22nd Annual Summer Undergraduate Research Fest

Hosted by the College of Natural and Mathematical Sciences

Wednesday, August 7, 2019

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Event Schedule

Wednesday, August 7, 2019

8:15 am: Poster Set-up & Presenter Check-In Begins

Ballroom Lobby, University Center, 3rd Floor

UC 312 Presenters' Complimentary Continental Breakfast

9:00 am – 10:30 am: Introductions & Oral Presentations

CHARACTERIZING THE DYNAMIC CAPSID-SP1 JUNCTION HELIX OF THE HIV-1 GAG POLYPROTEIN AND MATURATION INHIBITOR INTERACTION
Hanna Flores
MARC U STAR Scholars Program*

SYNTHESIS OF IMMUNOSUPPRESSIVE NANOPARTICLES FOR THE TREATMENT OF SYSTEMIC LUPUS ERYTHEMATOSUS
Alexandra Seas
MARC U STAR Scholars Program*

EDGE DETECTION USING RADON TRANSFORMS AND DYNAMIC PROGRAMMING FOR INDOOR ROBOTIC NAVIGATION
Signe Golash
COEIT Summer Research Program

ROLE OF N-MYC DOWNSTREAM REGULATED GENE 1 (NDRG1) IN THE ADAPTATION OF THE KIDNEY TO ANOXIA
Afeia Osei-Ntansah
*HHMI Scholar, MARC U*STAR Scholars Program, Meyerhoff Scholar*

10:30 am – 12:00 pm: Poster Presentations

Ballroom, University Center, 3rd Floor

10:30 am – 11:15 am – Poster Session 1
11:15 am – 12:00 noon – Poster Session 2

12:00 pm – 12:30 pm: Mentor Recognition and Closing

We ask that all research group pictures be taken after the closing.

Welcome

Welcome to the 2019 UMBC Summer Undergraduate Research Fest, which is hosted annually by the College of Natural and Mathematical Sciences. This marks the twenty-second year for this event. It is inspiring to see so many students participating and sharing the results of their summer research projects.

While some projects are the result of independent agreements, many have been made possible by grants or other funds dedicated to encouraging undergraduate research. All projects are associated with UMBC and require the support of research mentors. The mentors' passion for science and ongoing commitment to education are truly exceptional. I commend the students on their extraordinary efforts this summer. I particularly want to voice my appreciation of all the faculty, graduate student and peer mentors who have worked closely with them.

I especially want to thank the following staff members who coordinate this special event - Caitlin Kowalewski, Assistant Director for Undergraduate Academic Initiatives; Meika Samuel, Program Specialist; Kathy Sutphin, the Assistant Dean for Academic Affairs; and Justine Johnson, the Associate Director of the Meyerhoff Graduate Fellows Program.

Congratulations and best wishes for a very successful event,

William R. LaCourse, Ph.D.
Dean and Professor of Chemistry
College of Natural and Mathematical Sciences
University of Maryland, Baltimore County

Alphabetical Listing of Poster Presenters

First Name	Last Name	Poster Number	Poster Session
Zayied	Abubakar	1	Session 1
Theodore	Addo	2	Session 2
Afua	Adeck	3	Session 1
Rohan	Ahuja	4	Session 1
Christopher	Alfaro	10	Session 2
Ayah	Aligabi	5	Session 2
Aya	Alsabagh	6	Session 1
Noralhuda	Alyasiri	10	Session 1
Fabian	Amurrio	7	Session 2
Cameron	Anderson	8	Session 1
Nahum	Arefeayne	9	Session 2
Fiyinfolu	Atanda	10	Session 1
Bolutife	Baiyewu	85	Session 2
Sierra	Barber	75	Session 1
Sierra	Barkdoll	11	Session 2
Mahlet	Bauerle	12	Session 1
Holden	Beauzile	61	Session 2
Samar	Behdin	13	Session 2
Sana	Behdin	14	Session 1
Keynon	Bell	15	Session 2
Taylor	Bordes	16	Session 1
Dominique	Brooks	17	Session 2
Duyen	Bui	18	Session 1
Breanna	Byrd	19	Session 2
Amy	Calip	20	Session 1
Towanda	Carr	21	Session 2
Ridhi	Chaudhary	22	Session 1
Issac	Chaudry	23	Session 2
Patrick	Chen	24	Session 1
David	Chen	25	Session 2
Catherine	Chonai	94	Session 2
Sheridan	Danquah	26	Session 1
Ayushi	Dave	64	Session 1
Faith	Davis	27	Session 2
Simone	DeSouza	63	Session 1
Anna	Devadas	1	Session 1
Alexa	Diano	28	Session 2
Erick	Diaz	29	Session 1
Justin	Drummond	30	Session 2
Dianne	Eboh	21	Session 2
Bryce	Edwards	24	Session 2
Jason	Ejimogu	31	Session 1
Adilia	Espinoza-Jones	32	Session 2
Joseph	Evangelista	33	Session 1

Alphabetical Listing of Poster Presenters

First Name	Last Name	Poster Number	Poster Session
Zoha	Faraz	33	Session 2
Nathaniel	Felbinger	34	Session 1
Julianna	Fernandez	35	Session 2
Hana	Flores	36	Session 1
Garrett	Freeman	37	Session 2
Bailey	Godwin	38	Session 1
Signe	Golash	39	Session 2
Ken	Greenberg	40	Session 1
Anna	Greene	84	Session 2
Ewa	Harazinska	41	Session 2
Olivia	Hardy	42	Session 1
Murari	Harish	18	Session 2
Julia	Harmon	16	Session 2
Lauren	Harris	43	Session 1
Sydney	Haywood	44	Session 2
Andrew	Hennigan	45	Session 1
Joana	Hernandez	46	Session 2
Malika	Hiyam	47	Session 1
Ryan	Hoffman	48	Session 2
Nneamaka	Iwobi	49	Session 1
Jafira	Johnson	50	Session 2
Grace	Jones	51	Session 1
Sanaa	Jones	52	Session 2
Elisabeth	Kan	27	Session 1
Kasra	Kaviani	35	Session 2
Daniyal	Khan	4	Session 2
Yeihawa	Kulanda	53	Session 2
Brittany	Lafaver	9	Session 1
Judy	Lau	40	Session 2
Juelle	Lee	21	Session 1
Jennifer	Lenhoff	54	Session 2
Logan	Lineburg	55	Session 1
Abigail	Livingston	63	Session 2
Jiana	Lopez	56	Session 2
Natalie	Lucas	1	Session 2
Malavika	Mahendran	57	Session 1
Darius	McKoy	58	Session 2
Rodney	Mensah	35	Session 1
Alexandra	Misciagna	25	Session 1
Darrick	Moore	59	Session 2
Yasmin	Molkara	53	Session 1
Tevyur	Mosley	60	Session 2
Jamie	Mushrush	61	Session 1
Nidhi	Naik	62	Session 2
Crystal	Najib	63	Session 1
Zachary	Nicholas	64	Session 2

Alphabetical Listing of Poster Presenters

First Name	Last Name	Poster Number	Poster Session
Favour	Nwagugo	65	Session 1
Mawuyon	O Okesola	66	Session 2
Achuna Brian	Ofonedu	67	Session 1
Chelsea	Okeh	68	Session 2
Berniece	Okhaifor	69	Session 1
Oluwatomiwa	Oladunni	70	Session 2
Zaria	Oliver	71	Session 1
Ezimma	Onwuka	1	Session 2
Afia	Osei-Ntansah	72	Session 1
Cheyenne	Palm	12	Session 2
Jessica	Park	73	Session 2
Connor	Parker	31	Session 2
Stephen	Peltzer	74	Session 1
Melissa	Pena	75	Session 2
Charlene	Pfinayi	5	Session 1
Gabrielle	Pozza	41	Session 1
Maila	Raphael	76	Session 2
Arhamur	Rauf	77	Session 1
Kierra	Regis	78	Session 2
Alizay	Rizvi	79	Session 1
Alexandra	Rodriguez	96	Session 2
Gabriela	Rodriguez	64	Session 1
Dildora	Salimjonova	80	Session 2
Teiona	Sanders	85	Session 2
Alexandra	Seas	81	Session 1
Jasmine	Shaibani	14	Session 2
Noor	Shaikh	79	Session 2
Rashad	Sindhi	93	Session 1
Briana	Slater	82	Session 1
Cameron	Sloan	83	Session 1
Tamia	Tabourn	48	Session 2
Amber	Thompson	84	Session 1
Moriah	Thompson	85	Session 1
Neil	Tran	86	Session 1
Onyeka	Udoye	95	Session 1
Eric	Upton	87	Session 2
Jordan	Van Doren	88	Session 1
Phuong	Vi Le	89	Session 2
Ami	Vodi	38	Session 2
Claudia	Walker	90	Session 1
Gabriel	Wilkins	91	Session 2
A'lyssa	Williams	48	Session 1
Lorrayya	Williams	92	Session 1
Rianna	Zacharias	68	Session 1

Oral Presentations

CHARACTERIZING THE DYNAMIC CAPSID-SP1 JUNCTION HELIX OF THE HIV -1 GAG POLYPROTEIN AND MATURATION INHIBITOR INTERACTION
Hanna Flores
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SYNTHESIS OF IMMUNOSUPPRESSIVE NANOPARTICLES FOR THE TREATMENT OF SYSTEMIC LUPUS ERYTHEMATOSUS
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*HHMI Scholar, MARC U*STAR Scholars Program, Meyerhoff Scholar*

