Metropolitan Association of College and University Biologists
54th MACUB FALL 2021 Conference

From the Ocean Comes the Light

Saturday Oct 30th, 2021- 9:00 AM – 2:30 PM

Keynote Speaker: Nobel Prize Winner Martin Chalfie, Ph.D. Columbia University
"The Continuing Need For Useless Knowledge"

Keynote Speaker: Nidhi Gadura, Ph.D. QCC, CUNY Chair of Department of Biological Sciences and Geology
"A Sense of Belonging in STEM"

QUEENSBOROUGH COMMUNITY COLLEGE | CUNY

https://macub.qcc.cuny.edu/

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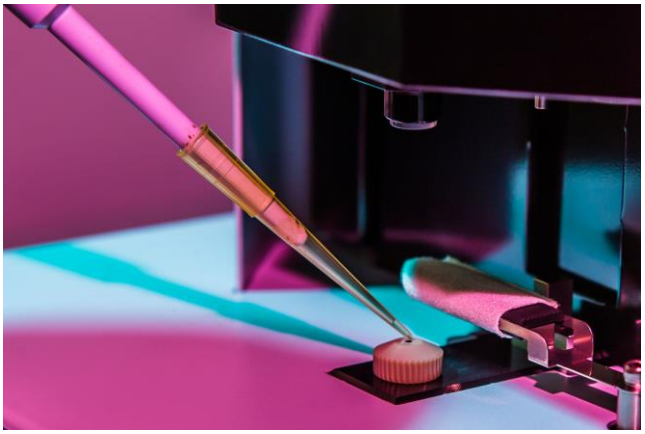


Program Overview

Welcome to the 54th Annual Metropolitan Association of College and University Biologists (MACUB) Conference!

9:00-9:05 AM: Welcoming Remarks by Nidhi Gadura, Ph.D., Chair and Professor QCC, CUNY
9:05-9:10 AM: Welcoming Remarks by Christine Mangino, Ed.D., President of QCC, CUNY
9:10-9:15 AM: Welcoming Remarks by Kathleen A. Nolan, Ph.D., President of MACUB

9:15-9:55 AM: Keynote Speaker - "The Continuing Need For Useless Knowledge" by Nobel Prize Winner Martin Chalfie, Ph.D. Columbia University

10:00-11:00 AM: Member presentations for Faculty (2 Zoom Rooms)
10:00-11:00 AM: Post Undergraduate Q&A Panel for Students (Main Zoom room)

11:00AM-11:05 AM: Introduction to Student Presentations by Brian Mitra Ed.D., Vice President for Student Affairs & Enrollment Management of QCC, CUNY (Main Zoom Room)

11:05-12:30 PM: Student Presentations (13 Zoom Rooms)

12:30-1:15 PM: Lunch Break (On your own)

1:15-2:00 PM: Keynote Speaker- “A Sense of Belonging in STEM” by Nidhi Gadura, Ph.D. QCC, CUNY (Main Room)

2:00-2:15 PM: Awards Ceremony Presented by Dr. Kathleen Nolan, President of MACUB

2:15-2:30 PM: Closing Remarks by Punita Bhansali, Ph.D. & Peter Novick, Ph.D. Co-Chairs of MACUB 2021

About MACUB

Metropolitan Association of College and University Biologists (MACUB) is a professional organization of college and university biologists in the New York-New Jersey-Connecticut Metropolitan Region.

Founded in 1967, MACUB's purpose is to stimulate dialogue among college and university biologists, provide members with a forum to present the results of their scientific and educational research, and to resolve transfer, and articulation problems between two and four year colleges.

Recently, MACUB initiated a number of grants and awards available to its members in support and recognition of research and scholarship.

MACUB, a federally recognized and tax-exempt non-profit corporation registered in New York State, is governed by an Executive Board elected by its members. The actions of the Board are governed by the Constitution and Bylaws of the Association.

Dr. Kathleen Nolan
President of MACUB
Department Chairperson, Professor
Biology & Health Promotion, Environmental Studies, Honors

About Queensborough Community College

Queensborough Community College (QCC) proudly reflects the unique character of the local Queens community, the most diverse county in the United States. We distinguish ourselves from other higher education institutions in America because of that diversity, with nearly equal populations of African Americans, Asians, Caucasians and Latinos. As of Fall 2020 our students have 64 different languages and have 117 countries of birth.

More than 12,000 students are currently enrolled in associate degree or certificate programs, or attending continuing education programs on our campus. Accredited by the Middle States Commission on Higher Education, Queensborough Community College, through its 17 academic departments, offers transfer and degree programs, including Associate in Arts (A.A.), the Associate in Science (A.S.), and the Associate in Applied Science (A.A.S.) degrees. The college also offers non-credit courses and certificate programs.

Left: Queensborough Community College Campus. Right: Queensborough Community College, CUNY President Dr. Christine Mangino

Students attend Queensborough primarily as the gateway to transfer to a four-year college or university—and over half of our students transfer to a four-year CUNY college after earning their Associate degree—or to obtain the necessary skills for career advancement.

A key goal of the college is to provide an academic environment that strengthens our students' commitment to their own education, thus making it possible for them to graduate and complete their academic or professional goals in a timely manner.

Another hallmark of the college is research. Our faculty is actively engaged in community college pedagogical research to study and improve the teaching methodologies to further benefit our students. 393 out of 775 faculty (both full- and part-time), or 51%, hold a doctorate or other terminal degree. Of the full-time faculty, 272 out of 390, or 70%, hold a doctorate or other terminal degree. They also conduct research in their academic disciplines, publish their findings and compete internationally in academic forums. The faculty is equally dedicated to the success of their students and encourages them to pursue their own intellectual development.

Direct Links to Zoom Rooms

9:00AM-10:00AM

Introductions and Keynote Speaker: Dr. Martin Chalfie (Main Room)

https://us02web.zoom.us/j/82777003923?pwd=VHA2ek1mcjFxdy9Va0Y1SlhLL1NYUT09

Meeting ID: 827 7700 3923

Passcode: 534725

10:00AM-11:00AM

Member Presentations for Faculty- Room 1 - Empirical

https://us02web.zoom.us/j/82912262244?pwd=VHR3ZXV5SEw2SVNhUkNCaFV4R0tnUT09

Meeting ID: 829 1226 2244

Passcode: 807286

Member Presentations for Faculty- Room 2 - Pedagogical

https://us02web.zoom.us/j/85080764381?pwd=eDFmQUNPWWVvUFdkN0QvMXpzK0hVUT09

Meeting ID: 850 8076 4381

Passcode: 854048

Post Undergraduate Q&A Panel for Students

Stay in main room

11:00AM-12:30PM

Student Presentations ZOOM Links

Biochemistry, Biophysics and Biotechnology (BBB) Room 1
Biochemistry, Biophysics and Biotechnology (BBB) Room 2
Biochemistry, Biophysics and Biotechnology (BBB) Room 3
Clinical (CLI) Room
Developmental Biology and Genetics (DBG) Room
Environmental Biology and Ecology (EBE) Room 1
Environmental Biology and Ecology (EBE) Room 2
Microbiology and Immunology (MBI) Room 1
Microbiology and Immunology (MBI) Room 2
Microbiology and Immunology (MBI) Room 3
Physiology and Neuroscience (PNC) Room 1
Physiology and Neuroscience (PNC) Room 2
Physiology and Neuroscience (PNC) Room 3

12:30PM-1:15PM

Lunch Break on Your Own/Judges Scoring

1:15PM-2:30PM

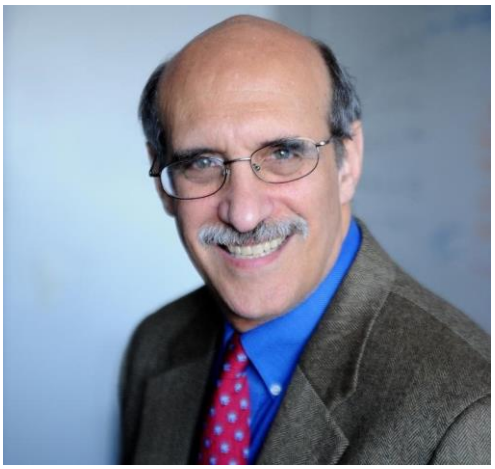
Keynote Speaker: Dr. Nidhi Gadura, Award Ceremony & Closing Remarks (Main Room)

https://us02web.zoom.us/j/82777003923?pwd=VHA2ek1mcjFxdy9Va0Y1SlhLL1NYUT09

Meeting ID: 827 7700 3923

Passcode: 534725

Keynote Speaker: Martin Chalfie, Ph.D.



"The Continuing Need For Useless Knowledge"

Martin Chalfie, Ph.D.

Professor

Columbia University, Irving Medical Center

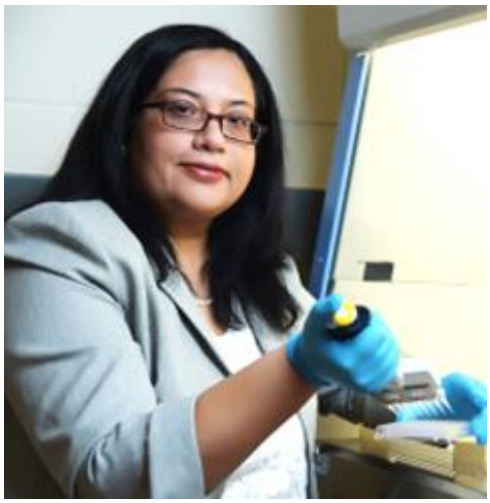
Martin Chalfie, University Professor in the Department of Biological Sciences at Columbia University, shared the 2008 Nobel Prize in Chemistry for his introduction of Green Fluorescent Protein (GFP) as a biological marker. Dr. Chalfie obtained his A.B. and Ph.D. from Harvard University and did postdoctoral research with Sydney Brenner at the MRC Laboratory of Molecular Biology, Cambridge, England. As a postdoctoral fellow, Martin Chalfie with John Sulston established the first genetic model for mechanosensation using the nematode *Caenorhabditis elegans*. He and his lab subsequently used molecular, genetic, and electrophysiological means to study neuronal specification, differentiation, outgrowth, and degeneration, microtubule structure and function, and mechanosensory transduction and its modulation in *C. elegans*. Dr. Chalfie is a past president of the Society for Developmental Biology and the current president-elect of the American Society for Cell Biology. He also chairs the Committee on Human Rights of the National Academies of Sciences, Engineering, and Medicine.

Keynote Speaker: Nidhi Gadura, Ph.D.

"A Sense of Belonging in STEM"

Nidhi Gadura, Ph.D.

Professor and Department Chair of Biological Sciences and Geology
Queensborough Community College, CUNY



Dr. Nidhi Gadura graduated with her Bachelor's degree from York College, received her M. Phil from Queens College and Ph.D. from The Graduate Center, CUNY. She joined the faculty of Queensborough Community College in 2007. Dr. Gadura has significantly contributed to curriculum development. She established a Dual/Joint AS/BS in Biotechnology at Queensborough in collaboration with York College. She developed honors courses in Biotechnology and Genetics. Additionally, she equipped a teaching biotechnology laboratory at Queensborough where she enjoys training students. Dr. Gadura strongly believes that hands-on research experience plays a pivotal role in the success of students who plan to pursue careers in STEM. To further her plans to foster research on campus, she spearheaded the creation of a Departmental Biotechnology research laboratory core facility with state of the art equipment. This core facility will continue to enhance the research activities of faculty and students at Queensborough for decades to come.

Dr. Gadura has secured funding from various agencies like the U.S. Department of Education MSEIP grant and NIH BioPREP grant aimed to help engage Queensborough students in research and increase STEM retention and graduation on campus. Her students' long-standing record of winning regional and national awards at prestigious scientific conferences is an additional testament to the caliber of research that is possible at Queensborough. Dr. Gadura practices several high impact pedagogical techniques in her classes. These include Writing Intensive courses, Academic Service –Learning, as well as Undergraduate Research integration into the curriculum. Her mantra is simple, you can never pay your mentors back, therefore, you must always pay it forward.

Postgraduate Q&A Panelists

Host: Dr. Rochelle Nelson, QCC, CUNY
Moderator: Dr. Peter A. Novick, QCC, CUNY

Amy Melok, DMD
Dentist, Brighter Smiles Dental
DMD, Case Western Reserve University
MS in Biology, Montclair State University
BS in Biology, Montclair State University

Jose Perez, PhD
Microbiologist II, Subject Matter Expert, Innophos
PhD in Molecular Biosciences, Seton Hall University
MS in Molecular Biology, Montclair State University
BS in Biology, Montclair State University

Megan Pirtle
PhD Candidate in Biomedical Science at Albert Einstein College of Medicine
BA in Psychology and Communication, Keene State College

Roksana Rahman, MS
Bioanalytical Quality Control Associate Scientist, Bristol Myers Squibb
MS in Microbiology, Seton Hall University
BS, Monmouth University

Ayuni Yussof, MS
PhD Candidate in Molecular Biosciences, Seton Hall University
MS in Molecular Biology, Montclair State University
BS in Biotechnology, Rutgers University

Faculty Member Presentations- Room 1 (Empirical)

10:00-11:00 a.m.

https://us02web.zoom.us/j/82912262244?pwd=VHR3ZXV5SEw2SVNhUkNCaFV4R0tnUT09
Meeting ID: 829 1226 2244
Passcode: 807286

1. 10:00-10:15 a.m.

A Preliminary Study of the vascular flora of Riverdale Park, Bronx, New York

Mark Yagudayev, Jingjing Tong, Rosivel Galvez, Pamela Arpi Pintado, Selin Ipe, Clara Maria L. Gata, Khadija Yousuff, Ariana Maks, Adam Leviyev and Kathleen Nolan

St. John's University, NY

The vascular flora at Riverdale Park, Bronx, New York were sampled during the growing season of 2021, April 14 to October 26, 2021. One hundred fifty-four species in 122 genera in 72 families were identified. Sixty non-native vascular plant species composed 39% of the flora. The largest families in the flora were the Asteraceae, 16 species and Rosaceae, 13 species. The largest genera were Acer 6 species, Quercus and Carex each with 5 species. The circumference and trunk diameter of Riverdale Park's big trees were measured with a diameter tape 1.37 meters above the ground. A double trunked Q. alba had a circumference of 515 cm, Q. rubra 338 cm, Q. velutina 335 cm while *Acer saccharinum, Platanus occidentalis, Carya ovata*, *and Liriodendron tulipifera* with circumferences over 300 cm. The parks protected status will enable researchers to conduct comparative floras in the future.

2. 10:15-10:30 a.m.

A Role for Thyroid Hormone Testing in COVID-19 Patients

Sara Danzi[1] and Irwin Klein[2]

[1] Department of Biological Sciences and Geology, Queensborough Community College, CUNY and [2] Department of Medicine, NYU School of Medicine

Thyroid hormone has profound effects on the heart and cardiovascular system. In thyroid hormone deficiency, cardiac function is impaired. The thyroid gland produces two hormones, T4 (~85%) and T3 (~15%). T4 is a prohormone that is deiodinated to T3, the active hormone. Reduced serum T3 levels can result from thyroid disease, (hypothyroidism), or indirectly as a result of decreased T4 to T3 conversion. In some hypothyroid patients, and in severe illness, surgery or trauma, there is decreased activity of the mono-deiodinase enzyme resulting in decreased serum T3, often with normal levels of serum T4 and the regulatory hormone, TSH (thyroid stimulating hormone). There is evidence that inflammatory cytokines play a role in this low T3 syndrome, sometimes referred to as nonthyroidal illness. The virus that causes COVID-19, the SARS-CoV-2 coronavirus, can damage heart muscle and affect cardiac function. Furthermore, in critical illness, including heart failure, there is evidence that low T3 states further impair cardiac function and have been shown to be a reliable prognostic marker. The low T3 state in critical illness and in heart failure has been associated with increased all-cause mortality.

To assess the current use of thyroid function testing, and the prevalence of nonthyroidal illness in a critically ill patient population, we retrospectively reviewed thyroid function testing in 720 COVID-19 patients at NYU

Langone's Tisch Hospital between March and May 2020. Of those patients, T3 testing was included in only 37 patients, (average age 60.86 years, range 19.7 – 86 years; 52.7% male; average days after positive COVID-19 test 20.04). All but 2 patients (94.6%) had serum T3 levels below the reference range [reference range 1.2 to 2.8 nmol/L]. Of those patients with reduced serum T3 levels, only two appeared to be hypothyroid with elevated TSH. Therefore, 89.2% of the patients who were tested for serum total T3 meet the criteria for nonthyroidal illness.

These data are significant in demonstrating the high occurrence of nonthyroidal illness in a large COVID-19 population with very severe illness. Low T3 states may have adverse effects in critical illness and serve as an independent predictor of increased risk of mortality. Additionally, experimental COVID treatment protocols with hydroxychloroquine would put this patient population at greater risk of cardiac effects. Hypothyroidism and hydroxychloroquine both prolong the QT interval, which predisposes to ventricular arrhythmias and sudden cardiac death.

In summary, in 720 COVID-19 patients, only 37 (0.05%) were assessed for serum total T3, despite the growing understanding in the medical community that the low T3 syndrome may have adverse effects in critical illness and is a reliable independent prognostic indicator of mortality. In those 37 patients, 94.6% had reduced serum T3, with 89.2% meeting the criteria for non-thyroidal illness. Replacement with liothyronine sodium injection (Triostat) has been shown to be safe and effective in treating the low T3 syndrome after cardiac surgery, and may prove to be beneficial in this setting.

3. 10:30-10:45 a.m.

mTOR pathway requirement for macrophage activation in innate immune responses

Maria Frias, Department of Biology and Health Promotion, St Francis College, NY

Innate immunity is characterized by host defenses involving anatomical barriers, sensor systems that recognize patterns associated with microbes or tissue damage, phagocytic cells, the inflammatory response and fever. Macrophages are a very important component of innate immunity. They are sentinel cells that can immediately detect foreign invasion or tissue abnormalities and trigger appropriate innate immune responses to clear the problem. Macrophages are present in nearly all human organs and tissues. A critical aspect of macrophages is that they are phagocytic cells, which engulf and degrade microbial pathogens, foreign objects, dead cell debris, and cancer cells. Upon stimulation and activation, macrophages regulate innate immune responses, as well as adaptive immune responses involving lymphocytes, by recruiting other immune cells to the local of invasion or damage.

In response to a microenvironment that has microbial cells or products, stimulated lymphocytes, or damaged cells, macrophages undergo final differentiation into one of two distinct activated or functional populations. The M1 macrophages are characterized by the generation of high levels of pro-inflammatory cytokines, antimicrobial properties, increased production of reactive nitrogen and oxygen species, and induction of helper lymphocyte responses. In contrast, M2 macrophages are characterized by their involvement in tissue remodeling and immune regulation.

The mechanistic target of rapamycin (mTOR) is a conserved serine/threonine protein kinase that responds to environmental signals, such as nutrient availability and presence of specific growth factors or hormones, to control cell growth, proliferation, metabolism, survival and differentiation. The mTOR pathway plays a critical role in mammalian cell, organ and organism homeostasis. The current model of mTOR activation suggests that a cytoplasmic mTOR translocates to the lysosome in response to nutrients. Once on the lysosome mTOR encounters its activator and becomes fully activated. Once activated, mTOR phosphorylates its targets to trigger protein translation initiation, lipid synthesis, ribosome biogenesis, and inhibition of macroautophagy.

Not much is currently known about the role of mTOR in macrophage polarization, and macrophage-mediated innate immune responses. Recent findings show that the mTOR pathway is required for macrophage differentiation from bone marrow derived progenitor cells. Moreover, recent studies suggest that mTOR triggers macrophage differentiation by inhibiting macroautophagy in the cell. Here, we propose to investigate the role of mTOR in macrophage polarization and activation. We hypothesize that mTOR translocates to the lysosome in response to pathogen signals, inhibits macroautophagy, and triggers during M1 polarization, but not M2 polarization, to ensure rapid phagocytosis of pathogenic invaders.

To investigate our hypothesis we are going to use monocytes isolated from peripheral blood. The monocytes will be differentiated into inactive macrophages in culture by the addition of phorbol 12-myristate 13-acetate (PMA). After that, we will trigger M1 or M2 polarization by using lipopolysaccharide (LPS, M1) or interleukin4 (IL-4, M2), in the absence or presence of the mTOR allosteric inhibitor rapamycin. We will then measure M1 or M2 cytokine production by specific ELISA assays, followed by fluorescence microscopy evaluation of mTOR subcellular localization and autophagosome formation.

4. 10:45-11:00 a.m.

Novel Bacteriophages and Enteric Bacteria Isolated from Kitchen Sponges

Bryan Gibb, NY Tech, NY

The humble and lowly kitchen sponge often sits neglected in a dish by the sink, marinating in the pool of water, soap, dirt, oil, and leftover food-- a perfect home for a rich microbial ecosystem. Following recent studies that explored the bacterial composition of kitchen sponges, we hypothesized that these sponges should harbor bacteriophages as well. A team of undergraduate students as part of a research course isolated bacteria from their own dirty kitchen sponges and used the isolated bacteria to find bacteriophages residing in the same sponge. All students had numerous bacteria from their sponges to choose for isolation, but only two successfully found a bacteriophage in the sponge that infected their isolated bacteria. Subsequent microscopy, biochemical and genomic characterization of the bacteria revealed that these two isolated strains are members of the Enterobacter cloacae subgroup. What was originally thought to be two isolated phages ended up being a single novel phage that is able to infect both of the isolated hosts from the two different sponges. Further host range testing with standard-related lab strains found that the phage can also infect *Cronobacter muytjensii.* Electron microscopy shows that phage is myoviridae. The genome of the phage does not show any strong similarity to other sequenced bacteriophages, and most of the identified genes have no known predicted function. Subsequent work has identified additional bacteriophages that infect these two bacterial isolates. Ongoing efforts continue to characterize these bacteriophages and the two related enteric bacteria. Many Gram-negative enteric bacterial strains are opportunistic pathogens that readily acquire resistance to antibiotics. These bacteriophages will help us understand the therapeutic potential of bacteriophages in treating infections caused by enteric bacteria.

Faculty Member Presentations- Room 2 (Pedagogical)

10:00-11:00 a.m.

https://us02web.zoom.us/j/85080764381?pwd=eDFmQUNPWWVvUFdkN0QvMXpzK0hVUT09
Meeting ID: 850 8076 4381
Passcode: 854048

1. 10:00- 10:15 a.m.

Triage and Recovery of STEM Laboratory Skills

Sujun Wei[1], Timothy Sonbuchner[2], Emily Mundorff[3], Jacqueline Lee[4], and Peter Novick [1]

[1]Queensborough Community College, CUNY, NY, [2]Adelphi University, NY,[3] Hofstra University, NY, and [4]SUNY Nassau Community College, NY

The global COVID-19 pandemic left universities with few options but to turn to remote learning. With much effort, STEM courses made this change in modality; however, many laboratory skills, such as measurement and handling equipment, are more difficult to teach in an online learning environment. A cohort of instructors who are part of the NSF RCN-UBE funded Sustainable, Transformative Engagement across a Multi-Institution/Multidisciplinary STEM (STEM2) Network (a working group of faculty from two community colleges and three 4-year universities) analyzed introductory biology and chemistry courses to identify essential laboratory skills that students will need in advanced courses. Seven essential laboratory proficiencies were derived from reviewing disciplinary guiding documents such as AAAS Vision and Change in Undergraduate Biology Education, American Society for Microbiology Recommended Curriculum Guidelines for Undergraduate Microbiology Education and American Chemical Society Guidelines for Chemistry: data analysis, scientific writing, proper handling and disposal of laboratory materials, discipline-specific techniques, measurement, lab safety and personal protective equipment, and interpersonal/collaborative skills. Our analysis has determined that some of these skills are difficult to develop in a remote/online setting but could be recovered with appropriate interventions. Skill recovery procedures suggested are a skill “boot camp,” department/college coordinated club events, and a triage course. The authors recommend that one of these three recovery mechanisms be offered to bridge this skill gap and better prepare STEM students for upper-level science courses and the real world.

2. 10:15-10:30 a.m.

Design, Synthesis and Testing of an Anti-Covid Gene Therapy: Integration of Authentic Research into an Undergraduate Laboratory Course

Martin Hicks and Flobater Gawargi, Monmouth University, NJ

Undergraduate biology students often graduate without exposure to authentic research experiences. Laboratory courses follow a one or two week fail-proof experiment resembling a cookbook recipe, lacking the uncertainty of genuine research. Techniques in molecular biology cover an array of skills essential to succeed in a biotechnological laboratory today. This lab course is based on the teaching of concepts while imparting the skills and applications of modern techniques, providing students with theoretical concepts and laboratory skills. We prepare students to carry-out scientific protocols that can be applied to a future workforce setting. Students are immersed in a 10-week series of labs with the objective to use molecular

cloning to make a novel gene therapy vector; therapies are designed to inhibit the expression of genes of the virus that causes Covid-19, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Students are introduced to PubMed and Genbank to research the background of SARS-CoV-2 and its target genes; the Spike gene (S), the membrane gene (M) the nucleocapsid gene (N) and the envelope gene (E). Students use the DNA software, Serial Cloner, as a tool to evaluate DNA sequences and mFOLD to analyze RNA structure. Students generate and visualize the design of an antisense gene therapy directed against one of the target viral genes. Using our gene therapy platform, students generate a vector with a unique target. Subsequently student-generated vectors were transfected into mammalian tissue culture cells that express the target genes (S, M, N or E) and RNA and protein was collected to measure the efficacy of the gene therapy vector to reduce the expression of the target viral gene.

3. 10:30-10:45 a.m.

Undergraduate Research in a classroom online vs. in person

Golebiewska, Urszula, Queensborough Community College, CUNY, Bayside, NY

Undergraduate Research is a powerful high impact practice, I use it in my honors General Biology 2 course, where students are engaged in analysis of bacteriophage genomes. The class is a part of the HHMI Sea-Phages program. Spring 2020 was the semester that started a challenging stretch of semesters. The Undergraduate Research class started its Bioinformatics project in person and finished online. I decided to compare the outcomes of the online classes to those of the in person. For the Spring 2020 the students' performance was comparable to an in-person modality. This can be attributed to the fact that students received ample in person instruction prior to conducting their independent investigations. They got a chance to build a community of learners, knew each other and could help each other. Starting from Fall 2020 the real challenge began. Initially, I thought that it should not make too much of a difference for the computational research to be conducted online rather than in person. However, from the start I learned that it was more challenging. Students seemed more confused and less confident about the research objectives. Explaining the use of various software was more difficult and building student support groups was more difficult. To compare the outcomes, I decided to look at the artifacts produced by students. Students were required to write research reports and present their findings to their peers at the end of semester. I developed rubrics to assess the presentations and the final reports. The results were compared to the oral presentations and written reports from the semester's taught fully in person. Spring 2020 semester was not compared as it was neither fully online nor fully in-person. The major challenges were the participation in synchronous sessions and keeping the timeline. Overall, the analysis of students' presentations showed that the level of understanding of the project was comparable to the in-person delivery. The amount of misconceptions propagated in the reports was a bit higher. One of the surprising observations was that students were more likely to ask for clarifications and help when meeting in person. Online delivery resulted in hesitancy to seek help and ask questions both from the instructor and from other students. I am going to discuss here the ways to engage students in their bioinformatics research. I will also describe the challenges, achievements and failures on my par while instructing students online in their bioinformatics projects.

4. 10:45-11:00a.m.

Preliminary study: Bimodal distribution of the exam scores in an asynchronous online microbiology course.

Katsuhiro Kita [1&2], Emily Vandalovsky[2], Abdul Aqeel[2] and Robert Highley[2]

[1]Department of Biology, St. Francis College, [2]Department of Biology and Horticulture, Bergen Community College, NJ

After COVID-19 pandemic in 2020 Spring, we all higher education instructors have been forced to change the delivery method of lectures as well as lab courses. Besides hybrid courses, there would be two different ways to deliver lectures; either synchronously or asynchronously. Although there is a study reporting that students in fully online programs showed more positive attitudes than traditional classroom settings (Perera et al. (2017) Life Sci. Edu., 16, ar60), it is very common to hear that there have been many struggles among higher education instructors for successful engagement of students in fully online settings, especially during COVID-19 pandemic. Here, we sought to compare the effectiveness of synchronous live streaming and asynchronous on students' learning outcome in Microbiology lecture. Both courses were taught by the same instructor, using the same material. Although the asynchronous mode does not allow live, interactive activities, interactive video quizzes using H5P and discussion board-based participation were done. When the score distribution of the first exam were compared, synchronous course (S; n=18) showed average 72.42 (S.D. 16.15) and median 73.5. On the other hand, one asynchronous course (AS1; n=18) showed the similar range (average 73.52, S.D. 9.73 and median 70.55), the other asynchronous course (AS2; n=18) showed significantly lower value (average 64.88, S.D. 17.25 and median 55.90). When two asynchronous sections are combined (n=36), the average is 69.20 (S.D.=14.48) and the median is 68.03. More interestingly, there are very clear, two peaks were observed in AS2 group's score distribution (higher peak: average 84.64, S.D.=5.75, median 85.8 vs lower peak: average 52.30, S.D.=6.19, median 54.30). As the asynchronous courses are still ongoing (2021 Fall), we cannot make the overall conclusion yet. Nevertheless, this preliminary data set would be very interesting to analyze the effect of the delivery modes in post-pandemic online teaching.

