter. In ordinary bridge design, the wind is allowed to pass through the structure by incorporating trusses. In contrast, in the case of the Tacoma Narrows Bridge, it was forced to move above and below the structure, leading to flow separation. Such flow separation, in the presence of an object, can lead to the development of a Kármán vortex street, as the flow passes through the object. In this short research work, we tried to find the exact reason for collapsing the bridge by considering vertical motion and torsional motion. A set of numerous basic models of suspension bridges were performed and the primary cause of collapsing was investigated. Since the torsional rotation of the bridge is what ultimately caused its failure, we deeply analyze the model of torsional rotation.

THE TROPHIC ECOLOGY OF BLACKNOSE DACE IN THE BRONX RIVER

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Urbanization, the transformation of natural landscapes into cities, is rapidly increasing and forces city rivers and streams to face challenges, including increased salinity, higher temperatures, runoff, nutrient pollution, and habitat loss. The Bronx River has low aquatic insect diversity and abundance is significantly reduced compared to non-urban rivers. The most abundant aquatic invertebrates in the Bronx River include caddisflies, midges, and amphipods, varying in both biomass and abundance. These insects are crucial food sources for fish in the river, including blacknose dace, *Rhinichthys atratulus*. Lower insect biodiversity and abundance could impact the fish trophic ecology in the river.

To study the trophic dynamics in the river, *Rhinichthys atratulus* was collected from June through July 2023. The lengths of the fish (cm) were recorded and then fish gut content was recovered. Invertebrate bodies both partial and whole were identified under a microscope and separated by taxa and location. Despite having the smallest biomass, midges were the preferred food choice for blacknose dace of all body sizes. This suggests that blacknose dace prefer the smaller prey and most likely must consume more to get the same energy in their diets that larger prey like caddis flies would provide.

USING MICROBIAL SOURCE TRACKING (MST) TO IDENTIFY WASTEWATER POLLUTANTS IN THE SAW MILL RIVER

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The Saw Mill River has frequently had levels of Enterococcus above the EPA limit, indicative of wastewater pollution. However, there has been debate over whether this pollution is of human origin. CURB (Center for Urban River at Beczak) has been monitoring fecal bacteria pollution in the river for almost 10 years. We worked in conjunction with CURB to sample water and look for bacterial DNA only found in humans' fecal matter. We extracted DNA from filtered water samples collected in the summers of 2022 and 2023. We then used quantitative PCR to identify ribosomal DNA from the HF183 cluster of the genus *Bacteroides,* bacteria found exclusively in the human gut microbiome. We found consistently high levels of HF183 rDNA in almost all samples. This evidence suggests that further work is needed to determine the specific sources of wastewater contamination in the Saw Mill River.

NONINVASIVE ACOUSTIC MONITORING OF BATS IN NEW JERSEY

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Noninvasive acoustic monitoring can be an effective method for collecting large amounts of data on otherwise elusive animals such as bats. This makes acoustic monitoring an indispensable tool for developing bat inventories and assessing activity and diversity. Our objective was to measure bat species abundance in a green space in urban New Jersey. Song Meter Mini Bat recorder (Wildlife Acoustics) was set up at Meadowlands Environmental Research Institute (MERI). The device recorded bat echolocation calls from June to September of 2021. Acoustic data was collected every month over a span of 8 nights. Data was processed using Kaleidoscope Pro acoustic analysis software. Initially it underwent an auto identification process which recognizes calls as either noise or a particular bat found in New Jersey. Later the calls were manually processed to ensure highest accuracy. Manually sorted data was used to perform month to month species abundance comparison using t-tests. The analysis confirmed a significant change in bat species abundance across the time. Our research showed that green spaces in urbanized New Jersey environments can act as centers for bat diversity.

MOLECULAR DIET ANALYSES OF PROBOSCIS BATS (*RHYNCHONYCTERISNASO*) FROM BELIZE

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The proboscis bat (*Rhynchonycteris naso)* is a small peri-aquatic bat species that roosts in conspicuous colonies and is common throughout the Central and South American tropics. Animals like *R. naso* that roost in exposed areas along active waterways may be vulnerable to disturbance from passing boat traffic, potentially leading to different foraging behaviors. In this study, we analyzed the diets of three groups of proboscis bats along the New River in Orange Walk, Belize– a heavily traveled waterway with less traveled tributary creeks. Between 2021– 2023, over 104 fecal samples were collected following immediate capture and release methods. We sampled three localities with different levels of human disturbance: Dawson's Creek, BarberCreek, and the Lamanai Outpost Dock. Fecal samples were used to construct cytochrome oxidase I (COI) libraries, which we used to identify insect prey species. While the number of prey species detected did not differ among the roosts, bats on the less disturbed creeks had unique prey species compared to the bats at the highly disturbed dock. This data suggests that differences in insect communities among the localities play an elemental role in determining distinct dietary patterns. Our results also show fine-scale differences in beta diversity despite theproximity between the roosts (~1–3 km). However, more information is required via additional samples to determine whether *R. naso* bats have any fitness consequence to the observed dietaryshifts, especially in other highly disturbed environments across their geographic range.

HONEY BEE COLONY POLLEN FORAGING PREFERENCES AND FOOD PLANT AVAILABILITY THROUGHOUT THE2023 SEASON IN NORTHERN NEW JERSEY

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Environmental stressors such as phenological mismatch between flowering plants and insect pollinators driven by climate change are leading to pollinator decline. Honeybees are an important model system for generalist pollinators because of the economic value of honeybee pollination and the role they play in ecosystems worldwide. This project investigates honeybee colony pollen foraging preferences and how they change over time in an urbanized environment.To determine honeybee colony pollen foraging preferences throughout the active season, 24-hourpollen samples from two roof-top apiary colonies were collected once per week. These pollen samples were used to identify and quantify abundances of source plants via hemocytometry overan entire season. To determine the food source plants from which the bees were choosing at eachpollen sample, regional bloom dates were determined via field assays twice per week within the foraging range of the focal colonies. The pending results will reveal patterns including the frequency of a colony's collection from long-term versus short-term blooming species, distinctions in foraging preferences between invasive and native species, as well as the extent of similarities and differences in foraging patterns between the two colonies throughout the season. This comprehensive analysis will allow for comparison with pollen collected since 2017 and provide a detailed benchmark for the pollinator-plant phenology to detect future potential phenological mismatch due to climate change.

EFFECTS OF WASTEWATER TREATMENT PLANT EFFLUENT AND ROAD SALT ON FRESHWATER ALGAE, SELENASTRUM CAPRICORNUTUM, POPULATION GROWTH

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Wastewater treatment plants (WWTPs) are essential for receiving, treating, and recycling residential and municipal wastewater. However, despite efforts to maintain water quality, WWTPs often release excess nutrients into receiving bodies of water. In addition, the application of seasonal road salts may runoff into freshwater systems and negatively impact organisms. This study investigated the population growth of freshwater algae, *Selenastrum capricornutum*, cultured within river water samples containing WWTP effluent mixed with two environmentally relevant concentrations of road salt. The hypotheses stated that (1) algal growth will increase with increasing WWTP effluent concentrations and (2) that the exposure to road salt will affect the algal growth. Water samples were collected from three locations in the Whippany River (Morris County, NJ), which receives WWTP effluent (upstream of the effluent source, at the effluent source, and downstream). To simulate road salt runoff, two concentrations (0.75 & 1.5 ppt) of a 50:50 mixture of calcium chloride (CaCl2), sodium chloride (NaCl) were then added to the river water to achieve the final exposures. Algae were then grown in the laboratory in the river water samples with the high and low salt concentrations, plus a control, for 18 days at 4100 lux and 26º C (N=5/TRT). Algal density was then recorded using a spectrophotometer (absorbance at 650 nm) three times weekly, which was then converted to cells/mL. Algal population density and growth rates were then calculated at the end of the experiment. Results indicated that river samples containing effluent had increased nutrients (N and P) compared to the upstream site. In addition, an increase in algal population density and growth rate was detected when cultured in with WWTP effluent, which may have bene due to the increased nutrients present. Road salt, however, had less of an effect than wastewater effluent on algal population growth. These results suggest that increased nutrients from wastewater treatment plants have a more prominent effect on algal growth compared to road salt.

UBC PRIMER 846 AS A TOOL FOR DETERMINING GENOTYPIC DIVERSITY OF *AMMOPHILA BREVILIGULATA* (AMERICAN BEACHGRASS) IN NEW JERSEY COASTAL DUNES

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New Jersey's coastal dunes provide natural beauty, critical habitat, and infrastructure protection for the state's coastal communities. Restoring New Jersey's coastal dunes typically involves single-genotype plantings of the 'Cape' variety of American Beachgrass (*Ammophila breviligulata*) for dune stabilization and development. However, it remains an important question whether single genotype plantings provide sufficient long-term sustainability and ecosystem function. To establish a benchmark of native diversity in New Jersey populations of *A. breviligulata*, Inter-Simple Sequence Repeat (ISSR) markers were used to demonstrate high genotypic diversity in three native New Jersey *A. breviligulata* foredune populations, but showed moderate diversity in the single mid-dune population analyzed (Slaymaker et al., 2015). Here we use ISSR markers to measure genotypic diversity across a successional gradient, from fore-dune to rear-dune, in a native New Jersey dune system. Initial work with UBC Primer 846 will be presented. This project will provide a better understanding of *A. breviligulata* biology and may inform future dune restoration practices.

A DECADE OF FEEDERWATCH: FOSTERING A DIVERSE AVIAN COMMUNITY ONE SEED AT A TIME

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Thirty-six avian species have been reported during the ten-year history of Project FeederWatch (PFW) on Saint Peter's University's urban campus. Analysis of the first eight years of data revealed an increase in total species seen per season and per week in the four years following partial native habitat restoration in the PFW study area. Our ongoing goals are to document species, create a supportive space for wintering and migrating birds in the midst of urban habitat, increase overall avian biodiversity, and encourage native bird species. Last year (2022-23), we experimented with a seed mixture at feeders that we hoped would discourage house sparrows, an invasive nonnative species that can be aggressive. This year (2023-24), thanks to a grant from the Society for Biodiversity Preservation, we expanded seed selections at feeders in an effort to provide food options that would support and attract a diversity of species. So far this season, we have identified 23 species, the highest number for any single PFW season to date. This total includes three native species seen for the first time: Tennessee warbler, hermit thrush, and red-winged blackbird. In addition, we are in the process of installing a camera system that will record birds that visit the feeders. This information will help us understand which species are primarily attracted to feeders versus those that are attracted to natural resources in the count area such as plant cover, berries, and wild seeds.

GLACIAL BOULDERS FROM THE SHAWANGUNK FORMATION AS EYEWITNESSES TO CLIMATE CHANGE: EVIDENCE FROM THE WILLIAM PATERSON CAMPUS REGION AND SURROUNDING COUNTIES

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Milky quartz pebble conglomerate boulders are scattered throughout the William Paterson Campus Region (WPCR) and surrounding northern counties in New Jersey. The monomineralic lithology of these boulders is uniquely distinct from local bedrocks found in these counties which consists primarily of basalt, brownstone, gneiss and shale. These boulders represent glacial erratics belonging to the Shawangunk Formation (GBSF) that outcrops in the Lower Hudson Valley Region and areas west of New Paltz, New York.

Detailed fieldwork indicates that GBSF have been transported as much as ~150km from their source provenance during the late Wisconsin glacial event in North America. GBSF allow components of the complex geologic history of the WPCR and northern New Jersey counties to be reconstructed. This geologic history documents several hundred million years of plate tectonism, sea level change, volcanic activity and glaciation and provides an opportunity to further reconstruct the glacial history of our suburban neighborhoods not normally recognized for continental ice sheets.

ANTIMICROBIAL AND ANTIBIOFILM PROPERTIES OF L-ASCORBIC ACID AND BITTER MELON FRUIT EXTRACT

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The growing number of emerging infectious diseases and antimicrobial resistance have become a worldwide concern for human health and welfare as available treatments are becoming inefficient. Biofilm formation, a multi-layer of microorganisms attached to each other and to surfaces, plays an important role in the development of antimicrobial resistance and makes it difficult to eradicate the infection with conventional treatment. The need for novel antibiofilm and antimicrobial compounds is crucial to combat the increasing occurrence of antimicrobial resistance. In this study, we investigate the antibiofilm and antimicrobial properties of the widely known vitamin L-Ascorbic acid, and the fruit extract of *Momordica charantia*, a commonly used plant in the Caribbeans. Both compounds were tested against 22 different bacterial and fungal strains using a broth assay and a biofilm assay. Initial results show that L-Ascorbic acid has significant antimicrobial properties against almost all bacterial strains tested but no effect on any of the fungi. On the other hand, *M. charantia* fruit extract had little to no antimicrobial properties but revealed a significant selective antibiofilm effect on bacterial strains including *Staphylococcus aureus*, *Staphylococcus epidermis*, *Bacillus subtilus*, *Escherichia coli, Pseudomonas aeruginosa,* and fungal strains including *Candida glabrata* and *Candida albicans.* Our results substantiated the antimicrobial benefits of L-Ascorbic acid and provided new insight into the antibiofilm properties of the fruit extract against a broad range of microorganisms. Further studies will be conducted to identify the active fraction of the fruit extract and investigate the antimicrobial and antibiofilm properties of the leaves of *M. charantia* plant.

EXPLORING ANTIMICROBIAL NANOPARTICULATES FOR ENHANCED SUNSCREEN PROTECTION

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In response to the detrimental effects of UV radiation on human skin, our study explored the antimicrobial properties of novel nanoparticulate composed of Zein-lupulone and Zein-chitosan polymers, for sunscreen application. Test nanoparticles were prepared by Dr. Leonida's team containing only GRAS substances and using an eco-friendly, inexpensive green antisolvent procedure. The ingredients used have properties that are beneficial to the skin. Zein, a biodegradable corn protein that maintain moisture, and shows effective absorption by cells. Lupulone, a hop derived antibacterial and antioxidant gent that has a stimulating effect on the collagen production in the body, and Chitosan a biocompatible polysaccharide well known safe antimicrobial agent.

Particulates containing different concentrations ratios of Zein/Lupulone and Chitosan were tested for their antimicrobial activities and their minimum inhibitory amounts (MIC) against opportunistic bacterial species relevant for the skin, *Staphylococcus aureus* (gram-positive bacteria), *Escherichia coli* and *Pseudomonas aeruginosa* (gram-negative bacteria), and *Candida albicans* (yeast) using agar well diffusion tests and 96 well plate. Our findings revealed that the nanoparticles inhibited bacterial growth, suggesting their potential as safe, effective ingredients in skincare products for mature skin, providing a preferable alternative to harmful substances in conventional topical formulations.

THE EFFECTS OF E-LIQUID ON THE GROWTH OF CANDIDA ALBICANS AND STREPTOCOCCUS SALIVARIUS ON BUCCAL EPITHELIAL CELLS

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E-cigarettes are alternative devices to the traditional cigarette. Many use it through the oral inhalation of aerosols created from the evaporation of e-liquid. During vaporization, propylene glycol, glycerol, vegetable glycerin, and other chemicals are released and may affect the overall health of the oral microbiome. A notable diversity of commensal bacteria and fungi can be found in the oral microflora. *Candida albicans* is a pathogenic fungus that is usually found in the mouth, genitourinary system, gastrointestinal tract, and skin. Excessive growth of *C. albicans* causes an opportunistic disease called candidiasis, which can damage the oral cavity among other regions of the body. One of the many bacteria that inhabit the oral cavity is *Streptococcus salivarius*, which also has one of the strongest attachments to epithelial cells. Previous studies had determined that 42.5% of individuals who smoke e-cigarettes are more likely to develop gum diseases compared to 28.2% of non-smokers.[1] Both strains of *S. salivarius* and *C. albicans* have the ability to adhere to epithelial cells. *C. albicans* attach to host surface cells and grow by thigmotropism through means of adhesin expressions.[2] The gram-positive bacteria *S. salivarius* has been known to attach through means of anchoring to the host's cell wall envelope.[3]

A number of environmental changes have been shown to interfere with the attachment of *S. salivarius* and *C. albicans* to oral cell surfaces. In this study, we used an e-cigarette and a vacuum filtering system to create various concentrations of e-liquid vapor solutions by drawing vapor through phosphate buffer for 15-sec, 30-sec, 1 min, and 3 min. Using a compound microscope, the attachment of *S. salivarius* and *C. albicans* to buccal epithelial cells was manually recorded over a range of concentration and incubation times. Under higher vapor concentrations, the attachment of *S. salivarius* and *C. albicans* to buccal epithelial cells demonstrated a significant decrease. However, *S. salivarius* appeared to have a more drastic decrease. There was no attachment of *S. salivarius* in the highest concentrated vapor solution. However, *C. albicans* attachment was still present and prominent in the highest concentrated vapor solution. Further studies should be conducted on the nature of the interference in attachment mechanisms of *S. salivarius* and *C. albicans* with vaping solutions.

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ANTIBIOFILM AND ANTIMICROBIAL PROPERTIES OF *SCHINUS TEREBINTHIFOLIA* FRUIT EXTRACT

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In the past few decades, the misuse and overuse of antimicrobials has led to an increase in the number of antimicrobial resistant infections, which according to the World Health Organization, has become a major worldwide concern and a threat to public health. The need to develop new therapeutic alternatives to address the ineffectiveness of conventional antimicrobialtreatments is crucial. The rising field of phytotherapy offers an efficient approach to addressing this global health crisis. In this study, we investigate the *Schinus terebinthifolia* plant fruit extractas a potential low-cost alternative to antibiotics. This highly available plant is widely used in gastronomy and known in folk medicine for its wound healing and health-promoting properties. In this study, we evaluate the plant's fruit extract antimicrobial and antibiofilm properties against22 different strains of bacteria and fungi using the broth microdilution, biofilm, and spot assays in microtiter plates. The results show that the fruit extract has a significant antibacterial effect onseveral gram-positive and gram-negative pathogenic bacteria including *Staphylococcus aureus, Enterococcus faecalis, Pseudomonas aeruginosa, Acinetobacter baumannii, Bacillus subtilis, Bacillus cereus, Escherichia coli, and Staphylococcus epidermidis.* In addition, the plant extract displays varying degrees of antibiofilm properties at different concentrations against bacteria andfungi. These findings suggest that the *S. terebinthifolia* fruit extract has the potential to be used as a novel antimicrobial alternative in the treatment of infectious diseases. Future studies will focus on further characterization of the fruit extract.

ANTIMICROBIAL AND ANTIBIOLFILM ACTIVITY OF LUTEOLIN AND BETULINIC ACID ON DIFFERENT STRAINS OF PATHOGENIC BACTERIA

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Biofilm is described as a colony of microorganisms that attach and stick to different surfaces. They account for over 70% of microbial infections. As a result, there has been a growing need to find natural compounds that possess strong antimicrobial and antibiofilm properties. Previous experiments revealed a CR root extract to have a strong antimicrobial and antibiofilm effect on different strains of pathogenic bacteria. Betulinic acid, Luteolin, Costunolide and Dehydrocostus lactone were identified to be components of this medicinal root plant. In this research, our goal centered around testing for the effectiveness of two of the components, Luteolin and Betulinic acid. Utilizing a biofilm and broth assay, we tested the two compounds against gram positive and gram-negative bacteria to identify the active compound in the CR root extract. Results showed that Betulinic acid and Luteolin had a strong antimicrobial and antibiofilm effect on gram positive strains, most notably, *Staphylococcus aureus* and *Staphylococcus epidermis*. These compounds appeared to not have exhibited similar anti-microbial strength on some gram-negative strains. However, a significant decrease in biofilm formation was observed with those set of strains tested.

TESTING ANTIMICROBIAL AND ANTIBIOFILM PROPERTIES OF NICOTINAMIDE (VITAMIN B3)

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Finding new treatments to address the emerging antimicrobial resistance crisis has become a major research priority. The misuse of existing treatments has fueled the spread of superbugs, which are microbes resistant to a range of conventional treatments. This problem has been exacerbated by the biofilm-forming abilities of certain microbes which contribute to the emergence of new antimicrobial resistance. In this study, we tested the antimicrobial and antibiofilm properties of Nicotinamide also known as Vitamin B3 on nineteen different strains of gram-positive and gram-negative bacteria and three different strains of fungi. Microbial growth and biofilm formation were tested at different concentrations using the broth assay and biofilm assay in 96-well microtiter plates. The data collected showed that high concentrations of Nicotinamide inhibited the growth of most tested microorganisms but had minimal antibiofilm effect. On the other hand, Nicotinamide appears to promote biofilm formation of Staphylococcus aureus, Staphylococcus epidermidis, and two strains of Candida albicans. The findings of this study suggest that Nicotinamide displays antimicrobial properties against a broad range of pathogens and can potentially be used in the treatment of infectious diseases.

ASSESSING ANTIMICROBIAL EFFECTIVENESS OF *CAMPIS RADICANS* STEM EXTRACTS

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Plants offer a vast array of phytocompounds, many of which have potential bioactive properties. This study seeks to investigate stem extracts of *Campsis Radicans* in order to evaluate its pharmacological potential. Previously, distinct fractions from the stem and wood of *Campsis radicans* were extracted and labeled based on their polarity through column chromatography. Agar well diffusion tests of crude extracts had shown antimicrobial activity against *gam-positive, gram-negative bacteria and yeast.*

This portion of the project used silica and cellulose thin-layer chromatography (TLC) plates to isolate flavanones, glycoflavones, isoflavones, cardiac glycosides, furanocoumarins, hydroxycoumarins, saponins, and iridoids. Compounds isolated from thin-layer chromatography were scraped from the TLC plates and purified. Each purified fraction was tested for their antimicrobial activity against common opportunistic microbes using agar well diffusion plates and 96 well plates. We obtained a total of 99 TLC fractions: 17 glycoflavones, 12 isoflavones, 16 cardiac glycosides, 21 furanocoumarins, 18 hydroxycoumarins, 12 flavanones, 2 saponins, and 1 Iridoid. Flavanones showed antimicrobial activity against *Staphylococcus aureus* (gram-positive bacteria), *Pseudomonas aeruginosa* (gram-negative bacteria), and *Candida albicans* (yeast). Iridoid and Saponins showed activity only against *Pseudomonas aeruginosa* (gram-negative bacteria).