Program Acronyms

COEIT Summer Research Program	College of Engineering and Information Technology Summer Research Program
HHMI Scholars	Howard Hughes Medical Institute
LSAMP	Louis Stokes Alliances for Minority Participation
MARC U*STAR	Maximizing Access to Research Careers—Undergraduate Student Training in Academic Research Program—NIH/National Institute of General Medical Sciences
NSF IRES BAHAMAS	National Science Foundation International Research Experience for Students - Conservation Biology of the Critically Endangered Bahama Oriole
NSF REM	National Science Foundation Research Experience and Mentoring
NSF REU	National Science Foundation Research Experience for Undergraduates Program in Chemical Sensing and Imaging at UMBC
SBTP	Summer Biomedical Training Program — CNMS and the UMBC Graduate School
SCI ART	Interface between Science and Art in the research laboratories of leading scientists, engineers and art conservators at the University of Maryland Baltimore County (UMBC), Johns Hopkins University, and the Walters Art Museum in Baltimore.
STEM BUILD at UMBC	Science, Technology, Engineering, and Math - Building Infrastructure Leading to Diversity at the University of Maryland, Baltimore County

CHARACTERIZING THE DYNAMIC CAPSID-SP1 JUNCTION HELIX OF THE HIV-1 GAG POLYPROTEIN AND MATURATION INHIBITOR INTERACTION

Hana Flores[1], Carly Sciandra[1], Emily Cannistraci[1], Pengfei Ding[1], Eric O. Freed[2], Michael Summers[1]

[1]Department of Chemistry & Biochemistry, Howard Hughes Medical Institute, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore MD 21250

[2]Virus-Cell Interaction Section, HIV Dynamics and Replication Program, Center for Cancer Research, National Cancer Institute, Frederick, MD 21702

Currently, 36.9 million people worldwide are living with the Human Immunodeficiency Virus (HIV) and new drug targets are in demand due to HIV's ability to rapidly mutate. Research efforts have been directed toward the replication cycle of HIV in order to identify landmarks crucial to the virus' infectivity as targets for inhibitory drugs. During assembly, thousands of the major structural protein for HIV-1, the Gag polyprotein, multimerize at the cell membrane and form a hexagonal lattice. Gag consists of Matrix (MA), Capsid (CA), Nucleocapsid (NC), and P6 domains, as well as two spacer peptides, SP1 and SP2. The transition of the CA-SP1 junction region from a random coil to six helix bundle is critical for Gag assembly. Assembled Gag is cleaved by the viral protease between different domains resulting in a mature infectious virus. The rate determining step of maturation is the cleavage between CA and SP1 with the scissile bond buried inside the six helix bundle. Maturation inhibitors, such as bevirimat, prevent the cleavage at CA-SP1. The CA-SP1 junction helix should have sufficient stability to allow Gag assembly, however, it should also have appropriate flexibility to allow viral protease access to the cleavage site. We hypothesize that the CA-SP1 junction helix is in a dynamic equilibrium between a tight alpha helix and loose random coil in order to mediate assembly and maturation. We aim to use solution Nuclear Magnetic Resonance (NMR) to elucidate the dynamic nature of the junction helix. NMR studies can also allow for the study of whether the cleavage-inhibitory effect of bevirimat is due to stabilizing the CA-SP1 junction helix. A greater understanding of the dynamics of the junction helix and its interaction with bevirimat provides more information to be used for the design of drugs that cease viral infectivity in those affected by HIV-1.

This research was sponsored by NIH/NIGMS MARC U*STAR T34 HHS 00026 National Research Award to UMBC, the NIH/NIGMS Grant #1P50GM103297 and the Howard Hughes Medical Institute (HHMI). All research was conducted at the Howard Hughes Medical Institute at UMBC.

SYNTHESIS OF IMMUNOSUPPRESSIVE NANOPARTICLES FOR THE TREATMENT OF SYSTEMIC LUPUS ERYTHEMATOSUS

Alexandra Seas[1], Marilyn Allen[1], James Dizon[1], Gregory Szeto[1]
[1]Department of Chemical, Biochemical & Environmental Engineering, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease that attacks healthy tissues and organs, such as the kidneys, heart, and lungs. SLE changes over time so that it affects each individual differently throughout their life, thus warranting various therapeutic techniques. Less severe cases are treated with low-dose steroids, pain medications, and antimalarial drugs, while more severe cases require high-dose immunosuppressives and corticosteroids. Disadvantages of such medications include toxicity to non-diseased tissues, opening the door for innovative SLE treatment techniques.

Poly(lactic-co-glycolic acid) (PLGA) is a biodegradable polymer that is often used to form nanoparticles: small particles that are used in several biological applications, particularly to target specific tissues, organs, or cells. Azathioprine and methylprednisolone are immunosuppressive and steroidal drugs, respectfully, both of which have therapeutic potential for the treatment of SLE. Corticosteroids are prescribed as anti-inflammatory medications, while immunosuppressives are given to slow the inflammatory immune response. A nanoparticle approach will allow for tissue-specific distribution of these drugs in order to decrease their toxicity.

Azathioprine and methylprednisolone nanoparticles were synthesized using an oil/water emulsion technique, followed by size and distribution testing via dynamic light scattering. Sizes ranged from 170-2000 nm with polydispersity of 0.1-0.2 depending on the drug identity and the ratio of drug to polymer. The methylprednisolone nanoparticles had a loading capacity of 10% and encapsulation efficiency of 20%, indicating that the drug was successfully incorporated into the nanoparticles. Finally, these particles will be used in both a cell-line study and a mouse model. The results of the in vitro and in vivo studies will provide a holistic understanding of how immunosuppressive drugs can be used to treat lupus, and how nanoparticle innovation can play a role in cutting-edge therapeutics.

This investigation was sponsored by NIH/NIGMS MARC U*STAR T34 HHS 00026 National Research Service Award to UMBC, Undergraduate Research Award from the UMBC Division of Undergraduate Academic Affairs, and the Lupus Foundation of America Gina M Finzi Memorial Fellowship.

EDGE DETECTION USING RADON TRANSFORMS AND DYNAMIC PROGRAMMING FOR INDOOR ROBOTIC NAVIGATION

Signe Golash[1], David Chapman[2]
[1]Department of Computer Science, Brown University, 69 Brown St Box 1822, Providence, RI 02912
[2]Department of Computer Science and Electrical Engineering, University of Maryland, Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250

The way computers and humans see differs greatly. Humans can recognize individual objects, like chairs and tables. A computer, however, sees only an assortment of colors arranged as a grid of pixels. It has no concept that these colors have any meaning. Computer vision is the study of algorithms and mathematical techniques that allow machines to comprehend the contents of images. Line detection is an important problem in computer vision where straight lines in images, like walls and door frames, are detected, which robots must use to effectively navigate boundaries and obstacles.

We evaluate the use of an optimal line detection algorithm known as the Approximate Discrete Radon Transform (ADRT). The Radon transform is an essential method used for digital reconstruction of Computed Tomography (CT), but is rarely applied to computer vision or line detection due to the slow processing time of a traditional implementation. Although faster processing times can be achieved by means of the Fourier transform with the projection slice theorem, this approach is subject to loss of quality due to discrete sampling of a continuous function.

The algorithm uses Dynamic Programming (DP) to remove redundant calculations. DP is a technique where complex problems are broken into smaller overlapping subproblems, whose results are stored in memory. This algorithm runs in $O(n^2 \log(n))$, improving processing time and enabling use in a wider variety of applications compared to the traditional technique's time of $O(n^3)$. Furthermore, this method does not suffer from sampling issues of the projection slice techniques.

We present the ADRT algorithm, its implementation, and performance analysis for the identification of linear edges in indoor photography. Finally, we discuss its applicability to robotic navigation as well as the potential benefits and limitations of ADRT as compared to standard line detection algorithms, including the Hough transform.

We would like to thank the Leadership Alliance, the VIPAR lab, and the UMBC College of Engineering and Information Technology for helping to support this research.