Student Presentations by Room

BBB ROOM 1

Moderator: Dr. Nidhi Gadura, QCC, CUNY
https://us02web.zoom.us/j/87973503136?pwd=SUltVGNoclVJU3orZ1pGdU8vRWVlQT09
Meeting ID: 879 7350 3136
Meeting Password: 877428

Presentation 1. 11:05AM - 11:17AM

A peek into the actions of "Molecular Scissors" of Biotechnology. Piechowska, Sabina & Ghoshal, Sarbani. Queensborough Community College, CUNY.

Presentation 2. 11:18AM - 11:30AM

ELISA: ENZYME-LINKED IMMUNOSORBENT ASSAY. Nasrin, Sumaiya & Gadura, Nidhi. Queensborough Community College, CUNY.

Presentation 3. 11:31AM - 11:43AM

Development inhibitors of Kinases via the synthesis of oxazepane compounds. Cui, Chang & Choi, Junyong. Queens College, CUNY.

Presentation 4. 11:44AM - 11:56AM

Uncovering the Mechanism of Heterotrimeric GTP-Binding Protein, Rap1a, in Hepatic Glucose Production. Sarecha, Amesh; Wang, Yating & Ozcan, Lale. Columbia University.

Presentation 5. 11:57AM - 12:09PM

Effects of Stimulants and HIV Proteins on Pyroptosis and Apopotosis Pathways in Human Brain Microvascular Endothelial Cells (hBMEC). Wei, Yufeng; Garzon, Luis & Joy Ikedife. New Jersey City University.

Presentation 6. 12:10PM - 12:22PM

Inositol Hexakisphosphate Kinase 1 (IP6K1) ameliorates diet induced obesity by enhancing energy expenditure pathway. Wanderley, Mayra; Piechowska, Sabina & Ghoshal, Sarbani. Queensborough Community College, CUNY..

Presentation 7. 12:23PM - 12:35PM

Ionic liquid-polymer gels for separations. (Nembhard, Shameir; Zmich, Nicole; Lall-Ramnarine, Sharon; Castner, Edward W. & Wishart, James F). Queensborough Community College, CUNY.

Presentation 8. 12:36PM - 12:48PM

The Impact of Curcumin on H460 cells. (Daniels, Dontaye; Noel, Angela; Bustamante, Monic & Moloney, Daniel). Queensborough Community College, CUNY & Stony Brook University.

BBB ROOM 2

Moderator: Dr. Peter A. Novick, QCC, CUNY

https://us02web.zoom.us/j/81231027417?pwd=R1ZOZnRkL1VYdEppaXRCdHRUUHJjZz09

Meeting ID: 812 3102 7417

Meeting Password: 576540

Presentation 1. 11:05AM - 11:17AM

Development of Small Molecule Inhibitors Targeting ssDNA-binding Protein Replication Protein. (A. Rodriguez, Diana; Hossain, Zakir & Choi, Jun Yong). Queens College.

Presentation 2. 11:18AM - 11:30AM

Differential Breast Cancer Cell Gene Expression after treatment with Single Walled Carbon Nanotubes. (Williams, Janice; Sullivan, Regina & Ghoshal, Sarbani). Queensborough Community College, CUNY.

Presentation 3. 11:31AM - 11:43AM

A Novel Protocol for Producing COVID-19 RBD Protein Vaccine. (Marnik, Arleta & Jahangir, ZMG Sarwar). Kingsborough Community College, The City University of New York.

Presentation 4. 11:44AM - 11:56AM

Back to Basics- Revisiting concepts for Sterile Techniques, Streaking & Serial Dilution. (Bhattacharya, Mira & Ghoshal, Sarbani). QCC, CUNY.

Presentation 5. 11:57AM - 12:09PM

DNA Fingerprinting "Detecting Alu Insertion". (Javellana, Shaun & Gadura, Nidhi). Queensborough Community College, CUNY.

Presentation 6. 12:10PM - 12:22PM

Affordable and rapid method for detection of Enterococcus spp. in NYC harbors using the Loop- Mediated Isothermal Amplification (LAMP). (Nasrin, Sumaiya & Nguyen, Andrew V). Queensborough Community College, CUNY.

Presentation 7. 12:23PM - 12:35PM

Aligned Crystal Growth of C60, n-type Organic Semiconductor. (Bilewu, Fathia & Kim, Bumjung). New Jersey City University.

Presentation 8. 12:36PM - 12:48PM

Designing an MTR4 Knockdown System to Investigate the Impact of lncRNA Accumulation on Differentiation Phenotype. (Udupa, Aditya; Vlasov, Pavel & Manley, James). Columbia University.

BBB ROOM 3

Moderator: Dr. Sarbani Ghoshal, QCC, CUNY
https://us02web.zoom.us/j/88053382082?pwd=V21PdjNoV3JXZFFCRWM1MWc3MlRLQT09
Meeting ID: 880 5338 2082
Meeting Password: 272316

Presentation 1. 11:05AM - 11:17AM

Fragment-based drug design in optimization of potent enzyme inhibitor of PptT from *Mycobacterium tuberculosis.* (Barrois, Elizabeth; Krieger, Inna & Mosior, John). Texas A&M University& Spring Hill College.

Presentation 2. 11:18AM - 11:30AM

The Effects of Sulforaphane on Non-Small Lung Cancer Cells. (Gao, Suncheng; Nacimba, Jordan & Moloney, Daniel). Queensborough Community College, CUNY & Stony Brook University.

Presentation 3. 11:31AM - 11:43AM

Synthesis of a Macrocyclic Analog of Pentamidine. (Haliru, Konyinsola & Aslanian, Robert). New Jersey City University.

Presentation 4. 11:44AM - 11:56AM

Gene Therapy for Brain Tumors: Identification of New Therapeutic Targets Based on RNA Structure. (Sine, Laura; DeMarco, Victoria; Hintelmann, Thomas; Sean Reardon & Hicks, Martin). Monmouth University.

Presentation 5. 11:57AM - 12:09PM

Development of drug- like inhibitors of Nek2 kinase using Nek2 overexpression fly model. (Hauter, Lamia; Bhuiyan, Ashif I; Reghuvaran Santha, Asha; Musayev, Rafael; Sweeney, Chloe; Dickson, Anna; Talele, Tanaji & Pathak, Sanjai). Queens College.

Presentation 6. 12:10PM - 12:22PM

GFP protein Expression. (Stella, Hill, Schneider, Patricia & Ghoshal, Sarbani). Queensborough Community College, CUNY.

Presentation 7. 12:23PM - 12:35PM

The Potential use of Inducible cAMP Early Represser (ICER) peptides in anti-cancerous treatment. (Homsi, Karim; Alves, Daniella; Cirinelli, Angelo; Lange, Keith; Molina, Carlos). Montclair State University.

Presentation 8. 12:36PM - 12:48PM

The Mechanistic Role of pVHL in the Ubiquitin-Mediated Degradation of Alpha-5 Integrin. (Shah, Prachi & Schoenfeld, Alan). Adelphi University.

CLI ROOM 1

Moderator: Dr. Mohammad Javdan, QCC, CUNY
https://us02web.zoom.us/j/82440752627?pwd=di9aY2t2SXVTWU54c2I0YW5BYlNmQT09
Meeting ID: 824 4075 2627
Meeting Password: 837347

Presentation 1. 11:05AM - 11:17AM

An Application of Artificial Intelligence to Diagnose Cancerous Cells. (Benoit, Marcus; Gromova, Valeria & Yanagisawa, Chiaki). Borough of Manhattan Community College.

Presentation 2. 11:18AM - 11:30AM

CHANGES IN BREAST CANCER CARE IN NEW YORK DURING THE COVID-19 PANDEMIC. (Rosado, Cheyenne; Fiederlein, Alexandra & Cutter, Noelle). Molloy College.

Presentation 3. 11:31AM - 11:43AM

Anti-COVID MicroRNA Therapy Blocks the Expression of the Spike Gene of SARS-CoV-2. (DeMarco, Victoria; Sine, Laura; Hintelmann, Thomas; Reardon, Sean & Hicks, Martin). Monmouth University.

Presentation 4. 11:44AM - 11:56AM

An Algorithm to Predict A Cancerous Cell With High Accuracy With Population Imbalanced Dataset. (Gromova, Valeria; Benoit, Marcus & Yanagisawa, Chiaki). Hofstra University.

Presentation 5. 11:57AM - 12:09PM

Generating cDNA Clones of the EGFR Transcript to Better Quantify EGFR Levels in GBM Tumors. (Reardon, Sean; Herrera, Jessica & Hicks, Martin). Monmouth University.

Presentation 6. 12:10PM - 12:22PM

Mesenchymal Stem Cell Paracrine-Mediated Repair in Diabetic Kidney Disease. (Stevic, Una; Gowan, Cody C.; Smith, Anastasia L.; Snow, Zachary K.; Summers, Jonathan C.; Conley, Sabena M.; Hickson, LaTonya J. & Nolan, Kathleen). St. Francis College.

Presentation 7. 12:23PM - 12:35PM

An Analysis of Multiple Factors on Stress in the United States. (Caparelli, Alexander; Chase, Owen; Fiamoncini, Maura; McMenamin, Connor; Prince, Ivy & Monaco, Pamela). Bucknell University.

DBG ROOM 1

Moderator: Dr. Rochelle Nelson, QCC, CUNY
https://us02web.zoom.us/j/87313877385?pwd=NzJHWWYvZVJCYjY4bzdpRmxTVkZYZz09
Meeting ID: 873 1387 7385
Meeting Password: 248056

Presentation 1. 11:05AM - 11:17AM

GENE THERAPY FOR BRAIN TUMORS: IDENTIFICATION OF NEW THERAPEUTIC TARGETS BASED ON RNA STRUCTURE. (Hintelmann, Thomas; Sine, Laura; Demarco, Victoria; Garwagi, Flobater & Hicks, Martin). Monmouth University.

Presentation 2. 11:18AM - 11:30AM

Changes in Hypothalamic Neuronal Transcriptome by the Dietary Fatty Acids: Oleic and Palmitic Acid. (Marino, Amanda & Poon, Kinning). SUNY Old Westbury.

Presentation 3. 11:31AM - 11:43AM

RNA Therapeutics for Brain Tumors: Targeting Pre-mRNA Splicing Motifs to Generate Therapeutic Gene Isoforms. (Hintelmann, Thomas; Sine, Laura; DeMarco, Victoria; Reardon, Sean & Hicks, Martin). Monmouth University.

Presentation 4. 11:44AM - 11:56AM

Detection of the FoxL2 gene *in Crassostrea virginica*. Sejour, Cassandra; Nielsen, Lilja & Hinkley, Craig. Kingsborough Community College.

Presentation 5. 11:57AM - 12:09PM

Identification of Telomere Regulating Genes in Drosophila melanogaster. Hanesworth, Isabella; Dalia, Abdelhamid; Barahona, Carla; Drammeh, Aisatou; Gonzalez, Elizabeth; Marquez, Felipe; Rahman, Elena; Stevens, Bryan C.; Torres, Edith R. & Zhou, Chun. Mercy College.

Presentation 6. 12:10PM - 12:22PM

Effects of anthropogenic noise on the vocal behavior of Song Sparrows (*Melospiza melodia*). Annon, Oshane; Nunez, Xiomara & Wydner, Katherine. Saint Peter's University.

Presentation 7. 12:23PM - 12:35PM

Influence of fungicide and nematicide on plant responses to drought and rainfall variability. Serrano Perez, Madaris; Jones, Jennifer & Evans, Sarah. Michigan State University, University of Puerto Rico.

EBE ROOM 1

Moderator: Dr. Alison Mello, QCC, CUNY
https://us02web.zoom.us/j/84430454335?pwd=MlVoUy9CNUhQSzYwSkdxR3NuLzRXQT09
Meeting ID: 844 3045 4335
Meeting Password: 737324

Presentation 1. 11:05AM - 11:17AM

Winging It for Seven Winters: Project FeederWatch Sheds Light on Urban Birds. (Rodriguez, Katherine; Annon, Oshane; Nunez, Xiomara; Amaya, Claudio; Regis, Ben & Wydner, Katherine). Saint Peter's University.

Presentation 2. 11:18AM - 11:30AM

Does Flower Color Attract Native Bees? Jimenez, Bianca; Dr. Eiden and Dr. Bukofser. Mercy College.

Presentation 3. 11:31AM - 11:43AM

Directional Orientation of Harbor and Gray Seals at Swinburne Island in New York City. Luong, Victoria; Woo, Kevin; Biolsi, Kristy & Radhakrishnan, Preethi. LaGuardia Community College.

Presentation 4. 11:44AM - 11:56AM

Monitoring Water Quality Parameters in NYS Parks Using Neulog Sensors Post Covid-19. Budhu, Eric; Bendeck Hincapie, Andrea; Liliah, Marisha; Ramos, Elizabeth & Schramm, Laura. St. John's University.

Presentation 5. 11:57AM - 12:09PM

A Study of Oyster Growth in Sheepshead Bay, Brooklyn, NY. Pena, Steven; Polizzotto, Kristin & Ortiz, Mary. Kingsborough Community College.

Presentation 6. 12:10PM - 12:22PM

WHY ARE MARINE VIRUSES IMPORTANT? Chitadze, Mariami & Nolan, Kathleen. St. Francis College.

Presentation 7. 12:23PM - 12:35PM

The Impact Rapid Temperature Change Has on the Swimming Ability of Larval Sheepshead Minnow (*Cyprinodon variegatus*). George, Sophia & Perez, Kestrel. St. Joseph's College New York (Brooklyn Campus).

Presentation 8. 12:36PM - 12:48PM

Microplastic Abundance in Lake Hopatcong. Gonzalez, Karla; Fitzgerald, & Allison. New Jersey City University.

EBE ROOM 2

Moderator: Dr. Sushma Teegala, QCC, CUNY
https://us02web.zoom.us/j/7624978469?pwd=UU5iVEkzNnlGK0VXNk4zRllnZDRiZz09
Meeting ID: 762 497 8469
Meeting Password: MACUB

Presentation 1. 11:05AM - 11:17AM

The Developmental Plan of Inflorescence Circumnutation in *Arabidopsis thaliana*. Brenner, Eric; Perez, Sofia & Brenner, Eric. Pace University.

Presentation 2. 11:18AM - 11:30AM

Zooplankton Biodiversity and Decapod Larvae Density in the Lower Hackensack River. Nguyen, Huy & Fitzgerald, Allison. New Jersey City University.

Presentation 3. 11:31AM - 11:43AM

The Effect of Urbanization on Avian Diversity at Purchase College, SUNY. Goddard, Rayna; Lemus, Jenifer; Connal, Nicole; Salazar, Kevin; Riccardi, Krystal & Jackson, Allyson. Westchester Community College.

Presentation 4. 11:44AM - 11:56AM

Connection between native plants, soil health, and soil biodiversity. Collier, Mac & Eiden, Margaret. Westchester Community College.

Presentation 5. 11:57AM - 12:09PM

STUDY OF MIGRATION PATHS, MATING, AND ABUNDANCE ALONG THE HUDSON RIVER. Calvagna, Vincent & Nolan, Kathleen. St. Francis College.

Presentation 6. 12:10PM - 12:22PM

Evaluation of Enterococcus Levels in the East River in Relations to Public Health. Mensah, Joshlyn; Kano, Briana; Gonzalez, Zenovia; Cardenas, Irma; Albro, David & Ellington, Jenna. St. Francis College.

Presentation 7. 12:23PM - 12:35PM

The Effect of Antifouling Biomaterials on Algal Growth and Biofilm Formation. Saleh-Esa, Mariam; Patel, Rich & Chu, Tinchun. Seton Hall University.

MBI ROOM 1

Moderator: Dr. Rondi Davies, QCC, CUNY
https://us02web.zoom.us/j/82468066288?pwd=QmYybWppZVNMdjBqY2VmNVVBMnh3QT09
Meeting ID: 824 6806 6288
Meeting Password: MACUB

Presentation 1. 11:05AM - 11:17AM

The Effects of Climate Change on Fatal Human Diseases. El Houzaly, Sara & Gupta, Richa. LaGuardia Community College.

Presentation 2. 11:18AM - 11:30AM

Microbial Contamination on Used Disposable Face Masks. Arias, Audrey; Clarke, Izabella; Asif, Kainat; Hill, Stella; Subramaniam, Raji & Schneider, Patricia. Queensborough Community College, CUNY.

Presentation 3. 11:31AM - 11:43AM

Understanding How Oomycete Plant Pathogens Interfere with The Immunity of Host Plant *Arabidopsis thaliana* Using Bioinformatic and Virtual Tools, Angie Jaramillo and Deb, Devdutta. Mercy College.

Presentation 4. 11:44AM - 11:56AM

Effects of Diminazene Aceturate on Human Cervical Cancer Cells. Boodhan Nicholas; Ofosu-Mensah; Jason Jeithy & Gharbaran, Rajendra. Lehman College, CUNY, Bronx Community College.

Presentation 5. 11:57AM - 12:09PM

Characterization of Penicillin Tolerance in Group B Streptococcus. Kobren, A; Memon, M; Tehrani, K; Kim, H; Hoque, F; Basu, P. Touro College of Pharmacy.

Presentation 6. 12:10PM - 12:22PM

To Determine How Oomycete Pathogens Interfere with Host Plant Defenses. McKenzie-Laury, Alexandrya; Bradley-Ortiz, Rashia & Devdutta, Deb. Mercy College.

Presentation 7. 12:23PM - 12:35PM

The Antimicrobial Properties of Curcumin and Green Tea Formulation on *B. subtilis* and *E. coli.* Gill, Harman; Patel, Radha; Chu, Tinchun. Seton Hall University.

Presentation 8. 12:36PM - 12:48PM

Antimicrobial and Antibiofilm Activity of N-Acetyl-L- Cysteine and L-Histidine on different Strains of Pathogenic Bacteria and Fungi. Alli, Muizzat; Sbateen, Nuha; Abbakass, Malika & Bendaoud Meriem. New Jersey City University.

MBI ROOM 2

Moderator: Dr. Sanjay Koul, QCC, CUNY
https://us02web.zoom.us/j/89947514786?pwd=QlhMdWRuRmZTeDdkaUp5dy9WSlNUUT09
Meeting ID:899 4751 4786
Meeting Password: 203518

Presentation 1. 11:05AM - 11:17AM

Antimicrobial and Antibiofilm Activity of Natural Compounds Produced by Unknown Marine Bacteria or the Human Body. Abakkass, Malika; Alli, Muizzat; Sbateen, Nuha & Bendaoud, Meriem. New Jersey City University.

Presentation 2. 11:18AM - 11:30AM

New Kid on the Block: Characterization of the Novel Multidrug-resistant Pathogen, *Candida auris*. Munoz, Javier; Birchwood, Adrielle; Bouklas, Tejas. SUNY College at Old Westbury.

Presentation 3. 11:31AM - 11:43AM

MuffinTheCat, Badulia, and DesireeRose Bacteriophages: Novel Members of the Tectiviridae Family. De Jesus, Angela; Beuhler, Brendan; O'Brien, Erin; Vargas Dominguez, Maria & Washington, Jacqueline. Nyack College.

Presentation 4. 11:44AM - 11:56AM

The Synergistic Antibacterial Effect of Patchouli with Antibiotics on *Klebsiella, Pseudomonas*, and *Staphylococcus* spp. Minnies, Jake; Postaski, Ashley; Saverimuttu, Augusta & Chu, Tinchun. Seton Hall University.

Presentation 5. 11:57AM - 12:09PM

COVID-19 Epidemiology. Cela, Sidorela; Ali, Manar & Sontag, Charles. Bergen Community College.

Presentation 6. 12:10PM - 12:22PM

The Antibacterial Effect of Ethanol-based Surgical Rub on *Bacillus* and *Mycobacterium* spp.Patel, Shivani; Wlodarski, Monika; Arellano, Emily & Chu, Tinchun. Seton Hall University.

Presentation 7. 12:23PM - 12:35PM

Antimicrobial and Antibiofilm Potential of a Medicinal Plant Root Extract. Sbateen, Nuha; Alli Muizzat; Abakkass, Malika & Bendaoud, Meriem. New Jersey City University.

Presentation 8. 12:36PM - 12:48PM

Two lytic *Citrobacter freundii* bacteriophages isolated from sewage with potential for phage therapy. Makedonska, Anna; Mosfique, Baizeed & Gibb, Bryan.New York Institute of Technology.

MBI ROOM 3

Moderator: Dr. Anuradha Srivastava, QCC, CUNY
https://us02web.zoom.us/j/85358302543?pwd=N2ZNSlhzaklWQUc2Z0w1YS9iREZldz09
Meeting ID: 853 5830 2543
Meeting Password: 552642

Presentation 1. 11:05AM - 11:17AM

To determine how oomycete pathogens interfere with host plant defenses. Bradley-Ortiz, RJ; Laury, Alexandrya & Deb, Devdutta. Mercy College.

Presentation 2. 11:18AM - 11:30AM

Inseparable partners: Phage follows enteric bacteria to non-poopy places. Wang, Jessica; Nagarwala, Hamza; Patel, Yamini & Gibb, Bryan. New York Institute of Technology.

Presentation 3. 11:31AM - 11:43AM

Localized Developmental and Functional Signatures Define Early Life Tissue Resident Memory T cells. Verma, Shivali; Guyer, Rebecca; Dogra, Pranay; Connors, Thomas; Szabo, Peter; Gray, Joshua & Farber, Donna. Columbia University.

Presentation 4. 11:44AM - 11:56AM

Antibacterial Effect of Phthalocyanine Zinc. Yussof, Ayuni & Chu, Tinchun. Seton Hall University.

Presentation 5. 11:57AM - 12:09PM

Analyzing the interaction between the oomycete effector protein, RxL23, and the plant defense gene, NPR-1. Daye, Mylaisha & Deb, Devdutta. Mercy College.

Presentation 6. 12:10PM - 12:22PM

Antibacterial Properties of Carvacrol on *P. fluorescens* and *S. epidermidis.* Patel, Rich & Chu, Tinchun. Seton Hall University.

Presentation 7. 12:23PM - 12:35PM

EFFECTOR PROTEINS DISRUPT PLANT IMMUNITY BY TARGETING CRITICAL PLANT DEFENSE GENES. Florentino, Gilda & Deb, Devdutta. Mercy College.

PNC ROOM 1

Moderator: Dr. Punita Bhansali, QCC, CUNY
https://us02web.zoom.us/j/89473623771?pwd=c3Z1ZnZlaWk2ZmE4aDlJL2xlRTA4dz09
Meeting ID: 894 7362 3771
Meeting Password: 291876

Presentation 1. 11:05AM - 11:17AM

THE USE OF SEM COMPOSITE IMAGES OBTAINED FROM STRUCTURES OF ADULT ZEBRAFISH OPTIC TECTUM MAINTAINED IN ORGANOTYPIC CULTURE TO STUDY CELLULAR DISTRIBUTION. Bimbo-Szuhai, Andras; Peguero, Ricardo; Roach, Kevin; Fulop, Zoltan & Corbo, Christopher. Wagner College.

Presentation 2. 11:18AM - 11:30AM

Genomic Study of GABA Receptor Ligand Binding Sites of the Bivalve Mollusc *Crassostrea virginica. (*Foster, Tia; Phoenix, Tamia; Hinkley, Craig; Carroll, Margaret, A. & Catapane, Edward, J). Medgar Evers College.

Presentation 3. 11:31AM - 11:43AM

The Regulation of GABARAP and LC3 During Autophagy. Kanaan, Omar; Gill, Karanvir; Motan, Nihal; Ozkaya, Kudret & Carroll, Reed. New Jersey City University.

Presentation 4. 11:44AM - 11:56AM

The Effect of Intergroup Interaction on Flexible Thinking and Behavioral Displays. Anderson, Kayla; Briones, Nadia; Matamoros, Rosa; Perez, Vanessa & Kostel-Hughes, Faith. Westchester Community College.

Presentation 5. 11:57AM - 12:09PM

Alterations in Glial Morphology in the Chronic Pain Hippocampus. (Amrami, Michael; Tajerian, Maral; Betancourt, John-Michael & Tajerian, Maral). Macaulay Honors College at CUNY Queens College.

Presentation 6. 12:10PM - 12:22PM

Changes in Metabolic Factors in Alzheimer's Disease. (Joseph, Patricia & Poon, Kinning). SUNY College at Old Westbury.

Presentation 7. 12:23PM - 12:35PM

The effect of adenosine kinase on neurogenesis and neuronal survival after traumatic brain injury. (Campbell, Andrea; Gebril M, Hoda; Fedele, Denise; Boison, Detlev & Short, Timothy). Queens College, City University of New York.

PNC ROOM 2

Moderator: Dr. Andrew Nguyen, QCC, CUNY
https://us02web.zoom.us/j/87900766379?pwd=VUsrSVkzSnhVL0dwNjUwcXg1NDliUT09
Meeting ID: 879 0076 6379
Meeting Password: 643721

Presentation 1. 11:05AM - 11:17AM

A potential drug target for treating Non-Alcoholic Fatty Liver Disease (NAFLD). McGowan, Natasha & Ghoshal, Sarbani. Queensborough Community College, CUNY.

Presentation 2. 11:18AM - 11:30AM

Molecular Plasticity of the Gonadotropin-releasing hormone-1 Neurons in the *Astatotilapia burtoni* Sassoon, Tsipora & Alvarado, Sebastian. Queens College, CUNY.

Presentation 3. 11:31AM - 11:43AM

Sexual dimorphism in microglial behavior and its effect on glioblastoma multiforme. Ahmed, Sameer; Mian, Mohammad & Nissen, Jillian. SUNY College at Old Westbury.

Presentation 4. 11:44AM - 11:56AM

Genomic Study of Dopamine Receptor Ligand Binding Sites of the Bivalve Mollusc *Crassostrea virginica.* Small, Shatema; Hinkley, Craig; Carroll, Margaret, A. & Catapane, Edward, J. Medgar Evers College.

Presentation 5. 11:57AM - 12:09PM

Role of Radixin, an ERM protein, in the control of endothelial barrier function. Mena-Khoury, Carol; Singh, Piarry & Mujica, Patricio E. Mercy College.

Presentation 6. 12:10PM - 12:22PM

Investigating Effects of GABARAP and Induced Autophagy on GABA Receptor ɣ2 Expression in HEK 293 Cells. Motan, Nihal; Ozkaya, Kudret; Gill, Karanvir; Kanaan Omar & Carroll, Reed. New Jersey City University.

Presentation 7. 12:23PM - 12:35PM

Role Of Extra Cellular Matrix In Brain Plasticity In Context Of Pain Chronification. Maghsoudi, Amirabbas & Tejerian, Maral. Queens College, CUNY.

PNC ROOM 3

Moderator: Dr. Urszula Golebiewska, QCC, CUNY
https://us02web.zoom.us/j/83197827467?pwd=ZE1EM0ZpUlcwRU40NmhEaGVxTlE2Zz09
Meeting ID: 831 9782 7467
Meeting Password: **666201**

Presentation 1. 11:05AM - 11:17AM

Astrocytic Volume Regulated Anion Channels: Potential Role in Enhancing Neuronal Glutathione Levels. Garana, Anne; Francois, Roodley; Matamoros, Melissa; Santiago, Andrea & Haskew-Layton, Renee. Mercy College

Presentation 2. 11:18AM - 11:30AM

Identifying potential SSRI treatments to cancer proliferation. Ihejirika, Patrick; Galvin, Cooper & Drigot, Zoe CUNY Brooklyn College.

Presentation 3. 11:31AM - 11:43AM

Microvascular Plasticity in the Pain Brain. Bouda, Abdoul & Tajerian, Maral. Queens College, CUNY.

Presentation 4. 11:44AM - 11:56AM

Involvement of the endosomal recycling system in the control of endothelial barrier function. Singh, Piarry; Mena-Khoury, Carol & Mujica, Patricio E. Mercy College.

Presentation 5. 11:57AM - 12:09PM

Inositol Hexakisphosphate Kinase1 (IP6K1) is a Potential Target in Treating Insulin Resistance. Piechowska, Sabina; Wanderley, Mayra & Ghoshal, Sarbani. Queensborough Community College, CUNY.

Presentation 6. 12:10PM - 12:22PM

Genomic Study of Histamine Receptor Ligand Binding Sites of the Bivalve Mollusc *Crassostrea virginica* Mansfield, Kera[1]; Wallach, Rosanne[1]; Catapane, Edward, J[1]; Hinkley, Craig[2]; & Carroll, Margaret A[1]. [1]Medgar Evers College, [2]Kingsborough Community College.

Presentation 7. 12:23PM - 12:35PM

Acorn Barnacles (*Semibalanus balanoides*) Density on Horseshoe Crabs (*Limulus polyphemus*) Carapace in Correlation with Carapace Condition in Jamaica Bay, New York. Jean Baptiste, Shiva; Colon, Christina & Hsiang, Chih Fu. Kingsborough Community College.