EVALUATING THE ANTIBACTERIAL ACTIVITY OF INSECT-INDUCED PLANT GALLS USING A NOVEL SURFACE COATING ASSAY

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Antimicrobial resistance is a critical global health threat contributing significantly to death rates. As concerns about multidrug-resistant (MDR) bacteria continue to rise, a shift from antibiotic use toward plant-derived antimicrobials is gaining traction. Plants produce an abundance of secondary metabolites as a defense against pathogens, including bacteria. Interestingly, these defense compounds even accumulate within insect-induced gall tissue – tumor-like structures residing on plants that serve as a nutritional source and protective barrier for larvae; however, there is limited research into the antimicrobial mechanisms and potentials of these galls. This project aimed to assess the relative antibacterial activity of insect-induced galls relative to their surrounding healthy plant tissue and commonly used antibiotics using a novel surface coating assay. Liquid chromatography-mass spectrometry (LC-MS) was also employed to identify differences in the metabolic profiles between galls and healthy tissues.

We found that our oak gall extract more effectively inhibited the growth of *Staphylococcus aureus* than the antibiotic, spectinomycin. Additionally, there were differences between the surface antibacterial activity of the gall and healthy tissue extracts and our LCMS findings suggest that the chemical profiles of the gall tissue are significantly different from the surrounding healthy tissue. This study explored the potential of insect-induced plant galls as a new source of surface antibacterial products that can be exploited for the development of more effective topical antibacterial agents in the post-COVID era.

EFFECT OF LABORATORY HIBERNATION ON OXIDATIVE DAMAGE AND ANTIOXIDANT CAPACITY IN THE RUBBER BOA (*CHARINA BOTTAE*)

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Winter hibernation in many ectotherms represents a prolonged period without feeding that may be accompanied by changes in metabolism and immune activity as energy-saving strategies. However, little is known about the physiological changes associated with hibernation in snakes. In this study, we examined seasonal variation in markers of oxidative stress in Rubber Boas (*Charina bottae*) using blood samples collected prior to and during laboratory hibernation. We assessed the seasonal dependence of plasma oxidative stress markers using the d-ROMs and OXY-Adsorbent tests, which quantify oxidative damage and non-enzymatic antioxidant capacity, respectively. We expected oxidative damage and antioxidant capacity to be lower during hibernation due to decreased reactive oxygen species production occurring in association with reduced host metabolism and immune activity in winter. We analyzed the effects of season (pre-hibernation or hibernation), sex (female or male), and their interaction on oxidative damage (mmol/L H_2O_2) and antioxidant capacity (μmol HClO/mL) using two-way rmANOVA. Our results indicated a significant effect of season and sex on mean oxidative damage. Mean oxidative damage was significantly higher during hibernation compared to pre-hibernation. We also found that female snakes exhibited higher oxidative damage compared to males, regardless of season. We did not find a significant effect of season or sex on mean antioxidant capacity. Our results suggest that, during hibernation, Rubber Boas have an increase in oxidative damage without an associated upregulation in non-enzymatic plasma antioxidant capacity.

ULTRASONIC VOCALIZATION, MATERNAL CARE, AND POSTNATAL SURVIVAL IN SEROTONIN-DEFICIENT *PET-1* KNOCKOUT MICE

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Effective maternal care in rodents depends in part on ultrasonic vocalizations by the pups that trigger survival-promoting behaviors by the dam. The ability of pups to produce effective calls and the ability of dams to hear and respond appropriately to these calls are crucial for pup survival. Defects in either call transmission or call receipt could lead to suboptimal maternal care and increased pup mortality. Deletion of the *Pet-1* gene results in a 70% loss of central serotonin neurons that is associated with increased mortality of *Pet-1* knockout pups. Specifically, over a large number of litters, 20-25% of knockout pups born to *Pet-1* heterozygous dams die within five days of birth compared to only 3-7% of wild type or heterozygous littermates (Erickson et al., 2007. *Respir. Physiol. Neurobiol.* 159:85-101). We hypothesize that abnormal call production by *Pet-1* knockout pups may contribute to this increased mortality. Previous work from our lab has shown that the general maternal behavior of wild type and *Pet-1* heterozygous dams is indistinguishable. However, a comparison of ultrasonic vocalizations from wild type and *Pet-1* knockout pups over the first five postnatal days suggest that calls made by wild type pups are more complex and louder than calls produced by knockout littermates. The present study is designed to confirm these previous observations and to extend these observations by assessing the maternal response of heterozygous dams to playback calls recorded from wild type and *Pet-1* knockout pups that were recorded under conditions of mild distress. We hope that these studies will help define the underlying reasons for the increased neonatal mortality that we have documented in *Pet-1* knockout neonates born to *Pet-1* heterozygous dams.

MELATONIN INHIBITS CIRCUMNUTATION IN ARABIDOPSIS THALIANA

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Melatonin (N-acetyl-5-methoxytryptamine) and auxin (indole-3-acetic acid/IAA) are both tryptophan-derived hormones found in Arabidopsis thaliana, the model plant for research (Meinke et al., 1998). Auxin transport and responses regulate circumnutation, a helical organ movement influenced by many variables such as light and chemicals (Stolarz, 2009); studying circumnutation allows researchers to better understand how and why plants have autonomous, endogenous movements without apparent stimuli (Stolarz, 2009). Melatonin in animals is correlated with circadian rhythms (Lewy et al., 1992); circumnutation in plants is also correlated with circadian rhythms (Niinuma et al., 2005). Melatonin negatively regulates auxin biosynthesis, the expression of PIN proteins (protein family of auxin transporters), and auxin responses in Arabidopsis (Wang et al., 2016). Melatonin and auxin are thought to act through different pathways to alter gene expression, with melatonin affecting 16 auxin-related genes (Zia et al., 2019).

No study has been published solely regarding melatonin's role in circumnutation, even though melatonin is involved with auxin biosynthesis and transport, which in turn can affect circumnutation. This study aims to test melatonin's effects on circumnutation in Arabidopsis due to melatonin's role in negatively regulating auxin biosynthesis and transport. Arabidopsis plants were sprayed with 400 μM of melatonin in water with tween-20, then video time-lapses of plants treated with melatonin were compared to a control of water and tween-20. MT-treated Arabidopsis plants had 24.33 fewer nutations than WT Arabidopsis on average.
Preliminary results indicate melatonin is inhibitory to circumnutation in Arabidopsis thaliana, given the decrease in back-and-forth (XY-axis) nutations.

THE EFFECT OF PERFLUOROOCTANESULFONIC ACID (PFOS) ON OVARIANFOLLICLES

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This study investigates the impact of perfluorooctanesulfonic acid (PFOS) on ovarian function, given its persistence in the environment and associated health concerns such as liver damage, cholesterol increases, immune dysregulation, and reproductive development issues. The ovary plays a pivotal role in female reproductive health, being in charge of the production of eggs and the synthesis of hormones critical for reproductive and general health. Within the ovary, ovarian follicles, fluid-filled sacs containing developing eggs, are instrumental in these processes, making them an essential system for exploring the impacts of environmental contaminants. We hypothesized that PFOS exposure would disrupt hormone synthesis and negatively affect female reproductive health. Using ovarian follicles from adult female CD-1 mice, we exposed follicles to PFOS doses ranging from 0.1 µg/mL to 100 µg/mL for 5 days and measured hormone levels via enzyme-linked immunosorbent assay (ELISA). We found significant changes in androstenedione and testosterone in 100 µg/mL PFOS treatment groups. Results also show significant impairment of 100 µg/mL PFOS treatment group on follicle growth within 96 hour period. Additionally, in the PFOS 1 µg/mL group, the inhibition was statistically significant at24, 48, and 72 hours. Lastly, all treatment groups were statistically different from the control group after 24 hours. The impairment of androstenedione and testosterone levels, along with disrupted ovarian follicle growth, are significant findings as they indicate potential adverse effects of PFOS on female reproductive health, which could lead to irregularities in ovulationand fertility issues. My research will also explore PFOS's effects on gene expression in the ovary,using Quantitative Polymerase Chain Reaction (qPCR) to assess the impact on steroidogenic enzyme gene expression in follicles cultured with PFOS. This research will deepen our understanding of how PFOS potentially alters reproductive function at the molecular level, paving the way for targeted interventions.

TOXICITY OF PHTHALATE ALTERNATIVE DI-2-ETHYLHEXYL TEREPHTHALATE (DEHTP) ON THE MOUSE OVARY

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Phthalates have been a key component of plastic materials since they were first introduced in the mid-1900s. Di-2-ethylhexyl phthalate (DEHP) has been the most widely used of this class of compounds as it has been added to plastics to ensure durability and flexibility, and it has been found in plastic materials such as food packaging, medical devices, toys, and personal care products. It was not until more recent years that DEHP began to be removed from its use in plastic materials due to increasing evidence of its ability to interfere with female reproduction. A rising replacement for DEHP is a chemical known as di-2-ethylhexyl terephthalate (DEHTP), which differs in structure only in the location of the ester side chains on the central benzene ring. DEHTP metabolites have been measured in human urine at a greater concentration than DEHP metabolites, yet there is little information about its potential health effects, specifically on the ovary. The ovary is an important organ for the female reproductive process as it is the location of egg development and release, as well as hormone production. In order to evaluate whether or not DEHTP is a safer alternative to DEHP, we looked at several crucial processes within the ovary that have been found to be disrupted by DEHP exposure, including steroid hormone production and cell cycle progression since many important processes within the ovary are growth-dependent.

To study these effects, young adult female CD-1 mice were orally dosed with DEHTP at a concentration of 10 µg/kg, 100 µg/kg, or 100 mg/kg or vehicle control for 10 days. Upon completion of the dosing period, the mice were euthanized, and their ovaries were extracted to conduct gene expression analysis using quantitative polymerase chain reaction (qPCR). In addition to gene expression analysis, we also performed enzyme-linked immunosorbent assays (ELISAs) to measure hormone expression in serum. Treatment with DEHTP did not significantly alter the expression of steroidogenesis enzymes or the concentration of hormones; however, a downward trend was observed with increasing exposure to DEHTP for enzymes *Cyp11a1* and *Cyp17a1*. Additionally, those exposed to DEHTP at 100 µg/kg and 100 mg/kg exhibited a borderline significant decrease in testosterone. DEHTP exposure also significantly decreased genes involved in the G1 phase of the cell cycle, including *Cdk4*, *Ccnd2*, and *Cdk2* expression for the group exposed to 100 mg/kg DEHTP. These results suggest that DEHTP exposure may not interfere with steroidogenesis within the ovary but could potentially impact the cell cycle. Ultimately, additional testing is needed to understand the effects of lower doses more relevant to human exposure and whether or not DEHTP is truly a safe and effective replacement for DEHP. Supported by NIH R00ES031150, P30ES005022, and R00ES031150-03S1.

A DESIGN-BASED STEREOLOGICAL APPROACH FOR QUANTIFYING SEROTONIN NEURON INNERVATION DENSITY IN BRAINNSTEM TISSUE

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Pet-1 is a transcription factor that is required for development of a full complement of serotonin (5-HT) neurons in the mammalian brainstem. Targeted deletion of the *Pet-1* gene in mice results in a 70% reduction of brainstem 5-HT neurons that is associated with a depressed and irregular breathing pattern, an increased incidence of spontaneous apneas, abnormal autoresuscitation responses to hypoxia-induced apnea, and increased neonatal mortality. These data are interesting in that abnormal 5-HT neuron development has been associated with Sudden Infant Death Syndrome (SIDS) in humans. A number of risk factors for SIDS are known, including prenatal exposure to cigarette smoke, which contains as a major ingredient the neuroteratogen nicotine. We hypothesized that the breathing deficits of the *Pet-1* knockout mice would be exacerbated by prenatal exposure to nicotine. Surprisingly, however, nicotine exposure actually *improved* breathing behavior in these mice. The underlying mechanism for this improvement is not known. One possibility is that nicotine "rescues" the population of 5-HT neurons that are normally lost as a result of *Pet-1* gene deletion. Alternatively, the improved breathing behavior may be due to a nicotine-induced preservation or functional re-innervation of respiratory control centers by the small subpopulation of 5-HT neurons that remain in the *Pet-1* knockout. We have eliminated the first possibility through a careful quantitative comparison of 5-HT neuron number in brainstem tissue taken from wild type and *Pet-1* knockout mice following developmental exposure to nicotine or saline (control). The purpose of this study is to develop unbiased immunohistochemical labeling and analysis procedures for accurately comparing and quantifying 5-HT fiber innervation of the preBötzinger Complex (the presumed site of central respiratory rhythm generation) in neonatal wild type and *Pet-1* knockout mice following developmental nicotine exposure. We hope that this analysis will help to better define the underlying basis for the recovery of an apparently normal breathing phenotype in the nicotine-treated *Pet-1* knockouts.

BIOCOMPATIBILITY ASSESSMENT OF MICROPLASTICS DURING ZEBRAFISH CAUDAL FIN REGENERATION

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Plastic pollution is a pervasive, contemporary issue. Previous research from our lab demonstrated that exposure of developing zebrafish to specific microplastics, namely polymethyl methacrylate (PMMA) and polyethylene terephthalate (PET), resulted in adverse developmental effects, including decreases in pericardial sac size, body length, and interocular distance. The goal of this study was to examine the impact of these two microplastics, as well as another common plastic, synthetic polyamide (PA), on tail fin regeneration in the zebrafish model. PMMA microplastics derive from a shatter-resistant form of glass, used in windows, aquariums, and medicine/dentistry, while PET is a strong and lightweight plastic, used in packaging, single use bags/bottles, and microfiber cloths. The PA-12 microplastics used in this study are common, durable plastics that derive from the breakdown of textiles, automotive parts, and electronics. The growing abundance of these plastics in the oceans increases the likelihood of them entering marine organisms and humans. Tail fin regeneration is a rapid method to examine the impact of compounds on cellular proliferation, migration, and tissue pattern formation, and can be effectively measured using the zebrafish model because of their rapid tissue regrowth capabilities. Our selected larvae had their tail fins amputated at 48 hours post fertilization and through live imaging of zebrafish larvae at 24 hours post amputation, exposure to PA-12 microplastics resulted in no significant impact to regeneration or mortality. However, PMMA and PET exposure was found to negatively impact regeneration and mortality. These findings support the hypothesis that microplastics in the environment can have negative impacts on tailfin regeneration and future experiments will examine impacts on cellular proliferation and apoptosis.

ANALYSIS OF SHOOT CIRCUMNUTATION DEVELOPMENTAL PROFILE IN *ARABIDOPSIS THALIANA*

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Circumnutation is the mysterious back-and-forth elliptical swaying conducted by plant appendages. Even though circumnutation was well characterized, defined, and named by Darwin over 150 years ago (Darwin, 1880), the purpose of circumnutation in non-twining plant shoots is still unknown. To better understand the purpose of circumnutation in shoots, my project aims to create a 3D developmental profile of the circumnutating growing flowering stems of the genetic model plant, *Arabidopsis thaliana*. The use of 3D time-lapse photography tracking the X, Y, and Z axis allows for full movement analysis. Preliminary data shows that there are 4 stages of circumnutation topology during the development of the inflorescence: "Micro-, Meso-, Macro- circumnutation" and "Horizontal Swinging Stage". Only meso-circumnutation has been analyzed in previous studies. The mean height of the primary inflorescence of the first nutation and the mean nutation frequency were identified. This research may set the foundation for discovering the purpose of circumnutation and indicates the selection of stages for circumnutation research should be taken into consideration. These findings may contribute to uniformity in circumnutation research. Stimuli (phototropic & thigmotropic) priorities in plant circumnutation may be tested in those developmental stages.

THE TOXICITY OF NANOPLASTICS IN THE OVARY

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New Jersey Institute of Technology, Newark, NJ

Plastics are compounds that slowly degrade into micro and nanoplastics. Microplastics have been found in human tissue and urine samples and nanoplastics may have the same, if not more, permeability into the human body. Once in the human body, they can interact with normal bodily functioning and may cause disruption. This study investigated how nanoplastics can interfere with processes like gene expression and what impact they have on the ovary, which is an essential female reproductive organ. Previous studies looked into the effects of nanoplastics on other organs such as the spleen, kidney, and testes. Little is known about the effects nanoplastics have on the ovary. We hypothesized that nanoplastics administered at environmentally relevant doses affect the expression of genes relating to steroidogenesis, cell cycle regulation, apoptosis, receptors, and oxidative stress. To test this, we conducted quantitative polymerase chain reaction (qPCR) on RNA extracted from mouse ovarian tissue cultured in 0.05% Tween20 (vehicle control) or 200 nm polystyrene nanoplastics at either 1 µg/mL, 10 µg/mL, and 100 µg/mL doses for 96 hours. The results show cell cycle regulators *Cdk4* and *Cdkn1a* were inhibited in the 100 µg/mL treatment group compared to control. *Cdk4* was borderline increased in the 10 µg/mL treatment group compared to control. Antioxidant *Sod1* was inhibited in the 100 µg/mL treatment groups. Pro-apoptotic *Bax* and *Casp3* genes were inhibited in the 100 µg/mL treatment group and *Casp3* was increased in the 10 µg/mL treatment group compared to control. Expression of the androgen receptor was inhibited in the 100 µg/mL treatment group. This indicates that gene expression is affected by nanoplastic exposure which may affect normal ovarian function.

EFFECTS OF VARIOUS SUGAR ALTERNATIVES ON THE WEIGHT OF ZEBRAFISH

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Department of Biology
Felician University, Lodi, NJ

A study from the mid-1900s has shown that saturated fat is the real cause of illnesses. However, it's known that the human body is like a chemical laboratory since it alchemizes sugar into fat. Correlation between sugar and conditions such as heart disease, diabetes, and obesity has been shown, but do all sugars have the same effect? To find out if the type of sugar has the same or different effect, three different types were chosen to determine if there was a deviation caused by the type of sugar. Sugar cane, agave syrup, and D-ribose were incorporated in each tank containing four zebrafish. Their average weight has been measured and recorded before starting the experiment and every week while the experiment is still in progress. The water concentration has also increased by 3g every week in 10 liters of distilled water. Since the research is still in progress, the results will be presented at the research conference.

DE NOVO SYNTHESIS OF THIOPHENE NATURAL PRODUCTS VIA [3+2] CYCLOADDITION OF SULFUR YLIDE AND NITROALKENE

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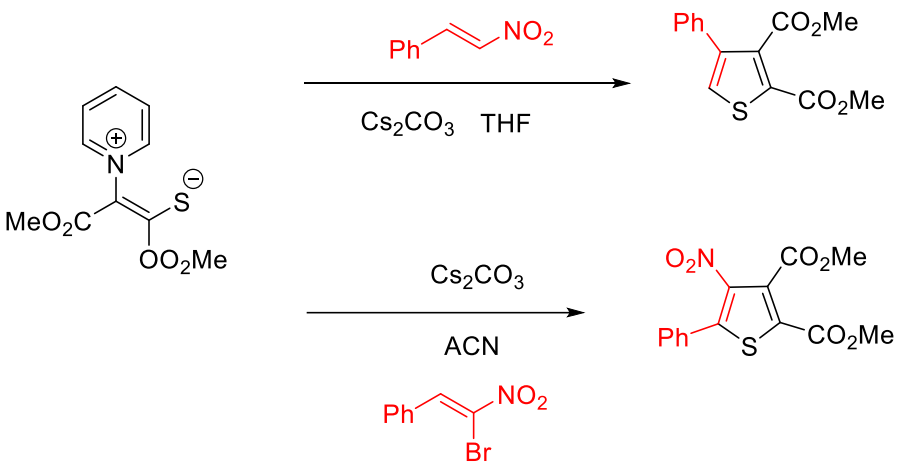
William Paterson University of New Jersey, Wayne, NJ

Thiophene compounds are widely distributed in plants, fungi, and bacteria, known for their diverse medicinal properties such as anti-inflammatory, anti-cancer, and antioxidant activities, rendering them potential candidates for therapeutic applications. In this study, we present a de novo approach to synthesizing targeted thiophene compounds. The reported method involves a [3+2] cycloaddition reaction utilizing nitroalkene and bromonitroalkene with sulfur ylides. Our research focuses on improving the reaction conditions to achieve a moderate to high yields of thiophene derivatives. Furthermore, we aim to extend these methodologies to the synthesis of thiophene derived natural products with notable biological activities.