ROLE OF N-MYC DOWNSTREAM REGULATED GENE 1 (NDRG1) IN THE ADAPTATION OF THE KIDNEY TO ANOXIA

Afia Osei-Ntansah[1], Jong Park[1], Rachel Brewster[1]
[1]Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250

The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

Posters

Poster	Session	Presenter's Name	Program Affiliation	Faculty Mentor
1	Session 1	Zayied Abubakar	SCIART	Cynthia Wagner, UMBC
1	Session 1	Anna Devadas	SCIART	Cynthia Wagner, UMBC
1	Session 2	Natalie Lucas	SCIART	Cynthia Wagner, UMBC
1	Session 2	Ezimma Onwuka	SCIART	Cynthia Wagner, UMBC
2	Session 2	Theodore Addo	HHMI Scholar	Rachel Brewster, UMBC
3	Session 1	Afua Adeck	LSAMP	Renee Dickie, Towson University
4	Session 1	Rohan Ahuja	NSF REU	Don Engel, UMBC
4	Session 2	Daniyal Khan	NSF REU	Don Engel, UMBC
5	Session 2	Ayah Aligabi	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
5	Session 1	Charlene Pfinayi	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
6	Session 1	Aya Alsabagh	LSAMP	Maricel Kann, UMBC
7	Session 2	Fabian Amurrio	NSF REU	Lee Blaney, UMBC
8	Session 1	Cameron Anderson	LSAMP	Fernando Vonhoff, UMBC
9	Session 2	Nahum Arefeayne	HHMI Scholars, MARC U*STAR Trainee	Michael Summers, UMBC
9	Session 1	Brittany Lafaver	HHMI Scholars, MARC U*STAR Trainee	Michael Summers, UMBC
10	Session 2	Christopher Alfaro	STEM BUILD	Mark Marten, UMBC
10	Session 1	Noralhuda Alyasiri	STEM BUILD	Mark Marten, UMBC
10	Session 1	Fiyinfolu Atanda	STEM BUILD	Mark Marten, UMBC
11	Session 2	Sierra Barkdoll	NSF IRES	Kevin Omland, UMBC
12	Session 1	Mahlet Bauerle	Meyerhoff Scholars	Michael Summers, UMBC
12	Session 2	Cheyenne Palm	Meyerhoff Scholars	Michael Summers, UMBC
13	Session 2	Samar Behdin	Independently working w/ mentor	Michael Summers, UMBC
14	Session 1	Sana Behdin	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
14	Session 2	Jasmine Shaibani	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
15	Session 2	Keynon Bell	MARC U*STAR Trainee	Minjoung Kyoung, UMBC
16	Session 1	Taylor Bordes	SBTP Trainee	Michael Summers, UMBC

Posters

Poster	Session	Presenter's Name	Program Affiliation	Faculty Mentor
16	Session 2	Julia Harmon	SBTP Trainee	Michael Summers, UMBC
17	Session 2	Dominique Brooks	HHMI Scholar, MARC U*STAR Trainee	Rachel Brewster, UMBC
18	Session 1	Duyen Bui	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
18	Session 2	Murari Harish	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
19	Session 2	Breanna Byrd	NSF IRES	Kevin Omland, UMBC
20	Session 1	Amy Calip	Independently working w/ mentor	Brad Peercy, UMBC
21	Session 2	Towanda Carr	NSF REM	Steven Miller, UMBC
21	Session 2	Diane Eboh	NSF REM	Steven Miller, UMBC
21	Session 1	Juelle Lee	NSF REM	Steven Miller, UMBC
22	Session 1	Ridhi Chaudhary	HHMI Scholar	Michael Summers, UMBC
23	Session 2	Isaac Chaudry	Independently working w/ mentor	Michael Summers, UMBC
24	Session 1	Patrick Chen	SBTP Trainee	Michael Summers, UMBC
24	Session 2	Bryce Edwards	Independently working w/ mentor	Michael Summers, UMBC
25	Session 2	David Chen	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
25	Session 1	Alexandra Misciagna	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
26	Session 1	Sheridan Danquah	NSF REU	Kevin Omland, UMBC
27	Session 2	Faith Davis	HHMI Scholar	Michael Summers, UMBC
27	Session 1	Elisabeth Kan	Independently working w/ mentor	Michael Summers, UMBC
28	Session 2	Alexa Diano	COEIT Summer Research Program	Erin Lavik, UMBC
29	Session 1	Erick Diaz	NSF REU	Lee Blaney, UMBC
30	Session 2	Justin Drummond	COEIT Summer Research Program	Carlos Romero-Talamas, UMBC
31	Session 1	Jason Ejimogu	MARC U*STAR Trainee	Michael Summers, UMBC
31	Session 2	Connor Parker	Meyerhoff Scholars	Michael Summers, UMBC
32	Session 2	Adilia Espinoza-Jones	Independently working w/ mentor	Michael Summers, UMBC
33	Session 1	Joseph Evangelista	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC

Posters

Poster	Session	Presenter's Name	Program Affiliation	Faculty Mentor
33	Session 2	Zoha Faraz	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
34	Session 1	Nathaniel Felbinger	Independently working w/ mentor	Philip Farabaugh, UMBC
35	Session 2	Julianna Fernandez	STEM BUILD	Fernando Vonhoff, UMBC
35	Session 2	Kasra Kaviani	STEM BUILD	Fernando Vonhoff, UMBC
35	Session 1	Rodney Mensah	STEM BUILD	Fernando Vonhoff, UMBC
36	Session 1	Hana Flores	MARC U*STAR Trainee	Michael Summers, UMBC
37	Session 2	Garrett Freeman	Independently working w/ mentor	Michael Summers, UMBC
38	Session 1	Bailey Godwin	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
38	Session 2	Ami Vodi	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
39	Session 2	Signe Golash	COEIT Summer Research Program	David Chapman, UMBC
40	Session 1	Ken Greenberg	Institute of Fluorescence	Christopher Geddes, UMBC
40	Session 2	Judy Lau	Institute of Fluorescence	Christopher Geddes, UMBC
41	Session 2	Ewa Harazinska	SCIART	Lisa Kelly, UMBC
41	Session 1	Gabrielle Pozza	SCIART	Lisa Kelly, UMBC
42	Session 1	Olivia Hardy	McNair Scholar	Andrea Kalfoglou, UMBC
43	Session 1	Lauren Harris	MARC U*STAR Trainee	Lee Blaney, UMBC
44	Session 2	Sydney Haywood	LSAMP	Erin Lavik, UMBC
45	Session 1	Andrew Hennigan	LSAMP	Phyllis Robinson, UMBC
46	Session 2	Joana Hernandez	LSAMP	Fernando Vonhoff, UMBC
47	Session 1	Malika Hiyam	LSAMP	Fernando Vonhoff, UMBC
48	Session 2	Ryan Hoffman	SBTP Trainee	Michael Summers, UMBC
48	Session 2	Tamia Tabourn	SBTP Trainee	Michael Summers, UMBC
48	Session 1	A'lyssa Williams	SBTP Trainee	Michael Summers, UMBC
49	Session 1	Nneamaka Iwobi	LSAMP	Fernando Vonhoff, UMBC
50	Session 2	Jafira Johnson	LSAMP	Rachel Brewster, UMBC
51	Session 1	Grace Jones	Independently working w/ mentor	Erin Lavik, UMBC

Posters

Poster	Session	Presenter's Name	Program Affiliation	Faculty Mentor
52	Session 2	Sanaa Jones	SBTP Trainee	William LaCourse, UMBC
53	Session 2	Yeihawa Kulanda	SBTP Trainee	Fernando Vonhoff, UMBC
53	Session 1	Yasmin Molkara	LSAMP	Fernando Vonhoff, UMBC
54	Session 2	Jennifer Lenhoff	LSAMP	Gregory Szeto, UMBC
55	Session 1	Logan Lineburg	HHMI Scholar	Charles Bieberich, UMBC
56	Session 2	Jiana Lopez	NSF REU	Zeev Rosenzweig, UMBC
57	Session 1	Malavika Mahendran	Independently working w/ mentor	Hye-Won Kang, UMBC
58	Session 2	Darius McKoy	HHMI Scholar, MARC U*STAR Trainee, Mey-erhoff Scholar	Rachel Brewster, UMBC
59	Session 2	Darrick Moore	LSAMP	Michael Summers, UMBC
60	Session 2	Tevyur Mosley	HHMI Scholar	Charles Bieberich, UMBC
61	Session 1	Jamie Mushrush	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
61	Session 2	Holden Beauzile	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
62	Session 2	Nidhi Naik	LSAMP	Erin Lavik
63	Session 1	Crystal Najib	STEM BUILD	Erin Green, UMBC
63	Session 1	Simone DeSouza	STEM BUILD	Erin Green, UMBC
63	Session 2	Abigail Livingston	STEM BUILD	Erin Green, UMBC
64	Session 2	Zachary Nicholas	Independently working w/ mentor	Michelle Starz-Gaiano, UMBC
64	Session 1	Gabriela Rodriguez	STEM BUILD	Michelle Starz-Gaiano, UMBC
64	Session 1	Ayushi Dave	STEM BUILD	Michelle Starz-Gaiano, UMBC
65	Session 1	Favour Nwagugo	LSAMP	Phyllis Robinson, UMBC
66	Session 2	Mawuyon O Okesola	COEIT Summer Re-search Program/LSAMP	Erin Lavik, UMBC
67	Session 1	Achuna Brian Ofonedu	COEIT Summer Re-search Program	Jianwu Wang, UMBC
68	Session 2	Chelsea Okeh	HHMI Scholar	Rachel Brewster, UMBC
68	Session 1	Rianna Zacharias	HHMI Scholar	Rachel Brewster, UMBC
69	Session 1	Berniece Okhaifor	NSF REU	Michael Summers, UMBC