Student Presentation Abstracts (in alphabetical order by name)

Ahmed, Sameer; Mian, Mohammad
Sexual dimorphism in microglial behavior and its effect on glioblastoma multiforme
SUNY College at Old Westbury
PNC Room 2

Glioblastoma multiforme (GBM) is the most common and most aggressive primary tumor of the brain, and is associated with one of the worst 5-year survival rates among all human cancers. Extensive analysis of patient data has shown a sex-based disparity in GBM, reporting that males are 1.5 to 3.5 times more likely to develop brain tumors than females, and subsequently have more extensive tumor necrosis and reduced survival compared to females. Contributing to progression of this disease are the resident immune cells of the brain and spinal cord known as microglia; while inflammatory microglia function in an anti-tumorigenic manner, gliomas can disrupt this by releasing factors that polarize microglia to an immunosuppressive phenotype, which in turn secrete cytokines that support tumor growth and spread. Therefore, a shift in microglial populations towards more pro- or anti-inflammatory behavior could greatly impact GBM progression. We hypothesized that the sexual dimorphism seen in GBM could be explained by differential responses of male- and female-derived microglia, in that male cells would potentially respond in a more anti-inflammatory manner than female microglia. To investigate this hypothesis, we obtained two microglial cell lines – N9 cells, which are of male origin, and BV2 cells, which are of female origin. These cell lines were investigated for their ability to release pro- and anti-inflammatory cytokines in response to lipopolysaccharide and interleukin-4 stimulation. We noted a differential expression pattern of cytokines between these cell lines, and thus wanted to further observe the effects of these cells on the growth and proliferation of GL261 glioblastoma cells. As the sex-linked steroid hormone estrogen is more prevalent in females, we hypothesized that estrogen may play a role in promoting a pro-inflammatory shift in microglial populations, as well as function in a suppressive manner towards glioblastoma cells. Interestingly, we found that estrogen polarizes N9 microglia to an anti-inflammatory phenotype, but suppresses GBM migration. In conclusion, N9 microglia showed a more anti-inflammatory, pro-tumorigenic phenotype than BV2 microglia, yet estrogen surprisingly acts in an immunosuppressive manner. These data indicate that the worse outcomes seen with GBM in males could in part be due to sexually dimorphic microglial function outside of hormonal effects.

Alli Muizzat, Sbateen Nuha, Abbakass Malika, and Dr. Meriem Bendaoud
Antimicrobial and Antibiofilm Activity of N-Acetyl-L- Cysteine and
L-Histidine on different Strains of Pathogenic Bacteria and Fungi
New Jersey City University
MBI Room 1

Over the years biofilm formation has become one of the leading causes of infections in hospitals due to their resistance to antibiotic treatments as well as the immune system. There has been dire need for new compounds that possess antimicrobial properties that not only inhibit the growth of biofilm but also potentially kill pathogens. As a result, many scientists have turned to natural compounds as a possible solution to the ongoing concern. In this research, our goal was to determine antimicrobial and antibiofilm activity of two amino acids, N-acetylcysteine, and L-histidine, on pathogenic bacteria and fungi. To achieve this goal, we tested the antibiofilm and antimicrobial effect of the two amino acids against 14 different strains

of bacteria and 3 strains of fungi using a biofilm and broth assay. Results showed that N-acetylcysteine had a strong bactericidal effect against all the tested pathogenic bacteria at 8mg/ml. N-acetylcysteine was also capable of biofilm inhibition in some bacteria. L-histidine demonstrated minor inhibition of biofilm formation activity against Staphylococcus aureus and Escherichia coli, and no bactericidal activity against all tested pathogens. Future studies will focus on studying the cytotoxic effects of the amino acids on human cells.

Amrami, Michael; Tajerian, Maral; Betancourt, John-Michael
Alterations in Glial Morphology in the Chronic Pain Hippocampus
Macaulay Honors College at CUNY Queens College
PNC Room 1

Worldwide, chronic pain (CP) affects over 1.5 billion people. Pain is an existing problem that is difficult to treat because we don't quite yet understand what causes it. One way pain becomes chronic is if the brain changes post-injury. Evidence has emphasized the role of the hippocampus as central to the experience of pain itself and to CP's associated comorbidities such as memory impairment, psychiatric mood alterations, and cognitive deficiencies.
Research in animal models has demonstrated that following CP conditions, there are cellular changes in the hippocampus. While most research regards neuroinflammation simply in terms of the number of activated glia, our laboratory strives to understand chronic pain by analyzing hippocampal glial cell morphology and arborization, giving insight into the complexity of glial processes beyond the mere quantification of cells. We hypothesize that peripheral injury results in neuroinflammation and morphological changes in astrocytes and glia in the chronic pain hippocampus.
Our laboratory used both the spared nerve injury (SNI) and tibia fracture model of CP. At three time points (3-week, 7-week, 20-week) post-injury, mice were tested for memory function (Y maze, social memory) and nociceptive indices (von Frey mechanical allodynia). Immunohistochemical (IHC) analysis was performed following the behavioral tests to measure glial presence (Iba1 and GFAP). Glial morphology and arborization were analyzed through Sholl analysis using Neuron J and Image J.
Sholl analysis of microglia revealed a reduction in glial processes and in increase in glial cell length post-injury, which are indicative of increases in glial complexity. Further analysis of glial complexity in terms of arborization and pruning will be conducted to reveal whether the morphology of the injured brain can provide insight into the pruning of neurons by glia in control versus injured conditions.
By looking at glia more closely, we may develop a better understanding of neuroinflammatory processes. In the future, we aspire to link these morphological changes to functional changes in glia, with the prospect of finding novel therapeutic treatments for the chronic pain patient.

Anderson, Kayla; Briones, Nadia; Matamoros, Rosa; Perez, Vanessa
The Effect of Intergroup Interaction on Flexible Thinking and Behavioral Displays
Westchester Community College
PNC Room 1

Interaction within and between communities is an inevitable and important part of daily life. Previous research has surfaced a causal relationship between interracial interactions and a temporary depletion of executive functioning, namely, inhibitory control. Understanding the mechanisms involved in this phenomenon can shed light on how societal infrastructures and policies can be better informed and prepared to mitigate and account for these effects. One important translation of that intent into scientific practice is to extend the lens of past work to include study on the branch of executive functioning known as flexible thinking. It is also vital in reaching a wholistic conclusion to further the existing studies on the

mechanism of anxiety on this phenomenon, to see what other behavioral displays can provide new insights into this matter. With this foundation, the question becomes: What is the effect of interracial interaction on flexible thinking and behavioral displays. This will be examined using the traditional model of recorded interactions between the participants and a confederate of either the same minority status as them, or a different minority status in which they will be asked to answer questions both from racially charged topics as well as neutral ones. These interactions will ultimately be coded for specific quantitative behavioral display markers such as interaction length in seconds, number of pauses, perceived stress level, number of body movements, and number of smiles. The interaction will be followed by the participants performing the Wisconsin Sorting Task (a known measure of flexible thinking.) Which will then be followed by a demographic survey, a debriefing, and finally, the participants will be compensated for their time. The results of this study were that some behavioral displays did show a statistically significant difference between groups, namely the interaction length for both racially charged and neutral topics, as well as body movements. The Flexible Thinking data was not statistically significant, though did show an interesting trend, particularly in percent error, which demonstrates a similar finding as that of past research on this topic. While these results leaves us curious, it points toward an abundance of potential research that if done under more traditional circumstances, such as in person rather than over Zoom, show promise for some worthwhile discoveries. The intention to explore this phenomenon is fundamental in advancing our scientific awareness of this human response to interaction with those we perceive as different. Understanding this can lead to supporting much needed reform in our educational policies, our healthcare system, our legal system, and so much more.

Angie Jaramillo and Dr. Devdutta Deb
Understanding How Oomycete Plant Pathogens Interfere With The Immunity Of Host Plant Arabidopsis thaliana Using Bioinformatic And Virtual Tools
Mercy College
MBI Room 1

Plants lack an adaptive immune system and instead rely on an innate immune system that allows them to defend themselves against microbial pathogens. Some of these pathogens include bacteria, viruses, fungi, oomycetes and nematodes. Pathogens are either very host specific or can affect a wide arrange of plants. These pathogens enter through wounds, natural openings, vectors, stylets or mechanical pressures. Once in the host, pathogens then use molecular strategies to cause disease to the plant and begin colonization. Our research focus is on oomycetes as a plant pathogen. Oomycetes use sophisticated molecular strategies called effector proteins to sabotage the defenses of their hosts. These proteins often manipulate signaling pathways in the plant in order to cause disease. Various plant hormones such as salicylic acid, jasmonic acid and ethylene trigger these signaling pathways and are the target of pathogen effectors. These pathways induce several immune responses in the host plant such as those inhibiting pathogen proliferation (PAMP-triggered Immunity or PTI) and those recognizing the effector right away (Effector-triggered immunity or ETI). Each year, agronomically important crops such as maize, wheat, rice and potatoes are lost due to pathogen attack, which not only cost the agricultural industry billions, but plays an effect on world hunger. Throughout this research, I used the Brugmansia to model how infection would arise in Arabidopsis thaliana to study plant-microbial interactions. The aim is to understand and possibly figure out how to avoid pathogen infection due to the action of effector proteins. Phytophthora sojae is an oomycete that causes stem and root rot of soybean. In this research, we aim to show that effectors from P. sojae act as suppressors of defense gene pathways in plants such as Arabidopsis. Using bioinformatics information, a virtual simulation and in-planta experiments, we have reached a better understanding of how effectors target the innate immunity that plants harbor.

Annon, Oshane; Nunez, Xiomara; Wydner, Katherine
Effects of anthropogenic noise on the vocal behavior of Song Sparrows (Melospiza melodia)
Saint Peter's University
DBG Room 1

Widespread anthropogenic noise acts as a sensory pollutant that presents a significant impediment to effective communication between birds. Noise from sources such as roadway traffic, airplanes, construction equipment, and landscaping equipment interrupts the flow of information between a sender and receiver while presenting both survival and fitness consequences. A songbird's vocalizations (songs, calls) are essential for purposes such as courtship, the establishment of territories, warning others of predators, and maintaining contact between family members. Previous studies have presented evidence that birds in noisy environments alter the frequency (pitch) of their songs and calls to rise above the generally lower pitch of man made noise sources. The goal of this study was to investigate whether songbirds changed their vocal behaviour in environments with high levels of anthropogenic noise. Song Sparrow (Melospiza melodia) recordings were made at three sites with varying levels of background noise: two sites, a suburban and rural site, in East Brunswick (Middlesex County), New Jersey and one site, an urban site, in Jersey City (Hudson County), NJ. Between June 8, 2020 and July 2, 2020, songs were recorded in .wav format using a Marantz Professional PMD-661 MKIII Handheld Solid-State Recorder with a sampling rate of 48 kHz and a Sennheiser MKE 600 Shotgun Microphone. A Tenma 72-945 digital sound level meter was used to measure real-time background noise at the locations where recordings were made. Bioacoustic measurements were made using Raven Pro 1.6 acoustic analysis software. Preliminary results suggest that Song Sparrows (Melospiza melodia) increased the minimum frequency of their songs and also sang shorter songs in areas that had higher levels of background anthropogenic noise. The soundscapes at many locations during the study period were altered due to widespread reductions in both human activity and noise due to mandated COVID-19 shutdowns. Next steps in this study include analysis and comparison of songbird vocalizations as soundscapes revert to more typical levels of varying anthropogenic noise.

Arias, Audrey; Clarke, Izabella; Asif, Kainat; Hill, Stella; Subramaniam, Raji; Schneider, Patricia
Microbial Contamination on Used Disposable Face Masks
Queensborough Community College
MBI Room 1

COVID-19 is spread primarily by respiratory droplets discharged into the air by coughing, sneezing or talking. In the spring of 2020, governments around the world recommended or mandated that the general public wear face masks as a barrier to droplet transmission. It has been known for some time that surgical masks are a potential source of bacterial shedding in hospitals. Recently, news media reported the detection of bacterial pathogens on six masks worn by elementary school children in Florida. Evidence indicates that bacteria on the external surface of a mask are likely from the wearer. Disposable face masks are frequently reused increasing the chance for contact transmission between hands and mask. This pilot study focused on isolating and characterizing bacteria and fungi on disposable face masks and assessing the relationship between mask reuse and contamination. Twenty-three used disposable masks were donated anonymously. The three-ply, non-woven, polypropylene masks were placed in sterile containers of Lauria broth for 20 minutes. The spread plate procedure was used to assess microbial contamination. Bacteria were cultivated on Lauria broth agar plates incubated at 37oC for 48 hours to estimate bacteria levels (cfu/ml/piece). Isolated bacteria were Gram stained and selected colonies were identified with 16S rRNA gene sequence analysis. All six isolates are potentially pathogenic including Staphylococcus aureus and five Enterobacteriaceae: Phytobacteria, Klebsiella pneumonia, Salmonella Thompson, Klebsiella

oxytoca, and Pluralibacter geroviae. Lauria broth from several masks was inoculated on 3M yeast fungi (YF) Petrifilm and incubated at room temperature for 5 days for fungal counts (cfu/ml/piece). Preliminary results indicate that mask reuse increases contamination. Future work will include 16S rRNA identification of the remaining bacterial isolates as well as processing of additional face masks. Establishing a direct link between reuse and contamination could lead to educational campaigns designed to increase hand-mouth cleanliness and decrease the reuse of disposable masks.

Barrois, Elizabeth; Krieger, Inna (Dr.); Mosior, John (Dr.)
Fragment-based drug design in optimization of potent enzyme inhibitor of PptT from Mycobacterium tuberculosis
Texas A&M University (research institution); Spring Hill College (home institution)
BBB Room 3

The prevalence of drug resistant tuberculosis is becoming a global health concern as tuberculosis is one of the leading causes of death from infectious disease worldwide. Developing new drugs is essential in preventing the spread of drug resistant tuberculosis strains. The Sacchettini lab recently identified 8918, a molecule that inhibits phosphopantetheinyl transferase (PptT), an enzyme essential to the lipid biosynthesis in Mycobacterium tuberculosis (Mtb). Use of 8918 to inhibit PptT led to Mtb cell death proving that PptT is a strong drug target; however, toxicity associated with 8918 makes it undesirable for further drug development. Recent screening identified a potent enzyme inhibitor of PptT, which unfortunately lacked whole cell activity. Crystal structure of PptT in complex with this inhibitor indicated the complete displacement of co-purified with PptT substrate CoA out of the active site, so it was chosen as a starting point for a fragment-based approach. We screened a fragment library of 880 compounds through nano-DSF and identified 26 molecules that increased the Tm by 3°C or higher, and 16 hits that decreased Tm by 3°C or lower. The top Tm shifting molecules are going through a co-crystallization with PptT process to obtain binding details information. Fragment binding information will be used to optimize our inhibitor for better cell permeability and to design new PptT inhibitors which may lead to developing a new effective drug treatment for tuberculosis.

Bhattacharya, Mira; Ghoshal, Sarbani
Back to Basics- Revisiting concepts for Sterile Techniques, Streaking & Serial Dilution
CUNY QCC
BBB Room 2

In biotechnology and molecular biology, different model organisms are used for experimental purposes. The most common of these model organisms is Escherichia coli (E.coli), as it is non-pathogenic, has a short generation time, its genome is well understood and can easily be manipulated for cloning and transformation purposes. While working with E.coli or other microorganisms, contamination may become a big problem and can ruin long hours of work. Thus, it is extremely important to master sterile techniques and learn correct procedures that will aid in designing further experiments with bacteria. In this presentation, we aim to review the details of sterile techniques commonly used in a biotechnology laboratory set-up. We also aim to discuss procedures and specific examples, about qualitative (streaking) and quantitative (serial dilution) methods for obtaining single bacterial colonies. For our presentation, we will focus on two bacteria- E.coli and Serratia marcescens (S marcescens) and present distinct illustrations about quadrant method of streaking, common problems that first-time college students make during such a laboratory procedure. Furthermore, we will present specific quantitation examples to demonstrate serial dilutions using stock

cultures of E.coli and S. marcescens grown overnight. Overall, the presentation will revisit important concepts and techniques about handling microorganisms commonly used in biotechnology.

Bilewu, Fathia
Aligned Crystal Growth of C60, n-type Organic Semiconductor
New Jersey City University
BBB Room 2

Semiconductors are available in hardware, for example, PDAs, tablets, PCs, and watches, and so forth Furthermore, most semiconductor gadgets use silicon as semiconductors and metal electrodes. These gadgets show extraordinary execution however need lightweight, adaptability, and straightforwardness, which are vital variables for cutting-edge hardware. Natural semiconductors, then again, show this load of properties and are considered appropriate materials for adaptable and transparent electronic devices. Organic semiconductors, on the other hand, exhibit all these properties and considered suitable materials for flexible and transparent electronic devices. Pristine C60 and its derivatives have been used for solar cells, superconductors, ferromagnets, photoelectric switches, magnetic tunnel transistors, field-effect transistors (FETs). As a high-performance organic semiconductor, C60 exhibited one of the highest electron mobilities among n- channel materials for FETs. C60 single-crystals have been widely grown from vapor or solution C60 has been known as an outstanding electronic material, composed of 60 fully conjugated p-electrons within each molecule . Compared to vapor growth, solution methods provide a platform to easily control the crystal growth of C60. For example, by simply changing the concentration of the solvents, the shapes of the crystals were varied from irregular, needles and clumped . The crystal shapes were shown to be associated with the structure and concentration of the solvents used. We, therefore, focused more on a solution growth method and controlled the growth parameters in terms of crystal alignment, shape, and dimensions to accommodate obtain single-crystals of C60. This research comprises of l growing C60 crystals using silicon a substrate. Single-crystals of C60 were grown using the vapor technique and hot plate technique was used to transfer small layer silicon wafer onto large silicon wafer (300um). Using both an electron microscope and optical microscope, C60 crystals were observed for length, size and density. Measured data shows that our best crystals had length of 10um. Obtained results show that we successfully grew crystals in different conditions , which give promise to using C60 as an organic semiconductor. We describe many processing methods such as Bis(trimethylsilyl)amine (HMDS) , Physical Vapor Deposition System (PVD) and Hotplate to grow different sizes arrays of aligned C60 single crystals. Our aligned C60 single-crystal needles and ribbons show(10um). By performing various experiments under different conditions to see what would work the best, we were able to successfully grow crystals of different sizes, different density with different directions. This experiments involved the use of hotplate and our results show that 500C has more closely aligned crystals than any other temperature and at 30 degrees, the result was less crystals . Using the HMDS method, 30 degrees was not very favorable because there were residue left but at 50 0C, there is a significant change as the crystals did not leave as much residue and are more aligned and lastly, using the (PVD)Physical Vapor Deposition System might not necessarily be a great solution to growing bigger crystals because as the temperature got higher, crystals were evaporating. We hope in the future to use this data to better get perfectly aligned C60 Crystals.

Bimbo-Szuhai, Andras; Peguero, Ricardo; Roach, Kevin; Fulop, Zoltan; Corbo, Christopher

THE USE OF SEM COMPOSITE IMAGES OBTAINED FROM STRUCTURES OF ADULT ZEBRAFISH OPTIC TECTUM MAINTAINED IN ORGANOTYPIC CULTURE TO STUDY CELLULAR DISTRIBUTION
Wagner College
PNC Room 1

In this study light microscopic study analysis of adult zebrafish optic tectum maintained in organotypic culture revealed that reactivated cells (potential stem cells) are able to form embryonic neural tube-like structures amongst spongiform, degenerating brain tissue. Furthermore, I kept optic explants in organotypic culture conditions for up to seven days. Tissue chunks from 24, 48, 96 hours, and seven days were fixed as-is and processed for scanning electron microscopic analysis. Structures were viewed at relatively low magnifying power at each surviving time, and about 10-20 individual images were captured and later stitched together to create a composite image (montage) in Adobe Photoshop. Cellular features such as size, surface appearance, surface protrusions, location, and grouping were analyzed. Interesting areas were further imaged under higher magnifying power. This composite image analysis allowed the authors to see three-dimensional, spatial relationships between surviving and damaged/dying cells. Based on the actual sizes of recognizable structures, formation of blood vessels, cellular aggregates, granulated cells, and surface membranes such as pia mater could be detected.

Boodhan Nicholas; Ofosu-Mensah Jason Jeithy
Effects of Diminazene Aceturate on Human Cervical Cancer Cells
Lehman College, CUNY, Bronx Community College
MBI Room 1

Cervical cancer is a type of cancer that affects the region of the women’s reproductive system called the cervix. This cancer attacks two different cells the glandular cells and the squamous epithelial cells but starts as Cervical intraepithelial neoplasia by healthy cervical cells going onto dysplasia. According to the American Cancer Society, the five-year survival of this neoplasm is 92%, 58%, and 17% for localized, regional, and distant disease. To improve the prognosis of this cancer, one line of study is to identify novel compounds with strong anti-cancer effects. Here, we studied the effects of diminazene aceturate (DIZE) on HeLa cells, a human cervical carcinoma cell line, after treatment for 48 hours. The cytotoxic assays we used include acridine orange-ethidium bromide (AO-EtBr) live-dead staining, casp3-7-specificstaining, and JC-10staining for detecting changes in mitochondrial membrane potential. Cell count of images from AO-EtBr assay revealed a greater percentage of dead cells associated with 100 uM DIZE (37.8% ±3.03%) compared to DMSO (Dimethyl Sulfoxide, solvent used to dissolve DIZE) -- (9.1% ±0.91%) ($p<<0.05$). In the AO-EtBr assay, AO which is membrane-permeable, stains live cells green, and EtBr which is membrane-permeable stains dead cells red (EtBr+). A similar counting procedure was carried for cells stained with a caspase3/7-specific dye, (Cell Event caspase3/7 green reagent). Caspase signaling consists of a series of enzymes that are involved in programmed cell death. In this assay, the cell count of images revealed a greater percentage of cells that stained green (indicating caspase 3/7 activation) with the dye at treatment with 100 uM DIZE (40.94% ± 1.05%) as compared to DMSO-- (6.67% ± 4.13%) ($p<<0.05$). We also study the effect of DIZE on mitochondrial membrane potential using the cationic dye, JC-10. The mitochondrion is a cellular organelle that is important for capturing energy from nutrients. A double-membrane structure, the mitochondria is a charged organelle (charge difference between the inside and outside of the mitochondrial membrane). Disruption of this charge can lead to cell death. With the JC-10 dye, the loss of mitochondrial membrane potential is followed by a red-to-green shift. Therefore, microscopically, live cells are stained with JC-10 dye contain red puncta or aggregates which are absent from or diminished in dead cells, which stain predominantly green with the dye. In our study, JC-10-stained cells treated with 100 uM DIZE predominantly green while those treated with DMSO stained orange to red. Our results suggest that

diminazene aceturate causes cytotoxicity via caspase activation and loss of mitochondrial membrane potential, in human cervical carcinoma.

Bouda, Abdoul; Tajerian, Maral
Microvascular Plasticity in the Pain Brain
Queens College
PNC Room 3

Chronic pain poses a heavy burden for the individual and society, comprising personal suffering, comorbid psychiatric symptoms, cognitive decline, and disability. Chronic pain is characterized by changes in nociception, affect, and cognition and is often resistant to classical treatment partly due to comorbid maladaptive plastic changes in the central nervous system (CNS). The mechanisms by which peripheral changes can influence CNS plasticity in the context of pain are not well understood. We hypothesize that peripheral injury is accompanied by blood-brain-barrier (BBB) compromise and microvascular changes in select brain regions, thereby resulting in pain chronification and the establishment of pain-related co-morbidities.
We will use the spared nerve injury (SNI) model of peripheral neuropathy to measure behavioral signs of nociception, anxiety, and cognitive decline. Evans Blue dye staining will be used to quantify BBB compromise, laser speckle imaging will be used to quantify cerebral blood flow, and microfil perfusion followed by micro-computed tomography will be used for the quantification of anatomical changes in brain microvasculature. Biochemical analysis will be conducted to measure the regional changes in vascular markers and tight junction proteins.
The proposed experiments will help identify the link between peripheral changes and CNS plasticity in the context of painful injuries. Our results will provide a mechanistic understanding of chronic pain as well open entirely novel therapeutic venues for the treatment of chronic pain.

Bradley-Ortiz, RJ; Laury, Alexandrya
"To determine how oomycete pathogens interfere with host plant defenses
Mercy College
MBI Room 3

The Food and Agriculture Organization of the United Nations estimates that between 20 and 40 percent of crop production is lost to pests worldwide each year. Plant diseases cost the global economy approximately $220 billion in crop loses annually. This blight on crops has led to a massive decrease in food supply allowing 800 million people to suffer from hunger and starvation. Pathogens and pests are the major cause of such crop losses and account for many issues that we see in plants. Bacteria, fungi, nematodes, and oomycetes are examples of different types of pathogens that lead to such high losses. These pathogens use sophisticated molecular strategies called effector proteins to sabotage the defenses of their host. Effectors from these pathogens are secreted into the interior of plant's cells, corrupting specific organelles such as the mitochondria, nucleus, cytoplasm, and even chloroplasts to suppress host defense and cause disease. In defense of this onslaught, plants preserve their health via their immunity response, which has been found to be a cascade of events and responses. The first phase is called Pathogen-Associated Molecular Pattern Triggered Immunity (PTI) where the plant triggers a primary immune response such as releasing reactive oxygen species to stop the pathogen. If the pathogen evades this phase, it can secrete its effectors leading to Effector Triggered Susceptibility (ETS) causing the plant to become compromised or diseased. The final phase is called Effector Triggered Immunity (ETI) where the effectors are recognized by plant resistance proteins (R Proteins) leading to cell

death in the affected area. Our research focuses on effectors and their effect on plant defenses. In order to understand how the pathogen effectors interact with host defense for the purpose of causing disease, we designed and executed an experiment that would allow us to test our theories. We hypothesized that effectors from oomycete plant pathogens would interfere with the expression of host defense genes that are important in plant defense hormonal pathways such as jasmonic acid and salicylic acid. We virtually tested this theory using a simulation-based software, Plant Simulation Laboratory where we identified genes that were most critical in the host. We then confirmed our virtual results through in planta experiments where we performed qRT-PCR to determine whether the effector proteins where able to suppress the host defense genes in pathogen-treated plants. Our results show that oomycete effectors Avh73 and RxL23 were unable to target the defense genes in question and did not suppress their expression. We are currently testing other host defense genes that may be the targets of these effectors in planta.

Brenner, Eric ; Perez, Sofia
The Developmental Plan of Inflorescence Circumnutation in Arabidopsis thaliana
Pace University
EBE Room 2

Circumnutation is the swiveling movement of plant appendages that is most pronounced in growing organs. Roots use circumnutation to burrow into the soil like a cork screw into a cork whereas trellising vine shoots circumnutate in order to find structural support. Currently, it is not known why shoots of non-twining plants circumnutate. One theory suggests that cyclical variation in the volume of pressure (potential) between the convex and concave areas of the bending zone in the stem is what causes circumnutation. These differences in water content are related to turgor and concentration of ions (Niinuma, K et al, 2005). Darwin produced the first seminal work on circumnutation in The Power of Movement of Plants (Darwin, Charles. 1880.) where he proposed the existence of an internal oscillator as the source of circumnutation. His work foretold the discovery of actual molecular oscillators involved in plant circadian rhythms (McClung, C Robertson. “The Plant Circadian Oscillator.” Biologyvol. 8,1 14. 12 Mar. 2019). As a first step towards understanding why circumnutation occurs in non-twining plant shoots a developmental profile of circumnutation is being analyzed in Arabidopsis thaliana inflorescences. The time lapse movement capture program Plant Tracer (planttracer.com) is being used to quantify the amplitude of nutation throughout the duration of inflorescent stem growth. Preliminary results indicate that there is a dramatic fold increase in circumnutation amplitude as the inflorescence elongates from the time emergence up to 5 cm in length. The purpose behind this dramatic increase in circumnutation amplitude is unknown.

Budhu, Eric; Bendeck Hincapie, Andrea; Liliah, Marisha; Ramos, Elizabeth; Schramm, Laura
Monitoring Water Quality Parameters in NYS Parks Using Neulog Sensors Post Covid-19
St. John's University
EBE Room 1

Regular, detailed monitoring of New York State Parks’ lakes post COVID-19 is of environmental concern. For multiple state and federal parks, COVID-19 restrictions caused researchers to miss fieldwork and sampling during spring and early summer, disrupting water, wildlife, and phenology studies. Our goal is to monitor the health of a sampling of NYS freshwater lakes on Long Island using sustainable methods to analyze water quality parameters. NYS parks selected for the study had an average increase of 31% in visitor attendance, comparing data available for 2019 and 2020. Weekly water samples were collected from NYS Belmont (40° 43’ 58.230” N, 73° 20’ 29.592” W) and Hempstead (40° 40’ 45.708” N, 73° 38’ 38.910”

W) Lake Parks using Neulog sensors monitoring conductivity, pH, temperature, and turbidity from June 9 through September 21, 2021. Data collected were analyzed using the non-parametric statistical Mann-Kendall (MK) procedure to determine monotonic trends. Interestingly, the MK trend analysis indicates conductivity is probably decreasing at Hempstead Lake Park (COV = 0.27, S = -14, CF = 94.6%). Also, the pH trend is probably decreasing at Hempstead Lake Park (COV = 0.11, S = -12, CF = 91.1%). We observed no trend or stable trends for temperature and turbidity at both Hempstead and Belmont Lake Parks. Together, these data suggest that Neulog sensors may be a reliable and sustainable means to monitor water quality parameters. However, additional monitoring is required to determine seasonal trends and at additional NYS parks.