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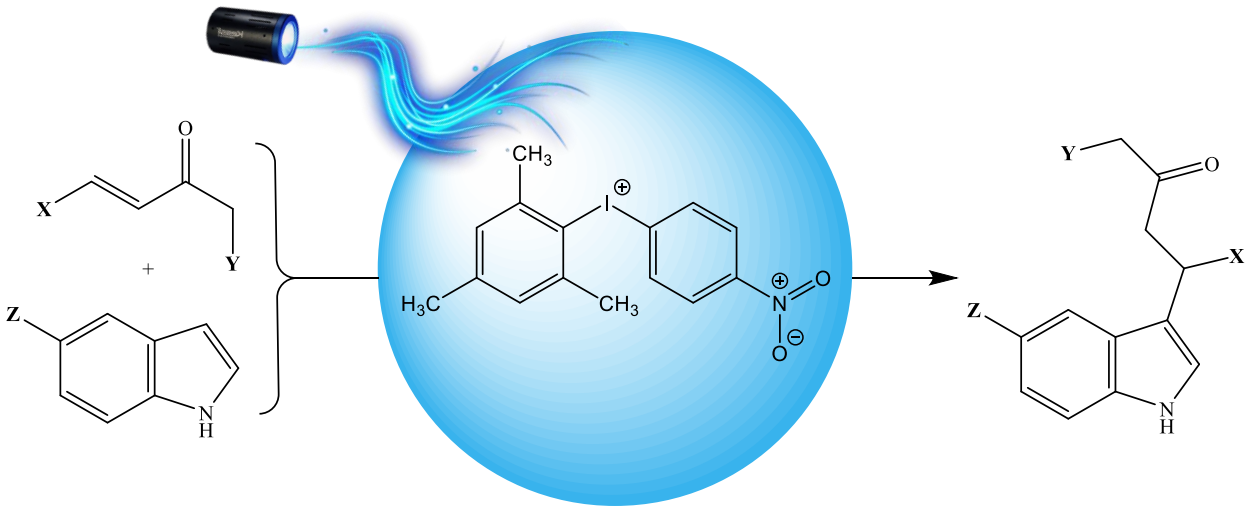
PHOTOACID GENERATOR CATALYSIS FOR CONJUGATE ADDITION REACTIONS

Sahil D'Souza and Dr. Joseph Badillo
Department of Chemistry & Biochemistry
Seton Hall University, South Orange, NJ



Visible Light Induced PAG Catalysis

Photoacid generators (PAGs) have been of interest in the scientific community because they are able to be used in green and sustainable chemical processes having various applications, including pharmaceutics for cancer treatment, microfluidics for the microelectronic industry, and for stereolithography material science related to polymers. Recent studies have identified PAGs to function exceptionally well as catalysts for organic synthesis. In this project, we propose that various PAGs, primarily mesityl(4-nitrophenyl)iodonium triflate, can catalyze the Michael addition between various substituted indoles and a range of alkyl vinyl ketones to form the corresponding β-indolyl ketone derivatives. PAGs when used for Michael Addition reactions are useful because they offer high chemo selectivity, a broad scope, and require only mild conditions. This protocol is amendable to a wide range of Michael acceptors such as cyclohexanone, malonate, and coumarin, as well as a variety of electronically diverse indoles and Michael donors to facilitate the desired 1,4-conjugate addition. Mechanistic studies and pH analysis have shown that light is required for reaction initiation. Catalyst photodegradation studies show control of acid generation in the system upon irradiation.

PHOTOPHYSICAL PROPERTIES OF ANCHORING GROUPS BINDING TO TiO_2 FILMS

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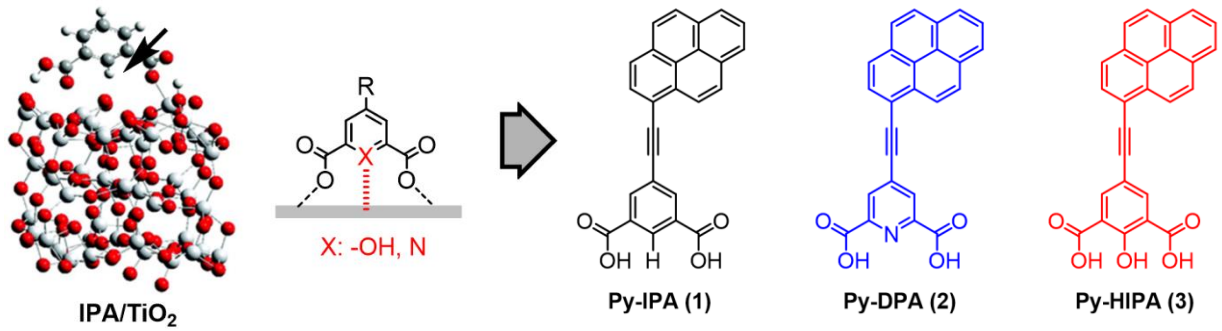
The binding of catalysts and light harvesters on nanostructured semiconductors is dependent on the structure of the anchor groups that form covalent bonds to the surface. Multipronged anchors, such as benzene-1,3-dicarboxylic acid, or isophthalic acid (IPA), are often used to ensure strong attachment to the surface using several covalent bonds. Here we introduced a third coordination unit X in C2 of IPA in three isophthalic acid derivatives: C2-OH in 2-hydroxyisophthalic acid (HIPA), C2 replaced by N in 2,6-dicarboxypyridine (DPA), and C2-NH in 2,6-dicarboxypyridin-1-ium (DCP). Each anchor was substituted with 1-ethynylpyrene (Py) as a fluorophore to study the anchor group effect in solution and on nanostructured TiO_2 films. Py-HIPA, Py-DPA, and Py-DCP were compared with the Py-IPA homologue. The protonation of nitrogen in DPA was observed after hydrolysis step of synthesis. Therefore, Py-DPA photophysical and geometric properties were calculated using DFT and TD-DFT calculations and the results were compared to the other dyes. The calculations indicate that substitution in C2 influences the HOMO and LUMO energies and orbital distributions. All ATR FT-IR spectra of the dyes on TiO_2 suggest the formation of bonds using the carboxylate group. UV-Vis absorption spectra indicate a high extinction coefficient for Py-HIPA and a significant red shift for Py-HIPA/TiO_2 and Py-DCP/TiO_2, compared to Py-IPA/TiO_2. A desorption experiment indicates that the HIPA anchor has the greatest binding strength to TiO_2 films. This study shows that replacing the C2-H of isophthalic acid with a coordinating group influences the binding and electron communication with the surface, and points to a more general approach of multipronged anchor with differentiated functional groups.

Scheme 1. Pyrene-based dyes for studying the binding of different anchor groups on TiO_2



COMPUTATIONAL INVESTIGATION OF SULFONAMIDE-ALDEHYDE DERIVATIVES

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Department of Chemistry
New Jersey City University, Jersey City, NJ

The increasing microbial resistance to antibiotics underscores the pursuit of novel antibacterial compounds. Sulfonamides, known for affordability and low toxicity, have been vital in combating infections. However, persistent bacterial resistance necessitatesa deeper understanding of their molecular intricacies. In this investigation, a repertoire of theoretical techniques, encompassing semi-empirical and ab-initio methodologies, is harnessed to scrutinize the stability, reactivity, and antioxidant attributes of the followingsulfonamide-aldehyde derivatives:

4-(2-(1,3-dioxo-1-(p-tolyl)propan-2-ylidene)hydrazinyl)benzenesulfonamide (M1),
4-(2-(1,3-dioxo-1-(p-tolyl)propan-2-ylidene)hydrazinyl)-N-(pyrimidin-2-yl)benzenesulfona mide(M2),
4-(2-(1,3-dioxo-1-(p-tolyl)propan-2-ylidene)hydrazinyl)-N-(4-methylpyrimidin-2-yl)benzen esulfonamide (M3). The semi-empirical method PM3 is employed to attain geometrical optimization of the compounds, while the theoretical methods Hartree-Fock (HF) and Density Functional Theory (DFT) are harnessed to unravel chemical properties.

Computational simulations are meticulously executed using Gaussian 16 and GaussView software packages, lauded for their precision in electronic structure calculations grounded in quantum mechanics. Our findings elucidate the preferential electrophilic attack at ketone sites, highlighted by their prominent Highest Occupied Molecular Orbital (HOMO) lobes. In vacuum, M3 exhibits the highest electrophilicity index, whereas, in a polar solvent, HF results favor M2, while DFT consistently suggests M3. Intriguingly, in cyclohexane, HF predicts that M1 has the highest electrophilicity index, while DFT predicts that M3 has the highest value. Also, Molecular Electrostatic Potential (MEP) analysis unequivocally maps the highest electron density regions to the aldehyde groups, juxtaposed with the lowest electron density regions attributed to amine and amino groups. In addition, based on the energy gap between HOMO and LUMO using both theoretical methods HF and DFT results, M2 was the most reactive on a polar solvent, while M1 was the most reactive on a non-polar solvent. These revelatory insights pave the way for the strategic design, reactivity and development of novel antimicrobial agents, addressing the critical need for efficacious alternatives amidst the relentless tide of bacterial resistance.

A GREENER ROUTE TO THE SYNTHESIS OF ANTIDEPRESSANT (*S*)-DULOXETINE (CYMBALTA)

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Caldwell University, Caldwell, NJ

Major depressive disorder (MDD) is a significant global health concern, with over 300 million individuals affected and a high association with suicide rates. Pharmacotherapy, particularly the use of antidepressants, is a crucial treatment strategy for MDD. (*S*)-Duloxetine (Cymbalta) is a widely prescribed antidepressant that elevates neurotransmitter levels to alleviate symptoms of depression. The industrial route for synthesizing (*S*)-duloxetine involves a Mannich reaction that requires harsh reaction conditions and lengthy reaction times, and also a kinetic resolution with low yield, lengthy steps, and the usage of multiple chemicals. We aim to develop a safer, faster, and more environmentally friendly synthesis route for (*S*)-Duloxetine using a microwave-assisted reaction and chemoenzymatic reduction. We first investigated the Mannich reaction of 2-acetylthiophene, paraformaldehyde, and dimethylamine using microwave technology. We experimented with different solvents and reaction temperatures and determined methanol at 180 Celsius degrees yielded the best results so far and led to about 50% conversion in 10 min under microwave conditions. Further optimization of reaction conditions to improve the yield is underway. We also carried out model reactions using Baker's yeast to enantioselectivity reduce ketone to its corresponding alcohol. We anticipate testing the product from microwave reaction for chemoenzymatic reduction soon using prepared immobilized Baker's yeast beads.

NICKEL-CATALYZED OXIDATIVE ESTERIFICATION

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Transition metals are often used as catalysts in the synthesis of esters due to their unique electronic properties and ability to facilitate the formation of new chemical bonds. In this project,we focused on the approach of oxidative coupling using one-step esterification to synthesize esters using benzoic acids and cyclohexene. Normally, the catalyst used for this reaction is palladium (a precious metal) or copper, but a few cases of nickel catalyzed oxidative coupling reactions have been reported. Nickel is a non-precious metal; meaning it is inexpensive and abundant. However, we have been struggling to reproduce the consistent reaction profile, so we are currently looking into using the nickel-terpyridine excited state catalysis approach for this esterification. Nickel-terpyridine excited state catalysis offers a potential strategy for promoting esterification reactions under mild conditions. This approach has the advantage of using light as an external energy source, which can be precisely controlled to initiate and regulate the catalytic process.

GOLD NANOPARTICLE INDUCED STEREOSPECIFIC BENZYLIC OXIDATION TO SYNTHESIS δ-HYDROXYALKYNONES: TOTAL SYNTHESIS OF CATECHOL PYRAN ISOLATED FROM PLECTRANTHUS SLYVESTRIS

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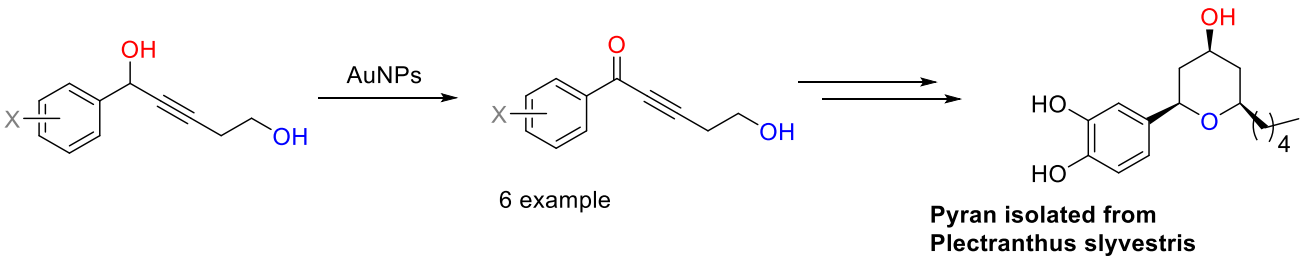
Department of Chemistry,
William Paterson University of New Jersey, Wayne, NJ

Oxidation is essential in synthesizing many biologically natural products and drug molecules. The stereospecific oxidation of alcohol remains a challenge, as one must pivot on protection/deprotection, precious metals, or harsh conditions to achieve stereospecific oxidation. This work illustrated the green approach towards stereospecific benzylic oxidation in the presence of primary alcohol. The reaction conditions formed an array of δ-hydroxyalkynones in good yields. The synthesized alkynones will be further utilized to rearrange reactions to synthesize catechol pyran natural product isolated from Plectranthus slyvestris.



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PRUSSIAN BLUE, FROM ARTISTS' PALETTE TO A PROMISING SOLUTION TO RECOVERY OF PRECIOUS METALS FROM ELECTRONIC WASTE

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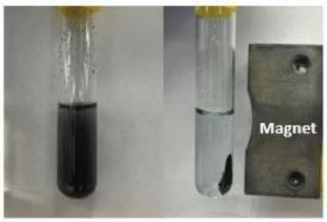
School of Natural Sciences
Caldwell University, Caldwell, NJ

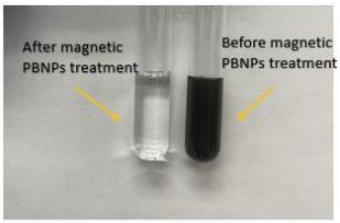
According to the Global E-waste Monitor, more than 59 million tons of electronic waste was dumped in landfills in 2019 alone and an estimated $57 billion worth of gold, silver, copper, platinum, and other recoverable metals was dumped and burned rather than recovered and reused. Meanwhile, the demand for these precious metals is growing exponentially due to technological advancements and industrial expansion; therefore, it becomes crucial to explore practical methods for the recovery and reuse of these precious metals from e-waste.

We first studied the preparation of PB pigment and its application to cyanotype print. We then investigated PB's ability to absorb heavy metal and recover precious metals. After synthesizing PB by mixing iron (III) chloride and potassium hexacyanoferrate, we harvested the precipitate through three different routes: sedimentation, centrifugation, and filtration, all of which proved to be time consuming. Through binding PB to a core of magnetite nanoparticles, we synthesized magnetic Prussian Blue Nanoparticles (PBNPs). Introducing Magswitch, a powerful magnetic device that can be turned on and off with a simple half turn of a knob, allowed us to accelerate the separation process exponentially with a guaranteed purification of magnetic PBNPs. The binding of PB and magnetite was confirmed using Infrared Spectroscopy. We tested the ability of magnetic PBNPs to trap lead in water and discovered that they effectively adsorbed the lead. Subsequently, we conducted tests on simulated gold and silver solutions, revealing a remarkable absorption of over 95% for both gold and silver. Further investigation of magnetic PBNPs to recover platinum group metals and test their effectiveness on real electronic waste is under way.

A recreation of "Great Wave Off Kanagawa" using Cyanotype (Sun Print) in our lab



Magnetic Prussian Blue



Sulfide Test for Lead-containing Water

REACTIVE OXIDATIVE SPECIES IN CANCER FOLLOWING NANOPARTICLE TREATMENT

Darshan Danak, Ashish Kokkula, Aida Lopez-Ruiz, and Dr. Kathleen McEnnis
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Dept. of Chemical and Materials Engineering, New Jersey Institute of Technology, Newark, NJ

There has been increasing interest in using metallic nanoparticles, such as gold and silver nanoparticles, as therapeutics for cancer treatments. Specifically, platinum nanoparticles (Pt NPs) have become potential cancer therapeutic due to their significant anticancer effects as well as low toxicity to healthy cells (compared to other types of nanoparticles such as Cisplatin). Previous data has shown that Pt NPs are effective against triple negative breast cancer (TNBC) cells. TNBC is a very aggressive and metastatic form of breast cancer. Current literature claims that Pt NPs induce cell death by increasing concentrations of reactive oxidative species (ROS) in extracellular cancer environments. We proposed that, due to platinum's antioxidative properties, the addition of Pt NPs would decrease ROS levels. In this study, we measured the effect of several concentrations of Pt NPs on ROS concentrations in various cell lines. We conducted ROS assays on three separate cancer cell lines, double positive breast cancer (DPBC) cells, triple negative breast cancer (TNBC) cells, and cisplatin-resistant uterine sarcoma cells, all with differing responses to Pt NPs.

In order to determine the effect of Pt NPs on reactive oxidative species (ROS) concentrations, we used several cell lines including TNBCs, DPBC, and cisplatin-resistant uterine sarcoma. We measured the ROS concentrations after either 1, 3, or 5 days for each cell line after treatment with Pt NPs. There was a significant increase in ROS after day 1 across all cell lines. Across all cell lines, ROS levels decreased after 3 to 5 days even at high concentrations.

The results of this study reflect our hypothesis that Pt NPs decrease ROS levels due to platinum's antioxidative properties. The decrease in ROS levels are indicative of platinum's antioxidant effects, which contradicts current literature. The results and data from this study can aid in the understanding of the mechanism of Pt NPs on ROS levels in TNBC, DPBC, and cisplatin-resistant uterine sarcoma cells.

Future studies will continue to examine the mechanism of action for Pt NPs in TNBC as well as determine their efficacy in mice models.

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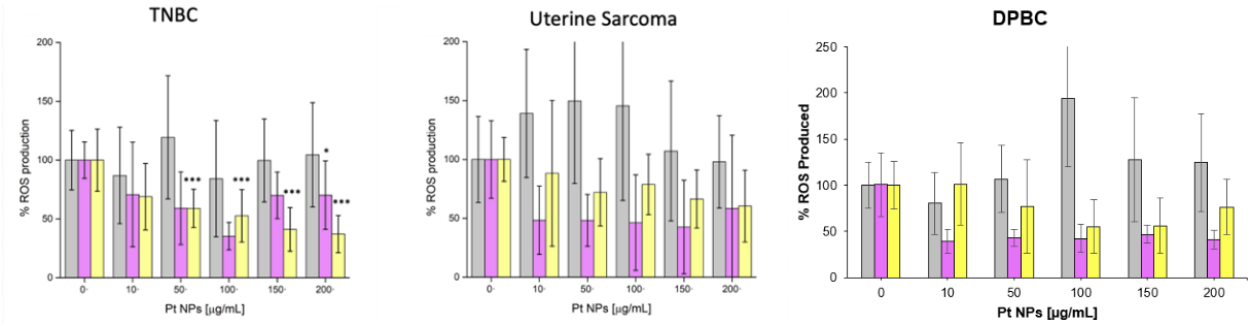
Acknowledgements: This research was supported, mentored, and overseen at the New Jersey Institute of Technology by Ashish Kokkula and Dr. Kathleen McEnnis.



LUPULONE ENCAPSULATED IN ZEIN/CHITOSAN NANOMATRICES

Antonio Ocampo, Sajin Philip, Jennifer Song, Dr. Mihaela Leonida, and Dr. Ish Kumar
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Zein (Z) is an alcohol-soluble prolamin protein found in corn and is typically dissolved in 70–80% aqueous ethanol before dispersion into water to precipitate zein as nanoparticles. Simultaneous addition of various lipophilic compounds co-dissolved in aqueous ethanol leads to their encapsulation. However, strategies are needed to eliminate the use of flammable ethanol in industrial processes. The objective of this work was to replace ethanol with nonflammable propylene glycol in the preparation of zein nanoparticles, subsequently stabilized electrostatically using gum arabic (GA). An antisolvent method was used (Fig. 1) in this study. Lupulone (L) was added as an ingredient in the zein nanoparticle synthesis due to its antibacterial and antimicrobial properties, as well as its stimulating effect on collagen production. Chitosan (C) is a biopolymer that can be used as a drug delivery agent. It shows antimicrobial properties against both gram-positive and gram-negative bacteria and has promising antioxidant and antifungal properties. Chitosan was added in the nanocomposites to enhance the antibacterial activity of L and to modulate its release.

Figure 1. Synthesis of the nanocomposites

The nanocomposites were characterized by FTIR, composition, encapsulation efficiency and loading capacity for lupulone, antioxidant assays, and modulatory effect on MMP-1 (collagenase I, matrix metalloproteinase-1) activity. The zein-based nanoparticles showed high encapsulation of L, antioxidant activity and modulatory effect on MMP-1 activity. All components, propylene glycol, Z, L, C and GA have generally regarded as safe status (GRAS) but have not been extensively used in skin care products. The method presented herein enables the preparation of stable zein nanoparticles which have potential for use in skin care products beneficial in preventing aging/photoaging and in topical applications to limit scarring during wound healing.

ONE POT ROUTE TO CYCLIC SILANES STABILIZED SILVER NANOPARTICLES.

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and Dr. Bhanu P. S. Chauhan
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In this research, we investigate cyclic hydro silanes as reducing and stabilizing agents in the synthesis of silver nanoparticles. These compound, also impart a passivation layer on the metal's surface. Through the manipulation of silane concentration and functionality we are able to tailor this passivation to enable a diffusion of small molecules for a controlled catalytic activity. Additionally these added surface functionalities allow for additional chemistry such as ligand exchange around the metal core nanoparticle to influence its surface properties and altering its application[1]. Silane concentration also affect the size of nanoparticles and growth rate[2]. Previously our group investigated the preparation of nano-sized metal systems involving long alky chains silanes with successful results[3]. Using this one pot synthesis under inert atmosphere, two cyclic silanes,1,3,5,7-tetramethyl cyclotetrasiloxane D_4^H a cyclic substituted siloxane and 1,2,3,4,5,6,7,8-octamethyl cyclotetrasilazane D_4 a cyclic substituted silazane were studied. The variation of the silane compound to the metal salt ratios resulted in nanoparticles of different sizes and morphology. The characteristic features of products were obtained using IR, UV-Vis, and TEM

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KINETIC STUDIES OF THE RELEASE OF LIPOPHILIC BIOACTIVE AGENTS IN FORMULATIONS FOR THE SKIN

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Formulations for the skin containing active principles which can act only after penetrating into the skin structure meet the *stratum corneum* (SC), a rate limiting barrier. Particles having at least one external dimension in the nanorange show better absorption through the skin while offering protection to bioactive agents encapsulated therein. Three different types of nanoparticles (NP) were synthesized involving different ingredients beneficial for the skin and the release profile for each type of nanoparticle in hydrophilic and lipophilic environments was studied.