Posters

Poster	Session	Presenter's Name	Program Affiliation	Faculty Mentor
70	Session 2	Oluwatomiwa Oladunni	HHMI Scholar, MARC U*STAR Trainee	Marie-Christine Onuta, UMBC
71	Session 1	Zaria Oliver	Meyerhoff Scholars	Lee Blaney, UMBC
72	Session 1	Afia Osei-Ntansah	HHMI Scholar, MARC U*STAR Trainee, Meyer-hoff Scholar	Rachel Brewster
73	Session 2	Jessica Park	NSF REU	Zeev Rosenzweig, UMBC
74	Session 1	Stephen Peltzer	STEM BUILD	Brad Peercy, UMBC
75	Session 2	Melissa Pena	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
75	Session 1	Sierra Barber	STEM BUILD	Steven Caruso/Joshua Wilhide, UMBC
76	Session 2	Maila Raphael	NSF REU	Lee Blaney, UMBC
77	Session 1	Arhamur Rauf	Independently working w/ mentor	Erin Lavik, UMBC
78	Session 2	Kierra Regis	HHMI Scholar	Michael Summers, UMBC
79	Session 1	Alizay Rizvi	Independently working w/ mentor	Daniel Lobo, UMBC
79	Session 2	Noor Shaikh	Independently working w/ mentor	Daniel Lobo, UMBC
80	Session 2	Dildora Salimjonova	McNair Scholar	Salem Abo-Zaid, UMBC
81	Session 1	Alexandra Seas	MARC U*STAR Trainee	Gregory Szeto, UMBC
82	Session 1	Brianna Slater	McNair Scholar	Carolyn Tice, UMBC
83	Session 1	Cameron Sloan	NSF REU	Lee Blaney, UMBC
84	Session 1	Amber Thompson	STEM BUILD, SCIART	Marcin Ptaszek, UMBC
84	Session 2	Anna Greene	SCIART	Marcin Ptaszek, UMBC
85	Session 2	Teiona Sanders	STEM BUILD	Jeff Leips, UMBC
85	Session 1	Moriah Thompson	STEM BUILD	Jeff Leips, UMBC
85	Session 2	Bolutife Baiyewu	STEM BUILD	Jeff Leips, UMBC
86	Session 1	Neil Tran	Independently working w/ mentor	Rachel Brewster, UMBC
87	Session 2	Eric Upton	Independently working w/ mentor	Phyllis Robinson, UMBC
88	Session 1	Jordan Van Doren	Independently working w/ mentor	Phyllis Robinson, UMBC
89	Session 2	Phuong Vi Le	Institute of Fluorescence	Christopher Geddes, UMBC

Posters

90	Session 1	Claudia Walker	HHMI Scholar, MARC U*STAR Trainee	Michael Summers, UMBC
91	Session 2	Gabriel Wilkins	Independently working w/ mentor	Matthew Fagan, UMBC
92	Session 1	Lorrayya Williams	COEIT Summer Re-search Program	Sanjay Purushotham, UMBC
93	Session 1	Rashad Sindi	Institute of Fluorescence	Christopher Geddes, UMBC
94	Session 2	Catherine Chonai	Independently working w/mentor	Brad Peercy, UMBC
95	Session 1	Onyeka Udoye	Independently working w/mentor	Belay Demoz, UMBC
96	Session 2	Alexandra Rodriguez	McNair Scholars	Tamara Bhalla, UMBC

Poster Abstracts

(Ordered by Poster Number)

USING DNA ANALYSIS FOR SPECIES IDENTIFICATION OF ANIMAL PARCHMENT

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In the field of art conservation chemists, biologists, engineers, and experts in the humanities collaborate to preserve artwork, documents, artifacts, and other items of cultural heritage. The purpose of this research was to ascertain the provenance of one category of such artifacts: ancient manuscripts written on animal parchment. Parchment, or highly stretched and cleaned animal skin, was the predecessor to paper and the most readily available medium for written works prior to the modern printing press. By extracting DNA from this material and identifying the species from which they were made, historians and conservators can better understand the cultural context of parchment manuscripts.

This project had three goals: extracting DNA from parchment, using the extracted DNA as a template for polymerase chain reaction (PCR) amplification with subsequent sequencing for species identification, and performing STR (short tandem repeat) analysis for individual identification. DNA samples were collected using destructive mechanisms by dissolving small portions of parchment in enzyme solutions as well as non-destructively using a triboelectric technique (dislodging and gathering follicle cells with excessive friction). Previous scientists have had some success extracting DNA (destructively) from parchment and performing whole genome sequencing or whole genome amplification (WGA) and then PCR.

A PCR primer pair capable of annealing to sequences from three species (bos taurus, capra hircus, and ovis aries) which flanks the D-loop region of mitochondrial DNA was identified and synthesized. Species identification was successful using control DNA with this primer pair. Attempts to amplify these same DNA segments directly from parchment DNA were unsuccessful. Experiments are underway to perform WGA with the parchment DNA, which will then be used as a template for PCR. If this method proves successful, the process will be repeated using the non-destructive extraction technique and extended to include STR analysis for individual identification.

This project is supported in by the Baltimore SCIART program which is funded by the Andrew W. Mellon Foundation Award 1806-0596. We would also like to acknowledge the Walters Art Museum, Abigail Quandt and Terry Weisser.

POSTER 1

IS THE DOWNREGULATION OF THE NA+/K+-ATPASE DUE TO CLATHRIN-MEDIATED ENDOCYTOSIS UNDER ANOXIA?

Theodore Addo[1], Jong Park[1], Dr. Rachel Brewster[1]
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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 2

EFFECT OF EGF PATHWAY INHIBITION ON RE-EPITHELIALIZATION AND REGENERATION RATE IN SALAMANDERS

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Salamanders have one of the most extensive regenerative abilities among most adult vertebrates. The Epidermal Growth Factor Receptor (EGFR) gene in salamanders is crucial for the maintenance of successful cell growth, cell proliferation and survival. AG-1748 is an inhibitor of EGFR pathways in cells. The objective of this study is to investigate the effects of the inhibition of EGFR pathways by AG-1748 on re-epithelialization and regeneration of amputated salamander tails. We hypothesize that the Inhibition of EGFR pathways in cells will lead to low levels of re-epithelialization, thereby causing low levels of regeneration. Salamanders were pre-treated in either the treatment – DMSO and AG1748 stock solution in Holtfreters (10nM) or control – DMSO in Holtfreters. The salamanders were then amputated and administered Methylene Blue (MB) dye to see which salamander re-epithelializes faster. High time of MB dye traces on stained tail is indicative of less re-epithelialization. It was observed that the salamander in treatment had less re-epithelialization compared to that in the control, since it displayed a lengthier timeframe of ~2 h before the loss of MB dye, compared to the salamander in the control solution which took ~1.4.

POSTER 3

A DIGITAL DASHBOARD FOR SUPPORTING ONLINE STUDENT TEAMWORK

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Teamwork skills are crucial for college students, both for their learning while in school and for their employability and career success after graduation. However, there are relatively few tools available that effectively assess the teamwork skills of students and provide a basis for improving them, and those that do exist suffer from a variety of shortcomings. In addition, almost all tools provide only episodic information: snapshots of team and team member performance at widely spaced intervals, with the major and sometimes only evaluation often taking place at the end of a team's activities.

We present a tool which collects the interactions of students who are using online platforms to complete a sustained task as a team; conducts a range of analyses of these data; and then presents information about team and team member behaviors in real time on a digital dashboard. This dashboard provides instructors with a user-friendly picture of team and team-member dynamics, which can also be made available, as appropriate, to both teams and team members, and enables instructors to provide regular and ongoing feedback to support teams and team members.

This project uses the data collected in a pilot study in Fall 2018 to demonstrate proof of concept and to do some initial analytical work. While some behaviors have been shown to be (or are self-evidently) beneficial or harmful to team performance, these data and analyses also make possible exploration of whether less obvious behaviors affect team outcomes and performance.

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POSTER 4

NANODROP VS. QC GEL, WHICH IS MORE ACCURATE?

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The purpose of this experiment is to isolate and characterize a bacteriophage from a soil sample that infects Bacillus thuringiensis (Bt). Bt is a gram positive rod that is used as a natural pesticide. In the coming age of antibiotic resistance, phage therapy has become a popular consideration towards treating bacterial infections, an important factor in this is the DNA of the phage. As a bacterial virus, the DNA of a phage is located in the capsid. This experiment identifies a potential variation between the measurement of DNA concentration by a Nanodrop Lite and quantification and analysis by comparison to mass standards in a QC Gel. There are pros and cons to both methods. For example, the Nanodrop is more time efficient, however the values are usually overestimated. On the other hand, the QC Gel is more accurate but time consuming. This project compares the two methods of DNA concentration analysis of phages. After isolation from the phage lysate, DNA was examined spectrophotometrically using a NanodropLite for each phage. Also, 1 µL of each DNA sample was examined by gel electrophoresis alongside known mass standards. Data analysis was completed using ImageJ. It was noted that the data collected for this experiment was done collectively as a cohort, which could introduce human error. The resulting R2 value of 0.3661 suggests there is a weak correlation between QC Gel and Nanodrop. While there are advantages to both methods, the QC Gel provided more accurate results.