Calvagna, Vincent
STUDY OF MIGRATION PATHS, MATING, AND ABUNDANCE ALONG THE HUDSON RIVER
St. Francis College
EBE Room 2

The Hudson River originates in the Adirondack Mountains and flows down the eastern half of New York State and ends in the Upper New York Bay. The river is home to a variety of aquatic life. Throughout the year there are seasonal distributions of animals, that either crossing the Hudson along their migration paths (birds) or use it as a conduit during an annual migration (fish). The Hudson River Almanac, hosted by the New York State Department of Environmental Conservation (NYDEC) is a project which documents noteworthy animal sightings along the Hudson throughout each year. We examined this almanac as a resource to uncover patterns of animal characteristics from August 2020 to January 2021. Migration routes, mating, and abundance were studied and then each trait charted on a map of the Hudson Valley.

Campbell, Andrea; Gebril M, Hoda; Fedele, Denise; Boison, Detlev
The effect of adenosine kinase on neurogenesis and neuronal survival after traumatic brain injury.
Queens College, City University of New York
PNC Room 1

Traumatic brain injury (TBI) is a significant public health concern that remains a leading cause of death, disability, and socioeconomic burden because there exist little to no therapeutic treatment. After a traumatic brain injury, the brain attempts self-repair through TBI-induced neurogenesis. However, the new neurons' capacity for recovery is restricted by changes in the microenvironment, such as reactive astrogliosis, which affect neuronal survival and axonal regeneration. Adenosine kinase (ADK), the critical adenosine-metabolizing enzyme, has been studied in several brain disorders, including epilepsy, schizophrenia, and stroke. Data from recent lab study reported an association between ADK expression levels and TBI-induced neurogenesis and cell proliferation in adult mice. Due to this data, we hypothesized that ADK inhibition promotes neuronal survival and differentiation after TBI. To address the underlying mechanistic links between ADK and TBI- induced neurogenesis, we used an in vitro model of a scratch-induced injury and immunocytochemistry. Neuronal cells derived from the cortices of wild-type embryos were cultured on coverslips and a scratch injury was induced four days after plating. Subsequent to the injury, each coverslip was treated with either media, the ADK inhibitor ITU, or vehicle (DMSO). Six days after the injury, the cells were stained with various markers to indicate cell death (TUNEL), neuronal growth (BDNF), neuron differentiation (MAP-2) and neuron activation (ERK1/2). Results indicate that ITU promoted cell survival after TBI. In addition, there was an increase in axon growth after the treatment with ITU. However, we observed that ITU-treated cells had fewer dendrites with shorter dendrite lengths, indicating a more

immature phenotype as compared to VEH-treated cells. In summary, these data suggest that inhibition of ADK may promote cell survival and growth in an in vitro model of TBI.

Caparelli, Alexander ; Chase, Owen ; Fiamoncini, Maura; McMenamin, Connor; Prince, Ivy
An Analysis of Multiple Factors on Stress in the United States
Bucknell University
CLI Room 1

Anxiety is an issue that has long beset the United States for decades. From economic productivity to familial life, the nature of worrying and stress over time has changed, and as discovered in the last three decades, has become less controversial in American culture. During this national reorientation with mental health, many questions in the medical field have emerged such as: when the onset of anxiety is likely to develop, the duration of these symptoms, and what specific stimuli and conditions are correlated with higher stress levels among the population. By utilizing Integrated Public Use Microdata Series (IPUMS) Health's database from 2000 to 2018 among 1,762,659 Americans, this two-fold observational study was able to break down anxiety indicators of Worry Frequency against the effects of one's age. The latter half of the study observes the compounded effects of the former's test with socioeconomic status, workloads, race, and gender. This presented several trends in how anxiety originates among the American population. In conjecturing that anxiety would increase as one ages, the regressionary analysis yielded results that indicate worry frequency on age alone is of a significant, positive relationship. Further studies provide greater clarity to the regression's explanatory power, where in regressing aforementioned control variables, there too, was a significant and positive relationship that also exposed the existence of omitted variable bias in the first iteration. From these results, this investigation finds that anxiety does tend to increase as one ages; however, these factors are variable across people and relative to the control variables considered. Moving forward, this study is useful in applications within America to target groups that are most vulnerable to anxiety. Following this, recommendations propose that states ought to expand treatment options, counseling, and education for the general public in the near future.

Cela, Sidorela; Ali, Manar
COVID-19 Epidemiology
Bergen Community College
MBI Room 2

Viruses are microscopic parasites that enter the body and infect the body by replicating. Covid-19 is a novel virus that attacks the respiratory system mainly but will also attack the circulatory system. Covid -19 is transmitted mainly through the air droplets. Asymptomatic carriers of the virus are particularly dangerous because they have the ability to spread the disease silently. Past studies have been focused on reviewing the emergence of pathogenic human coronavirus and public health strategies (De Wit et al., 2016), stay at home order (Murray, 2021), demographic, clinical, and epidemiologic characteristics (McGovern et al., 2021), epidemic trends from July 2020 to January 2021 (Zheng et al., 2021), and the relation between the percent of Black residents and COVID-19 cases and deaths (Cunningham at al., 2020). But none have completed the multivariate covariance analysis comparing the Social Regulations versus the effect on Social Choice by infection, morbidity, and mortality rates.
This study aims to fill this gap by comparing the infection and mortality rates of COVID-19 in all states (county-by-county and day-by-day) based on the density, public transport, social restrictions, politics, and population using online New York Times data and mobility data in COVID-19 Community Mobility Reports

by Google .The results will show the highest and lowest points of the virus, as well as the variables that might account for why the virus spread so fast in some states and more slowly in other states.

Chitadze, Mariami
WHY ARE MARINE VIRUSES IMPORTANT
St. Francis College
EBE Room 1

The discovery of novel viruses and new mechanisms underlying virus distribution and diversity exemplify the fascinating world of marine viruses - which orchestrate life in the ocean. The past decades' research has revealed viruses as key players in the marine ecosystem, from driving bacterial and algal mortality and evolution at the nanoscale, to influencing global-scale biogeochemical cycles and ocean productivity. The large number of unknown viral populations in the marine metagenome emphasizes the need for further isolation, characterization and sequencing of specific marine viruses. By using and comparing the Sample Inventory and the Conventional Extraction methods scientists have developed some new insights and understandings of marine viruses. Another method that further enriches our knowledge of viruses is a Targeted Viromics approach. The oceans greatly shape Earth's climate, hold 1.37 billion km3 of seawater, produce half of the oxygen in the atmosphere, and are integral to all known life. In a time where life in the oceans is under increasing threat (global warming, acidification, pollution, economic use), it is pressing to understand how viruses affect host population dynamics, biodiversity, biogeochemical cycling and ecosystem efficiency.

Collier, Mac
Connection between native plants, soil health, and soil biodiversity
Westchester Community College
EBE Room 2

To gather data on how native plant species interact with the ecosystem, four weeks were spent observing Penstemon digitalis plants in three different trial beds on the Westchester Community College campus. Of particular interest was the relationship between native plants and pollinators, and the relationship between native plants and soil health and soil biodiversity.
Native plants play an important role in the ecosystems in which they naturally occur. They coevolved alongside native insects and wildlife, and can be critical sources of food and habitat for these species. Compared to non-native plants, native plants are adapted to the soil and climate conditions of the region, requiring less fertilizer than non-natives and being linked to potential mitigation of soil erosion and conservation of plant-microbe-soil interactions.
The trial bed located in Westchester Community College's Native Plant Center would be expected to have more indicators of soil health than the two trial beds located elsewhere on campus, because the Native Plant Center's environment had the most plant diversity and the least disturbed soil.
To compare the indicators of soil health present in the three trial beds, several tests were performed in each trial bed. The presence of bacteria was measured through serial dilution of soil and plating onto an agar medium. The activity level of decomposers and detritivores in general, including bacteria, fungi, and certain animals was measured with a buried cotton test. The presence of insects and other arthropods was evaluated by using a Berlese-Tullgren funnel as well as setting pitfall insect traps, and comparing the number of organisms counted from each trial bed.
The results of these tests indicate that there is a greater amount of biotic soil factors in the Native Plant Center trial bed, compared to the other two trial beds on campus.

These results are currently preliminary, as future research could repeat these experiments to obtain a more representative sample size, and potentially obtain additional data on the correlation between soil health and the rate of plant growth. Further study of this topic is needed in order to build a greater understanding of how the use of native plant species could potentially improve soil health compared to non-native species.

Cui, Chang
Development inhibitors of Kinases via the synthesis of oxazepane compounds
Queens College
BBB Room 1

Kinases is an enzyme that adds phosphate groups to other molecules, such as sugars or proteins. They cause other molecules in the cell to become either active or inactive. Kinases play essential roles. Many human diseases are caused by mis-regulated kinases, which can be activated or over-expressed in human diseases such as cancer. FDA has approved small molecule kinase inhibitors as anti-cancer drugs. The research focuses on the development of kinases inhibitors via the synthesis of oxazepane compounds such as 9-methoxy-7-(o-tolyl)-2,3,4,5-tetrahydrobenzo[f][1,4]oxazepane.
The start reagent tert-butyl(2-hydroxyethyl)carbamate was reacted with methanesulfonyl chloride and triethylamine in dichloromethane at room temperature. This reaction converted alcohol group to methanesulfonate. This mesylation reaction provided good yield (90%). Then through SN2 reaction and reductive amination reaction successively, the primary amine was converted to secondary amine compound, which is 7-bromo-9-methoxy-2,3,4,5-tetrahydrobenzo[f][1,4]oxazepane. Based on this compound, the intermediate compound was be obtained via Suzuki coupling reaction. Varieties of analogs have been synthesized from this intermediate compound. We will test these analogs to determine whether they inhibit kinases.

Daye, Mylaisha
Analyzing the interaction between the oomycete effector protein, RxL23, and the plant defense gene, NPR-1
Mercy College
MBI Room 3

According to the USDA, approximately 40 to 50% of crops, including agronomically important crops such as corn, wheat, soybean, and cotton, are lost in the developing world due to plant disease, pests, or post-harvest losses. Plant pathogens such as bacteria, fungi, nematodes, and oomycetes infect these crops and cause crop losses in billions of dollars annually. Oomycetes such as Phytophthora infestans, P. sojae, and P. capsici, are the cause of diseases in several agronomically important crop plants such as potato, soybean, and tobacco. This loss results in the starvation of much of the world's population. We now know that oomycetes use sophisticated molecular strategies to cause diseases. They do so by secreting proteins called effectors into the interior of host cell. In this study, we studied the relationship between oomycete effectors and several defense proteins in the host plant. We specifically investigated the relationship between the host defense protein, NPR-1, and the oomycete effector protein, RxL23. NPR-1 is a defense gene found in several plants including the model host plant, Arabidopsis thaliana. It is a critical gene that promotes the onset of Systemic Acquired Resistance or SAR in plants. NPR1 is a positive regulator of salicylic acid, a hormone that is essential for plant resistance. On the other hand, RxL23 is an oomycete effector protein which belongs to the RxLR family of secreted effector proteins. To analyze their relationship, we first performed bioinformatic characterization of both the effector and defense gene using databases such as GenBank and UniProt. Then, using a plant simulation software called PlantSimLab, we replicated

the defense pathway of NPR-1 and performed virtual knockdown experiments of the genes included in this pathway. Our virtual experiments suggested that the knockdown of NPR-1 would result in the plant becoming diseased. Using this information, we predicted where the pathogen effector would target the defense pathway. To confirm our virtual results, we performed in-person experiments using qRT-PCR to determine the extent to which NPR-1 was expressed with or without pathogen infection. We concluded that the effector RxL23 was successful in inhibiting the expression of NPR-1 thereby successful in suppressing SAR in host plant.

De Jesus, Angela; Beuhler, Brendan; O'Brien, Erin; Vargas Dominguez, Maria; Washington, Jacqueline;
MuffinTheCat, Badulia, and DesireeRose Bacteriophages: Novel Members of the Tectiviridae Family
Nyack College
MBI Room 2

Students at Nyack College have isolated three new bacteriophages, MuffinTheCat, Badulia, and DesireeRose using Microbacterium testaceum as a host, which is an endophytic, gram positive Actinobacteria. The phages were sequenced, characterized and assigned to the cluster GE. These phages have an average genome size of 15,482bp and 54.9% GC content. Sequence analysis performed by Pittsburgh Bacteriophage Institute showed that the three phages had similarities to the Tectiviridae family. We hypothesized that by performing wet bench experiments and bioinformatic analysis, we could confirm these novel phages, MuffinTheCat, Badulia, and DesireeRose, belong to the Tectiviridae family. In order to verify the morphology of these phages, we obtained transmission electron microscope images and it was observed that the phages are tail-less and have a lipid-containing inner membrane some with a protruding nanotube, all characteristics of tectiviruses. Chloroform sensitivity assay was performed to test the effects on the phage virion stability and results showed the phages were sensitive to chloroform. Furthermore, by using bioinformatics programs such as Phamerator, HHpred, and NCBI BLAST, similarities and differences between the genome sequences from the other genera of the Tectiviridae family were found. We suggest that these phages are new members of the Tectiviridae family, however, they are sufficiently different from the other members to potentially form a novel genus.

DeMarco, Victoria; Sine, Laura; Hintelmann, Thomas; Sean Reardon; Hicks Martin
Anti-Covid MicroRNA Therapy Blocks the Expression of the Spike Gene of SARS-CoV-2
Monmouth University
CLI Room 1

Emerging viral diseases have increased in recent decades. In December 2019, an epidemic with low respiratory infections emerged in Wuhan, China. The disease, Covid-19 was found to be caused by a novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). As of October 14, 2021, WHO has confirmed greater than 239,000,000 global cases, nearly 5 million deaths worldwide, including greater than 720,000 in the USA. Fortunately, a vaccine has been approved and distributed, yet there are no approved therapeutics for infected individuals, and the threat of emerging vaccine-resistant strains remain. From advances in biotechnology, the genome and structure of SARS-CoV-2 is known. Three proteins are anchored in the viral envelope, Spike (S), Envelope (E), and Membrane (M), which is linked to the Nucleocapsid (N) protein connecting to the viral RNA genome. Our lab is developing an innovative therapy that delivers multiple therapeutic microRNAs to block the expression of distinct Covid viral proteins. The design of the anti-Covid microRNAs 1) mimics human microRNA cluster 17-92a structural stability, 2) forms guide-RNA substrates for the RNA induced silencing complex, and 3) are complementary to specific regions of the SARS-CoV-2 RNA genome without off-targets effects in the human genome. Twenty-one microRNA sequences were designed to target the S gene, six for N, two for M, and one for E. These were cloned into our microRNA-17-92 therapy vector which expresses six distinct anti-Covid RNA therapeutics

simultaneously. We have transfected the S gene into our tissue culture model to measure the efficacy of the anti-Covid microRNA therapy to down-regulate the S gene expression. In our preliminary experiments we show a significant 2.5-fold reduction in the relative abundance of the Spike mRNA in the treated cells ($p < 0.05$). We are currently testing additional therapies and verifying changes in spike protein levels. Next steps are to examine the secondary structure of our RNA therapy using SHAPE-MAP to optimize RNA therapeutic stability in comparison to the stable structure based on the human gene, microRNA Cluster 17-92a.

Dontaye Daniels; Angela Noel; Monica Bustamante; Daniel Moloney PHD
The Impact of Curcumin on H460 cells
Dontaye M Daniels
BBB Room 1

The objective of this research project is to explore the effects of curcumin on H460 lung cancer cells. In countries where the spice turmeric is a household staple and is regularly consumed in the diet, people have lower instances of colon, breast, and lung cancer. Previous studies have shown that curcumin, a component of turmeric, inhibits the proliferation and survival of many types of tumor cells. Curcumin may inhibit tumor growth by regulation of multiple signal pathways including cell proliferation (cyclin D1, c-myc), cell survival (Bcl-2, Bcl-xL, cFLIP, XIAP, c-IAP1), apoptosis activation (caspase-3, 8, 9), tumor suppressor (p53, p21) death receptor (DR4, DR5), and protein kinase pathways (JNK, Akt, and AMPK). Cell microscopy, cell proliferation assays, and a fluorescent apoptosis assay were used to measure Curcumin's effectiveness on H460 cells. We found that curcumin inhibits cell proliferation and induces apoptosis with a 50% inhibitory concentration (IC50) value of 7.5 mM. Curcumin's ability to selectively kill tumor cells and not normal cells makes it appealing as a preventive agent or anticancer therapy.

El Houzaly, Sara ; Gupta, Richa
The Effects of Climate Change on Fatal Human Diseases
LaGuardia Community College
MBI Room 1

The impact of climate change is being felt worldwide: global temperature is rising, snow covers are decreasing, glaciers are retreating, ice sheets are shrinking, sea levels are rising, extreme weather events are more frequent, and oceans are warming and acidifying. Humanity is facing a big environmental challenge which not only impacts our habitat and life of all other organisms on our planet but will also have ramifications on our health. In our research study, we have conducted a detailed examination of the scientific evidence proving the relationship between climate change and various fatal human diseases. Our findings indicate that variations in climatic conditions, such as temperature, rainfall patterns, and humidity, can increase the incidence of respiratory infectious disease- tuberculosis, and alter the incidence of waterborne diseases, especially diarrheal diseases. Also, an increase in the longevity of mosquitos and the development of malaria parasite, and consequently, transmission of malaria has been noted. Climate change could alter the dispersion of primary pollutants and secondary pollutants such as ozone gas. These pollutant gases have been linked to increased incidence of congestive heart failure and acute myocardial infarction. Furthermore, the incidence of allergic diseases and asthma are also likely to increase with climate change. From our studies, we conclude that identifying emerging disease risks is crucial to assess our vulnerability, and to determine specific areas where public health efforts are required.

Florentino, Gilda
EFFECTOR PROTEINS DISRUPT PLANT IMMUNITY BY TARGETING CRITICAL PLANT DEFENSE GENES
Mercy College
MBI Room 3

Diseased crops have impacted many lives worldwide. For example, it has brought great limitations on food supply and economic deficits to the agricultural industry. To help our cause, we must increase our knowledge on plant pathogens; and the molecular strategies they use to cause disease in plants. These invaders are known for causing infection in plant host cells by increasing susceptibility. The most common infectious organisms known to cause disease in plants include fungi, oomycetes, bacteria, viruses, viroid, phytoplasmas, protozoa, nematodes, and parasitic plants. Although, plants have evolved an inmate immune system that enables them to recognize these invaders and their molecular patterns through the use of membrane receptors (PRRs and PAMPs)pathogens continue to evolve their mechanisms. This initial recognition, results in a PTI (pattern-triggered immunity) response. Which provides a broad level of basic disease resistance against a variety of microbes. To counteract the negative effects of PTI, pathogens have developed effector molecules, these are proteins which are delivered to the host apoplast or into host cells to effectively suppress immunity and cause infection. In turn, plants have developed a second type of intracellular receptors in the form of pathogen resistance proteins. These PR proteins can then trigger an ETI(effector-triggered immunity) response in the presence of an effector protein; allowing for the plant to fully recover or self- distrust. This response is accomplished by the use of ROS, or through the biosynthesis of plant hormones, such as ET (ethylene) and JA (jasmonic acid). Effector proteins are known to suppress plant host immunity through targeting defense pathways and their critical genes, such as pathogenesis and antimicrobial related proteins. The main objective is to identify a critical gene known to activate ETI response in plants, and to conclude where in the signaling cascade might the effector protein target the host to increase susceptibility. This hypothesis was tested through the plant simulation software (PlantSimLab), which allowed for the re-construction and modeling of specific defense pathways(ET/JA pathway) found in plants such as (Arabidopsis thaliana). In addition, several knockout experiments were tested to model and identify those critical genes in the defense pathways.The results indicate that effector proteins can in fact disrupt and suppress plant immunity by targeting critical defense genes involved in the ETI response, such as PDF1.2 (DEFENSIN).

Foster, Tia; Phoenix, Tamia; Hinkley, Craig; Carroll, Margaret, A.; Catapane, Edward, J.
Genomic Study of GABA Receptor Ligand Binding Sites of the Bivalve Mollusc Crassostrea virginica
Medgar Evers College
PNC Room 1

GABA (γ-aminobutyric acid) an inhibitory neurotransmitter in molluscs and other animals has not been well studied in bivalves. In humans, impairment of GABA neurotransmission can cause epilepsy. In the bivalve mollusc Crassostrea virginica, as well as other bivalves, serotonin is an excitatory neurotransmitter that increases beating rates of gill lateral cell cilia. Previously our lab demonstrated in C. virginica serotonin's increase of cilia beating rates is blocked by applying GABA to the visceral or cerebral ganglia. Additionally, bicuculline methchloride, a GABAa receptor antagonist, blocked the effects of GABA. By using HPLC we previously detected GABA in low ng amounts in cerebral and visceral ganglia of C. virginica. Our immunofluorescence studies showed the presence of GABA neurons in cerebral and visceral ganglia; and that some serotonin neurons had GABA receptors on their soma. Recently the genome of C. virginica and other bivalves has begun to be mapped. By conducting BLAST searches of the NCBI (National Center for Biotechnology Information) database using DNA and protein sequences of C. virginica and other

invertebrate and mammalian species we found matches for GABAa and GABAb receptor genes on C. virginica chromosomes 3 and 5, respectively. Various invertebrates had Percent Identity above 60%, while humans and mice had Percent Identity of about 40% to 50% for GABAa and GABAb. We hypothesize that the ligand binding sites (LBS) for GABAa and GABAb receptors in C. virginica are evolutionarily conserved and will closely match those of other animals. To study this, we conducted searches of the NCBI database for GABAa and GABAb LBS of C. virginica and compared them to other animals. We found GABAb LBS contained 4 amino acids (N, L, A, Y) in positions 34, 122, 123, 267 that were highly conserved in LBS of other bivalves, gastropods, insects, mice, rats and humans. GABAa LBS for C. virginica has not yet been identified. We did find LBS of other animals contained 2 amino acids (L, Y) that were highly conserved among the animals in which it has been identified. The C. virginica GABAa receptor does contain L and Y amino acids. The study complements our earlier physiology and cell biology studies demonstrating the presence and a function for GABA in C. virginica and shows the genome of C. virginica contains genes to produce GABA receptor LBS that are similar to those of other animals. This new information is valuable as it shows the simple nervous system of C. virginica can be used to conduct studies on GABA neurotransmission. This work was supported in part by grant 2R25GM06003 of the Bridge Program of NIGMS, NIH grant K12GM093854 07A1 IRACDA Program of Rutgers University and PSC CUNY grants 62344 00 50 and 63434 00 51.

Gao Suncheng; Nacimba Jordan
The Effects of Sulforaphane on non-small Lung Cancer Cells
Queensborough community college and Stony brook university
BBB Room 3

Non-Small Cell Lung Cancer (NSCLC) is the most common type of Lung cancer found in 80-85% of the cases. The Environmental Risk Factors for NSCLC are: smoking, secondhand smoke, the consumption of occupational carcinogens, e.g., asbestos and radon, and malnutrition, such as the lack of vitamin C. Genetics and Epigenetics alterations also lead to NSCLC through mutations that activate the Oncogene RAS and inactivates the Tumor Suppressor Gene (TSG) P53. These changes affect the cell cycle, causing the cells to proliferate and avoid apoptosis leading them to form malignant tumors. The current treatment is surgical removal, and many tumors resist radiation therapy and chemotherapy treatment. The objective of this study is to investigate the effectiveness of an alternative treatment for Large Cell Carcinoma (LCC) {a subtype of NSCLC} on H460 lung cancer cells using Sulforaphane (SFN) extract as the treatment compound. SFN, found at high level in broccoli seeds and sprouts, has been recently studied as a novel anticancer compound. We hypothesized that SFN will inhibit the proliferation of H460 cells via reducing RAS signaling and increasing P53 activity. We examined the effectiveness of SFN on H460 cells through Cell Proliferation Assays, Trypan Blue staining, Fluorescence Apoptosis Assays, and Western Blot analysis for the determination of expression levels of P53. Our results indicate that SFN induces cell cycle arrest and apoptosis through the re-activation of the P53 gene and the inactivation of the RAS gene.

Garana, Anne; Francois, Roodley; Matamoros, Melissa; Santiago, Andrea
Astrocytic Volume Regulated Anion Channels: Potential Role in Enhancing Neuronal Glutathione Levels
Mercy College
PNC Room 3

Glutathione plays an important role in protecting the brain from oxidative stress, a major factor contributing to cell death in neurodegenerative diseases such as Alzheimer and Parkinson disease. Astrocytes are integral in facilitating glutathione production in neurons. The volume regulated anion channel (VRAC) represents a potential mechanism by which astrocytes release glutathione and its precursor molecule glutamate; however, VRAC's role in coupling astrocyte-neuron glutathione synthesis is unknown. We hypothesize that VRAC activation in astrocytes leads to increased glutathione production in neighboring neurons. To address this hypothesis, primary neural cells (astrocytes and neurons) were cultured from chick embryonic brain tissue. Astrocytes were swollen with hypoosmotic media to activate VRACs and astrocyte conditioned media was transferred to neurons, followed by neuronal measurements of glutathione through an enzymatic assay. While preliminary results do not show an increase in neuronal glutathione in response to hypoosmotic astrocyte-conditioned media treatment, our data suggests that the hypoosmotic conditioned media itself may contribute to glutathione loss in neurons through the VRAC channel pore (negating any potential increases in glutathione production in response to an astrocytic mechanism). Experiments are hence underway to determine if isosmotic conditioned media from VRAC-activated astrocytes contributes to neuronal glutathione production. Understanding the precise mechanism by which astrocytes increase neuronal glutathione production will aid in the development of neurotherapeutics aimed at combating oxidative stress.

George, Sophia; Perez, Kestrel
The Impact Rapid Temperature Change Has on the Swimming Ability of Larval Sheepshead minnow (Cyprinodon variegatus)
St. Joseph's College New York (Brooklyn Campus)
EBE Room 1

Global climate change affects the world's oceans having potential impacts on oceanic current patterns, average water temperature and variation in water temperature. Larval stages of fish populations are critical to study because mortality in the early life is typically extremely high, and they may be vulnerable to temperature changes and variation. The purpose of this experiment is to study the swimming ability, growth, and mortality of larval sheepshead minnow (Cyprinodon variegatus) under rapid temperature changes. Three treatments were created: warm/cold, which started at 28℃ for 6 days then decreased to 21℃, cold/warm which started at 22℃ for 6 days then increased to an average of 24℃, and variable which started at 22℃ for 4 days, increased to an average of 27℃ for 2 days, decreased to 22℃ for 3 days, then increased to an average of 26℃ for 3 days. Utilizing a video camera, frame by frame footage was tracked to calculate various measures of larval sheepshead minnow swimming including average velocity, maximum speed, and distance traveled. Fish maintained in the warm/cold treatment swam fastest, on average 90 mm/s compared to fish under the cold/warm treatment which swam 48 mm/s on average and variable which swam 54 mm/s on average. The data obtained from the warm/cold treatment suggests statistical significance in regards to average velocity, however, more trials with a larger sample size would need to be conducted. There were no statistically significant differences found between the initial length and final length of fish across all treatment groups although other swim differences existed. Ecologists can use this data to better understand fish populations in aquatic communities with rapid, unstable temperature changes. Since swimming ability may impact how effectively larval fish can escape predators and find food, this data can be used to further study population variability of different fish populations in the wild.

Gill, Harman; Patel, Radha; Chu, Tinchun
The Antimicrobial Properties of Curcumin and Green Tea Formulation on B. subtilis and E. coli

Seton Hall University
MBI Room 1

Curcumin, derived from the plants of the Curcuma longa species, more popularly known as turmeric. Prior studies reported that curcumin possesses antimicrobial, anti-inflammatory, antioxidant, and antiparasitic activities. F2, a formulation containing patented lipid-soluble green tea polyphenols, was also included in this study to test its antimicrobial effect. The bacteria used in this study were Escherichia coli (E. coli) and Bacillus subtilis (B. subtilis). E. coli, a Gram-negative bacterium, can cause various bacterial infections including urinary tract infections (UTIs), pneumonia, and cholecystitis. B. subtilis, a Gram-positive pathogen, is known to cause pneumonia, endocarditis, and bacteremia. This study aims to evaluate the antimicrobial effect of curcumin, F2, and the combination of both compounds against B. subtilis and E. coli with various assays including microplate, colony-forming unit (CFU), and disk diffusion assays. The growth analysis results indicated that the minimum inhibitory concentrations (MICs) for curcumin and F2 on B. subtilis and E. coli are 100 µg/mL and 10%, respectively. The CFU data showed growth inhibition ranging from 42.86% to 95.29% against B. subtilis and 87.17% to 99.93% against E. coli after treating with curcumin. As for F2, the CFU data showed inhibition ranging from 68.97% to 98.28% against B. subtilis and 98.22% to 99.88% against E. coli after treatment. A time-course (1, 5, 10, and 30-min) and study was carried out to determine the antibacterial efficacy of F2. The results indicated that F2 can reach 2.32 and 2.53 log reduction in E. coli and B. subtilis, respectively, suggesting that the lipid-soluble green tea polyphenol-containing formation could be a natural alternative bactericidal agent.