The first type of nanoparticles encapsulated nisin (N, a bacteriocin that is used as a natural preservative in foods), in chitosan (C), an inexpensive biopolymer. Chitosan, known for its antibacterial and antifungal activity, is used as drug delivery agent and, being hydrophilic, targeted the fast release of N in fatty environments. The effect of the C matrices was beneficial but afforded a release too low (1.5% over 8 days) for practical applications [1]. Tannic acid (TA), antimicrobial and strong antioxidant, was added in the synthesis as a potential modulator of N release. Its presence enhanced release of N in buffer by a factor of 4, with higher effect at lower N:TA ratios. The release in lipophilic media was conducted in lotions (oil-in-water, o/w, water-in-oil, w/o), and in simulated human sebum (HS). The highest release of N over time occurred in o/w (less lipophilic formulation) and increased as the N:TA ratio decreased. HS, the most lipophilic medium, afforded the slowest kinetics of N release from nanoparticulate C.

The second type of NP encapsulated lupulone (L), a hop (*Humulus lupulus*) compound with antibacterial, antioxidant, and anticarcinogenic properties, in zein (Z), an alcohol-soluble prolamin protein from corn. Z has many characteristics of an ideal topical delivery system such as high biodegradability and biocompatibility, superior binding ability, moisture attracter, and effective absorption by target cells. Zein-based NP displayed sustained L release in a hydrophilic environment (buffer pH 5.0) over 13 days. However, the levels were low for industrial applications [2]. We studied the release in lipophilic environments which was conducted in o/w cream and in HS. It was higher in o/w compared to HS and increased as Z:L ratio decreased. The kinetics of L release was still too low for applications in cosmetic formulations.

To address this problem, in a third set of NP, chitosan was added to the ingredients used in the second NP syntheses targeting modulation of L release. The release in buffer was highest at highest L content and higher C content afforded enhancement of release kinetics.

All NP discussed were produced using green processes, contain only GRAS substances, are inexpensive, and demonstrated potential for use in formulations for the skin as antioxidants, moisturizers, and preservatives.

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BIOCIDAL ACTIVITY OF PEROXIDE RADICALS GENERATED FROM A FUNCTIONALIZED NANO-FeOOH SYSTEM

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Bacterial infections can develop from medical implants and devices, posing a serious and life-threatening problem for patients. Approximately 32 million Americans have an implanted medical device, and they are at risk to develop a multitude of bacterial infections. *Staphylococcus aureus* is a gram-positive bacteria and one of the main causes of orthopedic-implant associated infections. There is current research on the use of Reactive Oxygen Species (ROS) as potent antimicrobial agents against Gram-positive and Gram-negative bacteria. Although iron nanoparticles (FeNPs) were proven to have viable antibacterial effects due to its capacity to catalyze H_2O_2, a type of ROS, the process was slow due to its short duration of activity.

In this project, iron oxyhydroxide (FeOOH) nanoparticles were synthesized and tested on the growth of *S. Aureus*. To do so, FeNPs were deposited on PDA (polydopamine) to accelerate ROS production and enhance the catalytic activity. Through ROS selective scavenging, it was confirmed that when PDA-FeNPs catalyzed H_2O_2, they mainly produced superoxide radicals, not hydroxyl radicals as expected. The PDA-FeNPs coated cotton fabrics showed antibacterial effects especially after being treated with argon plasma, which inhibited bacteria growth even after being exposed to 10^5 CFU *S. Aureus*.The importance of this research is to better understand the effects of metal nanoparticles as antimicrobial agents, in an effort to lower the rate of medical device-associated infections and prevent the increase of antibiotic resistance. Additionally, this method provided a cheap and simple nano-FeOOH system improving antibacterial efficiency for medical devices.

COMPARATIVE STUDY OF CATALYTIC EFFICIENCY BETWEEN NANOPARTICLES AND BULK METALS

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Our research focuses on devising new and novel methods for aromatic hydrosilane polymerization using different catalysts. Polysilanes, are Si-Si bonded molecules with organic substituents. They offer enticing benefits but pose difficulties in polymerization. To address these issues, scientists developed different methods for polymerization such as ring opening, Wurtz reductive coupling, or dehydrogenative coupling method.[1-4] Dehydrogenative coupling is a method in which monomers are catalyzed by transition metals, as an alternative to the harsh conditions like that of Wurtz coupling. Our research delves into a deeper area of silicon polymers and polysilanes catalysis in which we are focusing on the efficiency of catalysis. While promising results have been observed in this specific polysilane synthesis, the utilization of nanoparticle catalysts has shown more potential and favorable outcomes due to their increased surface ratio, enhanced potency and efficacy.

In this work we have synthesized polysilanes of phenylsilane and *p*-tolylsilane in presence of 1% Pt-catalyst ratio. The reactions were conducted at 90 °C under inert conditions and were monitored using IR and UV-vis spectroscopy. All products were characterized using NMR analysis for structure identification, GPC for molecular weight observation, UV-Vis spectroscopy coupled with IR for functional group analysis, and TEM for morphology examination. These studies provide a comprehensive approach to characterization of polymers. The details will be presented in this study.

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QUANTIFYING DYE UPTAKE BY UV-VIS SPECTROSCOPY

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In collaboration with a local tie dye shop, a method was developed to determine the concentration of Procion Red MX-5B bonded to cotton fabric during the dyeing process. A series of MX-5B solutions in various concentrations was used to dye fabric. Using UV-VIS, the maximum dye uptake was determined to be 15.03 ±0.02g/L. A similar process was used to observe how aging dye solutions affects dye uptake. Over a four week period the dye uptake decreased 12.5% for the highest concentrated MX-5B solutions and a 29.7% decrease for the lowest. The method was effective in determining the concentration of dye uptake on fabric as well as analyzing the effects of time on dye uptake. This method can be applied to different colored dyes.

A METHOD OF ANALYZING A TIME DEPENDENT VARIATION OF PROTEIN ELECTROSTATICS

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DNA supercoiling changes are managed by a class of enzymes called topoisomerases, which cleave, relax supercoiling, and relegate single- or double-stranded DNA. Our lab investigates topoisomerase IA, which is found in prokaryotes. Currently we are modeling the interaction between topoisomerase IA and ethacridine, a non-intercalating inhibitor of the enzyme which also demonstrates sequence specific behavior. However, the inhibition mechanisms are yet unclear. To further our investigations, we are modeling the electrostatic potentials to evaluate long-range phenomena. Our study findings are complicated by the number of simulations with different DNA sequences in the presence and absence of ethacridine. Since the structural characteristics influencing electrostatics differ with time, we are investigating mechanisms to categorize the time-dependent difference in electrostatic potentials. The study's findings indicate that there may be a smaller, more ideal selection for examination.

INVESTIGATING LIGAND-INDUCED LOCAL CONFORMATIONAL CHANGES OF FLUORESCENTLY LABELED G-QUADRUPLEX STRUCTURES

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DNA sequences rich in guanines readily fold to form quadruplex structures (GQs), which are bound by Hoogsteen-type hydrogen bonding of four guanine nucleotides (G4). GQs are important structural components in many physiological functions, including limiting telomerase activity seen in 85-90% of human tumor cells. Telomerase activity can be influenced by introducing small molecules that can interact with GQs. This interaction of small molecules can alter the stability and local conformations of the GQ at the guanine tetrad level, which in turn can affect the telomerase activity and cancer progression.

To identify changes in the local conformations of the telomeric sequence upon interaction with small organic molecules, we incorporated 6-methylisoxanthopterine (6MI), a circular dichroism (CD)-active fluorescent base analogue of guanine in place of guanine at distinct positions in the human telomeric GQ sequence. Several variations of DNA sequences were used to monitor the conformational changes at different locations of the GQ structure using UV-Vis, CD, and fluorescence spectroscopic methods. Past studies investigated the binding of TmPyP4 (5,10,15,20-Tetrakis-(N-methyl-4-pyridyl) porphyrin), a telomerase-inhibiting ligand, to the GQ but only addressed their interaction in a global conformational perspective. In this study, we used fluorescent base analogues to track the local conformation at individual G-tetrad levels using spectroscopic methods. The results demonstrated an initial stabilization followed by destabilization of the human telomeric DNA sequence with increasing ratios of TmPyP4, whereas the modified strands showed stabilization or destabilization depending on the position of the probe. The results suggest that site-specific fluorescent probes can be used as an "intrinsic sensor" to monitor the global and local structure and stability changes in GQs upon ligand binding. Understanding the effect of different drugs on the local GQ conformation will help to develop targeted drugs to treat cancer and other telomere-related diseases.

MECHANISTIC INVESTIGATION OF SUSTAINABLE BIOCATALYTIC SYNTHESIS OF CYCLOPROPANES FOR CHALLENGING SUBSTRATES

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Unactivated and electron-deficient olefins are important substrates for chemical synthesis, particularly for cyclopropanation, which offers access to many pharmaceuticals and biologically active products. However, transforming these olefins into higher-value chiral products is challenging because of their high activation energy and conformational flexibility, and there is no current mechanistic information to aid in the design of efficient heme-based biocatalysts. Despite this, unactivated and electron-deficient olefins are attractive substrates due to their low cost and their limited reactivity allowing for controlled selectivity. Thus, a systematic quantum chemical study was performed to investigate the effects of olefin substituents, non-native amino acid axial ligands, and natural and non-natural macrocycles on cyclopropanation. Comparison studies of various derivatives are done featuring a concerted, nonsynchronous mechanism for cyclopropanation via an Fe^{II}-based iron porphyrin carbene. The results show that electron-deficient substrates are indeed more challenging and suggest the value of the macrocycles containing electron-withdrawing groups aside from the native and commonly used porphyrin in significantly enhancing cyclopropanation catalysis for such substrates. Moreover, this study is the first of its kind to report a study on the axial ligand effect on such reactions involving challenging olefins. This study is thus expected to facilitate the design of efficient biocatalysts for cyclopropanation with unactivated and electron-deficient substrates using sustainable chemical approaches.

TESTING THE PREDICTIVE POWER OF MOLECULAR DYNAMICS SIMULATIONS

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The *E. coli* tryptophan repressor is a DNA binding protein that plays a regulatory role in the transcription of genes that encode the enzymes that synthesize L-tryptophan. The repressor is known to bind to both L-tryptophan as its natural corepressing ligand and to indole propionic acid as a natural inducing ligand. According to protein-ligand crystal structures the two ligands, despite having similar molecular structures, bind the repressor in opposite orientations, and with essentially equivalent binding affinities in biochemical assays. We would like to know whether such unexpected results could be predicted. We are using molecular dynamic simulations to assess whether computational methods can replicate these results. Simulations using Gromacs will analyze the interactions between tryptophan repressor and each ligand in both orientations. The results from the four simulations and the calculated binding energies will allow us to assess the value of molecular dynamics for predicting receptor and ligand binding interactions with the Tryptophan repressor as a model case.

SYNTHESIS OF FUNCTIONALIZED BICYCLIC MOLECULES THROUGH CYCLIZATION OF ANILINES AND PHENOLS USING PINCER IRIDIUM COMPLEXES

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(^{iPr}PCP)Ir(C_2H_4), an iridium catalyst primarily used for C-H activation, had previously shown moderate succession in its ability to cyclize certain styrenes into their indene derivatives[1], this work looked at the ability to perform similar cyclizations with different heteroatoms. Catalytic ability for the formation of indoles was tested with 2-ethynyl-aniline derivatives. The ability for complete conversion to the indole in two hours was demonstrated, as well as easy isolation of the product. Derivatives of 2-allyl-phenol were also tested and showed the ability to cyclize into saturated benzofuran derivatives. The yield of the benzofuran derivatives was measured with different electron donating and electron withdrawing groups, with yields generally ranging from 40 to 90% of the saturated benzofuran. Products were characterized through GC-FID, ESI-MS, column chromatography, 1D ^{1}H and ^{13}C NMR as well as 2D-^{1}H NMR. The mechanism to this cyclization was also investigated using experimental and density functional theory.

DESIGNING FUNCTIONAL CYSTEINE-LESS PROTEIN VARIANTS USING MACHINE LEARNING

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The ability to site-specifically label biomolecular complexes with small molecules such as fluorophores is a fundamental requirement for many biophysical assays that involve visualizing the localization, interactions, and mechanism of vital biological processes. For proteins, the most common method of labeling is *via* attachment of the small molecule to a cysteine residue. However, to achieve site-specific labeling at one position, all native cysteines must first be removed from the protein to avoid labeling any non-targeted locations. One of the major challenges of this task is thus to mutagenize the protein-encoding gene to remove native cysteines without disrupting the protein's functionality. Here, we leverage recent machine learning advances in large language models (LLM) of protein sequences to computationally design cysteine-less protein variants without perturbing their stability or function. LLMs, such as evolutionary scale modeling 2 (ESM2), encode the evolutionary patterns from past natural evolution of protein sequences and have recently been shown capable of predicting protein structure with high confidence. In this study, we have developed a method using ESM2 to efficiently create cysteine-less protein variants. As proof-of-concept, we have created a cysteine-less variant of the fluorescent protein mRuby3. Fluorescence activity assays in *Escherichia coli* are being performed to confirm that the modified mRuby3 maintains its functionality. By enabling the design of functional cysteine-less protein variants, our method will facilitate the subsequent step of site-specific labeling at particular sites of interest and thus open new possibilities for detailed studies of how proteins function.

SYNTHESIS AND CHARACTERIZATION OF PYRROLE-BASED PNP MOLYBDENUM COMPLEXES FOR NITROGEN FIXATION

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The reduction of dinitrogen gas to ammonia using transition metal catalysts at ambient temperature and pressure has potential as an environmentally conscious alternative to the Haber-Bosch process. Researchers have identified molybdenum as a promising candidate for an effective organometallic catalyst. One proposed mechanistic pathway for nitrogen reduction involves the formation and cleavage of a dinitrogen-bridging bimetallic complex, which avoids intermediates with high-energy partially-reduced nitrogen species. Electron-poor molybdenum is associated with better catalytic ability—the anionic electron-rich alkylamido PNP pincer complex is capable of nitrogen cleavage, but does not do catalysis, while a more electron-withdrawing diarylamido PNP variant is able to catalytically produce ammonia through a bimetallic N_2-bridged intermediate. Due to its aromaticity, the anionic pyrrole-based pincer ligand is even more less likely to donate π electrons to the metallic center, which may indicate its potential for catalytic nitrogen reduction.

To further investigate the bimetallic N_2 cleavage pathway, an anionic pincer ligand with a pyrrole center and bis-phosphine arms was synthesized. Initial attempts to metalate the ligand with molybdenum proved unsuccessful—therefore, in order to facilitate the initial deprotonation of the pyrrole moiety, a lithium-containing base was used to substitute the proton with a lithium cation. The compound was coordinated to a metal using Mo^{III} halide precursors, which formed the desired Mo^{III} complex as shown by paramagnetic nuclear magnetic resonance spectroscopy (NMR). Additionally, a diamagnetic Mo^{IV} pincer complex with an oxo ligand bound to the metallic center has been characterized using NMR and X-ray diffraction.

COMPREHENSIVE COMPUTATIONAL ANALYSIS TO IDENTIFY DUAL-TARGET INHIBITORS FOR THE NIPAH VIRUS THROUGH THE REPURPOSING OF APPROVED DRUGBANK SMALL MOLECULES

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The Nipah virus (NiV), with a significantly higher fatality rate compared to COVID-19, presents a grave threat as a potential future pandemic, particularly if ongoing mutations bolster its transmissibility. To impede NiV's entry into host cells, disrupt the viral envelope formation, and encapsulate the nucleocapsid, targeting the interaction between the Nipah attachment glycoprotein and the human ephrin-B2 receptor, alongside the matrix protein, is crucial. Leveraging already approved small molecules for drug repurposing offers a strategic advantage in expediting NiV treatment discovery, capitalizing on compounds with established safety profiles. Through precise docking methods and comprehensive Absorption-Distribution-Metabolism-Excretion Toxicity (ADMET) profiling of small molecules cataloged in DrugBank, we identified the top four candidates, subsequently subjecting them to 500 nanoseconds of molecular dynamics (MD) simulations and analysis via the Molecular Mechanics-Generalized Born Model and Surface Area Solvation (MM-GBSA) method. Further scrutiny, including examination of the free energy landscape, principal component analysis, and assessment of protein secondary structures, revealed Iotrolan (DB09487) and Iodixanol (DB01249) as potent dual inhibitors.

CHARACTERIZATION OF THE 5' ENDS OF POLYKETIDE SYNTHASE TRANSCRIPTS IN THE HARMFUL ALGAL BLOOM SPECIES, *KARENIA BREVIS*

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The dinoflagellate *Karenia brevis* causes harmful algal blooms containing brevetoxins that lead to death of marine life and health complications in humans. Understanding mechanisms of brevetoxin biosynthesis can help predict bloom toxicity and mitigate harmful effects in the future. Brevetoxins are made by polyketide synthase (PKS) enzymes. Several PKS genes have been previously characterized in *K. brevis* that contain single catalytic domains and a spliced leader (SL) sequence suggesting they are regulated post-transcriptionally. A newer transcriptome from 2017 has revealed that *K. brevis* also contains multi-domain PKS sequences; however, the SL sequence was not identified on any of the PKS transcripts. The objective of this study was to identify the presence of the spliced leader sequence on the 5' end of two of the newly identified PKS transcripts to determine if these new sequences are regulated through a similar mechanism as the previously identified PKSs. 5' RACE was performed on two PKS contigs, contigs 81604 and 54805. RACE PCR products were ~300 bp for both contigs suggesting some additional sequence has been obtained at the 5' ends. RACE PCR products were cloned using a TOPO cloning kit (Invitrogen) and transformed into *E. coli*. Restriction digests confirmed the inserts for most of the clones, and they have been submitted for sequencing. Sequences will then be analyzed for the presence of the SL sequence on both contigs. This work will increase our understanding of gene regulation of toxin-related sequences to ultimately lessen the negative impacts of bloom events.

EXPLORING THE EFFECTS OF AUTOPHAGY ON GABA RECEPTOR EXPRESSION IN HEK 293 CELLS

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Autophagy is a crucial cellular process responsible for degrading and recycling damaged components in cells. Autophagy initiates with the formation of an autophagosome, a double membrane structure that engulfs targeted components. The autophagosome fuses with a lysosome, triggering waste degradation and amino acid recycling. Gamma-aminobutyric acid receptor-associated protein (GABARAP) is thought to be essential for autophagosome maturation, trafficking, and lysosome fusion. GABARAP also binds to the γ2 subunit of GABA A receptors (GABARCs), a neurotransmitter receptor, crucial for receptor trafficking and synapse stability. However, the connection between GABARCs and autophagy remains unclear.

This study investigates the interplay between autophagy and GABA Rs using HEK 293 cells. GABA R γ2 subunits tagged with Green Fluorescent Protein (GFP) were transfected into HEK cells, followed by autophagy induction through various treatments. Immunocytochemistry labeled autophagy markers (LC3) and assessed GABA R clustering under these conditions. Colocalization between GABA Rs and autophagosomes was also examined. The results showed increased LC3 clustering, suggesting active autophagy. GABA R clustering also intensified under autophagy induction, suggesting a potential connection between autophagy and GABA R regulation. Colocalization between GABA Rs and LC3 was also observed, implying GABA R targeting to autophagosomes. GABA R intensity decreased with Rapamycin treatment, indicating autophagic breakdown. Furthermore, autophagy induction, especially with starvation, increased the surface-to-total GABA R ratio, suggesting at a role in GABA R expression regulation. These findings provide insights into the relationship between autophagy and GABA R regulation, promising future investigations into their dynamic interplay and underlying mechanisms.

THE INFLUENCE OF HPV+ CANCER ON GENOMIC STABILITY AND HUMAN NUCLEI

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The research focuses on Human papillomaviruses (HPVs) which are a significant etiological factor in the development of cervical cancer and head and neck cancers, two prevalent and clinically impactful conditions within the United States. To comprehensively explore the effects of HPVs on nuclear size, this research has focused on the examination of four distinct cell lines, each serving as a model system for HPV+ cancers. The cell lines employed were CasKi derived from cervical carcinoma and frequently used in research to study cervical cancer and its underlying cellular and molecular mechanisms; SCC-47 originating from head and neck squamous cell carcinoma; SCC-25 also derived from head and neck squamous cell carcinoma; HaCaT an immortalized human keratinocyte cell line. It is commonly used in dermatological research and serves as a model for studying skin-related diseases, including carcinogenesis and wound healing. CasKi and SCC47 cell lines are infected with Human papillomavirus type 16 which is strongly associated with cervical and head & neck cancers. We have been looking at HPV+ and HPV- tumors in the nuclei compared with healthy cells. SCC25 and HaCaT cell lines are HPV-negative controls, meaning they do not naturally carry any HPV infection. SCC47 and CasKi cell lines are HPV+, meaning they carry the HPV infection. We saw a lot of changes such as changes in shape, size, and number of micronuclei. There is a huge difference in HPV+ Cancer cells compared with HPV- Cancer cells and healthy cells.