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POSTER 5

MOLECULAR COMMONALITIES BETWEEN CANCER AND ALZHEIMER'S DISEASE, A BIOINFORMATICS APPROACH

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For decades, cancer as well as Alzheimer's disease, and neurodegenerative diseases, in general, have been receiving close review and examination due to their complex and multifactorial nature. Even though aging is a leading factor for both diseases, the relationship between them needs further investigation. From a broad perspective, the etiologies and pathways for cancer and Alzheimer's disease are at opposite ends of the spectrum. Cancer is associated with an increased rate of proliferation, while Alzheimer's disease is characterized by apoptosis and neurodegeneration. Consequently, (1) a population-based study found an inverse relationship between cancer and Alzheimer's disease in which cases with cancer history had a lower risk of Alzheimer's disease. However, molecular differences and similarities have yet to be determined thoroughly and proposed mechanisms have to be proven. Finding similarities between cancer and Alzheimer's disease rise the possibility of finding novel therapies that have not been used before to cure cancer or Alzheimer's disease.

Here, we will design bioinformatics and statistical network to construct molecular interaction networks between Alzheimer's disease and cancer. For this purpose, we will use several molecular-input such as protein-protein interactions, genetic markers, histone methylation, gene expression, protein domain connections and data from the Database of Genotype and Phenotype to integrate a connection network. Using protein-protein interaction analysis, several proteins related to cancer were found to be interacting with proteins related to Alzheimer's disease. Nonetheless, a protein domain connection related to Alzheimer's disease and cancer was also observed once. In the future, more data will be mined and analyzed to build a more comprehensive network of connections.

POSTER 6

PHOSPHORUS RECOVERY FROM POULTRY LITTER AND WASTEWATER SLUDGE USING DONNAN DIALYSIS

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Animal manure and wastewater sludge can serve as alternative sources of crucial nutrients like orthophosphate (P(V)). Donnan dialysis, which uses chemical potential gradients to transport ions across ion-exchange membranes, can be used to extract P(V) ions (i.e., H2PO4-, HPO42-, PO43-) from waste streams and replace the nutrients with inert ions like chloride (Cl-) from a draw solution. The objectives of the present work were as follows: (1) investigate the effect of pH on Donnan dialysis-based recovery of P(V) from poultry litter; and, (2) use complexation agents to release solid-phase P(V) from wastewater sludge for subsequent recovery by Donnan dialysis. To address the first objective, a 40 g L-1 poultry litter slurry (waste) was treated using a 500 mM NaCl draw solution. The following slurries were prepared: poultry litter slurry at pH 6.9 □ 0.1 (control); and, poultry litter slurry dosed with 1 M citric acid at pH 5.7 □ 0.8. The initial P(V) concentration in the control and citric acid-amended slurries were 198 mg L-1 and 358 mg L-1, respectively. After 7 d of operation, 39 and 43% of P(V) was recovered from the control and citric acid-amended slurries, respectively. These data suggest that recovery efficiency was not greatly affected by the initial slurry pH or phosphorus concentration. To address the second objective, batch equilibration experiments were conducted to determine the impact of ethylenediaminetetraacetic acid (EDTA) addition on P(V) release from wastewater sludge. After 24 h of mixing, the aqueous P(V) concentration increased from 2 mg L-1 (no EDTA) to a maximum value of 18 mg L-1 (35 mM EDTA) due to EDTA complexation of polyvalent cations that bind P(V). Overall, Donnan dialysis demonstrated promise for P(V) recovery from municipal and agricultural wastes, and P(V) recovery may be further improved through EDTA addition.

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POSTER 7

INVESTIGATING THE FUNCTIONAL PROPERTIES OF AUTISTIC GENES IN DROSOPHILA MELANOGASTER

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Autism is a spectral developmental disorder that affects patient communication and behavior in social interactions. Although autism affects 1 in 59 children, very little is known about the genetic aspects of the disease. Recent studies have identified 8 genes (ARID1B, ASH1L, CHD2, CHD8, DYRK1A, POGZ, SHANK3, and SYNGAP1) associated with autism in humans. Interestingly, orthologs of all eight genes are present in the genome of the fruit fly Drosophila melanogaster. Drosophila is an efficient model organism to study genes associated with neurological diseases because of its powerful genetic tools and tractable neuroanatomy. We used the pain-sensitive rolling pathway in Drosophila larvae to investigate the molecular function of the autism genes at the anatomical and behavioral level. Available tools allow us to manipulate specific genes exclusively in nociceptive neurons that regulate the well-characterized rolling behavior, which can serve as a readout of output changes after network impairment.

To mimic the escape mechanism of larvae in nature, we determined the gender of each organism and induced rolling behavior by mechanically poking control and experimental organisms with targeted manipulation of autism genes in nociceptive neurons exclusively. We recorded whether larvae showed successful rolling or not. We found that knockdowns of the genes Chd1, Prosap, and Brahma affected rolling frequency as compared to controls. Interestingly, rolling frequency of male larvae was stronger affected by Brahma overexpression, whereas rolling in females was stronger reduced by Brahma inhibition indicating a dimorphic role of Brahma. Since Chd1 and Brahma genes are known to be involved in epigenetic mechanisms, future experiments involve examining changes in histone modifications. Additional future directions include dissection of both male and females larvae for the anatomical analysis of neuronal networks using confocal microscopy.

This project was supported by the NSF USM LSAMP Program and the UMBC Natural Sciences Pre-Professoriate Fellowship to Fernando Vonhoff.

POSTER 8

STRUCTURAL CHARACTERIZATION OF HIV-1 MAL_3WAYBOTTOMCG

Nahum Arefeayne[1], Brittany Lafaver[1], Taylor Bordes[1], Julia Harmon[1], Darin Gilchrist[1], Kennedy Chioma[1], Noel Getachew[1], Phoebe Somani[1], Canessa Swanson[1], Dr.Michael Summers[1]
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Human Immunodeficiency Virus (HIV-1) is a retrovirus that targets CD4 T-cells of the immune system. This then can result in the development of acquired immunodeficiency syndrome (AIDS). Many drug therapies currently used, target regions of the viral replication cycle that are highly mutagenic. Through sequence analysis, it was found that the 5'-Leader of the viral genome is highly conserved and also responsible for regulating portions of the replication cycle such as genome recognition. Previous research has determined the minimal region within the 5'-Leader necessary for viral genome packaging known as the Core Encapsidation Signal (CES). Earlier studies in the Summers lab solved the three-dimensional structure of the CES for the widely used chimeric isolate, NL4-3. Our project focuses on the MAL isolate in order to investigate the possibility of a structure function relationship between the two different isolates. To determine the structure of the CES for the MAL isolate we use Nuclear Magnetic Resonance (NMR), which allows us to determine how biological molecules fold in a three-dimensional space. Studying the whole structure of the minimal packaging unit presents multiple issues due to the large size of the RNA, which results in overlapping and crowding of signals when interpreting NMR spectra. To alleviate this problem we use truncated regions of the CES called control oligomers.This specific project focuses on elucidating the structure of the MAL_3WAYBottomCG control oligomer which will in turn help to solve the structure of the full-length CES. Overall, an understanding of this potentially conserved structure will aid in the process of determining new therapeutics to inhibit this potent virus through its genome.

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POSTER 9

CONNECTING KINASES TO SIGNAL TRANSDUCTION PATHWAYS USING CHEMICAL PHENOTYPIC PROFILING

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Pathogenic fungi have a significant negative impact on human health and cause billions of dollars of crop damage annually. In contrast, different fungal species are used prevalently in the biotechnology industry to create an array of products, ranging from enzymes to antibiotics, which generate billions of dollars of revenue every year. In both pathogenic and beneficial fungi, the cell wall plays an important, protective role that can be exploited. For example, a better understanding of wall biosynthetic regulation may lead to novel antifungal therapeutics to combat fungal pathogens. This understanding might also be used to design genetic strategies to increase productivity in industrial fungal fermentations. To expand our understanding of cell wall biosynthesis and gene expression in fungi, we studied kinase mediated signal transduction in Aspergillus nidulans. We used toxins or chemicals known to perturb specific targets in fungal cells. With toxins, we first worked to determine a critical concentration (CC) (i.e., concentration just before wild type cells show reduced growth). Then, we used this CC to test a number of kinase deletion mutants for kinases previously identified in “omics” experiments as possibly playing a role in the regulation of cell wall biosynthesis or repair. Fungal spores of both a kinase deletion mutant and an isogenic control strain were grown on plates both with and without the toxin. Reduction in the growth of a deletion mutant indicates the deleted kinase may play a role in the pathway affected by the toxin. Thus helping us understand how various cellular pathways may be connected. We found that ΔmpkA and Δhk-8-9 deletion mutants had significantly impaired growth when compared to controls at the CC of 2,3-butanedione monoxime. Additionally, Δprka and Δmpka deletion mutants had a statistically significant growth defect when compared to the control strain at the CC of miconazole.

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POSTER 10

SHINY COWBIRD BROOD PARASITISM THREATENS THE CRITICALLY-ENDANGERED BAHAMA ORIOLE

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The Bahama Oriole is a critically endangered songbird endemic to Andros island. Known as a brood parasite, the Shiny Cowbird lays its eggs in oriole nests to be raised by the oriole parents. To ensure parasitism success, cowbirds peck and kill existing oriole eggs. Our goal was to rigorously document the severity of the threat cowbirds pose for the Bahama Oriole. Using a wireless nest-monitoring camera, we monitored oriole nests in two main habitat types including developed areas and undeveloped forest during the 2018 and 2019 breeding seasons. We found evidence of cowbird parasitism in Bahama Oriole nests. Using a chi-squared test, we compared nests found in both habitat types. We found that the rate of cowbird parasitism was significantly greater in developed areas near settlements and agricultural land than in undeveloped forest. These results suggest cowbird parasitism is a significant threat to orioles in developed areas.