Goddard, Rayna; Lemus, Jenifer; Connal, Nicole; Salazar, Kevin; Riccardi, Krystal; Jackson, Dr. Allyson
The Effect of Urbanization on Avian Diversity at Purchase College, SUNY
Westchester Community College
EBE Room 2

Urbanization is an ever growing problem as the conversion of natural habitats into urban areas. A negative impact includes loss of biodiversity. We want to determine how urbanization and the human disturbances affect native bird diversity on Purchase College campus (Westchester County, NY). We used trail cameras on 10 areas on Purchase campus. This allowed us to be able to see disturbances such as human activities and motorized (cars/trucks/lawn maintenance) from early May to mid June 2021. These cameras were set up on developed land, grasslands, and forested areas on campus. For calculating avian diversity, we performed point counts in the 10 areas, in a 50 meter radius. The natural habitat data was collected by the use of ArcGIS, a software that allowed us to determine the percentage of land type in a 75 meter buffer for each location. The point count data allowed us to calculate Shannon diversity for native and non-native birds. Our results showed that there was more bird diversity in the natural areas on campus. Also, the data indicated that disturbances did not have any effect on bird diversity. Based on our data, avian diversity seemed to be more affected by habitats, rather than disturbances. This shows that to conserve birds, we should focus on protecting natural habitats.

Gonzalez, Karla; Fitzgerald, PhD
Microplastic Abundance in Lake Hopatcong
New Jersey City University
EBE Room 1

Lake Hopatcong is one of the largest freshwater bodies of water in New Jersey and it once provided freshwater from southern New Jersey to Northern New Jersey (Smith, 2015). Due to the increase in plastic production in recent years this lake, like many others, is subject to plastic pollution. While there have been studies about plastic pollution in the ocean there is not much known about plastic pollution in lakes. To date, no microplastic survey has been completed at Lake Hopatcong. The purpose of this study was to provide a primary survey of the quantity and type of microplastic in Lake Hopatcong to visualize which areas are most affected due to higher microplastic count. To conduct this study a Manta Trawl net was used to capture microplastics at 11 different sites for 10 minutes. After preserving the samples, they were analyzed in the lab to determine what type of microplastics were found and where they were most abundant. It was hypothesized that the southern end of the lake would have more microplastics due to there being a dam where the lake empties out from. From the study it was concluded that the eastern edge of the lake had the highest amount of microplastics, and the southern edge had the second highest amount. This suggests that the microplastics are not flowing throughout the lake evenly and that they are getting trapped around the edge of the lake instead of flowing out of the lake.

Gromova, Valeria; Benoit Marcus
An Algorithm To Predict A Cancerous Cell With High Accuracy With Population Imbalanced Dataset
Hofstra University
CLI Room 1

With the diagnosis and early detection of breast cancer the 5-year survival rate of many patients increases. One method of detection of breast cancer is to extract cells from suspicious lump in the patient's breast using Fine Needle Aspiration (FNA) technique, and to look at characteristic of individual cells or cell nuclei. This method is not as invasive as the standard biopsy that requires a surgery. A small dataset is publicly available with 30 features of sample cells (malignant and benign). Early data analyses of such data showed mixed results, depending on examiners' skills. Among studies with the dataset, most of them ignored proper error analysis for the small statistics of the data as well as a bias due to imbalanced mixture of the data of malignant and benign cells (212 vs. 357 samples, respectively). We explore the use of modern machine learning (ML) to diagnose whether given cells are malignant or benign without human intervention. For this study we chose one of ML algorithms called Support Vector Machine (SVM) to demonstrate the power of ML methods with proper error estimate on some metrics to evaluate effectiveness of the algorithm and of the FNA technique to diagnose breast cancer. To evaluate the metrics and their errors for performance, we adapted nested-cross-validation method that is appropriate for analysis of small data samples in this type of study. Our emphasis is on the effect of population/class imbalance in the dataset. In our previous work done in 2020, we studied the effects of the population imbalance both in the training and the test dataset at the same time. In this study, we keep the population ratio constant in the training dataset, while changing the population ratio in the test dataset. This is more relevant in practice, as in reality the practitioners want to use the fixed training dataset to train their algorithm together with new test datasets collected by them without the category information (malignant vs. benign) and the population ratio. With SVM we find that over a wide range of the population imbalance it can achieve the sensitivity of 93% with 0.6 % of an uncertainty to correctly identify malignant cells, while only 2.0% with an uncertainty of 1.5% of benign cells were mis-identified as malignant. The practitioners can choose a better sensitivity value with a slight increase in the probability of mis-identification of the benign cells. We also find some biases imposed by imbalanced data and will present the result.

Haliru, Konyinsola.
Synthesis of a Macrocyclic Analog of Pentamidine

New Jersey City University
BBB Room 3

Pentamidine is a water soluble diamidine that has been used for over eighty years. It is a potentially toxic antiprotozoal and antifungal drug known to treat African trypanosomiasis (African Sleeping Sickness). Pentamidine works by inhibiting DNA synthesis with RNA polymerase activity. It does this by entering the protozoal cell and binding to DNA. The goal of this research was to make analogs of pentamidine that would have a greater biological effect, better oral bioavailability and be less toxic by locking the acylic structure of pentamidine into a macrocycle using the Grubbs Reaction. An advanced intermediate in the synthesis of a 15-membered ring analog has been prepared.

Hanesworth, Isabella; Dalia, Abdelhamid; Barahona, Carla; Drammeh, Aisatou; Gonzalez, Elizabeth; Marquez, Felipe; Rahman, Elena; Stevens, Bryan C.; Torres, Edith R.; Zhou, Chun
Identification of Telomere Regulating Genes in Drosophila melanogaster
Mercy College
DBG Room 1

Telomeres are the natural end of chromosomes and work to maintain chromosome stability. Telomerase functions to extend telomere length in eukaryotic species. In comparison, the telomeres of Drosophila melanogaster are composed of and extended by non-LTR retrotransposons including HeT-A, TART, and TAHRE. Previous research identified two mutations, called Tel and E(tc), that are capable of regulating telomere length in fruit flies. Both mutations are located within a short region on the third chromosome. For this study, we set out to identify additional telomere-length regulating genes from the same region on the third chromosome. We hypothesized that the genes capable of regulating telomere length may function in modulating chromosome structure, like a previously identified telomere-regulating gene Su(var)2-5. We used bioinformatics to identify candidate genes in the above-mentioned chromosome region that are predicted to remodel chromosome structures. After the identification process, we extracted genomic DNA from fruit flies with mutated versions of the candidate genes. Using real-time PCR, we compared telomere length between the fly mutants and the wild-type controls. We have found a new gene called CG6026 whose mutation can result in elongated telomeres. To investigate whether the mutation of CG6026 also affects the telomere structure, we are performing polytene chromosome staining and analyzing telomere fusion. This research will further our understanding of the molecular regulatory mechanisms of telomere elongation and structure in fruit flies. Because of the importance of alternative telomere lengthening in cancer development, this study of unraveling non-telomerase mechanisms may also contribute to human cancer research.

Hauter, Lamia; Bhuiyan, Ashif I; Reghuvaran Santha, Asha; Musayev, Rafael; Sweeney, Chloe; Dickson, Anna; Talele, Tanaji; Pathak, Sanjai.
Development of drug- like inhibitors of Nek2 kinase using Nek2 overexpression fly model
Queens College
BBB Room 3

Human Never in Mitosis Kinase 2 (Nek2) is a serine/threonine protein kinase and a core component of the human centrosome. Nek2 is known for its critical role in regulating centrosome disjunction through phosphorylation of C-NAP-1 and beta-catenin. It plays an integral role in promoting spindle checkpoint assembly and mediating mitotic events. Aberrant activity of Nek2 kinase has been associated with highly invasive behavior of metastatic tumors, and drug resistance. Novel inhibitory agents of Nek2 kinase are

thus urgently needed for development of targeted anti-cancer therapeutics. Currently, no clinical agent targeting Nek2 kinase has been developed yet. Using a fly model in Drosophila melanogaster, we have shown that the overexpression of Nek2 kinase can promote activation of Akt/PI3K pathway and cancer metastasis. We also identified a novel non-toxic quinoline-based pharmacophore from inhibitory EGFR candidate library that inhibited Nek2 function in-vivo and reduced metastasis. The present work describes the development of a dual-action inhibitor library using the quinoline-based pharmacophore that inhibits Nek2 kinase as well as EGFR kinase potently. We anticipated that that developed inhibitory molecules will possess desirable anti-cancer activities in several triple negative breast cancer cell lines where the expressions of both Nek2 and EGFR kinase are abnormally high.

Hill, Stella
GFP protein Expression
Queensborough Community College
BBB Room 3

Biological science's quest has always been to understand the existence of life and to gain a deep understanding of the relationship between living organisms and how they interact both within and outside of themselves. GFP protein expression is an experiment that can help to better understand how character traits are developed from DNA encoded genes. In this experiment, the GFP gene or DNA particle in the form of plasmid is taken from Jellyfish (Aequorea victoria). This plasmid containing GFP gene and other characteristics are then inserted into bacteria cells. The cells are allowed to grow and then observed for the specific traits of interest, in this case; resistance to antibiotic ampicillin and the ability to glow under UV light. Plasmids are extrachromosomal circular DNA molecules. They have their own origin of replication and carry genes independent of the chromosomal DNA. The pGLO plasmid is designed to carry the gene for GFP protein and the BLA gene. The plasmid consists of Ori where replication begins and ensures that the plasmid is replicated in each daughter cell. It also has a BLA gene which is responsible for the antibiotic resistance by producing beta lactamase that neutralizes a group of antibiotics to which ampicillin belong. There is the AraC gene which controls or regulates the arabinose operon. The arabinose operon in not active unless there is a presence of arabinose sugar therefore arabinose serves as the inducer for the arabinose operon. It is modified to express the GFP protein in the presence pf arabinose. The GFP gene is downstream of the AraC gene. It codes for the green fluorescent protein. Its expression depends on the activation of the AraC gene.
The experiment is used to illustrate the central dogma of biology from DNA to protein expression in observable traits. There are many important uses for this experiment. It is useful in understanding gene regulation mechanisms. It can also be useful in medicine to understand how bacteria resistance can occur, gene therapy for treating diseased genes. In agriculture useful and desirable traits can be introduced into plants and animals.

Hintelmann, Thomas; Sine, Laura; Demarco, Victoria; Garwagi, Flobater
GENE THERAPY FOR BRAIN TUMORS: IDENTIFICATION OF NEW THERAPEUTIC TARGETS BASED ON RNA STRUCTURE
Monmouth University
DBG Room 1

Individuals diagnosed with glioblastoma multiforme (GBM) have a short life expectancy of 12-15 months. This project is to develop therapies for effective and continuous drug delivery to the brain, targeting cancer-driving genes. Tumor cell proliferation in GBM is often stimulated by epidermal growth factor receptor (EGFR) and is important for tumor cell survival. In our lab, we are developing RNA therapies to alter the splicing mechanism of EGFR to block its activation, thus stop tumor cell growth. Our approach uses an adeno-associated virus gene transfer vector encoding RNA therapeutics targeting critical elements of the EGFR pre-mRNA transcript. In this project, we cloned therapies into our therapeutic delivery platform and tested their efficacy to alter EGFR gene expression in tissue culture cells. Currently, we are evaluating in vitro, the therapeutic RNA interaction with the target sequence of the EGFR pre-mRNA transcript. We have found that our therapies have led to a shift in Intron 10A retention increasing alternative intronic polyadenylation generating a short soluble therapeutic decoy. Our antisense therapy targeted the 5' Splice Site of exon 10 of the EGFR pre-mRNA transcript, downstream region of intron 10 of EGFR with a G-quadruplex tail, with a 4GQ tail, the wild type 5'Splice site with no tail, and the Exonic Splicing Enhancer (ESE) with a 4GQ tail in comparison to no treatment with no therapies. The retention for 10A retention for the downstream region of intron 10 with a 4GQ tail was 61.9 ($p < 0.002$). The retention for the Wild Type 5'Splice site with a 4GQ tail, had a shift of 15.9 ($p < 0.001$). The retention for the Wild Type 5'Splice site with no tail was 10.4 ($p < 0.002$). The retention for the Exonic Splicing Enhancer (ESE) was 5.9 ($p < 0.04$).

Hintelmann, Thomas; Sine, Laura; DeMarco, Victoria; Sean Reardon; Hicks Martin
RNA Therapeutics for Brain Tumors: Targeting Pre-mRNA Splicing Motifs to Generate Therapeutic Gene Isoforms
Monmouth University
DBG Room 1

Individuals diagnosed with glioblastoma multiforme (GBM) have a short life expectancy of 12-15 months. This project is to develop therapies for effective and continuous drug delivery to the brain, targeting cancer-driving genes. Tumor cell proliferation in GBM is often stimulated by epidermal growth factor receptor (EGFR) and is important for tumor cell survival. In our lab, we are developing RNA therapies to alter the splicing mechanism of EGFR to block its activation, thus stop tumor cell growth. Our approach uses an adeno-associated virus gene transfer vector encoding RNA therapeutics targeting critical elements of the EGFR pre-mRNA transcript. In this project, we cloned therapies into our therapeutic delivery platform and tested their efficacy to alter EGFR gene expression in tissue culture cells. We have found that our therapies have led to a shift in Intron 10A retention increasing alternative intronic polyadenylation generating a short soluble therapeutic decoy. Our antisense therapies targeted the EGFR pre-mRNA transcript, specifically, regions of exon 10 and intron 10. Therapies were either designed to enhance recognition of the alternative intronic polyadenylation signal or block recognition of canonical exon 10/exon 11 splicing. We targeted the Exonic Splicing Enhancer (ESE) wild-type 5' Splice Site (wt-5'SS) of exon 10, and the regions surrounding the alternative intronic polyadenylation signal. Each target showed a significant increase in intron retention. Targeting the ESE showed a 5-fold increase in intron retention ($p < 0.04$), the wt-5'SS was 15-fold ($p < 0.001$), and the region surrounding the alternative intronic polyadenylation signal showed the strongest effect, with greater than 60-fold increase in intron retention ($p < 0.002$). Currently, we are examining additional antisense therapies, as well as generation of the therapeutic soluble decoy protein using ELISA.

Ihejirika, Patrick; Galvin, Cooper;Drigot, Zoe
Identifying potential SSRI treatments to cancer proliferation
CUNY Brooklyn College
PNC Room 3

Major Depressive Disorder (MDD) and Cancer are some of the major ailments ravaging across many major modern societies. While there is ample research aimed at treating either MDD or Cancer, there is substantially less research aimed at treating both MDD and Cancer concurrently. This project aims to provide further insight in this vacancy of knowledge by displaying that there is evidence for antidepressant treatment, specifically Selective Serotonin Reuptake Inhibitors (SSRI) effectively decreasing cancer proliferation through targeting specific genes associated with both SSRIs, depression and cancer proliferation. This was accomplished by first identifying the genes targeted a number of SSRIs and which display an inverse association between expression in MDD and cancer proliferation, thus that the up-regulation of said gene's expression in MDD is associated with cancer cell growth and down-regulation of the gene's expression in MDD being associated with cancer cell death. The gene targeted by the SSRIs, depression and cancer proliferation was the SLC6A4 gene. Upon analysis of the SLC6A4 gene dependency on cell death and SSRI treatments (Fluvoxamine, Zimelidine & Paroxetine) on cell death, there was sufficient enough evidence towards the claims that the increased presence of the SSRI treatments; Fluvoxamine, Zimelidine & Paroxetine led to the death of the cancer-cell lines through knocking out the SLC614 gene. Further research on the impact of Fluvoxamine, Zimelidine & Paroxetine treatment on epithelial cells may be required to provide further evidence to the claim of SSRIs having the ability to treat cancers and MDD.

Javellana, Shaun
Queensborough Community College
DNA Fingerprinting "Detecting Alu Insertion"
BBB Room 2

DNA fingerprinting is a technique that can examine variations and unique patterns in DNA. The technique involves identifying similar variable number of tandem repeats (VNTR) between different DNA samples. VNTR are sequences of DNA that are repeated multiple times in our genome at particular loci. Forensic analysis of DNA fingerprints checks different loci on the human genome to find variations or similarities in the VNTR patterns and then help link DNA found at a crime scene to a possible suspect. VNTR are polymorphic meaning they have many forms and is therefore difficult to identify similar VNTR patterns between DNA samples in a classroom setting. In our experiment, we determine the presence or absence of the dimorphic alu element on chromosome #16 PV92 locus amongst 15 students. Alu elements are similar to VNTR and are considered "jumping genes" which are repetitive DNA elements that can inserted hundreds of times in the genome. The dimorphic alu element on chromosome #16 PV92 locus is 300 bp and can only be present or absent on this chromosome. To identify its presence/absence, we designed forward and reverse primers that would flank the alu element 400 bp away. In our experimental method, we the students extracted genomic DNA from their cheek cells, added the primer mix and then amplified the DNA by PCR. The PCR samples were then run on a gel by electrophoresis. 4 students were homozygous +/+ and had the alu element on both chromosomes. 9 students were homozygous -/- and did not have the alu element on the chromosomes. 1 student was heterozygous +/- and had the alu element on one chromosome but not both. These results can highlight whether particular students who possess or lack the alu element are related to each other. The different ethnic backgrounds of these students can also provide evidence that the alu element appears in different geographic locations around the world and in different populations. It can also represent evolutionary characteristics of alu elements.

Jean Baptiste, Shiva; Colon, Christina; Hsiang, Chih Fu

Acorn Barnacles (Semibalanus balanoides) Density on Horseshoe Crabs (Limulus polyphemus) Carapace in Correlation with Carapace Condition in Jamaica Bay, New York
Kingsborough Community College
PNC Room 3

Horseshoe crabs have been around for more than 455 million years ago. Data from two coastal study sites showed that several species of hitchhikers live on the shell of most American horseshoe crabs (Limulus polyphemus), which includes the acorn barnacles (Semibalanus balanoides). Once attached, the settlement of those sessile organisms as an adult is permanent. It has been reported that high levels of chlorophyll-a concentration contribute to the growth of barnacles. Therefore, it was hypothesized that the density of acorn barnacles on horseshoe crabs in Jamaica Bay will be higher than other epibionts, and barnacle density will correlate with chlorophyll-a levels. Data was collected through field of observations of epibionts on horseshoe crabs in Jamaica Bay, NY (2012-2019). Epibionts on horseshoe crabs were identified and recorded on Excel Spreadsheets. In 2021, due to COVID, a pilot study consisting of 100 photographs of horseshoe crabs was used to further understand the dominance and percent cover of each epibiont. This new methodology will allow new students to participate virtually using photographs taken in the field. Preliminary data reveal support the hypothesis that barnacles exhibit higher density on the carapace compared to Crepidula. In addition, the frequency of barnacles in correlation with chlorophyll-a levels was analyzed by using years of data ranging from 2012 to 2020. Future work is needed to further expand on the correlation of barnacles' density with chlorophyll-a levels.

Jimenez, Bianca
Does Flower Color Attract Native Bees
Mercy College
EBE Room 1

Populations of native bees are declining partially because of a reduction in the numbers of native plants we have left in our ecosystem. However, scientists, botanists, and horticulturists, are advocating for and encouraging individuals to plant native plants in their own yards. Many of these native plants are bright in color and attract a wide variety of pollinators; however, what the human sees is not identical to what our pollinators see. Bees can see from roughly 300-650 nm (wavelengths of light) which explains why bees cannot see red. Bees are trichromatic and make up colors from a combination of blue, green, and ultraviolet light. Recent studies have shown that bees prefer blue, violet, and purple flower color. In this study, I hypothesized that native bees would have a preference for the purple colored flowers on the Penstemon digitalis 'Pocahontas' plant instead of the white flowers on the Penstemon digitalis 'Straight' plant. To determine this, the Chicago Botanical Garden's Budburst protocol was used where bee visits were determined by counting the total number of bees that landed on flowers during a ten-minute period. Additionally, temperature, cloud cover, and phenology were recorded. Flower color wavelength was determined using a spectrophotometer. After three weeks of research, it was determined that native bees did have a preference for the purple flowers over the white flowers. However, honeybees had a preference for the white flowers instead of the purple flowers.

Joseph, Patricia
Changes in Metabolic Factors in Alzheimer's Disease
SUNY College at Old Westbury
PNC Room 1

Alzheimer's Disease is a brain disease characterized by a buildup of amyloid plaques and tau tangles in the brain that leads to inflammation, and the death of neuronal cells. The risk factors for this disease include age, family history, head trauma, poor sleep patterns, and obesity. Some of the common symptoms of Alzheimer's include memory loss, difficulty focusing, and behavioral changes. One of the primary risk factors for developing Alzheimer's disease is obesity, with later onset to induce hypophagia and weight loss. Although this major change in metabolism is highly prevalent in Alzheimer's disease patients, the metabolic factors involved in the progression of the disease are poorly understood. This research aims to explore changes in metabolic factors associated with Alzheimer's disease using the App^{NL-Gf} amyloid beta knock-in mouse model. Through blood assays and behavioral tests, cytokine and leptin levels, and memory tasks were measured in Alzheimer's disease model mice at 6 weeks (young) and 7 months (old) of age. While memory in the App^{NL-Gf} was similar to control mice at 6 weeks of age, the mice failed memory tasks by 7 months of age. In young App^{NL-Gf} mice, a significant increase was found in 46 cytokines in blood sera, such as LeptinR, ProMMP-9, Lselectin, CTACK, Shh-N, Resistin, and TNF alpha. This rise occurred prior to plaque formation and cognitive decline. By 7 months, during moderate to severe disease, the changes were no longer significant. Young mice also had a significant decrease in leptin, a hormone signaling satiety, that increased by 7 months of age. These results show that metabolic changes occur prior to the symptoms of Alzheimer's disease and may be involved in its onset. Further investigation will shed light on how these metabolic changes are involved with the progression of Alzheimer's disease.

Kanaan, Omar; Gill, Karanvir; Motan, Nihal; Ozkaya, Kudret, Carroll, PhD
The Regulation of GABARAP and LC3 During Autophagy
New Jersey City University
PNC Room 1

Autophagy is a process in which cells degrade their unneeded or dysfunctional organelles or other components. Membrane originating from ER surrounds the components to be recycled and form autophagosomes. Autophagosomes fuse with lysosomes forming autophagolysosomes where the digestive enzymes of the lysosome breakdown the contents. Autophagy occurs under stressful certain condition including starvation, but may play a role in overall cellular maintenance in neurons.Decreased autophagosome activity has been associated with neurological-diseases such as Alzheimer's disease.
Multiple proteins are associated with autophagy and formation of autophagosomes such as GABARAP and LC3 proteins. LC3 is recruited to the autophagosomal membrane and used as measure autophagy. GABARAP plays an important role in recruitment to form autophagosomes, although the relationship between the actions of LC3 and GABARAP are still being investigated.. In this project, the regulation of GABARAP during starvation induced autophagy in HEK cells is investigated in comparison to LC3 investigated on various time. Results indicate that In 2 hrs but not 1 hr of starvation caused an increase of LC3 clustering, suggesting induction of autophagy. Co-expression of GABARAP while not not affecting the clustering of LC3 in unstimulated, did reduce LC3cluster in stimulated cell such as starvation condition.

Karim Homsi, Daniella Alves, Angelo Cirinelli, Keith Lange, Carlos Molina Ph.D
The Potential use of Inducible cAMP Early Represser (ICER) peptides in anti-cancerous treatment
Montclair State University
BBB Room 3

Although chemotherapy, radiation, immunotherapy, and surgery can be effective cancer treatments, cancer research is always on a mission to find a more efficient, less expensive way to treat cancer. The use of peptides in cancer-related treatments is not as common as the treatments mentioned above, but is a very

promising cancer research field. Cell-penetrating peptides have the ability to deliver anti-cancer therapeutics to cancer cells. Inducible cAMP Early Repressor (ICER) is a transcription factor that is found in all eukaryotes. Deregulation of ICER protein is a common phenomena in many cancers, including skin cancer melanomas. ICER possesses tumor suppressing abilities. Overexpression of ICER blocks cells in mitosis, eliciting cell death and therefore, halting the tumorigenicity of cancer cells. Our data shows that ICER possesses cell penetrating peptide properties and is able to penetrate melanoma cells in culture. This cell-penetrating characteristic of ICER protein could potentially be used to eliminate tumor cells by apoptosis, setting the stage for the development of novel treatments for cancer.

Kobren A; Memon M; Tehrani K; Kim H; Hoque F; Basu, P
Characterization of Penicillin Tolerance in Group B Streptococcus
Touro College of Pharmacy
MBI Room 1

Group B Streptococcus is the number one cause of neonatal mortality due to infections such as pneumonia, bacteremia and meningitis, by passing from mother during birth. The preferred treatment for GBS is Penicillin G, however there can be treatment delay if the bacteria strain is penicillin tolerant. When a GBS strain is tolerant it can temporarily withstand, which means that the bacteria can regrow once again after the penicillin treatment. This experiment is conducted to determine a specific gene that is related to penicillin tolerance and create an assay to develop a primer that can be utilized during PCR testing.
The first trial is to confirm tolerance using a macrobroth dilution for penicillin killing and a regrowth tolerance assay. In a 96-well plate, susceptible strain, A909 and the tolerant strain, O90R will be incubated and grown overnight before it is treated with Penicillin G at different concentrations. The plate is again incubated overnight, and treated with Penase, an enzyme- based product that inactivates Penicillin G. After a third incubation period, the final results are measured on a spectrophotometer. For the second trial, Both strains were stained with SYTO9 and PI to measure its cell viability, membrane permeability and damage. The plate was incubated for 10 minutes in the dark, then SYTO9 and PI were excited at 444 nm laser, and were detected at 538 and 612nm.
After the penicillin treatment,there was a decrease of cells for the O90R strain, and the A909 strain. After the Penase U treatment, O90R cells increased for all penicillin concentration. For A909, there was no growth for the cells with high concentration of penicillin. For the cells with low concentration of penicillin, there was some growth. The A909 strain showed a tendency of declining SYTO9 concentration as penicillin G increased and after penase treatment. The O90R strain showed an increase of SYTO9 after penase treatment. So it was concluded that the O90R strain is tolerant strain, therefore it did not get lysed during the penicillin treatment and had regrown after the penicillin was deactivated. Whereas the A909 strain was lysed during the penicillin treatment and was unable to regrow when the penicillin was deactivated.

Luong, Victoria; Woo, Kevin; Biolsi, Kristy; Radhakrishnan, Preethi;
Directional Orientation of Harbor and Gray Seals at Swinburne Island in New York City
LaGuardia Community College
EBE Room 1

Safety at rest is important for preserving time to restore the demands of metabolic functioning. However, during these periods of rest, social species that gather collectively risk their safety and are subsequently vulnerable to threats, such as habitat encroachment and predation. It is imperative that social groups are consistently aware of their environmental surroundings. In this study, we investigated the directional orientation of harbor seals (Phoca vitulina) and grey seals (Halichoerus grypus), two marine mammal

species typically found hauled out during peak low tide on Swinburne Island, which is an urban location within New York City. We examined archival photographs that were taken at Swinburne Island between 2014-2019, and we measured the orientation direction of each seal. We also recorded whether neighboring individuals, adults and juveniles, and similar/dissimilar species orientated in the same or different direction. Individuals must be vigilant to their immediate surroundings and potentially rely on social information cues imparted to them by conspecifics.

Maghsoudi, Amirabbas
Role Of Extra Cellular Matrix In Brain Plasticity In Context Of Pain Chronification
CUNY-Queens College
PNC Room 2

Chronic pain is one of the major healthcare issues in the United States and worldwide. Despite its prevalence, to date, there are no satisfactory, mechanism-based treatments available to patients. One mechanism by which an acute painful injury becomes chronic is due to alterations in select brain areas, including the hippocampus. In particular, we have found neuronal cytoarchitectural changes, increased numbers of glial and astrocytic cells, as well as decreased rigidity in the extracellular matrix.
In our murine model of chronic neuropathic pain (spared nerve injury), we plan on investigating how changes in the biochemical and biophysical properties of the extracellular matrix can affect glial morphology and function in vitro. We will study morphological (soma size, cell size, and shape) and functional (phagocytosis, proliferation, and migration ability) changes in BV2 microglial cells grown on artificial matrices of differing rigidities as well as decellularized hippocampi from injured and control mice. Our future studies will include neuron-glia co-cultures to evaluate neuronal dendritic pruning by microglia grown on different matrices.
Understanding microglial modulation by the extracellular matrix can help us understand how pain-related brain plasticity may evolve and how extracellular effects may modulate microglial behavior vis-a-vis neurons. Such efforts are crucial in developing mechanism-based therapies for the millions of chronic pain sufferers worldwide.