THE ROLE OF THE UNFOLDED PROTEIN RESPONSE IN THE MALFUNCTION OF A HUMAN PQ-TYPE CALCIUM CHANNEL

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Voltage-gated calcium channels (VGCC) are fundamental in nerve excitability as well as skeletal and cardiac muscle contraction. A particular channel variant, PQ-type ($Ca_v2.1$), is involved in central neurotransmission and mutations in PQ-type channels are implicated in neurological disorders, specifically epilepsy. Here we studied a truncation mutant of the PQ-type channel, Q1397X, associated with epilepsy, but whose role in epilepsy remains unknown. Following *in vitro* cRNA transcription, electrophysiology using TEVC demonstrated no currents in *Xenopus laevis* oocytes expressing Q1397X mutant. Additionally, coexpression of wildtype PQ channels and Q1397X, simulating a heterozygous phenotype, significantly reduced wildtype channel current amplitude compared to WT channels alone, exhibiting a dominant-negative manner. Existing literature suggests the Unfolded Protein Response (UPR) to be a possible mechanism for the dominant-negative effect occurring in mutant/wildtype coexpression. Current examinations of whether wildtype currents in coexpressed Q1397X/WT cells can be rescued by inhibiting the UPR through ER stress sensor pathways are being conducted using UPR inhibitor drugs, 4μ8c and GSK2606414, and the dominant-negative UPR inhibitor protein, PERK K618A. Results from these experiments will clarify this mutant's role in epilepsy and possible development of specialized treatment options for patients suffering from the disorder.

THE EFFECTS OF PERFLUOROOCTANE SULFONATE (PFOS) EXPOSURES ON TRANSCRIPTIONAL PROGRAMS IN FALLOPIAN TUBE NON-CILATED EPITHELIAL CELLS

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Perfluorooctane sulfonate (PFOS) is a man-made chemical once prized for its industrial applications due to its thermal stability and water-repellent properties. However, it is a persistent environmental contaminant that resists natural degradation and accumulates in human tissues. Given its ability to bioaccumulate, investigating PFOS's potential effects on gene regulation in epithelial cells, which are present in many organs, is crucial. To understand how PFOS exposure influences gene regulation, we employed a combination of human fallopian tube non-ciliated epithelial (FNE) cell cultures, high and low PFOS dose exposures, mass spectrometry to quantify cellular PFOS uptake, and transcriptomics to analyze gene expression changes. Our experiments yielded the following key findings: 1.Dose-Dependent Intracellular Accumulation: PFOS readily accumulated within the intracellular pool of molecules in FNE cells. Importantly, the level of accumulation was directly dependent on the strength of the exposure, with higher doses leading to greater intracellular PFOS concentrations. 2. Differential Gene Regulation: Exposure to varying PFOS concentrations resulted in the differential activation of gene transcription within the FNE cells. This suggests that the specific genes affected by PFOS depend on the level of exposure. These findings demonstrate that PFOS exposure can alter gene regulation in FNE cells, and the effect is dependent on the dose. We are currently elucidating the specific genes and pathways targeted by PFOS at different concentrations.

NANOPORE-BASED DNA BARCODING OF HERBAL MEDICINAL PRODUCTS REVEALS PLANT INGREDIENTS NOT DECLARED ON THE LABEL

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In the culturally diverse setting of New York City, a plethora of traditional herbal medicines are used, many sold as herbal supplements in the New York city market as well as online. However, the US Food and Drug Administration (FDA) does not regulate these herbal medicines, and there have been instances of fraudulent (i.e. substituted/adulterated) herbal products in the US market. The typical workflow for plant DNA barcoding involves extraction of plant DNA, amplification and Sanger-based sequencing of an appropriate plant marker, and comparative sequence analysis against a plant database to authenticate the product. However, Sanger-based sequencing can only be used when herbal products contain only a single plant ingredient, not herbal products with multiple/mixed ingredients. In this project, we used Nanopore sequencing to authenticate a total of 8 non-FDA regulated herbal medicinal products (HMP, 3 single+ 5 mixed). Of the 3 single-ingredient HMP, 3 were sequenced using Nanopore, with 2 confirmed by Sanger, though Nanopore was able to detect other ingredients not on the label (i.e. adulterated). Though some of the declared plant ingredients (not all) were in detected in five of the mixed-herb HMPs, all had some level of adulteration, with some of these plant contaminants known to be toxic. Our research underscores the significance of Nanopore-based DNA barcoding to authenticate HMPs, and of herbal pharmacovigilance, especially in settings lacking stringent government oversight of herbal supplements.

INFLAMMATORY EFFECTS OF HIV-1 TAT PROTEIN AND SUBSTANCES OF ABUSE ON THE BLOOD-BRAIN BARRIER

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Caspase-1 has recently emerged as an anti-inflammatory therapeutic target due to its roles in releasing pro-inflammatory cytokines and initiating pyroptosis. Caspase-1 is activated by inflammasomes that detect cytosolic perturbations from infections. Active caspase-1 cleaves pro-IL-1β and pro-IL-18 into their mature, secreted forms and induces pyroptosis by cleaving gasdermin D. We hypothesized that caspase-1 inhibition could prevent inflammatory damage at the blood-brain barrier (BBB). We studied gene expression of death-inducing signaling complex (DISC) and inflammasome components in brain microvascular endothelial cells (BMVECs) treated with illicit drugs and HIV-1 Tat using real-time reverse-transcriptive quantitative polymerase chain reaction (RT-qPCR). Both apoptotic and pyroptotic genes, as well as pro-inflammatory cytokines, have been examined. Our initial results showed that amphetamine and HIV-1 Tat (86-residue and 101-residue constructs) activate inflammasomes while suppressing apoptosis and pyroptosis. Inflammasome genes, such as NLRP3, NLRP7, and NLRP12, are increased in expression. Initiator proteins, caspase-1, 4, and 5 are also significantly upregulated, leading to the elevation of the expression of pro-inflammatory cytokine genes, including IL-1β, IL-6, IL-18, and TNFα. However, Gasdermin D, another substrate of caspase-1 and the initiator of pyroptosis, is down-regulated. In addition, the expression of caspase-3, -7, and -8 in the apoptotic pathway is also decreased, suggesting a suppression of cell death through either apoptotic or pyroptotic mechanisms. Δ9-tetrahydrocannabinol (THC), on the other hand, led to increased caspase-7 and 8, as well as gasdermin D, suggesting that THC significantly induced cell death in both apoptotic and pyroptotic mechanisms. Cocaine prominently activated caspase-7 and 8, which would induce apoptotic cell death. We are in the process of novel molecular design and will identify potential caspase-1 inhibitors with predicted efficacy and drug-like properties. These newly designed molecules will be experimentally validated including enzymatic assays to determine IC50 and cell-based assays measuring gene expression, cell viability, and BBB permeability.

INVESTIGATION OF MRP AND PHA GENE FUNCTION IN MARINOBACTER ADHAERENS

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Karenia brevis is a toxic dinoflagellate that forms blooms in the Gulf of Mexico, harming the surrounding ecosystem. *Marinobacter adhaerens* are gamma-proteobacteria that are marine community members with *K. brevis* and were isolated from laboratory cultures of *K. brevis.* A previous bioinformatic analysis revealed a high content of sodium and iron transport clusters of orthologous groups (COGs) and additional evaluation of the sodium transport-related COGs led to the identification of genes that encode for *mrp* (multi resistance and pH) and *pha* genes (pH adaptation) that occur in neighboring loci in the bacterial chromosome. The *mrp* and *pha* genes belong to a family of antiporters that have been shown to play roles in pH homeostasis, resistance to elevated levels of various cations, pathogenesis, and biofilm formation in a variety of bacteria. The tandem arrangement is fairly uncommon in sequenced bacterial genomes and published studies on the roles of genes in this arrangement are lacking, giving us an opportunity to carry out novel research to explore the roles of these antiporters in *M. adhaerens*, including any interplay/overlap/redundancy of function. We have made knockout variants for both the *mrp* and *pha* genes individually as well as a double deletion through the use of suicide vectors constructed for this purpose. Studies to be presented in this poster show that there is significant redundancy of function with respect to pH homeostasis and cation resistance, as the double knockout shows significantly more sensitivity than the individual knockouts to growth at elevated pH and growth in the presence of high concentrations of sodium chloride and potassium chloride. We will also present RT-qPCR results of the effects of high pH and salt concentration on the expression of the *mrp* and *pha* genes.

THE GABARAP PROTEIN AND ITS ROLE/LOCALIZATION DURING AUTOPHAGY

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Autophagy is a crucial process in which damaged organelles are recycled to maintain cellular functionality and homeostasis, particularly under stress. This process involves proteins such as LC3, which facilitates the formation of double-lipid-membrane vesicles known as autophagosomes. Autophagosomes engulf damaged cellular components and fuse with lysosomes, organelles containing enzymes, leading to degradation and recycling. This research focuses on the intricate process of autophagy, specifically examining LC3 proteins and the less-explored GABARAP component. Although not much is known about GABARAP, there have been studies highlighting its ability to facilitate autophagy. This study aimed to investigate the role, significance, and localization of GABARAP in autophagy.

The hypothesis under examination was whether LC3 proteins and GABARAP would co-localize during the process of autophagy. Using techniques such as transfection, microscopy, and treatments, a lack of interaction was observed between the GABARAP component and LC3 proteins when observed in HEK 293 cells. Overexpression of the LC3 protein led to its localization in both the cytosol as well as in the nucleus. Although GFP-LC3 and endogenous GABARAP clustered in the cytosol, they did not interact, as observed by their lack of colocalization. To study this phenomenon, the reciprocal of the first experiment was conducted, where GABARAP tagged with Green Fluorescent Protein (GFP) was transfected utilizing identical conditions, The results observed yielded similar results, where the transfected
GFP-GABARAP DNA localized in the nucleus as well as the cytosol without localizing with endogenous LC3. in both instances, the transfected proteins migrated to the nucleus without aligning with their endogenous counterparts, despite their close proximity.

OPTIMIZING *IN VITRO* TRANSCRIPTION TO STUDY PQ CHANNEL MUTATIONS IMPLICATED IN EPILEPSY

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Voltage Gated Calcium Channels (VGCC) allow for the depolarization of plasma membranes to allow for the entry of calcium (Ca2+), allowing for physiological responses to take place including secretion, gene expression, contractions, and neurotransmission. PQ-type VGCC's play a major role in synaptic transmission, mutations in PQ-type VGCC are implicated in epilepsy. PQ-type VGCC consist of 3 subunits: the α1 subunit which is known to contain the channel pore and gating machinery, the α2δ subunit known to enhance the function of the channel, and the β subunit which allows for the regulation of gating mechanics and channel properties. Mutations that are implicated in epilepsy have been identified in the β subunit, including the Q131L mutation. We studied how the Q131L mutation impacted VGCC activation. This mutation was introduced using site-directed mutagenesis, then expressed in Xenopus oocytes and VGCC activity was recorded using two-electrode voltage clamp recordings (TEVC) to compare electrical currents with either the β3 WT or mutant β3 subunit. We found that channel activation was left-shifted (lower voltages could activate the mutant channel). This suggests a molecular mechanism of epilepsy. In addition, we optimized in vitro transcription which increased our likelihood of successful RNA synthesis, which enabled our TEVC recordings.

INVESTIGATING THE EFFECTS OF GABARAP ON INDUCED AUTOPHAGY IN HEK 293 CELLS

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Autophagy is a cellular process that is characterized by the formation of autophagosomes around dysfunctional organelles or unneeded cellular components. This process involves binding of the autophagosome to the lysosome, degradation of its contents, and return of the breakdown products back to metabolic pathways. Autophagy is essential for the normal functioning and development of cells, especially obvious in neurons as the deficit of autophagy has been linked with diseases such as Alzheimer's and Parkinson's. There are many proteins that are involved in autophagy, including GABARAP and LC3. LC3 is important for the formation of autophagosomes, and its clustering is an indicator of autophagy. On the other hand, GABARAP is believed to have a role in the lysosome fusion process in autophagy, although its role in autophagy is still being investigated. In this study, we investigated exogenous GABARAP regulation, expression levels and impact on autophagosome formation under autophagy-inducing conditions. Here it is shown that GABARAP overexpression inhibits endogenous LC3 clustering initiated by multiple triggers of autophagy. Additionally, evidence suggested GARARAP may in part localize to the nucleus. Live imaging testing showed GFP GABARAP expression levels increased with induction of autophagy. This was further tested by disrupting transcriptional and translational processes, suggesting that more protein might be translationally synthesized under autophagic conditions.

MODELLING INTRACELLULAR CONCENTRATIONS OF FREE AMINO ACIDS IN CULTURED OVARIAN CANCER PRECURSOR CELLS

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Cancer cells accumulate free amino acids from the tumor microenvironment to support cell growth, proliferation, and survival. Profiling of the free amino acid content of ovarian cancer (OC) tumors derived from patient ascites revealed that taurine and proline, both osmolytes, were present at high concentrations (>100uM). Previous work in the Iwanicki Lab has uncovered that supplementation of taurine in culture media can restore intracellular taurine levels to those found within tumor samples. Accumulation of taurine has been shown to impede the proliferation of fallopian tube non-ciliated epithelial cells expressing mutant p53 (FNE-m-p53), a cell culture model representing OC precursors. Taurine's antiproliferative effect was attributed to restoration of the tumor-suppressor p53 pathway and activation of the cell-cycle inhibitor CDKN1A (p21). Whether proline supplementation produces similar effects in FNE-m-p53 cells has not been explored.

The purpose of this investigation was to determine the effects of taurine and proline supplementation on cultured cells using a variety of assays, including flow cytometry, western blot, and live cell imaging. Our work has shown that proline, like taurine, activates p21 in cell lines expressing either mutant or wild-type p53. Interestingly, taurine, but not proline, induced cisplatin resistance in FNE m-p53 cells. Furthermore, both amino acids induced changes in cell morphology, including modulation of cell size and adhesion through fibronectin production.
This investigation sheds light on the effects of taurine and proline supplementation, including the activation of the tumor suppressor p21, modulation of cell size and adhesion, and acquisition of chemotherapy resistance.

CREATING A COST EFFICENT METHOD TO DETERMINE THEOPHYLLINE RIBOSWITCH ACTIVATION

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A riboswitch is a small piece of RNA in structure that binds a molecule to itself to turn on or turn off a gene. As a result, riboswitch regulation provides an opportunity to develop targeted therapies for various diseases. Currently one of the only ways to determine activation of a riboswitch in an organism is to perform Fluorescent Activated Cell Sorting (FACS). This machine requires a large amount of upkeep and a trained technician to use. Most smaller research universities do not have the resources to be able to use this type of machine which greatly limits the amount of research that can be performed on riboswitches. This project is built based on 3 different cloning methods: Gibson assembly, golden gate assembly, and PCR assembly. To test this, the lab is currently taking plasmids and performing these assemblies using fluorescent genes, GFP-UV and mCherry, as well as the sequence for the theophylline riboswitch. Once these genes are cloned, the hope is to view under UV light which of the fluorescent genes are expressing. The amount of expression will be quantified using ratio-metric fluorescence. If GFP-UV and mCherry express this will tell that the theophylline riboswitch is active. If only mCherry is active this will tell theophylline is riboswitch is inactive. These measurements can be used to measure activation of other riboswitches as well.

AN RNAI SCREEN IDENTIFIED THE *P38 MAP KINASE*, PMK-1, AS A POTENTIAL REGULATOR OF CELL MIGRATION DURING *C. ELEGANS* EMBRYOGENESIS.

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In order to properly develop, organisms must undergo proper cell migration. Cell migration is a process that is meticulously regulated but all the details on how this happens are not fully known. Links have been established between abnormal cell migration and diseases like cancer and some neurodegenerative disorders. *Caenorhabditis elegans* is a model organism with a well-established cell migration pathway. In *C. elegans*, the WAVE/SCAR pathway has been shown to regulate epidermal cell migration during embryonic morphogenesis. There are three axonal guidance receptors (SAX-3, UNC-40 and VAB-1) that send signals to WAVE to nucleate branched actin and initiate cell movement. We performed an RNAi screen for potential cell migration genes and identified PMK-1 as a potential regulator of the WAVE pathway. PMK-1 is a member of the *P38 MAP kinase* family and is an ortholog of human *mitogen-activated protein kinases 11 and 14* (MAPK11 and MAPK14). PMK-1 has been suggested to play a regulatory role in cell development and differentiation. We found that loss of *pmk-1* in *C. elegans* causes embryonic lethality, and a portion of these embryos die due to a failure in morphogenesis. The ventral cells of the epidermis fail to properly migrate and seal in the internal organs leading to dead embryos. This phenotype resembles what is observed when known WAVE genes are mutated. Loss of PMK-1 in *vab-1* and *sax-3* mutant backgrounds showed enhanced embryonic lethality while it was additive in *unc-40*. The enhanced lethality results could mean that PMK-1 is functioning in a pathway parallel to SAX-3 and VAB-1 while the additive lethality in an *unc-40* background could mean that they are functioning in the same pathway. We will further investigate to verify that PMK-1 is functioning in the WAVE pathway and determine where in the WAVE pathway it functions. Future experiments will also investigate how PMK-1 affects branched actin nucleation.

MOLECULAR BIOPHYSICS: CLBS DYNAMIC DOCKING WITH AMINO ACIDS

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This research aimed to investigate the binding capabilities of the ClbS Colibactin Resistance Protein, an antitoxin found in E. coli, with all 20 naturally occurring amino acids utilizing dynamic simulations. The methodology involved global docking simulations using AutoDockTools, followed by molecular dynamics simulations with GROMACS and visualization through VMD. The binding energies were calculated using AutoDock Vina, and RMSD graphs were generated using GRACE software. The results demonstrated ClbS Colibactin Resistance Protein binding with 4 of the naturally occurring amino acids. Tryptophan (TRP), phenylalanine (PHE), and tyrosine (TYR), amino acids with similar chemical properties, exhibited favorable binding interactions with ClbS. Notably, arginine (ARG) displayed a superficial but stable binding interaction as well. The favorable binding interactions observed with TRP, TYR, PHE, and ARG were potentially attributed to their larger size. This research provides insight into the binding capabilities of the ClbS protein, offering new directions for exploration in the development of novel therapeutic approaches that could target proteins traditionally considered challenging to drug.

CHARACTERIZATION OF THE 5′ ENDS OF HYBRID NONRIBOSOMAL PEPTIDE SYNTHETASE/POLYKETIDE SYNTHASE TRANSCRIPTS IN THE HARMFUL ALGAL BLOOM SPECIES, *KARENIA BREVIS*

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Karenia brevis causes harmful algal blooms that lead to marine animal death and health complications in humans through the production of neurotoxins called brevetoxins. Brevetoxins are synthesized by polyketide synthase (PKS) enzymes, but *K. brevis* also contains nonribosomal peptide synthetases (NRPS) and hybrid NRPS/PKS enzymes that synthesize different secondary metabolites. Characterization of these pathways will provide information on the full metabolome of *K. brevis* and their regulation. PKS transcripts previously studied contain a trans-splicing signal on their 5′end called the spliced leader (SL), suggesting they are regulated post-transcriptionally. The objective of this study is to identify if the spliced leader (SL) is present on the 5′ end of hybrid NRPS/PKS transcripts in *K. brevis* to determine if they are regulated in a similar way. To examine the 5′end, 5′ RACE was performed on two hybrid transcripts, contigs 1930 and 10563. Based on the current sequence data, the PCR products for both contigs would be at least ~250 bp. RACE PCR products were 350 bp for Contig 1930 and 150 bp, 200 bp, and 300 bp for Contig 10563 suggesting RACE produced cDNAs longer than the original sequence. Products after restriction digest exhibited sizes of ~350 bp for 1930, and ~200 bp for 10563, confirming inserts of the expected sizes. RACE PCR products were cloned using the TOPO cloning kit (Invitrogen), transformed into TOP10 competent *E. coli* cells, and sequenced. Sequence alignments between RACE sequences and the original contig 10563 showed no additional sequence at the 5′ end of the 15063 contig. Sequence alignments showed a short extension of the 1930 contig, but the SL sequence was not identified. Additional clones are currently being sequenced to obtain additional sequence at the 5′ ends. This work will improve our understanding of the gene regulation of these NRPS and NRPS/PKS transcripts and regulation of secondary metabolism in this harmful algal bloom species.

THE ROLE OF TAURINE IN AGE-RELATED MACULAR DEGENERATION (AMD)

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Taurine, a non-essential amino acid that is found throughout the body, has recently been linked to protective, anti-aging effects. It is found in high concentrations in the Retinal Pigment Epithelium (RPE) cells, which serve as a barrier, supporting and maintaining the overlying photoreceptor cells. Age-related macular degeneration (AMD) is a disease characterized by RPE and photoreceptor cell degeneration and is the leading cause of blindness in individuals 55 and older. Mutations in the taurine transporter result in an early onset of AMD, suggesting taurine's role in keeping RPE cells healthy and functional. When supplemented into *in-vitro* RPE cell culture, taurine was seen to have a positive effect on proliferation. Sodium iodate, an oxidant that is known to induce retinal degeneration through RPE cell death, was added to the *in-vitro* RPE cell culture in varying concentrations alongside taurine supplementation. Thus, we aim to interrogate whether introducing taurine to the AMD-induced RPE cells may prevent further disease progression, and possibly reversing the harmful effects of sodium iodate. If successful, this experiment may offer a potential treatment candidate, taurine, for this belligerent disease.

INVESTIGATION OF GABARAP AND GABA RECEPTORS DURING AUTOPHAGY

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Autophagy is a process of degradation where the cell removes unnecessary or damaged components through a lysosome-dependent mechanism. It allows for regulated breakdown and recycling by packaging unnecessary cellular components in autophagosomes which then fuse with lysosomes. Autophagy is particularly important in neurons, since its disruption has been linked to diseases such as Alzheimer's and Parkinson's disease. Many proteins are involved in autophagy including GABARAP (Gamma-Aminobutyric Acid Receptor-Associated Protein) which may play a role in the formation and maturation of autophagosomes and has been reported as having a role in the fusion process between autophagosomes and lysosomes. GABARAP is also involved in the regulation of the trafficking of its binding partner, the GABAA receptor γ2 subunit, one of several subunits that make up the inhibitory neurotransmitter channel. In this study, the effects of GABARAP on autophagosome formation, as well as on the localization of the γ2 subunit of GABAA receptor, under different autophagy-inducing treatments were examined in HEK 293 cells. GABARAP overexpression was found to inhibit LC3 clustering, an indicator of autophagosome formation. Additionally, distribution of endogenous GABARAP during autophagy as well as its increased colocalization with GABAA receptors suggested GABARAP and GABARs might be targeted to autophagosomes during autophagy.