We would like to thank the National Science Foundation's International Research Experience for Students program, the Bahamas National Trust, the University of Maryland, Baltimore County, and the International Field Studies, Inc., for funding and support for our research.

POSTER 11

ESTABLISHING CONDITIONS TO CHARACTERIZE THE HIV-1 MA:tRNA COMPLEX

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The human immunodeficiency virus (HIV) is a retrovirus that is the causative agent of the acquired immunodeficiency syndrome (AIDS), a disease which compromises the immune system. While current therapies inhibit several processes of viral replication, the development of drug resistance remains a risk for the HIV-positive population. Membrane targeting, a process which offers potential as a new therapeutic target, involves the trafficking of Gag polyprotein (Gag) to the plasma membrane via interaction between Gag's matrix domain (MA) and phosphatidylinositol- 4,5-bisphosphate (PI(4,5)P2). Recent studies have shown that cellular tRNAs interact with MA's basic patch prior to assembly, preventing interaction with PI(4,5)P2, but the underlying mechanism for the shift from MA-tRNA association to MA-PI(4,5)P2 remains elusive. In order to better understand this mechanism, this work aims to characterize the structure and interactions of the MA-tRNA complex using nuclear magnetic resonance (NMR) spectroscopy, a method of structure determination that requires conditions in which the complex is stable. To identify these conditions, 1D NMR titrations were performed to determine conditions for proper folding of the tRNA, and electric mobility shift assays (EMSAs) were employed to determine the stoichiometric ratio of MA to tRNA necessary for complex formation. Ultimately, better understanding these aspects of HIV biology may aid in the design of novel therapies.

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POSTER 12

BIOCHEMICAL AND STRUCTURAL ANALYSIS OF HUMAN IMMUNODEFICIENCY VIRUS TYPE-1 SPLICED RNA

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The human immunodeficiency virus (HIV) is the causative agent for acquired immunodeficiency syndrome (AIDS) which affects over thirty million people worldwide. The current treatments are only able to keep the viral infection at bay, calling for additional research to further understand the virus.

During HIV infection, the unspliced RNA (gRNA) is selectively packaged as a dimer from a large excess of spliced RNAs through interactions between the nucleocapsid (NC) domain of the Gag protein and the 5′ untranslated region (5′ UTR) of the gRNA. The sequence upstream to the first splice site, which contains most of the packaging signals including the dimerization site, is shared in all spliced RNAs and gRNAs. However, the spliced RNA is found to be packaged much less efficiently. This work aims to provide structural insight into the inefficient packaging of the spliced RNAs. Since dimerization is a prerequisite to packaging, the dimerization behavior of the spliced RNA was investigated via native gel electrophoresis, which showed that the spliced RNA favors a monomeric conformation in physiological conditions. This emphasizes the importance of RNA structure for gRNA packaging. Therefore, two-dimensional nuclear magnetic resonance (2D-NMR) with selective deuteration and control oligo strategies were used to study the highly conserved 5' UTR of the spliced RNA. The current NMR data suggests that the spliced RNA is structurally similar to the unspliced monomeric RNA, which is exclusively translated and not packaged. This work lays the foundation for the further structural study of HIV-1 spliced genome variants with the hope to create more effective treatments for the virus.

This research was funded by NIH/NIGMS grant R01 GM042561, and was conducted at the Howard Hughes Medical Institute at UMBC with support in part by the Howard Hughes Medical Institute's Precollege and Undergraduate Science Education Program.

POSTER 13

COMPARING GENOME SIZE AND PHYSICAL CHARACTERISTCS OF BACILLUS BACTERIOPHAGES

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Bacteriophages, commonly referred to as phages, are genetically diverse viruses that infect bacterial hosts. Using specific bacterial hosts, it becomes possible to isolate and characterize phages from the environment. The purpose of this experiment was to discover and characterize phages that infect the bacterium Bacillus thuringiensis. In understanding more about the diversity of each phage, the question was asked of whether there is a correlation between genome size and physical characteristics of the phage, i.e. capsid/tail length and width.
Soil samples from multiple locations in the East Coast were collected and each phage was isolated. After completing multiple plaque assays to ensure that only one phage was present, genomic DNA, isolated from a high titer lysate, was obtained. Phage gDNA was restriction digested and examined by gel electrophoresis to estimate genome size. Overall, 14 phages were discovered from 13 environmental samples. Based on results obtained from electron microscopy, all of the phages found are myoviruses. From 5 phages, the genome size (34-98 kb), tail length and width measurements (150-203 nm and 14-24 nm respectively), capsid length and width (79-92 nm and 71-90 nm respectively) and capsid volumes (398239-712448 nm^3) were determined. Data showed that the linear correlation of tail width or length vs. genome size had R^2 values of 0.51 and 0.33 respectively, while the correlation between genome size and capsid volume was close to zero. In summary, it was determined that genome size from the phages studied is independent of myovirus morphological characteristics.

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POSTER 14

SPATIOFUNCTIONAL ENZYME CONDENSATES IN LIVING C

Keynon Bell[1], Erin Kennedy[1], Anthony Huynh[1], Patricia Boyd[1], Tao Zhang[1], Minjoung Kyoung[1]
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The rate-determining, cytoplasmic enzymes in the glucose metabolism are organized into multi-enzyme assemblies of varying sizes in human cells. It has been proposed that these assemblies shunt glucose flux shunt from energy production to anabolic biosynthetic pathways and vice versa. Smaller assemblies play an important role in directing metabolic flux to glycolysis, but they are difficult to observe because they are not very bright. In this project, we use 4D imaging using a home-built lattice light sheet microscope (LLSM) to show that the signal to noise ratio of assemblies can be improved by adding tandem tetracysteine motifs to phosphofructokinase, liver type (PFKL). Moreover, we reveal that a significant number of the enzyme assemblies are in proximity with mitochondria. We also monitor the reversible formation of the enzyme assembly upon the inhibition of mitochondrial metabolism. Our results shed light on how the enzyme assemblies are formed and positioned near cellular organelles to locally and efficiently orchestrate their metabolic functions. We envision that the presented "spatiofunctional" characteristics of the enzyme assemblies in the glucose metabolism are an unprecedented starting point for understanding how functional metabolic networks form in live cells.

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Eric Betzig, Janelia Research Campus, Howard Hughes Medical Institute, Ashburn VA
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POSTER 15

STRUCTURAL CHARACTERIZATION OF HIV-1 MAL CES CONTROL OLIGOMER

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Human Immunodeficiency Virus (HIV-1) is a retrovirus that compromises CD4 cells in an immune system, leading to Acquired Immunodeficiency Syndrome (AIDS). Current antiretroviral drugs, target proteins within the HIV-1 replication cycle that are encoded by extremely mutagenic regions of the viral genome. A highly conserved region of the viral genome known as the 5'-Leader has been proposed to be an important new target for drug therapies. Further investigation of the 5'-Leader has revealed a minimal packaging region, necessary for propagation of new virus particles termed, the Core Encapsidation Signal (CES). The three-dimensional structure for the CES HIV-1 NL43 isolate has been solved but it has yet to be characterized for other isolates. Our project focuses on elucidating the three-dimensional structure of the CES for the MAL strain of HIV-1, in order to determine if there is a conserved structure function relationship. In order to elucidate the structure, we utilize Nuclear Magnetic Resonance (NMR), a structural biology technique that allows us to understand how biological molecules fold in space. The CES for these strains have 90% sequence identity and are predicted to fold similarly using Mfold software. Structure determination of individual regions of the CES alleviates some of the complications with solving the entire Core Encapsidation Signal structure. If the structure for the CES is conserved among different isolates of HIV-1, then this common drug target could be used for new retroviral therapies that could reduce the adverse effects of drug toxicity and therapeutic resistance.

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POSTER 16

EVIDENCE FOR CONSERVED MECHANISMS OF NEURULATION IN THE ZEBRAFISH FOREBRAIN

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The formation of the neural tube, the developmental precursor of the central nervous system, is facilitated by the bending and folding of the neuroepithelium, a process termed neurulation. Neural tube defects (NTD) are the most common type of birth defect in humans, primarily caused by improper neural tube formation. Investigating the cellular and molecular mechanisms that drive neurulation will help identify genetic risk factors for NTDs. The morphogenesis of the neural tube is facilitated by the formation of hingepoints, subsets of neuroepithelial cells that undergo apical constriction to form a wedge shape. Apical constriction occurs when a cell acquires a molecularly defined apical surface through apically polarized tight junction molecules, such as zona occludens (ZO1) and PARD3, in addition to the recruitment of an actomyosin contractile ring. Live imaging of hingepoint dynamics would further advance our understanding of hingepoint formation; however, it is difficult to perform in traditional model organisms. In contrast, the transparency and early accessibility of zebrafish embryos make them amenable to live imaging. Hingepoints were previously not reported in the zebrafish neuroepithelium, but we have recently found evidence for the presence of these structures in the forebrain. Using immunolabeling and confocal microscopy, we show the apical localization of ZO1 and PARD3 in a cluster of medial, wedge-shaped cells in the anterior neuroepithelium. Furthermore, we reveal that disruption of the apical actomyosin contractile ring, using the myosin inhibitor blebbistatin and myosin morpholinos, prevents apical constriction. These findings provide evidence for the presence of hingepoints in zebrafish and highlight the conservation of neural tube morphogenesis in teleosts, which pave the way for future investigations on the cellular and genetic basis of NTDs using zebrafish as a model organism.