Makedonska, Anna; Mosfique, Baizeed
Two lytic Citrobacter freundii bacteriophages isolated from sewage with potential for phage therapy
New York Institute of Technology
MBI Room 2

Antimicrobial resistance (AMR) is a growing global health threat that reduces the effectiveness of current treatments for microbial infections. Finding alternatives to antibiotics, therefore, remains an important public health challenge. Phage therapy uses viruses (bacteriophages) that infect bacteria to treat bacterial infections. Despite its promising application, much is yet unknown regarding the interactions between a phage, bacterium, and human host. To this end, we have isolated, purified, and studied two separate phages that infect the same bacteria, Citrobacter freundii. C. freundii is a commonly encountered microbe that typically causes treatable opportunistic infections. Recently, strains with AMR have proven more challenging to treat, making it a more dangerous pathogen, and hence a good target for phage therapy. The two phages were isolated from wastewater and are extremely lytic to bacteria. TEM shows that they are tailed phages from the myoviridae family. One phage is refractive to restriction enzyme digestion and with a greater capacity to infect other Citrobacter hosts. Genome sequences show both phages have large genomes of roughly 180 kb. We explore the reason for the inhibition of restriction enzyme digestion, and conduct a comparative genomic investigation with other closely related bacteriophages to determine their

suitability for phage therapy.

Malika Abakkass; Muizzat Alli; Nuha Sbateen; Dr. Meriem Bendaoud
Antimicrobial and Antibiofilm Activity of Natural Compounds Produced by Unknown Marine Bacteria or the Human Body
New Jersey City University
MBI Room 2

The identification of new antimicrobial and antibiofilm compounds is becoming a research priority around the world to solve the growing concern of antibiotic resistance. Biofilms form when microorganisms produce extracellular polymeric matrix that enable attachment and growth on various surfaces. The aim of this research was to find new antimicrobial or antibiofilm compounds naturally produced by marine bacteria or the human body to fight an increasing number of infectious diseases. The disc diffusion, biofilm, and broth assay were used to test unknown marine bacteria extracts against different pathogens. We also tested the antimicrobial properties of Taurine, Beta Alanine, and Taurocyamine (GES), which are compounds naturally produced by the human body. Results indicated that the bacterial extract from unknown 1 (U1) affected biofilm formation of strains of Staphylococcus aureus, Escherichia coli, and Staphylococcus epidermidis, while other unknown extracts showed a moderate inhibition zone against pathogenic bacteria. Taurine, Beta Alanine, and GES displayed a significant inhibition against gram-positive pathogenic bacteria and no significant effect against gram-negative bacteria. In future studies, the focus will be on identifying the active compound in the unknown bacterial extracts and to test Taurine, Beta Alanine, and GES against more pathogens using difference concentrations.

Mansfield, Kera1; Wallach, Rosanne1; Catapane, Edward, J1; Hinkley, Craig2; and Carroll, Margaret A1
Genomic Study of Histamine Receptor Ligand Binding Sites of the Bivalve Mollusc Crassostrea virginica
1Medgar Evers College, 2Kingsborough Community College
PNC Room 3

Histamine is a biogenic amine found in a wide variety of invertebrates. Histamine is particularly well studied in arthropods and gastropods where it is involved in local immune responses as well as regulating physiological functions in the gut. Histamine also functions as a neurotransmitter, especially for sensory systems. Previous physiology work of our lab found that histamine activates the sensory system of Crassostraea virginica, eliciting a motor response in the gill. Our earlier cell biology and immunofluorescence work also showed the presence of histamine receptors in ganglia and mantle of C. virginica. Recently the genome of C. virginica and other bivalves have begun to be mapped. By conducting BLAST searches of the NCBI (National Center for Biotechnology Information) database using DNA and protein sequences of C. virginica and other invertebrate and mammalian species we found matches for histamine receptor H1R genes on chromosome 8; H2R on chromosomes 1, 2, 5 and 10; and H3R on chromosome 3. BLASTS of other invertebrates and mammals found matches with very low Expect Values (E Values) and moderately high Percent Identity, signifying similarities of H1R, H2R and H3R of C. virginica to those of other bivalves, gastropods, insects, mice, rats and humans. We hypothesize that the ligand binding sites (LBS) for H1R, H2R and H3R receptors in C. virginica are evolutionarily conserved and will closely match those of other animals. To study this, we conducted searches of the NCBI database for H1R, H2R and H3R receptors LBS of C. virginica and compared them to other animals. We found the LBS for H2R in C. virginica was identified and match some other invertebrates well, but did not match humans of other mammals very well. The LBS for H3R matched some other bivalves, invertebrates as well as humans and other mammals well. The LBS for H1R in C. virginica and other invertebrates we looked at has not yet

been identified. The LBS for H1R in humans and other mammals is very highly conserved. This study complements our earlier physiology and cell biology studies demonstrating the presence and function for histamine in C. virginica, and shows that the genome of C. virginica contains genes to produce histamine receptor LBS that are similar to those of other animals where it has been identified. This new information is valuable as it shows that the simple nervous system of histamine can be used to expand studies on histamine neurotransmission. This work was supported in part by grant 2R25GM06003 of the Bridge Program of NIGMS, NIH grant K12GM093854-07A1 IRACDA Program of Rutgers University and PSC-CUNY grants 62344-00 50 and 63434-00 51.

Marcus Benoit;Valeria Gromova;Chiaki Yanagisawa
An Application of Artificial Intelligence to Diagnose Cancerous Cells
Borough of Manhattan Community College
CLI Room 1

The advent of artificial intelligence (AI) found many applications of different techniques to data science and other fields including finance, engineering, medicine, physics, chemistry, biology and so on. A subfield of AI called machine learning (ML) is the first go-to place to find powerful and yet easy to implement to make multi-variate analysis where the input data consist of many properties of each sample in the dataset of your interest. In this presentation the results of application of several well-established algorithms in ML to diagnose breast cancer using characteristics/features of suspicious cells. With the diagnosis and early detection of breast cancer the 5-year survival rate of many patients increases. One method of detection of breast cancer is to extract cells from suspicious lump in the patient's breast using Fine Needle Aspiration (FNA) technique, and to look at characteristic of individual cells or cell nuclei. This method is not as invasive as the standard biopsy that requires a surgery. A small dataset is publicly available with 30 features of sample cells (malignant and benign). Early data analyses of such data showed mixed results, depending on examiners' skills. Among studies with the dataset, most of them ignored proper error analysis for the small statistics of the data of malignant and benign cells (212 vs. 357 samples, respectively). A rapid progress has been made in the past decade in the field of ML together with a steady increase in computational power. Thus, time is ripe to apply ML algorithms to distinguish two classes of the cells, malignant vs. benign, without human intervention to maintain consistency and good accuracy of the method. For this study we explore several ML algorithms such as Random Forest, Adaboost, XGBoost, and Support Vector Machine (SVM) to demonstrate the power of ML methods with proper error estimate on some metrics to evaluate effectiveness of the algorithms and of the FNAtechnique to diagnose breast cancer. To evaluate the metrics and their errors for performance, we adapted nested-cross-validation method that is appropriate for analysis of small data samples in this type of study. Furthermore, to avoid some bias due to population imbalance, we compare the algorithms using a balanced population from the original dataset as well as the original dataset itself. Although we found some differences among the algorithms, most of algorithms perform well with the average probability of identifying malignant cells at 94.5% and the average probability of mis-identifying benign cells at 2.2%.

Marino, Amanda
Changes in Hypothalamic Neuronal Transcriptome by the Dietary Fatty Acids: Oleic and Palmitic Acid
SUNY Old Westbury
DBG Room 1

Prenatal exposure to a high fat diet results in the neurogenesis of orexigenic peptide neurons in the hypothalamus of the offspring. This increase in the number of peptide neurons leads to hyperphagic

behavior and predisposes offspring to obesity. However, the molecular mechanism in which a high fat diet affects neurogenesis is unknown. The primary composition of a high-fat diet consists of the monounsaturated fatty acid, oleic acid, and the saturated fatty acid, palmitic acid. This study examined the effects of palmitic and oleic acid on the hypothalamic neuronal transcriptome and on two processes of neurogenesis, proliferation, and migration. Immortalized embryonic day 18 hypothalamic neurons were treated with 1,10, and 100 μm of palmitic acid or oleic acid. The RNAseq results show significant gene enrichment in cellular pathways involved in proliferation, migration, and apoptosis. Further investigation shows that low concentrations of oleic acid stimulate proliferation while elevated levels of both fatty acids cause apoptosis. High concentration of oleic and palmitic acid was also shown to reduce hypothalamic neuronal migration. These results indicate a direct relationship between fatty acids and proliferation, migration, and pathways associated with neurogenesis.

Marnik, Arleta and Jahangir, ZMG Sarwar
A Novel Protocol for Producing COVID-19 RBD Protein Vaccine
Kingsborough Community College, The City University of New York
BBB Room 2

Background: Protein vaccines are antigens. They are highly efficient in developing antibodies by the cells of recipients following intramuscular administration quickly. We have developed a novel, unique and virtual protocol for the production of RBD of the SARS-CoV-2 S-protein. The SARS-CoV-2 RBD-protein directly stimulates antibody production against SARS-CoV-2. Hence, it is a safer, fast acting, and effective vaccine against SARS-CoV-2 and also efficient for immune compromised individuals.
Methods: We will reconstruct a plasmid carrying RBD, FP and sfGFP cDNA in sequence in an orf, transform Escherichia coli, C2566H, carrying T7 RNA polymerase gene. The transformed cells will express RBD-FP-sfGFP fusion protein developing green fluorescent cfu. The RBD-FP-sfGFP fusion protein will be isolated from the transformed E. coli, cfu. The RBD-protein will be separated from the sfGFP by digesting the FP with an enterokinase specific for the FP. The RBD will be eluted using HIC. The eluent RBD will be confirmed by immunoreaction using BioVision Elisa kit and quantified using a spectrophotometer at UV280nm.
Results: The plasmid reconstruct will be selected by ampr cfu. In addition, the plasmid will also carry the T7 promoter controlling the expression of RBD-FP-sfGFP fusion protein. The transformed Escherichia coli will efficiently express the RBD-FP-sfGFP fusion protein. The highly efficient sfGFP fused with RBD-FP will turn the transformed cfu green. The RBD will get separated from the sfGFP by the FP specific enterokinase. Pure RBD protein will be produced by HIC and the eluate carrying the RBD proteins will test positive against SARS-CoV-2 antibodies present in the BioVision Elisa kit. The RBD content in the eluate will be quantified by the spectrophotometer at UV280nm.
Conclusion: A BioVision ELISA positive test detects presence of <10 pg RBD/ml of the sample. For the application of RBD protein as a vaccine, a larger sample can be produced following the same protocol, formulated following a standard procedure and safety protocols. The RBD-protein vaccine, once administered, will be recognized by the cells of the immune system of the recipient, and stimulate T and B lymphocytes to produce antibody against RBD and thus the SARS-CoV-2 virus. The RBD protein carry no potential to recombine with the genome of the recipient.

Abbreviations: ampr = ampicillin resistant, cfu = colony forming unit, HIC = hydrophobic interaction chromatography, ampicillin, FP = fusion peptide, orf = open reading frame, RBD = receptor binding protein, sfGFP= superfolder green fluorescent protein, S-protein = Spike protein, SARS-CoV-2 = severe acute respiratory syndrome-coronavirus-2.

McGowan, Natasha; Sarbani Ghoshal
A potential drug target for treating Non-Alcoholic Fatty liver Disease (NAFLD)
Queensborough Community College
PNC Room 2

The United States is currently home to an obesity epidemic where 34% of adults and 15-20% of children are obese. The high number of those suffering from obesity are also at risk of developing cancer, coronary artery disease and diabetes. Those with metabolic disorders, diabetes and high levels of fat in the blood are at risk of developing fatty liver disease. Non-alcoholic fatty liver disease (NAFLD), also known as metabolic (dysfunction) associated fatty liver disease (MAFLD), is excessive fat build-up in the liver without another clear cause such as alcohol use. Inositol hexakisphosphate kinase 1 (IP6K1) is an enzyme in the inositol phosphate pathway which has recently been found to play a major role in obesity and associated comorbidities. In this presentation, a detailed review of the effect of IP6K1 on NAFLD will be presented. Our presentation will focus on studies conducted on rodent models where IP6K1 gene was deleted or pharmacologically inhibited. Gene deletion and pharmacology studies will confirm that IP6K1 can be potential drug target for treating NAFLD.

McKenzie-Laury, Alexandrya; Bradley-Ortiz, Rashia; Devdutta, Deb
To Determine How Oomycete Pathogens Interfere with Host Plant Defenses
Mercy College
MBI Room 1

The Food and Agriculture Organization of the United Nations estimates that between 20 and 40 percent of crop production is lost to pests worldwide each year. Plant diseases cost the global economy approximately $220 billion in crop loses annually. This blight on crops has led to a massive decrease in food supply allowing 800 million people to suffer from hunger and starvation. Pathogens and pests are the major cause of such crop losses and account for many issues that we see in plants. Bacteria, fungi, nematodes, and oomycetes are examples of different types of pathogens that lead to such high losses. These pathogens use sophisticated molecular strategies called effector proteins to sabotage the defenses of their host. Effectors from these pathogens are secreted into the interior of plant's cells, corrupting specific organelles such as the mitochondria, nucleus, cytoplasm, and even chloroplasts to suppress host defense and cause disease. In defense of this onslaught, plants preserve their health via their immunity response, which has been found to be a cascade of events and responses. The first phase is called Pathogen-Associated Molecular Pattern Triggered Immunity (PTI) where the plant triggers a primary immune response such as releasing reactive oxygen species to stop the pathogen. If the pathogen evades this phase, it can secrete its effectors leading to Effector Triggered Susceptibility (ETS) causing the plant to become compromised or diseased. The final phase is called Effector Triggered Immunity (ETI) where the effectors are recognized by plant resistance proteins (R Proteins) leading to cell death in the affected area. Our research focuses on effectors and their effect on plant defenses. In order to understand how the pathogen effectors interact with host defense for the purpose of causing disease, we designed and executed an experiment that would allow us to test our theories. We hypothesized that effectors from oomycete plant pathogens would interfere with the expression of host defense genes that are important in plant defense hormonal pathways such as jasmonic acid and salicylic acid. We virtually tested this theory using a simulation-based software, Plant Simulation Laboratory where we identified genes that were most critical in the host. We then confirmed our virtual results through in planta experiments where we performed qRT-PCR to determine whether the effector proteins where able to suppress the host defense genes in pathogen-treated plants. Our results show that oomycete effectors Avh73 and RxL23 were unable to target the defense genes in question and

did not suppress their expression. We are currently testing other host defense genes that may be the targets of these effectors in planta.

Mena-Khoury, Carol; Singh, Piarry; Mujica, Patricio E.
Role of Radixin, an ERM protein, in the control of endothelial barrier function
Mercy College
PNC Room 2

The inflammatory response is characterized by a transient loss of function of the vascular barrier, manifested in a rapid increase in endothelial permeability (hyperpermeability) to macromolecules, which leads to tissue swelling. Pro-inflammatory molecules released by injured tissues or cells activate vascular endothelial cells (EC), which in turn respond by rearranging intercellular junctions, thus increasing paracellular transport of fluids and solutes across the vascular wall. EC activation leads to mobilization of the endothelial nitric oxide synthase (eNOS) from the cell membrane, and nitric oxide (NO) production and delivery to subcellular targets. We have observed that cAMP signalling via Exchange protein activated by cAMP-1 (Epac1) triggers the mobilization of eNOS back to the membrane, concomitant with the termination of hyperpermeability. However, less is known about the cellular localization of these factors in this context. Radixin, a member of the ezrin/radixin/moesin (ERM) family of proteins, has been shown to regulate the localization of exogenously expressed Epac1 to the plasma membrane, but whether this is a relevant mechanism in EC remains unclear. We hypothesize that radixin may regulate endothelial response to pro-inflammatory stimuli by modulating Epac1 localization. We used immunocytochemistry to test the localization of eNOS, Epac1, and radixin in EAhy926 cells stimulated with platelet-activating factor (PAF) to simulate inflammation, and with 8cPT-cAMP, an Epac1-selective cAMP analog, to model the cAMP-mediated termination of hyperpermeability. Our results indicate that radixin localizes to intercellular junctions PAF challenge, and that Epac1 stimulation with 8cPT-cAMP mobilizes an additional pool of radixin. Together, these data suggest that Radixin plays a relevant role in the termination of endothelial hyperpermeability.

Mensah, Joshlyn ; Kano, Briana ; Gonzalez, Zenovia ; Cardenas, Irma ; Albro, David
Evaluation of Enterococcus Levels in the East River in Relations to Public Health
St. Francis College
EBE Room 2

Brooklyn Bridge Park is a waterfront recreational ground along the East River in New York City. Compounding human use and illegal spilling of industrial waste can cause harmful effects on the environment, aquatic species, and human health. Enterococci levels are measured to evaluate the quality of water, as it is an indication of fecal contamination. Found in feces of humans and other mammals, the presence of Enterococci in water can have harmful effects on human health. In joint effort with the NYC Citizen Water Quality Testing Program, Enterococci levels were measured over a 20 week period from Brooklyn Bridge Park (Pier 2, Pier 4 and Dumbo Cove). We hypothesize greater Enterococci levels at Pier 4 due to the greatest amount of human activity and debris observed. To test this hypothesis, water samples

were collected from each pier and measured using the Enterolert IDEXX kit. All samples were placed in IDEXX quanti trays for enumeration and incubated at 41°C. The research revealed that Dumbo Cove had the highest amount of Enterococcus compared to the other two sites. The average Enterococci levels at Dumbo Cove were 304.4 colony forming units (cfu) per 100 mls of water, over 8 times the level deemed safe for recreational activities. Increased amount of Enterococcus levels at Dumbo Cove were presumably influenced by increased human and animal activity, extreme weather events, and a build up of debris. The sustained high levels of Enterococci may have potential public health implications with respect to antibiotic-resistant organisms that are present in the water.

Minnies, Jake; Postaski, Ashley; Saverimuttu, Augusta; Chu, Tinchun
The Synergistic Antibacterial Effect of Patchouli with Antibiotics on Klebsiella, Pseudomonas, and Staphylococcus spp.
Seton Hall University
MBI Room 2

Antibiotic resistance has become a prevalent issue with the over usage of antibiotics, leading to a global health crisis. A potential solution to this problem is patchouli oil which is extracted from the leaves of Pogostemon cablin and was used in complementary and alternative medicines. The main component of the Pogostemon cablin used in this study is patchouli extract (PE). This study aims to evaluate the synergistic antibacterial activities of patchouli and various antibiotics on the growth of two Gram-negative bacteria, Klebsiella aerogenes (K. aerogenes) and Pseudomonas fluorescens (P. fluorescens), and one Gram-positive bacterium, Staphylococcus epidermidis (S. epidermidis). All three are biofilm-forming bacteria that could serve as good model organisms to evaluate the antibacterial properties of natural products. Microplate, colony-forming unit (CFU), Kirby-Bauer, and Congo-red assay were carried out to investigate the antimicrobial and antibiofilm formation properties of PE. The results showed that the minimum inhibitory concentration (MIC) is 1.66 mg/ml PE for all tested bacteria. CFU assay results indicated a significant bacterial inhibition (greater than 7.24%) for all three bacteria when treated with PE. The results from the Kirby-Bauer assay exhibited that 0.66 mg/ml PE has the maximum synergism on antibacterial activity when combined with Tetracycline and Streptomycin. Thus, patchouli extract could be further explored as an alternative to combat antibiotic-resistant bacteria.

Motan, Nihal; Ozkaya, Kudret; Gill, Karanvir; Kanaan Omar; Carroll, Reed
Investigating Effects of GABARAP and Induced Autophagy on GABA Receptor ɣ2 Expression in HEK 293 Cells
New Jersey City University
PNC Room 2

Neurons do not undergo mitosis. They terminally differentiate into lifetime-lasting cells where their neurodevelopment and hemostatic maintenance depend greatly on the autophagy process. Autophagy is a cellular catabolic pathway that degrades dysfunctional cellular components, like mitochondria, endoplasmic reticulum, and proteins, and recycles the breakdown products into cellular metabolic pathways. Autophagy is of great interest in neurons, as defects in the process have been linked to many neurodegenerative diseases. Both Microtubule-associated protein 1A/1B-light chain 3 (LC3) and Gamma-aminobutyric acid receptor-associated protein (GABARAP) are vital proteins in the autophagy process.

While LC3 is involved in autophagosome elongation, maturation and is used as an autophagy marker, GABARAP is a receptor-associated protein that may be responsible for autophagosome fusion to the lysosome. GABARAP is also known to play a significant role in the regulation of its associated surface receptor, the gamma-aminobutyric acid (GABA) type neurotransmitter receptor (GABAR). Whether there is any link between the role of GABARAP in autophagy and its regulation of GABARs is unknown. In this study, the effect of GABARAP on the ɣ2 subunit of GABA receptor expression was examined in the presence and absence of autophagy-inducing treatments.
Results suggest GABARAP has an effect of increasing the GABARAP ɣ2 receptor expression in co-transfected cells. Preliminary results suggest that induction of autophagy through starvation and chloroquine treatment may enhance this effect.

Munoz, Javier; Birchwood, Adrielle; Bouklas, Tejas
New Kid on the Block: Characterization of the Novel Multidrug-resistant Pathogen, Candida auris
SUNY College at Old Westbury
MBI Room 2

Candida auris is an emerging pathogenic yeast that has become a leading cause of fatal hospital-borne infections worldwide. Since its discovery in 2009, over 900 cases have been reported across the United States, predominantly in New York. C. auris exhibits a multidrug resistance that has never been seen in fungal species, and is often misdiagnosed for non-pathogenic species. Further, little is known about the mechanisms behind its antifungal resistance and pathogenicity. Previously, our laboratory investigated 10 C. Auris isolates (CAU1-10) from New York and established that they replicated relatively fast, showed extensive resistance to the antifungal drug, fluconazole, were phagocytosed and killed in mouse macrophages at comparable rates, and showed variable virulence in both a waxworm and mouse infection model. To investigate the relationship between the extensive drug resistance and successful host outcome, we passaged these strains in sub-therapeutic fluconazole over 500 generations, and investigated the evolved strains (CAU1E-10E) for their ability to form the cell wall, resist high temperatures, and inhibit drugs. Both the evolved and original strains were gram-positive based on gram staining, with the exception of strain CAU-8E. All strains showed similar cell wall budding patterns based on calcofluor staining. All evolved strains were more sensitive to higher temperatures, showing diminished growth at 42° C. Based on minimum inhibitory concentrations, a significantly higher number of the evolved strains exhibited fluconazole resistance. Hospital-wide outbreaks of C. auris continue to rise worldwide. Our studies shed light on the mechanisms that contribute to their azole resistance and success as a human pathogen, namely their cell wall remodeling, temperature, and drug sensitivity. This is imperative and fundamental to the proper diagnosis and treatment of this emerging global threat.
Nasrin, Sumaiya; Gadura, Dr. Nidhi
ELISA: ENZYME-LINKED IMMUNOSORBENT ASSAY
Queensborough Community College
BBB Room 1

ELISA, or Enzyme-Linked Immunosorbent Assay is a diagnostic tool that detects and measures the antigens or, antibodies to determine whether a test subject is exposed to a disease or not. Additionally, if a test subject has a positive result for a disease, it is possible to determine the stage of the disease by using the ELISA method. In the ELISA technique, antigens, and antibodies or, in other words, immunocomplex is a very important factor. Antigens are referred to as "foreign substances" that causes the human immune system to respond and to be activated. In contrast, antibodies are a type of protein that contains four chains of amino acids and antigen-binding sites. One special characteristic of the antibody is that each antibody recognizes a very specific antigen that allows fighting against a very specific infection or, disease. ELISA

can be performed in four different ways such as direct, indirect, sandwich, or, competitive. Qualitative ELISA allows deciding whether a patient has a positive or negative result in terms of a disease diagnosis whereas quantitative ELISA allows us to quantify or, measure the optical density of the sample using a spectrophotometer. To analyze the data of this honors project experiment, a standard plot was created by entering known antigen concentration on the Y-axis and corresponding absorbance value on the X-axis. ELISA was performed in triplicate for the unknown patient samples. Triplicate testing allows us to determine an intra-assay variation within one test. Additionally, testing each patient sample in triplicate allows avoiding false-positive and false-negative results. After plotting our patient samples we were able to determine if the patient tested positive or negative for HI. All data and log plots will be shown in detail for our conclusion. Even though this ELISA was being used to test the HIV patient samples, it is possible to test the sample of COVID- 19 patients by using the same methodology.

Nasrin, Sumaiya; Nguyen, Dr. Andrew V.
Affordable and rapid method for detection of Enterococcus spp. in NYC harbors using the Loop- Mediated Isothermal Amplification (LAMP)
Queensborough Community College
BBB Room 2

Enterococcus spp. are gram-positive bacteria that colonize human and animal intestines. They can survive in aerobic or anaerobic environments as well as in extreme conditions, making them ideal microorganisms for testing of fecal contaminated environmental water. Rapid detection of Enterococcus spp. is needed to reduce the risk of exposure to contaminated water. There are several ways to test for the presence of Enterococcus spp. such as the Enterolert enzymatic assay or microbial DNA amplification by Polymerase Chain Reaction (PCR). Most tests are expensive or require special instrumentation like a thermocycler. We sought to explore the usage of an alternative method to PCR called Loop-mediated isothermal amplification (LAMP). Using LAMP, we analyzed for the presence of Enterococcus spp. in the water around New York City. The advantage of LAMP reaction is that it is inexpensive, requiring only a water bath between 60-68o C, 4-6 specialized primers and a processive Bst DNA polymerase. To make the assay rapid, we use DNA prepared by the boiling method instead of traditional chromosomal extraction and employ a colorimetric assay to detect positive LAMP reaction. Our preliminary data show that water sample contaminated with Enterococcus spp. can be detected using common household items and our own do-it-yourself detection apparatus.

Nembhard, Shameir; Zmich, Nicole; Lall-Ramnarine, Sharon; Castner, Edward W.; Wishart, James F.
Ionic liquid-polymer gels for separations
Queensborough Community College
BBB Room 1

The need for more eco-friendly refrigerant gas alternatives to hazardous chlorofluorocarbons (CFCs) (due to their ozone depleting properties) led to their replacement by mixtures of hydrofluorocarbons (HFCs). However, the required separation of these HFC blends before their recycling or disposal at the end of their life cycle is challenging. Ionic liquids (ILs), with their characteristic low vapor pressures and tunable properties, are potentially suitable for membrane-based separation of gases under vacuum conditions, but their viscosities are too low. Ion gels prepared from ionic liquid-polymer mixtures have shown promise as solid supports that facilitate the separation of gases while retaining IL properties. However, key attributes of ion gels are still poorly understood and both the structure of the IL and the IL/polymer ratio need to be optimized to achieve good separation of gaseous mixtures. This project aims to develop improved and

energy-efficient separation mechanisms that will reduce hazardous gas releases into our environment. We report on the preparation and physical characterization of selected ion gels. Ionic liquids based on tetraalkyl-phosphonium and ammonium cations and bis(trifluoromethylsulfonyl)amide anions were synthesized and purified in our labs. The alkyl groups on the IL cations were selected by design to form a significant non-polar region, and thus optimized for use as gas separation membranes. The polymeric material used in the ion gels is a common battery development diblock copolymer, PDVF-co-HFP. H-1 and C-13 Nuclear Magnetic Resonance (NMR) spectroscopy was used to confirm the structure of the ILs, and they were combined with five weight percent of the di-block co-polymer to produce ion gels. Preliminary results reveal soft, gel-like materials rather than thin membranes. The IL/polymer ratio will be varied to produce membranes optimized for gas separations and the ion gels will be characterized using differential scanning calorimetry, high-energy X-ray scattering and Pulse-Gradient Spin Echo NMR spectroscopy. These measurements will identify the best ion gel systems for gas separation tests.

Nguyen, Huy; Fitzgerald, Allison
Zooplankton Biodiversity and Decapod Larvae Density in the Lower Hackensack River
New Jersey City University
EBE Room 2

The lower Hackensack River estuary is a rich ecosystem, with a variety of microorganisms and filter-feeding invertebrates as well as fish and crustaceans. Some of these microorganisms will be zooplankton such as copepods, immature invertebrates and chordates, eggs, larvae, and juveniles of adult nekton, which are carried through the water. There is a lack of published research on the zooplankton of the lower Hackensack River, which would add to the existing literature on the Meadowlands ecosystem, including birds and fishes. The goal of this study is to determine the biodiversity of crustaceans in the zooplankton across a salinity gradient Hackensack River with special attention dedicated to crab (decapod) zoeae and megalopae. It was hypothesized that zooplankton biodiversity would increase as salinity increases towards the mouth of the river. Zooplankton samples were collected over an 8-week period at three locations along a salinity gradient. Samples were towed from a boat using a 150-micron net on an outgoing tide. Results indicate that estuarine crab larvae might be most comfortable with waters in a mid-saline range, which could be explained by the falling tide on both dates pushing more saltwater species out of the river. Zooplankton biodiversity measurements changed from the first sampling date to the third, with the emergence of new freshwater species and an overall increase in freshwater species abundance as summer went on; possible explanations for the difference may be due to an influx of lower salinity water from upriver. This research has established the presence of several species of crabs within the estuary, which provide a vital link in the food chain.