THE CELL WALL INTEGRITY PATHWAY IS REQUIRED FOR *FKS2*-MEDIATEDECHINOCANDIN DRUG RESISTANCE IN *CANDIDA GLABRATA*

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Candida glabrata is a fungal pathogen that can cause invasive infections in immunocompromised patients. These infections are treated with echinocandin antifungal drugs that inhibit fungal cell wall synthesis by targeting beta-1,3-glucan synthase. Mutations in *FKS1* or *FKS2* genes that encode for this target enzyme lead to resistance; however, multiple fungal tolerance pathways, including the cell wall integrity (CWI) pathway, are activated upon drug exposure prior to *FKS* mutation and yield hypersusceptibility to echinocandins when targeted. To determine the role of the CWI pathway in echinocandin-resistant cells, we first disrupted a CWI pathway gene (*SLT2*) in a drug-resistant *FKS2* mutant (S663P). Subsequent drug susceptibility assays performed showed that disruption of *SLT2* surprisingly led to a reversal of echinocandin resistance. Our next aim was to complement this phenotype with reintroduction of *SLT2* on a plasmid. We cloned *SLT2* onto *C. glabrata*-specific plasmids which were expressed inour *SLT2* knockout strains using a gap-repair cloning technique. More recent work generated additional plasmid-bearing control strains required for comparison. Drug susceptibility assays revealed successful complementation of the *FKS2* mutant that was disrupted for *SLT2*. With *SLT2* reintroduced, this strain demonstrated elevated MICs compared to wild type and empty- plasmid controls, as expected. In addition, the added presence of plasmid-borne *SLT2* did not alter susceptibility profiles of wild type or resistant cells that contained intact chromosomal copies of *SLT2*. These studies reveal that *SLT2* influences echinocandin resistance in *C. glabrata*and provide additional insight into how targeting the CWI pathway may increase echinocandin efficacy and how *FKS2* gene expression is controlled.

ASSESSMENT OF DIVERSITY OF SAPROXYLIC FUNGAL COMMUNITIES IN BOREAL FOREST USING THE MYCOPINS METHOD

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Fungi in boreal forests release nutrients into the ecosystems they inhabit by serving as primary decomposers of organic matter. This decomposition changes the structure of detritus over time, thereby improving habitat suitability for a rotation of new organisms over the course of decay. Succession after this fashion is impacted by many factors including the source material for decay. Forest tree species can be broadly divided into *angiosperms*, broadleaf trees, which produce hardwood, and *gymnosperms*, conifers, which produce softwood. These types of wood are mostly composed of cellulose and lignin but differ in the chemistry that determines characteristics such as hardness and resistance to microbial invasion. Deadwood is therefore a highly diverse nutritional resource and likely harbors an equally diverse group of specialized fungal species. Our research aims to identify various saproxylic fungi in a boreal forest where the ecosystem is minimally disturbed by anthropogenic factors, characterize their succession, and assess the effects of forest management strategies on forest diversity. We hypothesize that: 1). Succession of species will be observed in fungal communities in deadwood as communities change while decay progresses. 2. Fungal communities will differ in hardwood and softwood.

The MycoPins method was used to monitor fungal colonization in woody debris. Short, sterilized hardwood and softwood dowels were shallowly buried in 4 different environments in a boreal forest in Finland. The 4 transects: a swamp, a broadleaf forest, and a protected forest with and without access by reindeer, were sampled throughout 2022-2023. Dowels of each wood type were retrieved every 2 weeks (winter permitting) over the course of a year and analyzed to identify the colonizing microbes via metabarcoding. Our research group analyzed 35 MycoPins collected from the broadleaf forest. Metabarcoding was used to evaluate fungal diversity in the MycoPins: DNA was extracted from each sample, amplified using PCR, and sequenced using next-generation sequencing. Data was analyzed using the SCATA pipeline, statistical analysis was performed using R and the Vegan package, and species that were not identified via SCATA were manually identified by NCBI BLAST. Traits for each identified species were sourced from FungalTraits. The data provide preliminary support for both of our hypotheses and highlights the importance of continued investigation of the dependance of succession dynamics on the composition of detritus.
Our research emphasizes the ecological importance of fungi in boreal forests and provides data on the varied species and successional roles of saproxylic fungal guilds during wood decomposition. The insights gained from this study pave the way for further investigations emphasizing the need for informed strategies to conserve biodiversity and make use of these vital natural resources.

DEVELOPING TREE RING RECORDS FROM HIGH MOUNTAIN NEW JERSEY

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This paper presents a comprehensive exploration into the realm of dendrochronology, focusing on the methodologies and findings derived from extensive tree ring data collected from High Mountain Park Preserve in New Jersey. Dendrochronology, the study of tree rings, serves as a powerful tool for reconstructing past environmental conditions, providing valuable insights into climate variability, ecological dynamics, and anthropogenic influences over time. The research detailed in this paper encompasses the collection and analysis of tree ring samples from diverse tree species on High Mountain. Methodological approaches, including core sampling, cross-dating techniques with CooRecorder and statistical analyses with CDendro, are employed to establish an accurate and robust chronology. This paper aims to extend existing dendrochronological records and enhance our understanding of regional and global environmental histories. We used the data collected from High Mountain and compared it to known data collected from Norvin Green State Forest in New Jersey to find any strong correlations within the data sets. Our results show a stronger correlation during the summer months and a higher sensitivity to precipitation during this time. The goal is to use these tree ring records to uncover more information about precipitation and stream flow. Furthermore, this study underscores the potential of dendrochronology informing contemporary environmental management strategies and climate change mitigation efforts.

INVESTIGATING WATER QUALITY IN INTERCONNECTED BODIES OF WATER IN NORTHERN NEW JERSEY

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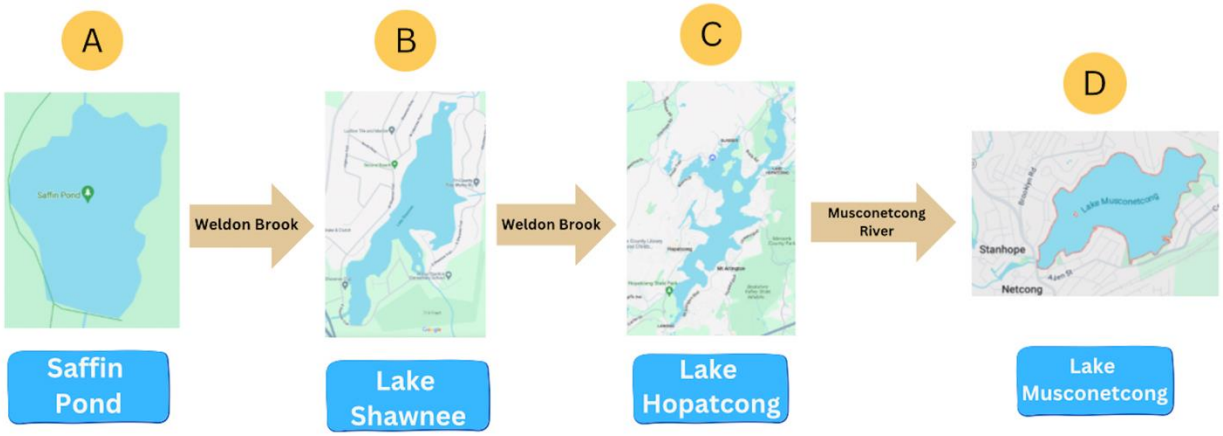
This study focuses on the flow of water from Weldon Brook through several lakes, including Lake Shawnee, Lake Hopatcong, Lake Musconetcong, Waterloo Lakes, and Tilcon Lake, before eventually reaching the Musconetcong River and the Delaware River. The water quality analysis for each individual body of water, followed by comparisons with all connected bodies, is crucial for understanding the potential impact of upstream water quality on downstream bodies. This project aims to measure and compare water quality in different bodies of water, analyze critical data such as pollutant concentrations, and provide valuable information for managing and preventing pollution incidents.



BUG ROADS: MODELING THE POTENTIAL DISPERSAL ROUTES OF HYMENOPTERAN POLLINATORS IN NEW YORK CITY

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Hymenopteran pollinators play a crucial role in natural ecosystems, and the presence of green spaces in cities is vital for supporting the diversity of these pollinators. However, in New York City, green spaces are not uniformly spread out, and obstacles such as buildings can hinder the dispersal of pollinators. It may be a challenge for pollinators in New York City to locate suitable habitats or food resources. The goal of this study was to model insect pollinator's possible travel routes ("bug roads") in Manhattan. To do this we used QGIS to model the shortest distance that insects would need to travel between green spaces (N = 373) while also having to navigate around buildings and other barriers. We also measured the connectivity of parks based on reported maximum foraging distance for different species of hymenopteran pollinators using community cluster analysis. Furthermore, we estimated potential pollinator habitat in each green space using Lidar land cover data.

In general, hymenopteran pollinators will travel between 250 m and 14000 m and after excluding paths that were longer than 14000 m, the average path between green spaces was 6362.5 ± 4.5 m. We also found that the number of community clusters decreased with increased foraging distance. Short foraging distances typical of solitary bees (< 1000 m) resulted in numerous small clusters. Longer distances typical of eusocial bees like European honey bees and bumble bees (> 2000 m) yielded a few large clusters. Furthermore, we found that ~98% of the green spaces in Manhattan do not have enough high or medium vegetation cover to support the full foraging ranges of solitary bees. These results suggest that green spaces in New York City may better support pollinators with large foraging distances, but local habitat quantity and quality may be more important for solitary bees, which do not travel as far from their nests.

THE BACTERIAL SYMBIONTS OF THE PARASITIC PLANT *RAFFLESIA*—MICROSCOPIC PARTNERS FOR CONSERVING THE WORLD'S LARGEST FLOWERS?

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Rafflesia (Rafflesiaceae), an endangered endophytic holoparasitic plant, spends most of its life within the tissues of its sole plant host, *Tetrastigma*, only emerging to bloom, producing the world's largest flower. Much of its life cycle is unknown including why and how *Rafflesia* infects only certain host species, making it very difficult to conserve and propagate by traditional horticultural techniques. However, bacterial endophytes have been shown to play a major role in promoting the growth of plants and may be involved in the life cycle of *Rafflesia*. Our study focused on characterizing the bacterial microbiome of seeds and flower buds of *Rafflesia speciosa* in comparison to *Tetrastigma* samples to understand how *Rafflesia* infection changes its host microbiome and vice versa. We observed that *R. speciosa* seeds have a more distinct microbiome compared to *Rafflesia* buds which are intimately connected to their hosts allowing bacterial exchange. Moreover, certain bacteria in *Tetrastigma* host species seem to be important for *Rafflesia's* growth inside the host. These findings may have applications in the horticultural propagation of *Rafflesia* for ex situ conservation.

BEEING TOGETHER: INVESTIGATING HONEYBEE FORAGING DYNAMICS AND POLLEN DIVERSITY

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The Honeybee is one of the most collaborative insects in the world. Each hive is made up of thousands of bees working together to build and sustain a colony.

Honeybees are remarkable generalist pollinators that forage on a wide variety of plants. Their foraging behavior is crucial for both the plants they pollinate and the survival of their own colonies. Their foraging habits are essential for colony survival. Foraging behavior of honeybees depends on both inside colony environment and external environment. This behavior mainly depends on diverse diet, nutritional needs, energy efficiency, colony health, and environmental adaptability.

The purpose of this study was to carefully comb and analyze pollination patterns. These pollination patterns mainly focused on how the number of food-plant species decreased or varied over the year 2023.

Pollen was collected from a hive sample and was homogenized in glycerin solution. A hemocytometer was used to count numbers of unique pollen types based on their differences in size, shape, and color. Overall, the data collected offers valuable insights into the foraging habits and dietary preferences of honeybees, as well as the botanical composition of their environment.

EFFECTS OF TEMPERATURE ON MANGANESE DEMAND IN A MARINE DIATOM, *THALASSIOSIRA PSEUDONANA*

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As global temperatures increase, coastal ocean temperatures increase, causing stressful environmental conditions for many marine organisms. One model coastal species is the diatom Thalassiosira pseudonana. Collectively diatoms help with around 25% of the world's carbon fixation.

A primary mechanism that T. pseudonana uses to tolerate thermal stress is Superoxide Dismutase (SOD), an important antioxidant enzyme that helps to protect diatoms from damage due to oxidative stress. At higher temperatures reactive oxygen species (ROS) increase, to mitigate this, diatoms employ manganese-dependent SOD (Mn-SOD). Mn-SOD helps neutralize superoxide radicals, protecting the diatoms from oxidative stress-induced cellular damage. Mn-SOD helps to reduce imbalances in cellular redox status, ensuring proper functioning of cellular pathways. By helping to mitigate the effects of oxidative stress, Mn-SOD ensures that there is efficient photosynthetic activity.

At higher temperatures we hypothesize that the growth rates of T. pseudonana will decrease due to heat stress, as manganese demand increases, ultimately limiting antioxidant potential, thus diminishing growth.

This study explores the impact of temperature variations on manganese (Mn) demand in diatoms, by exposing diatoms to elevated temperature conditions of 24, 27, and 30°C, with a control temperature of 18°C. Within these temperatures, diatom cultures were grown with varying Mn concentrations ranging from 160 pM to 9.7 nM available Mn. We investigated the relationship between temperature and manganese concentration, by examining the growth rates of each treatment. Diatom growth was monitored over time, assessed by measuring chlorophyll fluorescence, to determine the density of the culture, as there is a known relationship between chlorophyll fluorescence and cell density. To quantify the growth rate, the natural logarithm of relative fluorescence versus time was analyzed.

We found that 18°C low manganese cultures grew 30% slower than cultures in replete manganese. We also found that with elevated temperatures, this growth rate depression was further exaggerated. This suggests that T. pseudonana has a higher cellular demand for Mn when exposed to elevated temperatures. As oceans continue to warm with ongoing climate change, Mn demand could continue to increase in this species, outpacing what is naturally available in their environment. In the future we plan to measure Mn use efficiency across a range of temperatures.

UBC PRIMER 810 AS A TOOL FOR DETERMINING GENOTYPIC DIVERSITY OF *AMMOPHILA BREVILIGULATA* (AMERICAN BEACHGRASS) IN NEW JERSEY COASTAL DUNES

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New Jersey's coastal dunes provide natural beauty, critical habitat, and infrastructure protection for the state's coastal communities. Restoring New Jersey's coastal dunes typically involves single-genotype plantings of the 'Cape' variety of American Beachgrass (*Ammophila breviligulata*) for dune stabilization and development. However, it remains an important question whether single genotype plantings provide sufficient long-term sustainability and ecosystem function. To establish a benchmark of native diversity in New Jersey populations of *A. breviligulata*, Inter-Simple Sequence Repeat (ISSR) markers were used to demonstrate high genotypic diversity in three native New Jersey *A. breviligulata* foredune populations, but showed moderate diversity in the single mid-dune population analyzed (Slaymaker et al., 2015). Here we use ISSR markers to measure genotypic diversity across a successional gradient, from fore-dune to rear-dune, in a native New Jersey dune system. Genomic DNA preparation of mid-dune samples and initial work with UBC Primer 810 will be presented. This project will provide a better understanding of *A. breviligulata* biology and may inform future dune restoration practices.

VARIABILITY IN COMMON YELLOWTHROAT SONGS AND THE IMPACT OF ANTHROPOGENIC NOISE

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Bird songs play a crucial role in avian life, serving various communication purposes such as courtship, mate attraction, predator alarm, group cohesion, and territorial defense. However, anthropogenic noise poses a significant challenge to avian communication in urban and suburban environments, potentially impacting bird fitness and survival. Many bird species, including song sparrows, have been observed altering their vocalizations in response to anthropogenic noise. The objective of this study is to investigate song variability of common yellowthroats (COYE) (*Geothlypis trichas*) and possible correlations between their song characteristics and levels of urban noise in different areas of New Jersey. Song recordings of common yellowthroat songs were obtained during the summers of 2020 and 2021 at various sites. The selection of sites was based on the different levels of anthropogenic noise across New Jersey; a sound meter was used to record the ambient background noise respectively with each recording. The experiment focuses on several sites, including the Saint Peter's University campus (SP), East Brunswick Baseball Field (EBB), Heavenly Farms (HF), and Lincoln Park West (LPW). Spectrograms and measurements were analyzed using Raven Pro 1.6 software. Preliminary results point towards variation in bird songs between sites with different noise backgrounds, showing an increase in songs' bandwidth and a decrease in song complexity and duration as the noise level increases. The implications of this study are crucial for developing an understanding of the effects of anthropogenic noise on COYE populations and for making conservation efforts aimed at mitigating any potential consequences for future COYE populations.

THE EFFECTS OF CLIMATE ON THE GROWTH OF EASTERN COTTONWOOD IN AN URBAN PARK

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The role that highly disturbed areas play in affecting the growth of plants can be seen by analyzing how trees react to growing in highly disturbed areas. The purpose of this study is to see how over time *Populus deltoides* (Eastern Cottonwood) reacts to growing in Teaneck Creek Conservancy, a former dumping site and now recently restored wetland. *P. deltoides* is the most common tree species in this park. This study uses cores from ten *P. deltoides* trees across the conservancy (two cores from each tree). Each core was mounted, sanded, and digitally scanned. These scans were then used to digitally measure the length and amount of tree rings on each of the cores. A linear regression trendline was fit to the raw tree ring data to detrend the ring widths. Daily weather data was downloaded for Teterboro Airport, NJ, from 1980 to 2023. For each year the precipitation data were summed and temperature data were averaged for both the growing season (March to November) and water year (October to September). Notably, the growing season from 1980 to 2023 had an average maximum temperature that lay in the *P. deltoides* optimal growing range, however, the average minimum temperatures lay below the optimal growing range. The detrended tree ring width data will be compared to annual weather data to analyze the impacts of weather on tree growth. Understanding the relationship between tree growth and weather will provide information on how climate change could affect the growth of these trees.

EFFECT OF INCREASED WINTER TEMPERATURE ON METABOLISM AND OXIDATIVE DAMAGE IN OVERWINTERING LUNA MOTHS (*ACTIAS LUNA*)

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As the impacts of climate change are monitored, ongoing research aims to predict the effects of increased global temperature on animal physiology, morphology, and survival. In particular, increased winter temperatures may have adverse effects on fitness of insects that undergo overwintering and reproduce in the subsequent spring. During this period of scarce resources, many insects undergo diapause, halting development and lowering metabolism to conserve energy. To investigate the effects of winter warming on insects, we reared two groups of Luna Moths (*Actias luna*), which overwinter as diapausing pupae, into their overwintering stage: one at a typical overwintering temperature (6.5°C), and another at a higher temperature (10.5°C) to model a climate change scenario. We measured the effect of winter temperature on the following physiological variables: resting metabolic rate (RMR, as CO_2 production rate), evaporative water loss rate (EWL), discontinuous gas exchange cycle (DGC) period, and oxidative damage. Additionally, we measured the effect of winter temperature on body size (pupal mass throughout the overwintering stage and adult moth mass after eclosion) and eclosion timing. We predicted increased winter temperature would increase RMR and EWL, decrease DGC period, and increase oxidative damage. We also predicted that animals in the warmer temperature treatment would experience decreased pupal and adult mass, and accelerated eclosion timing. We found that warm treatment pupae experienced significantly increased RMR, decreased DGC period, and decreased pupal mass at the end of winter, compared to pupae in the nominal cold treatment. We found no significant effects of winter temperature on EWL, oxidative damage, adult moth mass, or eclosion timing. As we have demonstrated the effects of increased winter temperature on the energy expenditure and subsequent mass loss in Luna Moth pupae, future experiments exploring adult fitness consequences of a climate change scenario are warranted.

FLOPPING MOVEMENT AND DEVELOPMENT IN *MICROSTEGIUM VIMINEUM* RECORDED USING TIMELASE

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Microstegium vimineum, also known as Japanese stilt grass is an invasive shade tolerating C4 grass. Little research has been done regarding the movement patterns of this plant. This research analyzed *M. viminium* grown in 3-inch pots and recorded using timelapse cameras. Plant movement was then traced using the program PASCO Capstone to perceive trends in stilt grass behavior and movement.

M. vimineum seeds were collected from NJ and recorded for three weeks using timelapse. The shoot apex of each plant was tracked using PASCO Capstone and graphs marking X position over time and Y position over time were generated. The average duration of flops, number of flops and duration of preamble were all measured. The behavior of Japanese stilt grass flopping was able to be replicated in a lab setting indicating that it may be coded within the genome of the plant and may pose an evolutionary advantage for this species aiding in its invasive nature.