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POSTER 17

EFFECT OF BACTERIOPHAGE GENOME SIZE ON HOST RANGE

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Bacteriophages are viruses that can infect a specific range of bacteria cells, called its host range. The specificity of infection can be utilized in phage therapy to target and eliminate pathogens without compromising the human body's normal microbiome. The broader a phage's host range, the more probable it can treat pathogens. The focus of this research was to determine whether there is a correlation between genome size and host range size. To do so, phages (n=5) were isolated, characterized microbiologically and morphologically, analyzed by restriction digest of their genomic DNA (gDNA), and examined via their host ranges.

To calculate the genome size of each phage, gDNA was extracted from crude lysate and cut with restriction enzymes for gel electrophoresis. A standard linear curve of a DNA ladder was calibrated then used to estimate the final genome size of phages. The estimated genome size of each phage was 40, 60, 70, 77, and 98 kbp.

Host range analysis was completed by plating 9 different bacterial hosts by serially diluting phage lysate by a factor of 10 (9x). Each dilution was spot titered on each plate and incubated over 24 hours at 30°C and analyzed for plaque formations. For the 5 phages, B.t. konkukian and B.t. Al Hakam showed the highest resistance to infection. Whereas, hosts B. cereus Gibson 3571, B.t. DSM-350, B.t. israelensis, and B. anthracis delta Sterne were infected by each of the 5 phages.

The number of hosts the phage infected or lysed were then counted and plotted against the genome size of the phage. A linear trend was plotted ($R^2 = 0.410$) demonstrating a weak positive correlation between genome size and host range size. This indicates that as genome size increases, the host range size does not increase.

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POSTER 18

POPULATION ANALYSIS OF FERAL ISLAND CATS: PREDATION RISK TO ENDANGERED BAHAMA ORIOLE

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The Bahama Oriole is a critically endangered species endemic to Andros, The Bahamas. Of the many dangers that the Bahama Oriole faces, introduced mammalian predators, such as feral cats, pose a major threat to the species' survival. Cat predation is one of the largest sources of human related bird morality, particularly for island species that evolved in the absence of mammalian predators. This study estimated the abundance of feral cats inhabiting the pine forests of Andros. We placed motion sensitive wildlife camera traps at twenty-three locations within our selected six-square-kilometer study plot to detect the presence of feral cats. We found at least five adults as well as three kittens within the plot, indicating about one cat per square-kilometer. This preliminary analysis suggests that, not only are feral cats a likely predator, they are also reproducing successfully in the pine forest and pose a long-term threat to the Bahama Oriole population.

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POSTER 19

CHEMOATTRACTANT GRADIENT SENSING OF CELL CLUSTER MIGRATION IN DROSOPHILA EGG CHAMBERS

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Chemoattractant gradients can guide motile cells to their destination- this process is called chemotaxis. We are interested in the chemotactic forces needed for cell cluster migration in the Drosophila egg chamber. The egg chamber consists of sixteen germ line cells surrounded by a layer of somatic follicle cells. During mid-oogenesis, two non-motile polar cells at the anterior end of the chamber are surrounded by migratory follicle cells called border cells. The cell cluster detaches from the epithelium and begins its migration to the oocyte. We examined how the cell cluster senses and translates the chemoattractant gradient to motion in order to improve our model of chemical gradient sensing and implement it in the Stonko et al. migration model.

We compared the Stonko et al. model with the Cai et al. model. The former viewed the cluster as an aggregate of single cells while the latter viewed the cluster as one large group. The Cai model integrated the pulling force along the surface, a sphere for simplicity, of the cluster. The chemotactic force was assumed to be only along the x-axis. We aimed to find a way to get a fully 3D force generation of this chemotactic force using multivariable calculus and MATLAB to compare and possibly update our migratory force on the Stonko model.

POSTER 20

OVEREXPRESSION OF GENES FOR INCREASED GROWTH AND LIPID PRODUCTION IN ALGAE

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Biofuels are derived from biomass and are a sustainable source of renewable energy. Algal-based biofuels are especially promising because algae grow rapidly, can grow on wastewater, and do not use crop space. We are attempting to increase growth rate and lipid production in Chlamydomonas reinhardtii (Chlamydomonas), a green microalga that can be genetically manipulated to overexpress proteins of interest. Chlamydomonas is CO2 limited and makes low amounts of triacylglycerides (TAGs) that can be easily converted to biodiesel. To overcome these disadvantages, we are using standard cloning methods to make plasmid constructs that should overexpress in Chlamydomonas five carbon concentrating mechanism (CCM) proteins (CAH3, CAH6, CAH8, LCI1, NAR1.2) and a key TAG biosynthesis enzyme (DGAT1). Carbonic anhydrases CAH3, CAH6, and CAH8 interconvert bicarbonate and carbon dioxide to improve CO2 uptake from water, while LCI1 and NAR1.2 transport CO2 across membranes. Our cloning strategy involves ligating a ble-2a DNA fragment into previously constructed CCM and TAG vectors that were not able to drive expression of the CCM or TAG proteins in Chlamydomonas. The ble-2A fragment encodes resistance to the antibiotic bleomycin and also couples expression of the ble protein via viral 2a-peptide to our genes, increasing chances for expression. Then we use bacterial minipreps and restriction digests to test for proper ligation. We are still working to generate the CAH6, CAH8, and NAR1.2 constructs. Three constructs, for CAH3, LCI1, and DGTT1, are complete and we are transforming into Chlamydomonas to test for protein expression by western blot. Expressing transformants will be tested for growth rate and TAG production. If increased growth is achieved, the same procedure would be used for Chlorella vulgaris, a green alga better suited for industrial production of biofuels.

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POSTER 21

CHARACTERIZATION OF THE INITIAL GAG/RNA INTERACTIONS THAT ARE CRITICAL FOR HIV-1 SELECTIVE GENOME PACKAGING

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36.9 million people are currently infected with Human Immunodeficiency Virus (HIV), a retrovirus responsible for the onset of Acquired Immunodeficiency Syndrome (AIDS). Upon transmission, the virus attacks CD4+ T cells and assimilates its proviral genome into the host genome. During viral assembly, interactions between the 5'-leader (5'-L) of viral genomic RNA and its translated product, the Gag polyprotein, initiate the selective packaging of two copies of the HIV-1 genome from a cell environment containing large excess of non-viral RNA.
We seek to understand the molecular mechanisms of this selective packaging which may facilitate the exploration of new therapeutic targets to halt viral assembly. The Gag binding sites in the dimeric 5'-L were characterized by isothermal titration calorimetry (ITC). A total of 28 Gag binding sites were identified, among which four sites associated with endothermic isotherm showed much higher binding affinity. Those high-affinity binding sites were further mapped to the bottom junction of the core packaging signal (CES) using a series of truncated versions of 5'-L. NMR titration experiments revealed that nucleotides involved in these tight binding are clustered in the (UUUU)/(GGAG) region located at the stem of SL3. The endothermic binding was explained by the disruption of the GU wobble base pair in the (UUUU)/(GGAG) region. This is further confirmed by the fact that mutations stabilizing the (UUUU)/(GGAG) region eliminated the high-affinity endothermic binding. Our in vivo competitive packaging assay showed that these stabilizing mutations significantly hinder the selective packaging of the viral RNA. Thus, we identified a critical Gag binding site in the packaging signal of HIV-1 genomic RNA. High-affinity Gag binding leads to the unwinding of this region which is essential for selective genome packaging. These findings may lead to the development of novel therapeutics to suppress genome packaging, hence terminating viral replication.

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POSTER 22

STRUCTURAL CHARACTERIZATION OF THE U5-PRIMER BINDING SITE (PBS) OF THE MAL HIV-1 GENOME USING NUCLEAR MAGNETIC RESONANCE (NMR) SPECTROSCOPY

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The human immunodeficiency virus type 1 (HIV-1) is the causative agent for the human acquired immunodeficiency syndrome (AIDS). As a retrovirus, a critical sequence in the HIV-1 replication cycle is the reverse transcription of the viral RNA genome to DNA, integration of the proviral DNA into the host genome, and the transcription of the newly integrated DNA to viral RNA. After transcription, the unspliced transcribed viral RNA transcripts exists in an equilibrium between two conformations. RNA transcripts can remain as a single subunit – the monomer conformation – or two transcripts can dimerize at the palindromic U5 dimer initiation site (DIS) where they exist in the dimeric conformation. Previous studies have shown that the monomer and dimer conformations have distinct structural and functional characteristics where the monomer serves as traditional mRNA that is translated into viral proteins while the dimer is selectively packaged as the genomic material for daughter virions. Following the infection of a host cell, the HIV-1 RNA genome must be reverse transcribed into DNA by viral reverse transcriptase. Like most DNA polymerases, reverse transcriptase requires a primer to initiate the synthesis of the DNA daughter strand, and the U5-PBS describes the region in the 5' leader where the reverse transcriptase primer will bind. Currently, we use nuclear magnetic resonance (NMR) spectroscopy to aid in the elucidation of the structure of the U5-PBS in the dimer conformer by collecting and assigning data on multiple oligo fragments. We aim to use NMR spectroscopy to elucidate the structure of the U5-PBS in the dimer and monomer so our findings may lead to the development of novel inhibitors to serve as possible long-lasting treatment options for HIV-1 positive patients.