Patel, Rich; Chu, Tinchun
Antibacterial Properties of Carvacrol on P. fluorescens and S. epidermidis
Seton Hall University
MBI Room 3

Antibiotic resistance has been a growing issue of concern, especially post-pandemic. Therefore, a natural antibacterial alternative is in urgent demand. Carvacrol, the primary component in Oregano and other essential oils, is reported to exhibit antimicrobial activity on a broad range of bacterial species. The aim of this study is to evaluate the antibacterial activity against Gram-negative Pseudomonas fluorescens (P. fluorescens) and Gram-positive Staphylococcus epidermidis (S. epidermidis). P. fluorescens can be used as a surrogate for Pseudomonas aeruginosa (P. aeruginosa) which causes many nosocomial diseases including respiratory tract, urinary tract, and gastrointestinal infections while S. epidermidis is a bacterium

that causes endocarditis, dermatitis, as well as other pathogenic diseases harmful to human life. Growth analysis results indicated that the 0.50% and 1% carvacrol showed significant inhibition of P. fluorescens and S. epidermidis. Colony-forming unit (CFU) assay results indicated that bacterial viability reduced when treated with 1% carvacrol. Microscopic observation was also carried out to explore the potential mechanism of the carvacrol. In conclusion, the preliminary results suggested that carvacrol could be used as a potential broad-spectrum antibacterial agent.

Patel, Shivani; Wlodarski, Monika; Arellano, Emily; Chu, Tinchun
The Antibacterial Effect of Ethanol-based Surgical Rub on Bacillus and Mycobacterium spp.
Seton Hall University
MBI Room 2

Antibiotic-resistance bacteria is currently a major global health crisis due to the overuse and misuse of antibiotics. This study aims to assess the effectiveness of an ethanol-based surgical rub, F6 on two potential antibiotic-resistant bacteria, Bacillus subtilis (B. subtilis) and Mycobacterium smegmatis (M. smegmatis). B. subtilis is a Gram-positive, spore-forming bacteria capable of growing in soil and in the gastrointestinal tracts of animals. M. smegmatis is a Gram-positive, biofilm-forming bacteria found in soil, water, and plants; it exhibits many of the same characteristics as other species of Mycobacteria, which are highly pathogenic and can cause serious human disease. Microplate assay and colony-forming unit assay (CFU) were used to evaluate the antibacterial activity of F6 over a 24-hour period. Microplate assay results indicated that half-maximal inhibitory concentration (IC50) for F6 is around 5% and the minimal inhibitory concentration (MIC) is greater than 10% for both bacteria tested. The CFU results indicated that 10% F6 had inhibition of 95% or greater for both bacteria. Further experiments are needed to explore the potential synergism of F6 and antibiotics as well as the efficacy of anti-biofilm activity.

Pena, Steven; Polizzotto, Kristin; Ortiz, Mary
A Study of Oyster Growth in Sheepshead Bay, Brooklyn, NY
Kingsborough Community College
EBE Room 1

Oyster spats were placed in a cage in the water at the end of Sheepshead Bay, Brooklyn, NY to see if they would survive and grow. When oysters grow together, they create a natural barrier against storm waters. They also provide habitat for many different species. The hypothesis for this study is the oysters will grow while the number of survivors will decline. Four sets of growth measurements (Nov 2019, Jun 2020, Oct 2020, Jun 2021) were collected over time. Data collected included the number of surviving oysters as well as their size. Descriptive statistics were performed on all four datasets. Inferential (parametric and non-parametric) comparisons were also performed (ANOVA, Wilcoxon Rank-Sum, and Kruskal-Wallis tests) on the data. The results of all inferential tests were “extremely statistically significant”. The initial number of oysters was 144, and the final count was 22. The oysters went from an average size of 1.606 ± 0.609 cm to 5.154 ± 1.346 cm. Based on the results; the hypothesis is accepted. The number of oysters decreased while the average size increased. Monitoring of the oysters will continue.

Piechowska, Sabina; Ghoshal, Sarbani
A peek into the actions of "Molecular Scissors" of Biotechnology
Queensborough Community College
BBB ROOM 1

The ability to fragment DNA became the cornerstone of molecular biology and biotechnology. In 1978, Arber, Nathans and Smith were awarded a Nobel Prize for their discovery of restriction enzymes (RE), which are also called molecular scissors. RE can cleave dsDNA at specific sequences called restriction sites. There are four types of RE, of which type II is most preferred during cloning procedures. In this presentation, we will discuss detailed procedures for restriction digestion of the vector, pUC19 with two RE, namely EcoRI and BglI. We are also going to discuss in detail how restriction maps are created from data obtained by analyzing DNA fragments from agarose gels. Restriction maps show the relative location of a selection of restriction sites along linear or circular DNA and this type of mapping has contributed immensely towards our knowledge of vectors and plasmids. Restriction mapping has been known to identify unknown genes without sequencing. Additionally, such mapping contributed heavily to our ability to genetically engineer organisms and recombinant DNA technology where an organism's genes are manipulated, an example of this includes the generation of synthetic human insulin using transformed bacteria.

Piechowska, Sabina; Wanderley, Mayra; Ghoshal, Sarbani
Inositol Hexakisphosphate Kinase1(IP6K1) is a Potential Target in Treating Insulin Resistance.
Queensborough Community College
PNC Room 3

Present-day sedentary lifestyle and unlimited access to food caused an increasing number of people to get obese and suffer from Type-2 diabetes (T2D). T2D patients show insulin resistance (IR), when pancreatic hormone insulin fails to lower circulating blood glucose levels as cells cannot uptake glucose. AKT is an insulin sensitizing enzyme and research in both humans and rodents has shown abnormalities in phosphorylation of AKT in T2D. Our research targets an enzyme called IP6K1 (inositol hexakisphosphate kinase 1) of the inositol phosphate pathway. IP6K1 phosphorylates IP6 into a pyrophosphate IP7. IP7 has been shown to be a physiologic inhibitor of AKT and thus promotes insulin resistance. Our overall research hypothesis is that genetic deletion or inhibition of IP6K1 will improve AKT phosphorylation and in turn ameliorate IR. During our research, we reviewed the impact of genetic deletion as well as pharmacological inhibition of IP6K1 in mice fed a high fat diet (HFD). Our analysis shows that genetic deletion and pharmacological inhibition of IP6K1 in HFD fed mice significantly protect them from diet-induced obesity, as also improves insulin sensitivity in comparison to wild-type mice. In comparison to control mice, mice with genetic deletion or treatment with IP6K1 inhibitor showed improved glucose and insulin tolerance tests, as well as maintained phosphorylation of AKT in liver, skeletal muscle and adipose tissue as evident from Western Blotting experiments. In conclusion, IP6K1 can be a potential target for treating T2D and insulin resistance.

Reardon, Sean; Herrera, Jessica; Hicks, Martin
Generating cDNA Clones of the EGFR Transcript to Better Quantify EGFR Levels in GBM Tumors
Monmouth University
CLI Room 1

Epidermal growth factor receptor (EGFR) is dysregulated in 57% of patients suffering from Glioblastoma Multiforme (GBM). It is the most common central nervous system (CNS) malignancy with a median survival of only 14 months. In our lab, we are developing assays to quantify the abundance of EGFR using quantitative PCR and DNA and RNA sequencing technologies. In order to quantify the absolute value of EGFR samples using in vitro and in vivo studies, I have isolated cDNA clones of pre-mRNA and mRNA transcripts of the EGFR gene. I isolated total RNA from either the nucleus or the whole cell, reverse transcribed with gene specific primers to produce EGFR specific cDNA, which was PCR amplified and cloned into a vector through TA cloning, the sequences were verified using Sanger sequencing to verify that EGFR is present in the cloned vectors. I am currently testing the vectors in quantitative PCR using a serial dilution to determine how effective of a standard my clones are to quantify EGFR in comparison to isolated EGFR mRNA from tissue culture of HEK 293 cells and GBM tumor cells.

Rodriguez, Diana; Hossain, Zakir;
Development of Small Molecule Inhibitors Targeting ssDNA-binding Protein Replication Protein A
Queens College
BBB Room 2

Replication Protein A(RPA) is a single stranded DNA (ssDNA) binding protein. This protein has many biological functions, specifically to repair DNA and activate cell checkpoint pathways. Thus, the inhibition of RPA prevents the division of cells. Given its ability to prevent DNA repair and the proliferation of cells, chemicals agents that inhibit RPA can potentially be a viable therapeutic against cancer. Chemical agents that can be potential inhibitors of RPA are currently being synthesized through organic synthesis. These chemical agents are to be characterized through nuclear magnetic resonance (NMR) and Mass spectroscopy analyses.

Rodriguez, Katherine; Annon, Oshane; Nunez, Xiomara; Amaya, Claudio; Regis, Ben; Wydner, Katherine S.
Winging It for Seven Winters: Project FeederWatch Sheds Light on Urban Birds
Saint Peter's University
EBE Room 1

Birds in urban habitats face numerous survival challenges. In 2014, we began a multi-year research survey of birds that winter in urban areas with the Saint Peter’s University campus (Jersey City, NJ) as our study site. Our methodology makes use of the Project FeederWatch (PFW) protocol established by the Cornell Lab of Ornithology. From November to April, birds attracted to resources (including feeders) within a designated study area are counted and reported to a North American database managed by Cornell. After four seasons of PFW (2014-2018), it was clear that only a few species are present every season, with House Sparrows (Passer domesticus) being dominant by sheer numbers. In Summer 2018, a grant enabled us to renovate a portion of the study area by removing English ivy and beginning to restore native habitat by planting native plants and wildflowers, especially those beneficial to birds and pollinating insects. Three seasons later, we have evidence that supports our hypothesis that “Restoring native habitat in an urban area will increase the diversity of winter birds (species richness)”. Since the start of PFW (2014) at our site, twenty-seven species have been counted but only five species have been present throughout all seven seasons: House Sparrow, Mourning Dove (Zenaida macroura), European Starling (Sturnus vulgaris),

American Robin (Turdus migratorius) and Northern Mockingbird (Mimus polyglottos). In the two PFW seasons following the native plant garden (2018-19, 2019-20), the average number of species seen weekly increased compared to previous seasons with first-time reports of six native species: White-breasted Nuthatch (Sitta carolinensis), Fox sparrow (Passerella iliaca), American Goldfinch (Carduelis trista), Song Sparrow (Melospiza melodia), Blue Jay (Cyanocitta cristata), and Sharp-shinned Hawk (Accipiter striatus). In the most recent season (2020-21), the number of species reported weekly increased further. Native species reported for the first time in 2020-21 were Black-capped Chickadee (Poecile atricapilla), Cedar Waxwing (Bombycilla cedrorum), Hairy Woodpecker (Picoides villosus), and Ruby-Crowned Kinglet (Regulus calendula).

Rosado, Cheyenne; Fiederlein, Alexandra;
CHANGES IN BREAST CANCER CARE IN NEW YORK DURING THE COVID-19 PANDEMIC
Molloy College
CLI Room 1

The COVID-19 pandemic has prompted the current health system to reorganize and rethink the care offered by health establishments. Breast cancer is the leading cause of cancer-related mortality worldwide, with New York having one of the highest incidences of cases in the United States. Despite recent advances in breast cancer care, the pandemic left many medical facilities changing diagnostic and treatment procedures and frequencies. This study examined changes in breast cancer care (BCC) during the pandemic. A cross-sectional analysis was done for 200+ participants in NY. Surveys were sent out to breast cancer organizations and advertised on social media. Women ages 18 and over currently undergoing treatment or in remission for breast cancer completed the survey. Answers were recorded for analysis, and responses were analyzed using a word-emotion association lexicon to assess how patients felt regarding their BCC during the pandemic. Additionally, responses were analyzed using SAS-software, and we included results corresponding with a 95% confidence interval. Our results show a total of 98.7% of patients with breast cancer received cancer treatment despite the ongoing pandemic. Most patients with breast cancer were anxious and/or worried concerning their BCC during the COVID-19 lockdown. There was no delay of appointments seen in 81.3% of patients in remission, while 15.2% of patients had a delay due to appointment unavailability and wait time after previous treatment. A total of 94.4% of patients stated that remission care has not changed since before the pandemic. However, most patients felt unsettled and nervous about the possibility of postponed treatments or canceled appointments due to the pandemic. In this study, patients with breast cancer experienced anxiety with their cancer care. The majority of patients did not experience delay and/or a reduction in the level of care required. The patient responses evaluate how the pandemic has changed BCC in NY. Our data suggest that although patients expressed anxiety and worries, care remained relatively unchanged. Regardless, BCC during a pandemic calls for policies to support and resources to identify women in need of treatment. Future work is needed to understand the full impact of the pandemic on the quality of BCC for patients across the globe.

Saleh-Esa, Mariam; Patel, Rich; Chu, Tinchun
The Effect of Antifouling Biomaterials on Algal Growth and Biofilm Formation
Seton Hall University
EBE Room 2

An increase in algal blooms due to eutrophication promoted by urbanization has become a prevalent matter in water bodies across the country. Such harmful algal blooms have extensive detrimental effects on aquatic wildlife and public health. This study aims to evaluate how the synergistic effect of phthalocyanine

dimethylformamide (PC-DMF) coating, when exposed to light, produces reactive oxygen species (ROS) to inhibit algal growth and biofilm formation. Fluorescent GloFish™ Zebrafish were acquired and placed in an ambient tank and another tank absent of natural light for photoactivation. Temperature and pH levels were recorded during each feeding to ensure stability. Fish behavior was also documented over the course of several weeks. PC-DMF was observed to have no detrimental effect on the fish. It was noted that healthy fish were vibrant in color while the ill fish lose their fluorescence. Glass slides containing the PC-DMF coating were submerged in the tank to evaluate its antifouling effects. For the fish tank that was isolated from natural light, lumen projectors were used to provide lighting to activate the PC-DMF. The results indicated that the slides coated with PC-DMF had significantly less algal growth (up to 85.54% inhibition) compared with the control slides. Samples from both tanks were also collected and analyzed by microscopy. Several species of algae were identified including Chlorella and Diatoms. Filamentous cyanobacteria Anabaena spp. was also detected. In conclusion, light-activated PC-DMF has the potential to inhibit algal growth and biofilm formation which could be used for a wide range of applications.

Sarecha, Amesh; Wang, Yating; Ozcan, Lale
Uncovering the Mechanism of Heterotrimeric GTP-Binding Protein, Rap1a, in Hepatic Glucose Production
Columbia University
BBB Room 1

Diabetes Mellitus (DM) refers to a group of metabolic disorders characterized by chronic hyperglycemia and most commonly occurs from inadequate insulin production, inadequate sensitivity of cells to the action of insulin, or both. Diabetes falls under two main etiopathogenetic categories, I and II. Type I diabetes, which is called insulin-dependent diabetes mellitus (IDDM), is primarily due to a deficiency in insulin due to the autoimmune-mediated destruction of pancreatic β cells. Type II Diabetes Mellitus (T2DM), the most common form of diabetes, is a prevalent metabolic disorder and its pathogenesis is caused by a combination of peripheral insulin resistance and dysfunctional compensatory insulin secretory response from pancreatic β cells. Additionally, one of the mechanisms for why patients with T2DM have elevated fasting plasma glucose (FPG) levels is that there is aberrant activation of HGP in the post-absorptive state which fails to be properly suppressed by insulin.
Recent studies have provided insight on gluconeogenic signaling pathways in hepatocytes, which contribute to underlying abnormalities such as increased hepatic glucose production. However, little is known about the endogenous regulatory mechanisms that prevent aberrant activation of this pathway. With this project we focus on the protein and isoform Rap1a to show that Rap1a is a negative regulator of gluconeogenesis and prevents HGP's aberrant activation. Rap1a is a small G protein, which stands for Ras-related protein 1a and belongs to the Ras superfamily of GTPases and cycles between an inactive GDP-bound form and an active GTP-bound form. Upon binding to its receptors, glucagon activates adenylate cyclase and increases intracellular cAMP. GTPase-activating proteins, such as Rap1GAP, stimulate GTP hydrolysis and thereby inactivate Rap1. Through recent work, we have identified a heretofore unknown metabolic function of Rap1a in regulating plasma LDL-C metabolism and raised the possibility of targeted Rap1a activation as a new therapeutic strategy to treat hypercholesterolemia. Because Rap1a is downstream of glucagon and its role in glucose metabolism has never been studied, we became interested to see if Rap1a plays a role in glucose metabolism.
Mouse models relevant to diabetes and obesity-induced insulin resistance, such as Rap1afl/fl mice backcrossed onto C57BL/6J background, have been used to elucidate the role of, heterotrimeric GTP-binding protein, Rap1a in glucose metabolism. With the help of immunoblotting, real-time quantitative PCR, and novel assays, we have shown that Rap1a is a glucagon signaling effector, and activation of Rap1a suppresses hepatocyte gluconeogenic gene expression and glucose production. We identified Rap1a

deficiency worsens glucose metabolism and insulin tolerance in lean and diet-induced obese mice and are currently elucidating on the mechanism of action behind Rap1a. Our mechanistic work revealed that Rap1a does not regulate gluconeogenesis through affecting intracellular cAMP/PKA levels and our further studies investigating the mechanism of action by which Rap1a functions has led to the identification of one mechanism by which Rap1a inhibition increases glucose production which may be through regulating the activity of insulin-sensitive gluconeogenic transcription factors, Foxo1,3,4. These studies could reveal new dimensions to the pathophysiology of diabetes and be leveraged to design new prevention treatments of cardiometabolic disease.

Sbateen, Nuha; Alli Muizzat; Abakkass, Malika; Dr.Bendaoud, Meriem
Antimicrobial and Antibiofilm Potential of a Medicinal Plant Root Extract
New Jersey City University
MBI Room 2

Antibiotic resistance is a growing public health problem. Some bacteria such as Staphylococcus aureus and Staphylococcus epidermidis are capable of causing severe infectious diseases and are becoming more resistant to many commonly known antibiotics. This public health concern has prompted a worldwide interest in using natural anti-microbial compounds. In this study, we directed our focus on a root extract of a widely used medicinal plant (CR) in the treatment for diabetes and to improve the immune system. However, very little is known about the potential antimicrobial and antibiofilm properties of the CR root extract. In the present study, the antimicrobial effect of CR extract was tested on a wide range of gram-positive and gram-negative bacteria as well as fungi using the broth assay. CR was found to have a strong antibiofilm effect against Staphylococcus aureus and Staphylococcus epidermidis and various antimicrobial effects on other gram-positive and gram-negative bacteria as well as fungi. The active fraction appears to be greater than 100 KDa in size. Heat and Proteinase K treatment of the root extract had no effect on its activity. Further studies will be conducted to characterize and identify the active fraction of the CR medicinal plant.

Sejour, Cassandra; Nielsen, Lilja, Hinkley, Craig
Detection of the FoxL2 gene in Crassostrea virginica
Kingsborough Community College
DBG Room 1

The Eastern Oyster, Crassostrea virginica, is a mollusk that is native to eastern North America. Eastern Oysters are ecologically important since they filter water, removing chemical contaminants, and they also build reefs that serve as habitats for other marine organisms. Eastern Oysters typically begin life as males, however, due to a combination of environmental and genetic influences they can change to females later in life. We are interested in understanding the genetic pathway(s) that control sex determination in C. virginica. Sex determination has been studied extensively in humans and other mammals. Studies have identified several important sex determination genes including Sox9 for males and FoxL2 for females. These genes have been identified in a closely related mollusk, C. gigas, and we were therefore interested in detecting their presence in C. virginica. In this study, we decided to focus on FoxL2 (Forkhead box protein L2), a transcriptional activator that may play a role in ovarian development. Our hypothesis is that the FoxL2 gene is present in the Eastern Oyster genome. As a first step, we used the human FoxL2 protein to perform a BLAST search against the C. gigas genome database at NCBI. This search identified two potential C. gigas FoxL2 proteins, one with 47.8% identity to the human protein and the other with 70.3 % identity. We used the C. gigas protein with highest identity to the human protein to BLAST the C. virginica genome and

found two proteins with 90.3% identity to the C. gigas FoxL2 protein. The C. virginica proteins only differ from each other by one amino acid and are encoded by separate genes located on chromosome 5. Multiple sequence alignments showed that the C. virginica proteins have 48%-52% identity to the FoxL2 proteins from fruit flies, zebra fish, chickens, mice, and humans and this identity falls predominantly within the forkhead box of these proteins. These results support our hypothesis that C. virginica contains a FoxL2 protein. This work was supported by grant 2R25GM06003 of the Bridge Program of NIGMS and grant #0537-22-1091 of the CSTEP Program of NYSED.

Serrano Perez, Madaris - Jones, Jennifer - Evans, Sarah
Influence of fungicide and nematicide on plant responses to drought and rainfall variability
Michigan State University, University of Puerto Rico
DBG Room 1

Because increased drought and rainfall variability are affecting natural environments in the Midwest and across the globe, it is imperative to study how plant interactions with other organisms influence drought tolerance. Microbial organisms, such as fungi and nematodes, can have both symbiotic and pathogenic interactions with plants. Nevertheless, studies have shown there is a gap of information and understanding of how these microbial interactions are beneficial to plants. For this REU project I leveraged a new large-scale rainout shelter experiment with manipulations of fungal and nematode abundance to see 1. how fungicide and nematicide treatments alter plant growth and flowering and 2. how fungi and nematodes alter plant growth during drought and rainfall variability. Also, for this new experiment set up, I wanted to see how existing variation in plant communities differs across treatments. I measured plant growth in control, fungicide and nematicide treatments in irrigated, drought, and variable rainfall shelters on early successional vegetation. I recorded plant height, specific leaf area and leaf dry matter content (LDMC) on Red Clover (Trifolium pratense) and Goldenrod (Solidago canadensis) . Finally, I measured percent ground cover and percent flower cover for the whole plant community. I found that LDMC for red clover was lower in nematicide subplots than in fungicide subplots(p=0.02). For the community measurements, I found that between the two sample times percent flower cover decreased in fungicide subplots more than nematicide subplots (p=0.04). Finally I found that drought footprints had significantly lower initial ground cover than the other rainfall treatments. I showed that fungi and nematode abundance altered plant phenology and physiology in ways that could influence plant drought tolerance. With continued sampling, I will be able to test the impact of fungi and nematode abundance on plant drought tolerance.

Shah, Prachi; Schoenfeld, Alan
The Mechanistic Role of pVHL in the Ubiquitin-Mediated Degradation of Alpha-5 Integrin
Adelphi University
BBB Room 3

The Von-Hippel Lindau (VHL) tumor suppressor gene produces a protein known as pVHL, which regulates HIF-a by targeting it for ubiquitin-mediated degradation1. pVHL also regulates integrins, such as alpha-5 and beta-1, which are proteins essential for cell adhesion and migration. Mutations in VHL result in the upregulation of integrins, thereby promoting metastasis. Integrins are taken into the cell via endocytosis and recycled in order to travel and fuse with a new part of the cellular membrane, enabling cancer cells to move forward and invade body tissues.
Past experiments performed in the lab demonstrated that bafilomycin, a lysosomal inhibitor, blocks the regulation of integrins by pVHL. This indicates that pVHL requires lysosomes to regulate integrins and may be involved in the mechanism that targets integrins to the lysosome for degradation. A recently performed

experiment illustrated that lysosomes are necessary for tight junctions, which link cells together, suggesting that the degradation of integrins by lysosomes is important for cell linkage. This semester, RNA interference will be used to specifically lower the levels of alpha-5 integrin. Once confirmed by Western blotting, the goal is to see whether some of pVHL's tumor suppressor properties, such as tight junction formation and reduced cell migration, are due to alpha-5 regulation.
The overall purpose of this research project is to understand the mechanism by which pVHL regulates integrins. Since pVHL ubiquitinates target proteins like HIF-a, other pVHL substrates that could be involved in the lysosomal targeting of alpha-5 integrin are being considered. Sequestosome-1 (SQSTM1) and sorting nexin-17 (SNX17) are characterized as potential target proteins involved in the degradation of integrins. SQSTM1 is a possible target because it interacts with atypical protein kinase C, which is identified as a target of pVHL2. The interest in SNX17 is due to its possible role in protecting integrins from degradation by separating lysosomal and recycling pathways3. It is hypothesized that when these target proteins are present, integrins are recycled. However, when these target proteins are present in low levels or even absent, integrins are sent to the lysosome. SQSTM1 and SNX17 will be tested as possible target proteins of pVHL by first performing a Western blot to observe whether there are high levels in VHL- cells and low or absent levels in VHL+ cells. If these differences are observed, a proteosomal inhibitor will be utilized to see if the decrease is due to regulation by pVHL. Another method of investigation is to examine whether pVHL ubiquitinates integrins. Some integrins have ubiquitination patterns that may allow pVHL to target them to the lysosome. This will be tested by transfecting a tagged ubiquitin molecule and observing whether alpha-5 integrin is ubiquitinated. Alpha-5 integrin will be extracted from the cells through immunoprecipitation and a Western blot will be performed to observe the levels of ubiquitin. If pVHL ubiquitinates integrins, levels of ubiquitinated alpha-5 integrin will be higher in VHL+ cells in comparison to the VHL- cells.

Sine, Laura; DeMarco, Victoria; Hintelmann, Thomas; Sean Reardon; Hicks Martin
Gene Therapy for Brain Tumors: Identification of New Therapeutic Targets Based on RNA Structure
Monmouth University
BBB Room 3

This project is to develop therapies to bypass challenges to effective and continuous drug delivery to the brain, for the treatment of glioblastoma multiforme (GBM). Currently, individuals diagnosed with GBM have a short life expectancy of 12-14 months. Our approach has the potential to deliver one single dose of gene therapy directly to the GBM tumor environment and block the production of cancer-driving genes. Epidermal growth factor receptor (EGFR) is dysregulated in 57% of all GBM. Our approach uses an adeno-associated virus gene transfer vector encoding RNA therapeutics targeting critical elements of the EGFR pre-mRNA transcript. We have examined the 'pre-mRNA structurome' of EGFR to evaluate the accessibility of targetable regions. To advance our therapeutic strategy, we have analyzed the secondary structure of the EGFR transcript using selective 2' hydroxyl acylation and primer extension followed by mutational profiling (SHAPE-MaP). SHAPE-MaP reactivity profiles were generated revealing the structure of splicing and cryptic polyadenylation signal (PAS) elements within the targeted region. We identified enhancer binding motifs surrounding the 5' splice site and hidden elements of a cryptic polyadenylation signal. Based on these structural profiles, we generated RNA therapies that interact with structural elements to unravel the hidden polyadenylation signal with the potential to activate expression of the short therapeutic isoform. In this project, we cloned these therapies into our therapeutic delivery platform and tested their efficacy to alter EGFR gene expression in tissue culture cells. Currently, we are evaluating in vitro, the therapeutic RNA interaction with the target sequence of the EGFR pre-mRNA transcript.

Singh, Piarry; Mena-Khoury, Carol; Mujica, Patricio E.
Involvement of the endosomal recycling system in the control of endothelial barrier function
Mercy College
PNC Room 3

The inflammatory response is characterized by a transient loss of function of the vascular barrier, manifested in a rapid increase in endothelial permeability (hyperpermeability) to macromolecules, which leads to tissue swelling. Pro-inflammatory molecules released by injured tissues or cells activate vascular endothelial cells (EC), which in turn respond by rearranging intercellular junctions, thus increasing paracellular transport of fluids and solutes across the vascular wall. EC activation leads to mobilization of the endothelial nitric oxide synthase (eNOS) from the cell membrane, and nitric oxide (NO) production and delivery to subcellular targets. We have observed that cAMP signalling via Exchange protein activated by cAMP-1 (Epac1) triggers the mobilization of eNOS back to the membrane, concomitant with the termination of hyperpermeability. However, the mechanisms that enable the return of eNOS to the EC membrane are not known. We hypothesize that eNOS may interact with the recycling endosomal system in EC. To accomplish this, we established a culture protocol for immortalized (EAhy926) and primary human umbilical vein EC (HUVEC). We stimulated EAhy926 cells with platelet-activating factor (PAF) to simulate inflammation, and with 8cPT-cAMP, an Epac1-selective cAMP analog, to model the cAMP-mediated termination of hyperpermeability. We used immunocytochemistry to determine the localization of eNOS, actin, vascular endothelial (VE)-cadherin, and the recycling endosomal marker Rab11a. Our results suggest that the termination of inflammatory endothelial hyperpermeability may involve the endothelial endosomal recycling system.