THE PHYSIOLOGICAL AND BEHAVIORAL SUBLETHAL EFFECTS OF HEAVY METAL ZINC ON ADULT *AMERICAMYSIS BAHIA*

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Anthropogenic activities such as industrialization, modern farming, and vehicle use, release toxins into marine environments posing threats to marine organisms and human health through bioaccumulation (Oulton et al. 2014, Wu et al. 2019). While previous research traditionally focused on lethal toxicity tests, sublethal effects are becoming significant stressors on marine ecosystems (Mayer-Pinto et al. 2020). This study addresses the gaps in understanding how sublethal effects, such as heavy metals like Zinc, can impair marine organism physiology and behavior even at environmentally relevant concentrations permitted by regulatory authorities such as the US EPA (Huang et al. 2010, Oulton et al. 2014, US EPA 2015). Using *Americamysis bahia* (Mysid shrimp) as a model organism, we aim to investigate the sublethal impacts of Zinc exposure on growth, swimming behavior, and foraging over a 13-day period on both continuously exposed and previously exposed *A. bahia*. While our hypothesis predicting overall reduced behavior and growth in adult *A. bahia* exposed to sublethal concentrations of Zinc was not fully supported, our results did reveal significant impairments in swimming and foraging behaviors in continuously exposed individuals. Interestingly, our findings indicated that *A. bahia*previously exposed to Zinc exhibited signs of recovery, suggesting the possibility of mitigating the adverse effects of toxicant exposure. These results underscore the importance of considering sublethal effects in ecotoxicology studies and potentially revising regulatory standards for heavymetal concentrations to safeguard marine ecosystems and human health. Understanding the physiological effects of toxicants on marine organism is crucial for effective ecosystem management. By highlighting the potential for recovery from toxicant exposure, our research offers hope for the longevity of marine ecosystems and the preservation of the food chain.

THE EFFECT OF MELATONIN ON HERB PLANT

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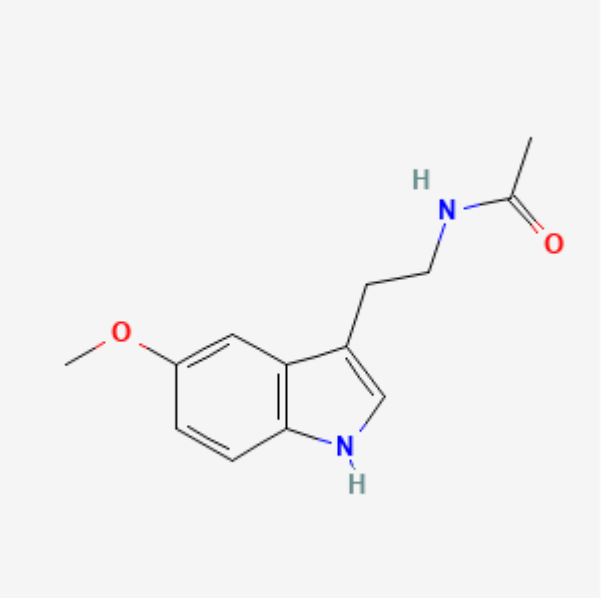
Plant melatonin is a multifactorial molecule similar to those found in animals with many specific plant physiological functions. Your brain releases the hormone melatonin when it is dark outside. It assists your body in maintaining a 24-hour clock and proper sleep patterns. Melatonin promotes flowering and fruit ripening, maintains redox equilibrium, lowers stress, improves gene expression and enzyme activity, prevents leaf senescence, stimulates root growth and development, supports plant development, and shields plants from pathogen attack (regulating plant innate immunity, initiating defense responses). In this project, five different tea plants (Lavender, Echinacea, Chamomile, Peppermint, Lemon Balm) Will be germinated and tested against live grown plants; there will be a control group and experimental group that will have melatonin diluted with water. The growth of each plant will be measured periodically and recorded.



IN SILICO MODELING OF AQUATIC TOXICITY OF ORGANIC CHEMICALS TO THREE TROUTS' SPECIES: AN ENVIRONMENTAL TOXICITY DATA GAP FILLING STUDY

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Oncorhynchus clarkii, *Salvelinus fontinalis*, and *Salvelinus namaycush* are trout species indigenous to North America, currently facing population declines attributed to environmental pollution and overfishing. Conservation efforts, including catch-and-release practices, have been initiated to mitigate these threats. This study aimed to evaluate the susceptibility of these species to common environmental pollutants by utilizing acute median lethal concentration (LC_{50}) toxicity data from the US EPA's ToxValDB database. We developed and applied quantitative structure-activity relationship (QSAR) and quantitative read-across structure-activity relationship (q-RASAR) models, leveraging chemical descriptors to predict the toxicity of a broad spectrum of chemicals to each trout species. Our models accurately estimated the toxicity of 1,172 external compounds, identifying the most hazardous substances for each species. For *O. clarkii*, the most toxic compounds were identified as Benzenamine, Dinitramine, and Benfluralin; for *S. fontinalis*, Propanil, 4-Methylbenzoic acid, and 3-Chlorobenzilydeneacetone; and for *S. namaycush*, Hexachlorphene, EDTA, and Ethanomethrin emerged as the top toxicants. These QSAR and q-RASAR models offer insights into the toxicological mechanisms of action and assist in bridging data gaps regarding aquatic toxicity for these species, which is crucial for conservation strategies in light of the pervasive pollution threatening North American waterways.

MUD PUDDLING BEHAVIOR IN BUTTERFLIES

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Mud puddling is a distinctive feeding behavior primarily seen in butterflies, but also in moths, and other insects. In mud puddling, butterflies congregate at dung, carrion, or mud to supplement their diets with micronutrients absent in their larval diets. This study consolidates existing knowledge of the patterns and benefits of mud puddling behavior, while also identifying gaps in ourunderstanding of this intriguing phenomenon. We examine both the proximate and ultimate causesof mud puddling including dietary supplementation, its effects on courtship and female choice, changes in fecundity, and its social aspect as a possible protection against predation. Additionally,we explore the social and sensory cues for this behavior as well as regional, sex, and taxonomic variation in mud puddling. Through this research we identify key questions for future investigationthat will allow us to better understand mud puddling.

THE ROLE OF THE MAIN OLFACTORY EPITHELIUM DURING MOTHERHOOD

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Motherhood is associated with significant, behavioral, emotional, and physiological changes. Mouse pups require significant parental care, making appropriate maternal behavior essential for their survival. Oxytocin has been shown to facilitate pup retrieval behavior in mothers and support social learning[1]. The exact role of oxytocin through the senses, specificallyduring motherhood is still unknown[2]. Focusing on the primary olfactory organ, the main olfactory epithelium (MOE), we are investigating how changes in pregnancy-related hormonal activity impact olfactory-guided maternal behaviors. *We aim to show how smell and oxytocin receptor presence in the MOE changes with motherhood.* We will assess olfactory driven behavioral changes during motherhood. We will place pup odor and a neutral odor on opposing sides of a behavioral track, called a tri-chamber. We predict mothers will prefer pup urine over aneutral odor. We will determine 1) whether oxytocin plays a key role in maternal behavior in response to pup related olfactory cues, and 2) if oxytocin receptor expression changes over the course of motherhood in the MOE. We have found that mothers, unlike virgin females, prefer pup odor at postpartum day 5, but not during pregnancy. Moreover, we have demonstrated that oxytocin receptors are expressed at some point in the MOE. This study will reveal key insights into the sense of smell in understanding how virgins transition into motherhood through changesin the MOE.

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bioRxiv 2023.02.23.529692;doi: https://doi.org/10.1101/2023.02.23.529692

UNRAVELING THE IMPACT OF MICROPLASTICS ON REGENERATION OF *DUGESIA TIGRINA* (PLANARIA)

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Living species coexisting with human civilization face the repercussions of environmental choices, with microplastics emerging as a concern due to their pervasive presence and potential health implications. This study investigates the impact of microplastic pollution on freshwater ecosystems, focusing on a particular species, *Dugesia japonica*, a planarian (flatworm) known for its regenerative capabilities. The hypothesis states that microplastics can affect neoblasts and stem cells, crucial for regenerating injured body parts, leading to inflammation. Drawing from recent research, *Dugesia japonica* exhibits microplastic-induced oxidative stress, microbiota dysbiosis, and altered regeneration processes. Moreover, investigations into nanoplastic exposure reveal inhibition of feeding behavior and delayed regeneration, emphasizing potential adverse effects. The experimental setup involves incubating planaria in solutions containing microplastics, including concentrations of 0.01% polystyrene, polypropylene, and polyethylene terephthalate. In each group, a planarian was placed on ice to amputate either in transversal, mid sagittal, and sagittal cuts during the two weeks of exposure to experimental conditions.

Qualitative assessments of motility and regeneration stages will be conducted. The qualitative analysis will assess the distribution and density of stem cells, as well as the composition of the microbiome, identifying specific microbial taxa and patterns in community structure and diversity. Photography using iPhone 11 and Leica Zoom 2000 stereoscope will aid in capturing visuals for analysis. In conclusion, this study aims to provide insights into the impacts of microplastic pollution on planarian regeneration and microbiome, shedding light on the broader implications for freshwater ecosystems and highlighting the need for measures to mitigate these.

HARD METALS LINKED TO AUTISM?: A STUDY IN NORTHERN NEW JERSEY COUNTIES

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Autism, also known as autism spectrum disorder (ASD), is a complex neurodevelopmental disorder with a multifactorial etiology, meaning it likely arises from a combination of genetic and environmental factors. Autism typically manifests in early childhood,with signs often becoming noticeable between the ages of two and three. Research has explored various potential risk factors for autism, such as genetic predisposition and prenatal exposure to certain chemicals or infections. Hard metals and different chemicals found in drinking water can severely affect the nervous system of adolescents and are a concern for overall health and development. However, it has not been definitively linked to autism as a sole or primary cause.

Various studies were conducted analyzing the rates of autism and the number of children with high lead, nitrate, nitrite, and carbonate levels in their blood. In this study, we sampled water samples from every county in Northern New Jersey and compared the presence of hard metals and chemicals to those in the water of Toms River, Ocean County. Toms River happens to have the largest number of Autism cases in New Jersey and by completing this study, we hope to conclude the correlation between contaminated waters and Autism rates in New Jersey.

EVALUATING THE IMMUNE AND INFLAMMATORY RESPONSES IN MICEFOLLOWING EXPOSURE TO THE ARTIFICIAL OXYGEN CARRIER OXYVITA®

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Artificial Oxygen Carriers (AOC) may be a solution to current blood shortages. Like hemoglobin, they carry oxygen around the body, which is vital for cellular respiration. OxyVita is an AOC composed of hundreds of polymerized bovine hemoglobin molecules produced in Middletown NY by OXYVITA, Inc. This novel AOC is currently in preclinical trials that evaluate its efficacy and safety. Our previous studies demonstrated a robust antibody response to the polymer, which increased with subsequent exposures. Previous research also found that mice exposed to OxyVita gained weight at the same rate as mice exposed to saline and displayed no signs of discomfort or systemic inflammation. Our current studies evaluate if OxyVita has any toxicity in mouse vital organs or tissues by looking at the innate and adaptive immune responses. We used RT-PCR to measure cytokine expression in organs of mice injected with either PBS or OxyVita every 2 weeks. Mice receiving multiple exposures of OxyVita expressed low to undetectable levels of inflammatory cytokines in kidney and liver tissues. We further examined antibody production using our established ELISA protocol. Our results demonstrate that OxyVita elicited an adaptive immune response measured by the increased production of antibodies following each exposure, which is consistent with previous observations. Importantly, the PBS and OxyVita treated mice again gained weight at the same rate. Therefore, OxyVita may not be affecting the health of the mice, even though there is a large amount of antibody production. These results suggest that OxyVita may be a viable solution for providing oxygen to vital organs in emergency situations.

DESIGNING GFP PURIFICATION PROTOCOL FOR TEACHING LAB

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Green Fluorescent Protein (GFP) revolutionized cell biology by enabling the visualization of cellular processes with its ability to glow under UV light. Its discovery was honored with the Nobel Prize in Chemistry in 2008. The fluorescence of GFP facilitates visual tracking of the purification process, creating captivating and memorable learning experiences. We developed a purification protocol of GFP expressed in *E. Coli* suitable for a summer STEM science course for high school students. The protocol involves extracting GFP from *E. coli* cultures transformed with GFP-expressing plasmid, followed by hydrophobic interaction and size exclusion chromatographic techniques. This purification protocol can be used to impart practical skills in the lab while generating enthusiasm and curiosity to inspire a new generation of scientists.

ISOLATION OF AN APTAMER SELECTIVE TO GLUCOSE

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Diabetes is a disease that hundreds of million people live with daily throughout the world. Although this is disease is typically not fatal, it can be if not treated properly. The day to day life of a person with diabetes consists of blood sugar monitoring by finger pricks, insulin injections and strict diet. The research for a glucose aptamer would be the first step to eliminate the need for all of this. This project uses Systematic Evolution of Ligands by Exponential Enrichment, or SELEX, to select RNA that binds specifically glucose. The process is a cycle beginning with a PCR from a pool of millions and billions different DNA sequences, then transcription to RNA, negative selection, positive selection, and reverse transcription back to DNA. The conclusion of the reverse transcription is the beginning of the next generation where each generation becomes more selective to glucose. Eventually the RNA would be sequenced and converted to a riboswitch. A riboswitch is a sequence of untranslated mRNA that can bind a specific ligand, in this case glucose, and transmit a signal to the expression platform to start the reaction to make a protein. For this project, the riboswitch would begin the production of insulin only in the presence of glucose. By making insulin outside of the pancreas, diabetes patients would no longer need insulin injections or constantly monitor their blood sugar levels. The project is currently on its 26^{th} generation and is continuing to move forward. Once we obtain a high ratio of positive over negative cleavage percentages we will begin the process to clone DNA and individually test sequences to find an aptamer that cleaves only in the presence of glucose.

INVESTIGATING THE ROLE OF THE BIR2 DOMAIN AS A CASPASE INHIBITOR

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Apoptosis is the controlled process of cell death. A cell can signal this pathway to occur when in stress or after sensing damage. Apoptosis is triggered by the caspase protein. Under normal conditions, these proteins are bound to IAP (inhibitor of apoptosis) proteins. IAP's inhibit the caspase proteins from activating the apoptosis signaling pathway. This ensures that apoptosis is only occurring when necessary. IAP's consist of 3 main regions/domains: The BIR1 domain, BIR2 domain, and the linker region. The BIR1 domain is known to cause inhibition on its own.

To investigate the mechanism the BIR2 domain uses to inhibit the caspase protein, the protein fragment was induced into bacteria with a maltose tag and purified using a Q-Sepharose column, followed by an amylose column. The quality of purification was assessed using gel electrophoresis. The inhibition capabilities of the BIR2 domain (with and without the linker region) at varying concentrations (0.05, 0.1, 0.2, 0.5, 1, and 2 μM) were compared to those of the BIR1 domain and the unmodified IAP. This was done by performing a caspase *in vitro* assay. The BIR2 region showed significantly less inhibition compared to the BIR1 domain and unmodified IAP. This suggests the BIR2 domain does not have inhibiting properties on its own. Further caspase binding studies will be performed to see if the BIR2 domain allows for a better active site junction.

REEVALUATION OF CATECHOL DERIVATIVES TOWARDS CATALYTIC DOMAINS OF MMPS

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Matrix metalloproteinases (MMPs) are a family of calcium-dependent enzymes primarily responsible for the remodeling and degradation of the proteins comprising the extracellular matrix (ECM). The tightly regulated activity of MMPs plays key roles in important physiological processes like wound healing and angiogenesis but contributes to pathologies like cancer if overexpressed. Therefore, the search for molecules that regulate MMP activity is a target of interest in clinical research. The modulators studied in this research are (-) epinephrine,(±) epinephrine, L-dopa, and dopamine, since previous studies indicate that catecholamines have MMP regulating potential. Using the BioTek Gen5^{TM} Microplate Reader and Imager Software, we performed enzyme kinetic assays in 96-well microplates to observe the effects of these catecholamines on MMP-9

INVESTIGATION OF THE KINETICS AND INHIBITION OF TM1785, AN ACETYLORNOTHINE AMINOTRANSFERASE FROM *THERMOTOGA MARITIMA*

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TM1785, a protein derived from the hyperthermophilic bacteria *Thermotoga maritima*, exhibits acetylornithine aminotransferase (AcOAT) activity. AcOAT plays a pivotal role in the biosynthesis of arginine, an indispensable amino acid in numerous organisms. Arginine serves as a vital intermediate in the catabolism of proteins, nitric oxide, creatine, and polyamines, owing to its diverse metabolic pathways. Its function involves the reversible conversion of N-acetylornithine and 2-oxoglutarate to ornithine and N-acetylglutamate. Notably, *E. coli* also catalyzes this conversion as part of the lysine biosynthetic pathway. The focus of this study is to investigate the kinetic and inhibitory properties of TM1785, as well as investigating the impact of environmental factors such as pH and temperature on enzyme function. In the laboratory setting, TM1785 was overexpressed in E. coli and subsequently purified via affinity chromatography. Kinetic assays were conducted utilizing a coupled reaction with glutamate dehydrogenase, enabling the measurement of NADPH generation rate via a spectrophotometer set at 340 nm. These assays facilitated the determination of TM1785's kinetic parameters with various substrates and inhibitors, alongside the characterization of inhibition constants. Initial kinetic analyses revealed a Km value of= 42 μM and a Kcat of = 0.506 s^{-1} for TM1785, comparable to reported kinetics data of established AcOATs, reaffirming its functional role. Our findings not only enhance our understanding of TM1785 under diverse conditions but also contribute to the broader comprehension of AcOAT kinetics. Furthermore, This study seeks to broaden our comprehension of TM1785's AcOAT activity by elucidating its kinetic parameters and. Additionally, inhibition studies with gabaculine, a recognized AcOAT inhibitor, are underway to provide further insights into TM1785's behavior. Additional experiments with diverse substrates and inhibitors further enrich our understanding of TM1785's kinetic behavior.

RANDOM PROTEINS BIND RANDOM LIGANDS

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NSF REU Training Site in Biophysics, Nové Hrady, Czech Republic, Summer 2023

Indirect evidence suggests that protein surfaces are teeming with potential sites for small molecules of all kinds, even when binding crevices are not detected in crystal structures. To test this hypothesis, we used docking and molecular dynamics simulations (MD) to explore whether arbitrary ligands have the capacity to bind to arbitrary proteins.

We selected 14 random *E. coli* protein crystal structures from the Protein Data Bank (PDB) that were water soluble, under 40 kDa, solved at resolution 1.5 to 2.0 Å, and with few unresolved residues. Each protein was docked with each of the 20 natural amino acids individually; none of the proteins has an amino acid as a natural ligand. Amino acids were parameterized with the AMBER forcefield and acpype topologies. AutoDock Tools version 1.5.7 predicts poses for small molecules binding to receptors. Promising amino acid poses were chosen by visual examination for diverse and extensive bonding interactions, and depth of recess from the surface. Each pose was evaluated with all-atom molecular dynamics simulations of up to one microsecond using GROMACS. The MD simulation results were modeled, analyzed, and visualized in Visual Molecular Dynamics.

Nine proteins bound one or more amino acids for 100ns or longer based on a stable RMSD level that could be replicated in an independent MD simulation. Binding energies were calculated in vacuum using an empirical scoring function in AutoDock Vina. Amino acid binding energies ranged from -2.70 to -5.44 kcal/mol. Several proteins bound the amino acid methionine (among others). Those proteins were also tested with S-adenosyl methionine (SAM). With several proteins SAM demonstrated a notable increase in residue interactions and calculated binding energies compared to methionine alone, staying bound for most of one microsecond and with calculated binding energies of -3.31 to -5.50 kcal/mol. Proteins that bound SAM were also tested with adenosine monophosphate (AMP). Several proteins exhibited favorable binding energies (-5.31 to -8.80 kcal/mol) in one microsecond simulations, comparable to the energy found in a 1 microsecond MD simulation with the known AMP-binding protein cystathione β-synthase (PDB:3DDJ; -6.23 kcal/mol).

The docking and simulations indicate that randomly selected *E. coli* proteins can bind random small ligands like amino acids, SAM, and AMP persistently and with binding energies comparable to those calculated for a natural AMP-binding protein. Unexpectedly, all ligands remain mobile within their binding locations, with changing bonding partners but similar binding energies. The calculated energies are a weakness of the results because they neglect contributions from solvent and will not be commensurate with experimental affinities. We are presently evaluating better tools for energy calculations; calculating binding energy for a native SAM-binding protein; and deciding on methods to examine the binding of SAM and AMP to the proteins experimentally.

These results indicate that protein surfaces indeed present potential binding sites for random small molecules. This conclusion suggests that many, perhaps all, soluble proteins may be viable targets for design of small molecules that can modulate protein function. Even when binding crevices do not pre-exist in crystal structures, ligands may exploit protein dynamics to find binding sites that can be further optimized.

INVESTIGATING AN ALTERNATIVE METHOD FOR ENDOGLUCANASE CELB2 PRODUCTION IN *E. COLI*

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CelB2 is a cellulase from *Streptomyces lividans* useful for cellulose breakdown, which is a key process in alternative fuel production. We are interested in the optimization of activity and stability of CelB2 for industrial applications. This project was intended to explore a simplified purification method with improved yield of CelB2 by using the pET28a expression vector in *E. coli*. The currently used pMAL vector system produces MBP-CelB2 fusion that requires protease digest, affinity, and ion-exchange chromatographies for purification. The pET28a vector can simplify the purification process by facilitating purification through Ni-NTA affinity chromatography directly. We hypothesized that the pET28a system would provide faster purification and higher yield compared to the pMAL system. However, after multiple trials, the target protein concentration was found significantly low in all protein fractions, suggesting that the target protein may have aggregated and fallen out into the pellet. This was confirmed with CelB2 activity in the resuspended pellet. We conclude that the pET28a system is not optimal for CelB2 expression due to the instability of recombinant CelB2 protein in *E.coli*.

I-R3 DNA ENZYME CATALYTIC CHEMISTRY THROUGH ION PROMOTED CLEAVAGE

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Deoxyribozymes are synthetically engineered short ssDNAs that function in hydrolyzing RNA. More recently, a small ssDNA enzyme was engineered to break the phosphodiester bond in DNA, that are important to the long-term storage of genetic information. For the single-stranded I-R3 DNA enzyme, the catalytic core of 17 nucleotides forms an asymmetrical bulge when it is annealed to its single-stranded DNA substrate. When this structure is in the presence of Zn^{2+} under neutral pH, the substrate strand will be cleaved between two adenosines in positions A15 and A16, resulting in a 5' product and 3' product. At the discovery of the I-R3 DNA enzyme, Zn^{2+} ions promoted cleavage activity, while Cd^{2+}, Co^{2+}, Cu^{2+}, Ni^{2+}, Mn^{2+}, Ca^{2+}, and Mg^{2+} did not promote the cleavage activity.

This project is designed to study the cleavage behaviors of the I-R3 DNA enzyme through the introduction of different metal ions in place of the known zinc ions that promote cleavage. Metal ions were chosen based on their atomic radii size and their overall similarities to the atomic radius size of the zinc ions. The current hypothesis is that metal ions with similar atomic radii to the zinc ions may promote cleavage of the DNA substrate when bound to the I-R3 DNA enzyme.

The chosen metal ions will be added to 100 pmol DNA enzyme, 10 pmol DNA substrate, 50 mM HEPES pH 7.05, and consistent salt concentrations after an initial annealing period. The sample will be quenched with a denaturing solution, ran on an acrylamide gel, and stained with SYBR gold to be analyzed by photodensitometry to find the percentage of cleavage.

Understanding the correlations between metal ions and cleavage of the I-R3 DNA enzyme would have a significant impact on the understanding of deoxyribozymes and their overall catalytic function. This research could also have further biological and medicinal applications with targeting and cutting single stranded viral DNA, such as parvoviruses.

SYNTHESIS AND UV-VIS/HPLC SPECTRA ANALYSIS OF NOVEL BENZIMIDAZOLE ANALOGUE HAVING SUGAR MOIETY AS CHEMOTHERAPEUTIC AGENT

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Cancer is fundamentally a disease of mitosis and microtubules' importance in the mitotic process has made it a key target in anticancer therapeutics. In an attempt to discover novel chemotherapeutic agent targeting microtubule a molecular docking based virtual screening was studied, which lent strong support for the potential of a newly designed benzimidazole derivative TL-2 (2-thio-*β*-D-{2',2'-di-*O*-[3"-(4-fluoro-phenylpropanoyl)]}glucosyl-5-nitro-benzimidazole) as a potent chemotherapeutic agent, by means of microtubule inhibition, exerting its effect in the colchicine binding pocket (***Figure 1***). In the present study, the novel benzimidazole derivative is being synthesized using a facile and recently developed synthesis procedure. The synthetic pathway includes the design of a chemically distinct intermediate **2a** (2-thio-*β*-D-(2',3',4',6'- tetra-*O*-acetyl)glucosyl-5nitro-benzimidazole), which was achieved by conjugating commercially available 2-mercapto-5-nitrobenzimidazole and freshly prepared 1-Bromo-*α*-D- glucose tetraacetate (the sugar moiety). To compare both biological and chemical properties, a second conjugate, **2b** (2-thioethyl-5-nitrobenzimidazole) was synthesized. These novel analogues of Benzimidazole having sugar moiety were subjected to UV-Vis/HPLC Spectroscopy analysis, which suggested the sugar intermediate as well as ethyl conjugation with 2-mercapto-5-nitrobenzimidazole was successfully achieved. The synthesis and characterization of these compounds will be described.

BIOPHYSICAL CHEMISTRY OF AGING

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Aging is a complex and little-understood process modulated by the activity of a vast variety of proteins. One protein long known to be involved in aging is pre-Lamin A/C, which, when processed to form Lamin A, is a critical component of cell (nucleus) structure, and which, prior to processing, is involved in cell proliferation (via interaction with the Notch signaling pathway) and aging. More recently, tyrosinase, the rate limiting enzyme in melanin production, has been found to modulate biochemical processes associated with aging, in particular protein carbonylation (which damages proteins) and the production of lipofuscin, a pigment indicated cellular wear-and-tear. Tyrosinase expression is also known to correlate to both reduced protein carbonylation and enhanced lipofuscin formation. We report our progress in development of optimal NMR and MS based techniques to monitor protein carbonylation *in vitro* and our application of those techniques to probe how tyrosinase reduces protein carbonylation while enhancing lipofuscin production. We also report our work exploring the role of protein flexibility in the function of both tyrosinase and pre-Lamin A/C, in particular how key disulfide-bridge forming cysteine residues and other sequence features modulate pre-Lamin A/C flexibility in potentially functionally important ways, such as modulating pre-Lamin A/C interactions with the Notch signaling pathway.

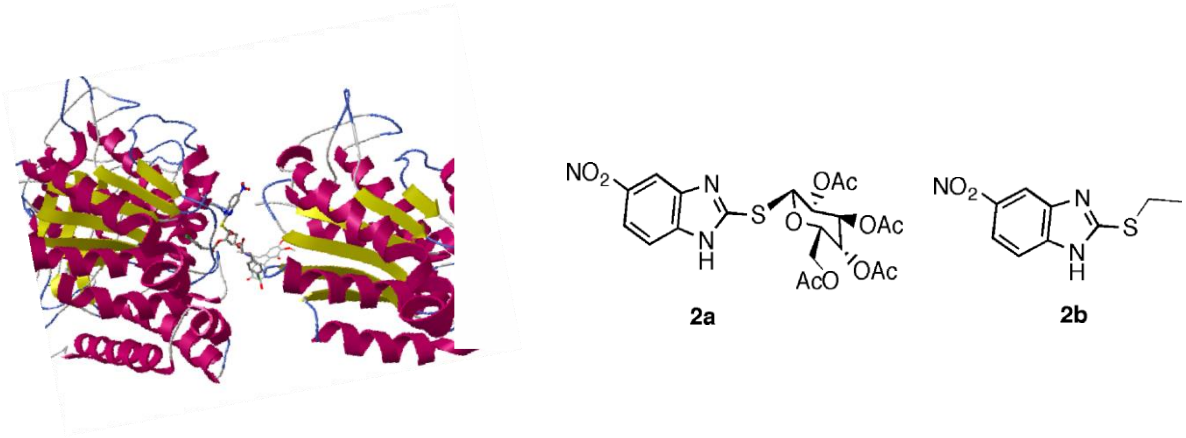

Figure 1. Target ligand TL-2 and native ligand Colchicine in situ at binding site (Left). **2a**, 2-thio-*β*-D-(2',3',4',6'-tetra-*O*-acetyl)glucosyl-5nitro-benzimidazole (middle); **2b**, 2-thioethyl-5-nitrobenzimidazole (right).

FUNCTIONAL INVESTIGATIONS OF TM1347: AN ESSENTIAL PROTEIN FOR CELL GROWTH AND PROLIFERATIN FROM THERMOTOGA MARITIMA

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In 2000, the NIH funded the Protein Structure Initiative (PSI), which focused on protein structure determination. Over 6900 structures were determined through the PSI; ~35% of those structures have completely unknown functions and even more have unconfirmed putative functions.

TM1347, a protein from the hyperthermophilic bacteria *Thermotoga maritima*, was putatively assigned the function of an inosine-5-monophosphate dehydrogenase (IMPDH), based on sequence comparisons. IMPDHs catalyze the first committed step in de novo guanine nucleotide biosynthesis, the NAD dependent oxidation of inosine monophosphate (IMP) to xanthosine monophosphate (XMP). As such, IMPDHs are the key regulators of the guanine nucleotide gene pool, which makes them critical for cell replication and proliferation, along with various other cellular functions such as signal transduction and energy transfer. In this study, we investigated the ability of TM1347 to act as an IMPDH using functional assays. TM1347 was cloned and overexpressed in E. coli, and purified using affinity chromatography. To experimentally investigate the function of TM1347, the production of NADH was measured using a spectrophotometer at 340 nm, which is a direct assay for IMPDH activity. Our results indicate that TM1347 does function as an IMPDH, and kinetic parameters are reported.

IMMOBILIZATION OF BIS(2-PYRIDYLMETHYL)AMINE FRAMEWORKS ONTO SOLID SUPPORTS

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The issue of climate change has become more imminent in recent years with an increasedeffort to reduce carbon emissions as finding a greener energy source compared to fossil fuels is vital to the protection and longevity of our environment. Methane monooxygenase (sMMO) enzymes initiate the oxidation of methane to methanol, and if this process could be mimicked synthetically, it would serve as a potential route for greener energy production. Towards this goal, current research involves the immobilization of pyridyl based ligands onto the surface of functionalized silica to yield heterogenous biomimetic ligands. These ligands could lead to heterogeneous organometallic catalysts that demonstrate capabilities equivalent to those of homogeneous catalysts with increased recyclability. Silica is functionalized with organic groups like amines to create a nucleophile that, with electrophilic methyl pyridyl groups, facilitates the immobilization. Preliminary reactions immobilizing 2-bromo-6-chloromethylpyridine onto functionalized silica as well as the formation of an aldehyde from 2-bromo-6-chloro methylpyridine and 4-aminobutyraldehyde diethyl acetal seem to have been successful. The product of the latter reaction, bis(2-bromo-6-pyridylmethyl)-4-aminobutyraldehyde (Br_2BPABA), seems to have also been successfully immobilized onto the surface of functionalized silica. A Suzuki Cross-Coupling between Br_2BPABA diethyl acetal and 2,3-dimethoxyphenylboronic acid was also successfully carried out to demonstrate the potential for further modification of the pyridyl groups for the immobilization of more complex organic groups. Ongoing studies include the characterization of the surfaces of the functionalized silica materials.

SYNTHESIS OF SILICA-METAL COMPOSITE NANOPARTICLES DECORATED WITH POLY-RHODANINE

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This research encompasses the investigation of silica-silver composite nanoparticles decorated with poly-rhodanine. When combining silver salts with silica at room temperature, silver ions preferentially adhered to the silica surface. Once rhodanine was added, polymerization of the rhodanine monomer leading to the formation of poly-rhodanine was observed. This poly-rhodanine layer preferentially formed around the silica-silver composite nanoparticle. The results were analyzed utilizing electron microscopy, infrared microscopy, and ultraviolet microscopy. Currently, other metal salts including copper acetate and gold chloride will be investigated to determine their influence in the formation of different morphologies of poly-rhodanine. Silica-silver composite nanoparticles are known to exert cytotoxic effects against *Escherichia coli* and *Staphylococcus aureus* by inducing oxidative stress to their DNA, and also by interacting with their cell walls[1]. Future studies will entail the investigation of these silica-metal-poly-rhodanine composite nanoparticles and their anti-microbial effects against various microbial strains.

(1) Song, Jooyoung, et al. "Enhanced Antibacterial Activity of Silver/Polyrhodanine-Composite-Decorated Silica Nanoparticles." *ACS Applied Materials & Interfaces*, vol. 5, no. 22, 7 Nov. 2013, pp. 11563–11568, https://doi.org/10.1021/am402310u. Accessed 12 Oct. 2020.

PHOTOGRAPHIC/X-RAY FIXER WASTE

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Photographic film printing and radiographic film development generate a considerable amount of silver waste. Driven by concerns over the impact of silver waste on the environment, we set out to develop practical and instrument-free ways for the sustainable recovery of silver from X-ray films and photographic/X-ray fixer waste. Based on the knowledge that the enzyme in fresh pineapple, bromelain is made up of chains arranged in a specific three-dimensional structure, where within the site of the enzyme there are amino acid residues that interact with and split peptide bonds found in proteins with basic amino acids such, as arginine and lysine. This enzymatic function allows bromelain to break down proteins, including gelatins such as the black silver layer from our x-ray film Adopting sonication in the process greatly speeds up the process. Further investigation on how the freshness, concertation of pineapple extract, and temperature impact the rate of silver removal from X-ray films is undergoing. We also delved into the use of polyanilines (PAN) for recovery of solver from photographic/X-Ray fixer waste. The reaction between PAN and silver nitrate solution proceeded beautifully, with silver crystals forming on the surface of PAN. We are positioned to use PAN to recover silver from the fixer solution next. By offering low-cost and eco-friendly ways for silver recovery, this research strives to tackle environmental issues while preserving the beauty of silver, for future generations.

THE IMPACT OF 3D PRINTING ON THE GROWTH OF BIOFILMS ON 316L STAINLESS STEEL

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316 L Stainless steel (SS) is one of the most used metals in orthopedic procedures. It is, however, prone to implant-related infections (IRI) which have a low treatment rate due to the difficulty of eliminating biofilms. This study tests how the unique surface characteristics of 3D Printed 316 L due to its distinct manufacturing processes impact biofilm adhesion compared to wrought 316 L. Pseudomonas aeruginosa (PA), a frequent contaminant of metal surfaces, was incubated on both 3D printed and wrought 316L samples and were modified in several ways to monitor bacterial adhesion. Various techniques were applied to visualize and quantify adhesion to the metal surfaces. The wrought 316L samples were found to be more prone to bacterial adhesion. Bacteria were also found to attach to corrosion pits that form on metal surfaces suggesting two different pathways for attachment. Future studies could determine what characteristics make 3D printed 316L SS less prone to biofilm adhesion and apply these properties to the more affordable wrought options.

RHEOLOGY – A METHOD OF MATERIALS CHARACTERIZATION

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Analytical rheology is the subject of determining the microstructure of a material from measurements of its viscoelastic response and can be applied to any material system where the rheological response depends on the microstructure. Correlation of the rheological behavior of different materials with interfacial chemistry and microstructure was used to probe the origin and nature of particle interaction forces.

Rheology is very sensitive to particle interactions and is characterized in terms of the apparent viscosity, shear yield stresses, critical shear stresses and elastic (G') and viscous (G") moduli. The connection between rheology, microstructure and interfacial chemistries is a function of applied stress and/or shear rate. Experimental methods of determining the linear viscoelastic functions are highly evolved such that accurate and reliable measurements can be made in a routine highly automated manner. Analytical rheology exploits this experimental capability and develops advanced methods of interpreting and utilizing standard rheological measurements.

SILVER NANOPRISMS WITH VINYL FUNCTIONALITIES

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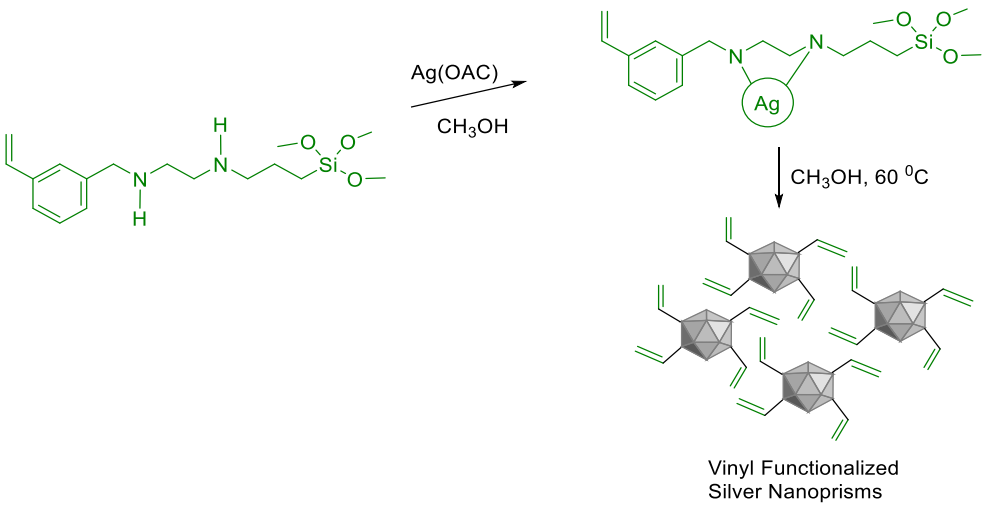
It has been suggested that morphologies can impact the catalytic, biological, and therapeutic properties of nanoparticles. Our group has been investigating the synthetic routes to reliably control and create new morphologies using silicon based surface functional groups which can be manipulated. In this research, 3-(N-Styrylmethyl-2-aminoethylamino) propyltrimethoxysilane hydrochloride (3-SAS) is used to synthesize these silver nanoparticles, mainly nanoprisms. This amino-silane is used as a reducing and stabilizing agent for formation of silver nanoprisms in a methanol. Because the amino-silane acts as both a reducing and a stabilizing agent, less chemicals are used during the process of synthesizing nanoparticles.[1] By controlling the ratio between silane and precursor silver salt, different shapes and morphologies of nanoparticles can be obtained. UV-Vis spectroscopy was used to measure the change in the formation of nanoparticles for around 4-6 hours. TEM, ^{1}H NMR, and IR spectroscopy were used to characterize the silver prisms and their surface passivation.



[1.] Chauhan, B. P. S.; Matam, S.; Johnson, Q. R.; Patel, A.; Moran, K.; Onyechi, B. Generation of Zerovalent Metal Core Nanoparticles Using N-(2-Aminoethyl)-3-Aminosilanetriol. *J. Vis. Exp. JoVE* **2016**, No. 108. https://doi.org/10.3791/53507

CONTROLLED MESOPOROUS SILICA GEL

***Arianna Yom*[1]**, Qiaxian R. Johnson[2], Clairissa Yom[2], and Dr. Bhanu P. S. Chauhan[2]*

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The use of gels made from solutions or sol-gels date back to over 26,000 years; however, for the manufacturing ceramics and other functional applications the earliest known example are around 11,000 years old.[1] Ceramics can be formed through the sol-gel process and materials produced can have great catalytic, antimicrobial, and thermo-resistant properties.[2] Based on the drying method such as critical point drying or aging, sol-gels can have applications in the fields of electronics, photonics, and medicine.

Through soft chemistry designer mesoporous silica gels were synthesized in a one part process via the reaction of bis(trimethoxysilylpropyl)amine (1124) with polymethylhydrosiloxane (PMHS). Gel porosity within the silica network can be altered through the control of precursor ratios and solvent. The mesoporous network can also incorporate non-hydrolytic chemical agents which could be used for drug delivery, fertilizer, or catalytic applications. Materials loaded within these pores such as metals can be reduced by the attached SiH groups and complex within the networked silica via the amino ligands to produce metallic nanoparticles. Analysis of generated materials were characterized via UV-Vis, FT-IR, TEM, SEM, NMR, and TGA spectroscopy.

(1) *Ceramic history*. https://depts.washington.edu/matseed/mse_resources/Webpage/Ceramics/ceramichistory.htm (accessed 2024-04-03).
(2) Hüsing, N.; Schubert, U. Aerogels—Airy Materials: Chemistry, Structure, and Properties. *Angew. Chem. Int. Ed.* **1998**, *37* (1–2), 22–45. https://doi.org/10.1002/(SICI)1521-3773(19980202)37:1/2<22::AID-ANIE22>3.0.CO;2-I.

COCHINEAL RED AS A PH-RESPONSIVE FOOD FRESHNESS INDICATOR, A NEW DESTINY FOR THE BUGS TO DYE FOR

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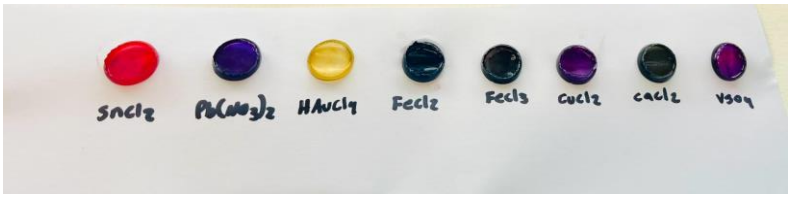
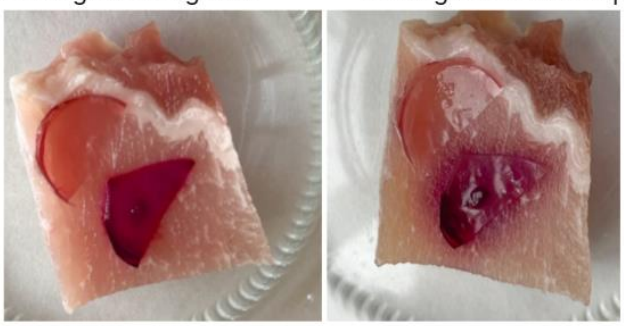
Cochineal, a red dye from bugs, is what gives red velvet cake, strawberry ice cream, fruit juices, and red Skittles their vibrant color. Our research started by extracting the red dye (carminic acid) from cochineal bugs, and studying its pH-dependent property. Since the use of expiration are solely rough estimates of the duration of meat freshness and it is well known that microbial growth and the enzymatic decomposition of meat release volatile alkaline compounds that change the pH of food, we aimed to identify a biodegradable polymer as the host matrix of cochineal red, and apply it to develop a pH-responsive label for real-time monitoring food freshness. We first embedded the red dye onto filter papers and also onto films synthesized from polyvinyl alcohol (PVA) and agar. We then established the reference colors of the host matrix using pH buffers (1-13) with a special focus on pH 5-6 where meat spoils. We discovered that PVA based films produced pronounced color changes in the pH range of interest. Initial results indicate cochineal red is effective in monitoring pork freshness. However, staining of the meat is an issue. To prevent staining, cleaning the films with water was proposed. Interestingly, we observed an unexpected color change of the cochineal-embedded PVA films upon contact with tap water as the film turned from red to black. A flame test on the residue of the sink water after boiling proved the main impurity in tap water contains calcium. We further confirmed that the blackening was due to calcium by adding a calcium chloride solution to the cochineal extract which resulted in the solution turning black. After this discovery, we further investigated cochineal red's color changing effect when chelating with different metal ions. We tested 22 different metal ions and observed that 8 of the 22 caused a color change, concluding that the films can potentially be used to detect the presence of certain metals in solutions.

Metal solutions that caused a color change in the Cochineal films





Cochineal Red As Meat Freshness Indicator

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4	Centenary University
5	Columbia University
6	Fairleigh Dickinson University
7	Felician University
8	Kean University
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11	Marymount Manhattan College
12	Monmouth University
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