Small, Shatema; Hinkley, Craig; Carroll, Margaret, A.; Catapane, Edward, J.
Genomic Study of Dopamine Receptor Ligand Binding Sites of the Bivalve Mollusc Crassostrea virginica
Medgar Evers College
PNC Room 2

Gill lateral cells of Crassostrea virginica are innervated by dopamine (DA) and serotonin nerves. DA slows down lateral cell cilia beating rates and serotonin accelerates them. DA receptors are classified as D1R and D2R. Physiology and cell biology work of our lab found the DA receptors involved in gill lateral cell cilia inhibition are D2R-like in the gill cells and D1R-like in the cerebral and visceral ganglia. Our HPLC studies found DA in various tissues, including gill, cerebral and visceral ganglia of Crassostrea virginica. Using immunofluorescence techniques, we showed the presence of DA neurons in cerebral and visceral ganglia as well as D2R-like postsynaptic receptors in gill lateral cells and D1R-like postsynaptic receptors in cerebral and visceral ganglia. Recently the genomes of C. virginica and other bivalves have begun to be mapped. By conducting searches of the NCBI (National Center for Biotechnology Information) database using DNA and protein sequences of C. virginica and other invertebrate and mammalian species we found matches for D1R genes on chromosomes 4 and 5, and D2R genes on chromosomes 3 and 5 of C. virginica. BLASTS of the receptors found matches with very low Expect Values (E values) and high Percent Identity of the D1R and D2R receptors to those in other bivalves, gastropods, insects, mice, rats and humans. Various invertebrates had Percent Identity above 60%, while humans and mice had Percent Identity of 30 - 40%. We hypothesize that the ligand binding sites (LBS) for D1R and D2R receptors in C. virginica are evolutionarily conserved and will closely match those of other animals. To study this, we searched the NCBI database for D1R and D2R LBS of C. virginica and compared them to other animals. We found D2R LBS contained 17 amino acids (W, D, V, S, F, T, L, S, S, S, W, F, F, N, F, T, Y) with very highly conserved (70

- 100%) to LBS of other bivalves, gastropods, insects, mice, rats and humans. D1R LBS have not yet been identified in C. virginica, nor in the other animals we searched for, except for humans where it contained 17 amino acids (W, D, I, S, T, S, A, S, S, S, W, F, F, N, F, V, W). The study complements our physiology and cell biology studies demonstrating the presence and function for DA in C. virginica, and shows the genome of C. virginica contains genes to produce DA receptor LBS that are similar to those of other animals. This new information is valuable as it shows that the simple nervous system of C. virginica can be used to expand studies on DA neurotransmission. This work was supported in part by grant 2R25GM06003 of the Bridge Program of NIGMS, NIH grant K12GM093854 07A1 IRACDA Program of Rutgers University and PSC CUNY grants 62344 00 50 and 63434 00 51.

Stevic, Una; Gowan, Cody C.; Smith, Anastasia L. ; Snow,Zachary K.; Summers,Jonathan C. ; Conley, Sabena M. ; Hickson, LaTonya J.
Mesenchymal Stem Cell Paracrine-Mediated Repair in Diabetic Kidney Disease
St. Francis College
CLI Room 1

Mesenchymal stem cells (MSC) possess paracrine activities which induce kidney repair. We aimed to assess the effects of MSC-conditioned medium (MSCcm) on diabetic kidney disease (DKD) injury in vivo and in vitro.
Male mice (10-11-weeks-old; NOD/SCID; optimal for testing xenogenic MSC therapy) were divided into 3 groups: 1) control (n=4), 2) streptozotocin (STZ 37 mg/kg i.p. for 4 days; n=3), and 3) STZ+MSCcm (n=2). MSCcm from human adipose tissue-derived MSC (7.4x106 MSC) was administered daily i.p. for 5 days. Mice were euthanized 7 days after MSCcm treatment. Ex vivo kidney tissue was assessed via qPCR for pro-fibrotic (collagen 1, activin A), pro-inflammatory (MCP-1), and kidney injury (KIM-1) markers. Fresh kidney tissue was stained for senescence marker, senescence-associated β-galactosidase (SABG). Macrophage marker F4/80 was analyzed by flow cytometry. In human renal tubule epithelial cell (HK-2) studies, HK-2 were incubated in high glucose (HG; 25mM) plus indoxyl sulfate (IS; 1mM) for 12 hours, to simulate DKD injury. HK-2 were then incubated with MSCcm for 48 hours. qPCR measured KIM-1 mRNA.
At 2 weeks following STZ injection, glucose levels (> 250 mg/dL) established diabetes in all mice. STZ induced an increase in collagen I, activin A, MCP-1, and KIM-1 which were reduced by STZ+MSCcm treatment (Figure). Decreases in cellular senescence abundance (blue SABG staining) and F4/80 (10%) were observed in STZ+MSCcm vs. STZ mice. In vitro studies confirmed a fall in HG+IS HK-2 mRNA KIM-1 expression after MSCcm treatment. In conclusion, these findings indicate a potential therapeutic role for MSC-derived cell-free therapy in DKD.

Tsipora Sassoon; Sebastian Alvarado
Molecular Plasticity of the Gonadotropin-releasing hormone-1 Neurons in the Astatotilapia burtoni
Queens College
PNC Room 2

The African cichlid, Astatotilapia burtoni, is a favorable model to communicate the cellular substrates of plasticity in connection with behavior. Adjustments in their immediate surroundings facilitate modified behavior through gradual modifications in neural processes and their inherent structure and function. A. burtoni can abruptly alter their color and behavior with varied habitats and social cues. To study this, we are looking at the anatomical differences in the Gonadotropin-releasing hormone-1 (GnRH1) neurons in animals that are blue or yellow. GnRH1 neurons are fundamental to the hypothalamic-pituitary-gonadal axis of an animal's reproductive behavior. Our approach uses coupled study of behavior and

neuroanatomical analysis of GnRH1 neurons with tissue clearing and genetic labeling with a green fluorescent protein (GFP). This project will contribute to our understanding of phenotypic plasticity and behavior. We hypothesize that environmental influences shape neural differences in the GnRH1 between blue and yellow male morphs. Based on our preliminary data, each color morph has its own behavioral profile. Blue males present as being more reproductively inclined than the yellow males who present to be more territorial and aggressive. This project will present a more nuanced view of neuroplasticity in this emerging model system for the study of neuroscience and social behavior.

Udupa, Aditya; Vlasov, Pavel; Manley, James
Designing an MTR4 Knockdown System
to Investigate the Impact of lncRNA Accumulation on Differentiation Phenotype
Columbia University
BBB Room 2

The nuclear exosome is an indispensable quality control mechanism that can oftentimes co-transcriptionally regulate the stability of nascent RNAs and have a significant impact on cellular processes like splicing, export, and recombination. The helicase MTR4 is a well-known component of this complex and functions to make RNAs amenable to degradation by the exosome. Given that the exosome itself has many functions in the cell and the RNAs (pre-mRNA and non-coding) it regulates the levels of both have a significant impact on cellular programs like differentiation, it is imperative to have an efficient system to stably introduce knockdown of key exosome subunits like MTR4. This paper reports the successful construction of a lentiviral plasmid containing tetracycline inducible anti-MTR4 shRNA, its delivery into HEK-293T cells, as well as the robust knockdown of MTR4 and accumulation of target eRNA following induction. Moreover, the findings in this paper demonstrate that under the regime of MTR4 knockdown, eRNAs accumulate around actively translating ribosomes to a greater extent. Ultimately, the generation of this stable MTR4 knockdown cell line will allow us to circumvent many of the inconveniences associated with traditional transient siRNA transfection, and make future endeavors trying to decode the precise mechanism in which non-coding RNA impacts differentiation phenotypes at a post-transcriptional level more manageable.

Verma, Shivali; Guyer, Rebecca; Dogra, Pranay; Connors, Thomas; Szabo, Peter; Gray, Joshua; Farber, Donna;
Localized Developmental and Functional Signatures Define Early Life Tissue Resident Memory T cells
Columbia University
MBI Room 3

Immune responses in barrier tissues are critical for protection against a host of infectious pathogens. Tissue Resident Memory T cells (TRM) are the major immune population that mediate this protection in adults by providing a potent frontline defense against previously encountered pathogens in various peripheral tissues (skin, lungs, intestines, brain, liver, salivary glands, and lymphoid organs). Despite their capacity to provide long-term enhanced protection during adulthood, we currently lack an understanding of the mechanisms of tissue-specific TRM development, maintenance, and regulation during early life that allow the formation of long-lived TRM. We performed bulk RNA-sequencing on TRM cells isolated from pediatric (0 – 10 years of age) tissue (intestine, lung, lymph nodes, and spleen) to discern the defining functional signatures and developmental stages of localized TRM subsets in early life. Gene expression analysis revealed a core TRM gene signature upregulated across all tissues, as well as tissue-specific distinctions between early life mucosal and lymphoid-derived TRM. Additionally, intestinal and lung TRM presented unique functional signatures that were dynamic over age. Intestinal TRM exhibited increasingly regulatory profiles over age,

with pathway analysis revealing upregulated suppression of cell proliferation, cytotoxic molecule production, and IFNγ-mediated signaling. Importantly, we found increased expression of critical cell adhesion markers associated with TRM maturation in both lung and intestinal TRM, however intestinal TRM were characterized by a dramatic upregulation during infancy and subsequent maintenance of expression levels, whereas lung TRM upregulated maturation markers steadily over the first decade of life. We further explored gene signatures through singe-cell RNA-sequencing of infant and adult intestinal and lung tissue TRM, and identified key putative transcription factors (IKZF2, LEF1) and canonical TRM markers (ITGA1, CXCR6, LGALS1) upregulated across age. Interestingly, intestinal TRM upregulated these earlier, to a higher level, and in a greater population of cells. Taken together, these results reveal a potential biasing towards intestinal TRM development during infancy, where the bulk of antigenic challenge is faced in early life. Our analyses underscore a specialized profile of site-specific functional development in early life TRM that potentially indicates their enhanced ability to respond to the immune challenges faced in their respective tissue microenvironments.

Wanderley, Mayra; Piechowska, Sabina ; Ghoshal, Sarbani
Inositol Hexakisphosphate Kinase 1 (IP6K1) ameliorates diet induced obesity by enhancing energy expenditure pathway
Queensborough Community College
BBB Room 1

The evolution of mankind resulted in physical inactivities and increased access to unhealthy and calorie dense food. This modern lifestyle is the principal cause of the silent and slow growth of the global pandemic called obesity. Obesity results when fat accumulation exceeds the storage-capacity of adipose tissue depots. Our research focuses on targeting IP6K1 to treat obesity and associated comorbidities. Previous research showed that insulin stimulates the inositol phosphate kinase IP6K1 to produce IP7 (5-diphosphoinositolpentakisphosphate), which in turn inhibits insulin sensitizing enzyme Akt, these result in obesity and type-2 diabetes. For this project, we reviewed extensively the effect of genetic deletion and pharmacologic inhibition of IP6K1 on obesity. Our review identified significant statistical differences in obese states among wild type mice, IP6K1 knockout mice, and mice which were treated with the inhibitor when fed high fat diet (HFD) or were allowed to age naturally. Our presentation will show IP6K1 deletion or inhibition leads to less body weight and less accumulation of body fat due to enhanced energy expenditure without altering food intake.

Wang, Jessica; Nagarwala, Hamza; Patel, Yamini
Inseparable partners: Phage follows enteric bacteria to non-poopy places
New York Institute of Technology
MBI Room 3

Bacteriophages, viruses of bacteria, are the most numerous biological particles on the planet. There are an estimated 10^31 particles, at least ten times more than the estimated number of bacteria. If true, there should be at least one phage for every bacterial species, and phages should be able to be isolated from any environment inhabited by the host. In spring of 2018, a group of students isolated two strains of Enterobacter cloacae and a bacteriophage from kitchen sponges. E. cloacae is a member of an enteric group of bacteria and also a facultative anaerobe, so we wondered if we could find bacteriophages in other environments that infect these hosts. By sampling a variety of different environmental sources, we identified novel bacteriophages that infect these strains from wastewater, brackish water in an estuary, a freshwater pond, and soil from a backyard. The diversity of these environments is consistent with the resilience of the

environmental range of E. cloacae. Phage Shaolin from the kitchen sponge has a genome of 51 kb, is a tailed phage of myoviridae morphology, and capable of infecting Cronobacter muytjensii. We are continuing to characterize the isolated bacteriophages and conducting host range experiments with other related strains of bacteria. All of the bacteriophages produce a hazy plaque morphology, so we are attempting to isolate lysogens. The variety of bacteriophages found in different environments reflects the environmental range of the host, and should encourage phage hunters to think outside the toilet when trying to isolate phages that infect enteric bacteria.

Wei, Yufeng; Garzon, Luis; Joy Ikedife
Effects of Stimulants and HIV Proteins on Pyroptosis and Apopotosis Pathways in Human Brain Microvascular Endothelial Cells (hBMEC)
New Jersey City University
BBB Room 1

Human Brain microvascular endothelial cells (hBMVEC) are a central element of the microvasculature that forms the blood-brain barrier (BBB) that shields the brain against toxins and immune cells via paracellular, transcellular, transporter, and extra cellular matrix proteins. Damaged hBMVEC cells may cause stroke, seizures and other ailments. The present experiment tested the effects of several stimulants (Cocaine, THC, and Amphetamine) and two HIV proteins (Tat-86 and tat-101) on hBMVEC cells to determine if Pyroptosis (cell inflammation) or Apoptosis pathways were induced. Western blot and Rt- qPCR techniques were used to determine if either pathway was induced. Through protein and cDNA gene Seeanalysis, it was determined that both pathways were induced, Apoptosis mostly. Four main protein markers were found: PEA-15, Casp1, Casp3, and Casp8. Further research is needed to establish how other stimulants and organic compounds affect and influence the BBB penetrance to treat ailments such as Alzheimer's and HIV.

Williams, Janice; Sullivan, Regina; Ghoshal Sarbani
Differential Breast Cancer Cell Gene Expression after treatment with Single Walled Carbon Nanotubes
Queensborough Community College
BBB Room 2

Triple-negative breast cancer (TNBC) is an aggressive disease with limited treatment options. Single-walled carbon nanotubes (SWCNT) have unique properties including stability under various conditions and high surface area. Biomedical applications of SWCNT have the potential to expand cancer treatment options. Previous results from our lab have shown that TNBC cells have reduced rates of migration after treatment with dispersed SWCNTs. Our study will test the hypothesis that SWCNT treatment inhibits migration by altering expression of Matrix Metalloproteinases (MMPs), tissue inhibitors of Metalloproteinases (TIMPs) and PRPF4B. When PRPF4B, a pre-mRNA splicing factor kinase, is down regulated breast cancer cell migration is inhibited. MMPs and TIMPs have been reported as putative tumor markers and specific types have been implicated in breast cancer. All gene expression studies will be performed by real-time PCR. Anticipated data from our gene expression studies may help reveal that SWCNTs can be potential therapeutics for treating breast cancer.

Yussof, Ayuni; Chu, Tinchun
Antibacterial Effect of Phthalocyanine Zinc
Seton Hall University

MBI Room 3

In recent years, the spread of resistant bacterial strain and a global pandemic led to the search for new antimicrobial agents to overcome this problem. Phthalocyanine zinc (PcZn) is a photosynthesizer that can be used in photodynamic inactivation (PDI) as it can generate reactive oxygen species (ROS) that ultimately kills the cells. This study investigates the antibacterial effect of PcZn as a PDI photosynthesizer with and without light, aerobically, and anaerobically on Escherichia coli (E. coli), Pseudomonas aeruginosa (P. aeruginosa), Bacillus subtilis (B. subtilis), and Staphylococcus aureus (S. aureus). Microplate assays, colony-forming unit (CFU) assay, and confocal microscopy were used to determine the antibacterial properties of PcZn. The microplate assay showed 0.012 mM PcZn inhibited bacteria in all tested conditions. The CFU results indicated that light-activated 0.2188 mM PcZn resulted in 95% or greater inhibition aerobically in all four bacteria. Furthermore, PcZn was able to inhibit bacterial growth between 9.09% to 34.98% anaerobically. In conclusion, activated PcZn could serve as an effective antibacterial agent.

List of 2021 MACUB Registrants*

Abakkass	Malika	New Jersey City University
Ahmed	Sameer	SUNY College at Old Westbury
Albro	David	Saint Francis College
Alcendor	Ralph	City Tech
Ali	Manar	Bergen community college
Alli	Muizzat	New Jersey City University
Amrami	Michael	Macaulay Honors College at CUNY Queens College
Annon	Oshane	Saint Peter's University
Aquino	Bianca	Kingsborough Community College
Aragon	Brittney	Queensborough Community College, CUNY
Arias	Audrey	Queensborough Community College, CUNY
Arnoldi	Alessandra	Pace University
Asif	Kainat	Queensborough Community College, CUNY
Barahona	Carla	Mercy College
Barrois	Elizabeth	Spring Hill College
Basu	Paramita	Touro College of Pharmacy
Bendaoud	Meriem	NJCU
Benoit	Marcus	Borough of Manhattan Community College
Berrouet	Marie-Francesca	Queensborough Community College, CUNY
Bethva	Robert	Queensborough Community College, CUNY
Bhansali	Punita	Queensborough Community College, CUNY
Bhattacharya	Mira	Queensborough Community College, CUNY
Bimbo-Szuhai	Andras	Wagner College
Birchwood	Adrielle	SUNY College at Old Westbury
Boodhan	Nicholas	Lehman College, CUNY
Bouda	Abdoul	Queens College
Bouklas	Tejas	Old Westbury
Bozeman	Gregory	Kingsborough Community College
Brenner	Eric	Pace University
Briones	Nadia	Westchester Community College
Brogun	Dmitry	Kingsborough Community College
Brown	Ann	Medgar Evers College
Brown	Lewis	Columbia University
Buehler	Brendan	Nyack College
Bukofser	Holly	Westchester Community College/Mercy College
Burdowski	Allen	St. Francis College
Cadet	Samantha	Kingsborough Community College
Callahan	Jill	Saint Peter's University
Calvagna	Vincent	Vincent Calvagna
Campbell	Andrea	CUNY Queens College
Canger	Anthony	Mercy College
Caparelli	Alexander	Bucknell University

Cardenas	Irma	St. Francis College
Carrera	Zulina	Kingsborough Community College
Carroll	Margaret	Medgar Evers College
Carroll	Reed	New Jersey City University
Catapane	Edward	Medgar Evers College
Cela	Sidorela	Bergen Community College
Chalakova	Maria	Saint Peter's University
Chalfie	Martin	Columbia University
Chan	Tia	Kingsborough Community College
Chitadze	Mariami	Mariami Chitadze
Chu	Tinchun	Seton Hall University
Clarke	Izabella	Queensborough Community College, CUNY
Collis	Robert	Westchester Community College
Colon	Christina	Kingsborough Community College
Corbo	Chris	Wagner College
Crescitelli	Louis	Bergen Community College
Cui	Chang	Queens College
Cutter	Noelle	Noelle Cutter
Daniels	Dontaye	Stonybrook University
Danzi Engoron	Sara	Queensborough Community College, CUNY
Daye	Mylaisha	Mercy College
De Jesus	Angela	Nyack College
Decker	Aubrianna	Aubrianna Decker
DELL	ALISON	St. Francis College
DeMarco	Victoria	Monmouth University
Drammeh	Aisatou	Mercy College
eiden	margaret	Westchester Community College
Ekdeshman	Elvira	Kingsborough Community College
El Houzaly	Sara	LaGuardia Community College
Ellington	Jenna	St.Francis College
Elshikh	Ammar	Seton Hall University
Faison	DeJanae	Saint Peter's University
Faucette	Azure	Kingsborough Community College
Feliciano	Omar	CUNY YORK COLLEGE
Ferrara	Isabella	Pace University
Fiederlein	Alexandra	Molloy College
Fitzgerald	Allison	NJCU
Florentino	Gilda	Mercy College
Florentino	Gilda	mercy college
Foster	Tia	Medgar Evers College
Francois	Roodley	Mercy College
Freilich	Xenia	LaGuardia Community College
Frias	Maria	St Francis College
Gadura	Nidhi	Queensborough Community College, CUNY
Gao	Suncheng	Queensborough Community College, CUNY & Stony Brook University
Garana	Anne Frances	Mercy College

Garzon	Luis	New Jersey City University
George	Sophia	St. Joseph's College New York
Ghoshal	Sarbani	Queensborough Community College, CUNY
Gibb	Bryan	NYIT
Gill	Harman	Seton Hall University
Gillis	Bill	SUNY Old Westbury
Goddard	Rayna	Westchester Community College
Golebiewska	Urszula	Queensborough Community College, CUNY
Gonzalez	Rosann	Nassau Community College
Gonzalez	Elizabeth	Mercy College
Gonzalez	Karla	New Jersey City University
Grew	John	New Jersey City University
Gromova	Valeria	Valeria Gromova
Gupta	Richa	LaGuardia Community College
Gussin	Arnold	retired
Haliru	konyinsola	New Jersey City University
Hammond	Penelope	Kingsborough Community College
Hanesworth	Isabella	Mercy College
Harb	Kristina	New Jersey City University
Hardy	Sydney	Kingsborough Community College
Haskew-Layton	Renee	Mercy College
Hassan	Rachel	Kingsborough Community College
Hauter	Lamia	Queens College
Herrera	Jessica	Monmouth University
Herstoff	Emily	St Francis College
Hicks	Martin	Monmouth University
Hidalgo	Ronnie	Kingsborough Community College
Hill	Stella	Queensborough Community College, CUNY
Hincapie-Bendeck	Andrea	St. John's University
Hinkley	Craig	Kingsborough Community College
Hintelmann	Thomas	Monmouth University
Ihejirika	Patrick	CUNY Brooklyn College
Jaramillo	Angie	Mercy College
Javdan	Mohammad	Queensborough Community College, CUNY
Javellana	Shaun	Queensborough Community College, CUNY
Jones	Stephanie	Kingsborough Community College
Jones	Kimberly	Suffolk County Community College
Joseph	Patricia	SUNY College at Old Westbury
Kanaan	Omar	New Jersey City University
Kano	Briana	St. Francis College
Kita	Katsuhiro	St. Francis College
Kobren	Andrew	Touro College of Pharmacy
Koul	Sanjay	Queensborough Community College, CUNY
Lall-Ramnarine	Sharon	Queensborough Community College, CUNY
Lee	Jacqueline	Nassau Community College
Liliah	Marisha	St. John's University

Lland	Kristen	Queensborough Community College, CUNY
Lloyd	Scarlett	Wagner College
Luong	Victoria	LaGuardia Community College
Maghsoudi	Amirabbas	CUNY-Queens College
Makedonska	Anna	New York Institute of Technology
Mangino	Christine	Queensborough Community College, CUNY
Mansfield	Kera	Medgar Evers College
Marino	Amanda	SUNY Old Westbury
Martinez	Stephanie	Saint Peter's University
Masi	Sal	Nassau Community College
Maughn	Cheryl	Kingsborough Community College
McFarlane	Andre	Kingsborough Community College
McGowan	Natasha	Queensborough Community College, CUNY
McKenzie-Laury	Alexandrya	Mercy College
Mello	Alison	Queensborough Community College, CUNY
Memon	Mahnoor	Touro College
Mena- Khoury	Carol	Mercy College
Mensah	Joshlyn	St. Francis College
Meza	Sandra	Bergen Community College
Minnies	Jake	Seton Hall University
Mitra	Brian	Queensborough Community College, CUNY
Mohamed	Serena	Saint Peter's University
Mohammad	Mian	SUNY Old Westbury
Mosfique	Baizeed	NYIT
Motan	Nihal	New Jersey City University
Mujica	Patricio	Mercy College
Munoz	Javier	SUNY College at Old Westbury
Nagarwala	Hamza	New York Institute of Technology
Nasrin	Sumaiya	Queensborough Community College, CUNY
Nasrin	Sumaiya	Queensborough Community College, CUNY
Nelson	Rochelle	Queensborough Community College, CUNY
Nembhard	Shameir	Queensborough Community College, CUNY
Nguyen	Huy	New Jersey City University
Nguyen	Andrew	Queensborough Community College, CUNY
Nielsen	Lilja	Kingsborough Community College
Nieto	Fernando	SUNY Old Westbury
Nieto	Fernando	SUNY Old Westbury
Nissen	Jillian	SUNY College at Old Westbury
Nolan	Kathleen	St. Francis College
Novick	Peter	Queensborough Community College, CUNY
O'Brien	Erin	Nyack College
Ortez	Corina	Corina Ortez
Ortiz	Mary	Kingsborough Community College
Patel	Radha	Seton Hall University
Patel	Rich	Seton Hall University
Patel	Shivani	Seton Hall University

Patel	Yamini	New York Institute Of Technology
Pena	Steven	Kingsborough Community College
Perez	Sofia	Pace University
Perez	Jose	Innophos
Perez	Kestrel	St. Joseph's College
Pfeifle	Noah	Pace University
Phoenix	Tamia	Kingsborough Community College
Piechowska	Sabina	Queensborough Community College, CUNY
Pirtle	Megan	Albert Einstein College of Medicine
Pitta	Samantha	Kingsborough Community College
Postaski	Ashley	Seton Hall University
Prabhakar	Kumkum	Nassau Community College
Proteasa	Gheorghe	Queensborough Community College, CUNY
Pucci	Brianna	Kingsborough Community College
Quamina	Travina	St. Francis College
Rahman	Elena	Mercy College
Rahman	Roksana	N/A
Ramos	Elizabeth	St. John's University
Raste	Zoe	Seton Hall University
Regis	Ben	St Peters university
Roach	Kevin	Wagner College
Rodriguez	Katherine	Saint Peter's University
Rodriguez	Diana	Queens College
Rosado	Cheyenne	Molloy College
Rozenboym	Anna	Kingsborough Community College
Saleh-esa	Mariam	Seton Hall University
Santiago	Andrea	Mercy College
Sarecha	Amesh	Columbia University
Sarinsky	Gary	Kingsborough CC
Sassoon	Tsipora	Queens College
Saverimuttu	Augusta	Seton Hall University
Sbateen	Nuha	New Jersey City University
Schawaroch	Valerie	Baruch College
Schneider	Patricia	Queensborough Community College, CUNY
Schoenfeld	Alan	Adelphi University
Sejour	Cassandra	Kingsborough Community College
Serrano Perez	Madaris	Michigan State University, University of Puerto Rico
Shah	Prachi	Adelphi University
Sherald	Kayla	Kingsborough Community College
Sine	Laura	Monmouth University
Singh	Piarry	Mercy College
Small	Shatema	Medgar Evers College
Sontag	Charles	Bergen Community College
Spence	Nickayla	Queensborough Community College, CUNY
Srivastava	Anuradha	Queensborough Community College, CUNY
Stalter	Richard	St. John's University

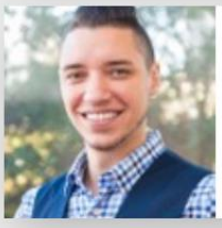
Stearns	Donald	Wagner College
Stevens	Bryan C.	Mercy College
Stevic	Una	St. Francis College
Sullivan	Regina	Queensborough Community College, CUNY
Tamari	Farshad	Kingsborough Community College
Tawde	Mangala	Queensborough Community College, CUNY
Teegala	Sushma	Queensborough Community College, CUNY
Tehrani	Khashayar	Touro College Of Pharmacy
Tehrani	Khashayar	Touro College of Pharmacy
Tolvo	Anthony	Molloy College
Tomala	Nyah	Mercy College
Tong	Jingjing	St. John's University
Torres	Edith R.	Mercy College
Trotman	Diana	Queensborough Community College, CUNY
Tsimounis	Areti	Queensborough Community College, CUNY
Twersky	Laura	Saint Peter's University
Vargas Dominguez	Maria	Nyack College
Vasquez	Cynthia	Kingsborough Community College
Velasquez	Nancy	Queensborough Community College, CUNY
Verma	Shivali	Columbia University
Wallach	Rosanne	Medgar Evers College
Wanderley	Mayra	Queensborough Community College, CUNY
Wang	Jessica	New York Institute of Technology
Washington	Jacqueline	Nyack College
Wayne	Jay	Suffolk County Community College
Wei	Sujun	Queensborough Community College, CUNY
Wlodarski	Monika	Seton Hall University
Wood	Lauren	Stony brook University
Wydner	Katherine	Saint Peter's University
Yagudayev	Mark	St. John's University
Yanagisawa	Chiaki	Borough of Manhattan Community College/CUNY
Yussof	Ayuni	Seton Hall University
Zenovia	Zenovia	St.Francis College
Zhou	Chun	Mercy College

*List as of 10/25/2021

The 2021 QCC, CUNY MACUB Team

Conference Co-Chairs

Dr. Punita Bhansali



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Dr. Anuradha Srivastava

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Dr. Sanjay Koul

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Dr. Sushma Teegala

Acknowledgements

We would like to thank….

- President Christine Mangino (QCC, CUNY) and Vice President Brian Mitra (QCC, CUNY) for their continued support of STEM
- David Moretti of Marketing (QCC) for helping our team construct the MACUB website
- Tony Gamino of Marketing (QCC) for helping with the development of the MACUB program
- Terry Chan, Dharmanand (Vick) Bijraj & Jasmine Chung of Information Technology (QCC) for hosting and monitoring the Zoom platform
- The entire post undergraduate student panel for sharing their experience with the MACUB participants
- All the hard working faculty who volunteered their time to moderate and judge the student presentations
- The MACUB board for helping the QCC, CUNY team plan the event
- All of the faculty presenters, and keynote speakers for their hard work disseminating recent research results
- The tremendous efforts of all student presenters for their dedication to advancing biological research

The MACUB Board thanks you for attending

Kathleen Nolan, Gary Sarinsky, Fernando Nieto, Edward Catapane, Margaret Carroll, Paul Russo, KumKum Prabakhar, Tin-chun Chu, Nidhi Gadura, John Grew, Jill Callahan, Martin Hicks, Jonathan Ouellet, Pam Monaco, Davida Smyth, Joshlyn Mensah, Donald Stearns, Christopher Corbo, & Anthony DePass.