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POSTER 23

EXPLORING THE EFFECT OF THE U5 PALINDROMIC SEQUENCE IN THE DIMERIZATION CHARACTERISTICS OF THE HIV-1 GENOME

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The human immunodeficiency virus type 1 (HIV-1), which attacks the immune system, affects over forty million people worldwide. HIV-1 is a retrovirus that uses its viral RNA genome to make DNA using the enzyme, reverse transcriptase. After reverse transcription is complete, the viral DNA is integrated into the host cell's genome, followed by transcription of viral RNA. The viral RNA can exist in two possible conformations - a monomeric or dimeric conformation, which are structurally and functionally unique. While the monomer conformation serves to translate into viral proteins, the dimer conformation is packaged as the genomic material for virions. A region of interest is the palindromic 5' dimerization initiation site (DIS) as this region has been shown to be the interface for the dimerization. Previous studies on the dimerization profiles of two specific HIV-1 strains, MAL and NL4-3, found two significant differences. Through nuclear magnetic resonance (NMR) studies, the MAL dimer is shown to be stabilized strictly by base pairs between the palindromic DIS region, an interaction we call a kissing dimer, and the dimer conformation of NL4-3 is stabilized by a rearrangement of the 5'-L, forming an extended dimer. Also, gel electrophoresis studies suggest that MAL requires magnesium to dimerize while NL4-3 does not. We hypothesize that this is due to the difference in the palindrome sequence. Comparing the NL4-3 palindrome, GCGCGC, to the MAL palindrome, GUGCAC, the NL4-3 palindrome is stabilized by a greater number of hydrogen bonds. We predict this difference in the palindrome between MAL and NL4-3 may be instrumental in explaining the difference in dimerization profiles. To test our hypothesis, we created mutant MAL and NL4-3 constructs switching the palindrome sequences. NMR and gel studies show that the mutagenesis studies of the palindrome significantly alters the dimerization of MAL and NL4-3 RNA transcripts.

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POSTER 24

DISCOVERING AND CHARACTERIZING BTP BACILLUS THURINGIENSIS KURSTAKI PHAGES

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Bacteriophages are viruses that infect bacteria. They are among the most diverse organisms on Earth and an estimated 10 31 phages are thought to exist. Phages are important because their ability to kill bacteria could provide an alternative way to combat bacterial drug resistance. Despite their abundance, only a small fraction of phages have been characterized. The purpose of this work is to isolate and characterize new phages from soil samples obtained from locations around Maryland, USA. To do this, enrichment and direct isolation techniques were tested by plaque assay on lawns of Bacillus thuringiensis subsp. kurstaki incubated for 24 hours at 30°C. Plaques were circular with diameters ranging from 1 - 5 mm. Bacteriophage were plate harvested then imaged by transmission electron microscopy (TEM). When measured the phages had the following average measurements; head dimensions: 86 nm by 79 nm, uncontracted tail 189 nm by 19 nm, contracted tail: 77 nm by 25 nm. A host range test was performed to find other bacteria that the phages could infect and kill. The phages had a narrow host range. In total, they only infected two of the eight other bacterial hosts introduced to them, but they can lyse all eight other hosts. A restriction enzyme digest to compare the DNA sequences of the phages were also performed. EcoRI and HindIII showed the most variation in the ability to cut the phages' DNA, suggesting they might be the most useful for discriminating between different phages based on DNA sequence. PET was used to predict the cluster arrangement of the phages using the restriction enzyme digest results, most phages were predicted to come from the cluster C3. Some were unclustered. All the phages are myoviruses likely of the family Herelleviridae. In the end, a total of 14 unique phages were found and characterized.

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POSTER 25

USE OF RADIO TRACKING TO STUDY TERRITORY SIZE OF THE BAHAMA ORIOLE

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The Bahama Oriole (Icterus northropi) is a critically endangered bird found only in Andros, Bahamas. Previous literature on these orioles suggested they mostly nested in developed areas in Coconut Palms (Cocos nucifera). With new knowledge that the Bahama Oriole also nests in pine forests (Pinus caribaea), we hope to make more accurate population estimates. Determining the home range of the Bahama Oriole is crucial to making reliable population estimates.

Using radio transmitters placed on three different orioles, we triangulated the position of tagged birds. These positions were used to generate territory maps for the three radio tagged birds. To access the validity of our equipment, and ensure the transmitter was still on sampled birds, we also periodically set out to sight the tagged orioles. The resulting home range maps show that the Bahama Oriole has a larger territory size than was previously assumed. These findings will be crucial in our ongoing efforts to estimate the total number of Bahama Orioles surviving.

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POSTER 26

NOVEL METHODS FOR ELUCIDATING THE STRUCTURE OF HIV-1 5' LEADER

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In 2018, 37.9 million people lived with HIV. Despite decades of study on this retrovirus, the structure of its genome remains unsolved. Our lab uses various methods to elucidate the structure of the highly-conserved 5' leader. NMR spectroscopy is a favored method of elucidation for RNA complexes. However, the use of traditional NMR methods is limited for RNA constructs larger than 60 nucleotides. This project is a continuation of a study that used paramagnetically-tagged reporter proteins to induce pseudocontact shifts (PCS) in the NMR spectra of an RNA construct. We can use these PCS to refine larger structural models than those typically generated using NMR.

The goals of this project are to expand upon this method of elucidation and apply it to the 5' leader of HIV-1. In a proof-of-concept study, we worked with various isotopic labeling schemes of a 46-nucleotide RNA construct. The different schemes serve two purposes: to help with the sequential assignment of nucleotides and to generate robust data through consistent spectra. We successfully measured PCS in the RNA of interest and refined an initial model of the protein-RNA complex. We collected an additional set of restraints arising from paramagnetic alignment of the protein-RNA complex in solution - residual dipolar couplings (RDCs). Fitting the experimental RDC data to our initial model showed excellent agreement with predicted values.

Our future directions are to collect the same type of spectra with various labeling schemes for a construct of the HIV-1 5' leader. As this is much larger than the previous construct, to verify the proper folding and binding of the reporter protein, we will calculate isothermal titration calorimetry data and conduct gel shifts. This will help elucidate the potential stacking of the TAR and Poly-A regions of the 5' leader, a section of the structure that is still unknown.

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POSTER 27

OPTIMIZING IMMUNE CELL METABOLISM FOR GROWTH AND FUNCTION

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Cellular metabolism is a complex group of chemical reactions that sustain life. Metabolic pathways regulate the use and availability of energy and nutrients, ultimately controlling cellular function. Monitoring the dissolved oxygen concentration and pH of culture media can allow us to see how metabolic stress or limited energy can affect cellular properties. Glycolysis is the primary metabolic pathway used by cells to produce energy by breaking down glucose. Decreasing glycolytic activity has been proven to increase the function of specific immune cells called T cells. T cells are expanded from millions to billions of cells to create cutting-edge cancer therapies. Increasing the proliferation and function of T cells is critical for treating cancer, but current technologies have not optimized their growth and function through control of metabolism.

We used non-invasive optical sensors to monitor the pH and dissolved oxygen concentration in cultures of Jurkats, a human T cell line. The sensors are patches installed in the bottom of a culture vessel. It is expected that both pH and dissolved oxygen will decrease over time, because as cells grow, they produce lactic acid which lowers the extracellular pH and they consume oxygen during cellular respiration. Preliminary testing showed an 80% decrease in dissolved oxygen over a 3-day period, correlating with the cell growth. Throughout the same time period, the pH only decreased slightly from 7.9 to 7.6. Subsequent testing can be used to optimize these metabolic factors and improve overall conditions for cell viability. Future studies will use sensors to maintain target pH and dissolved oxygen levels throughout T cell cultures to obtain desired proliferation and function.

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POSTER 28

OPTIMIZATION OF EXCITATION-EMISSION FLUORESCENCE SPECTROSCOPY FOR CHARACTERIZATION OF DISSOLVED ORGANIC MATTER IN BALTIMORE STREAMS

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Contaminants are discharged into surface water from municipal wastewater effluent, urban runoff, and agricultural waste. These waste streams also contain dissolved organic matter (DOM), which is generally nontoxic but can affect the fate of contaminants in aquatic systems. DOM is a mixture of thousands of unique molecules stemming from the breakdown of plant and animal matter. We hypothesized that the total organic carbon (TOC), total nitrogen (TN), and fluorescence spectra, measured as excitation-emission matrices (EEMs), of water samples can be used to identify leaking sewers in urban streams. The objectives of the present work were to (1) evaluate the TOC and TN content of water samples collected from 27 sites in the Gwynns Falls and Jones Falls watersheds and (2) optimize two parameters, namely the integration time and wavelength step size, involved with measurement of fluorescence EEMs. Measured TOC and TN concentrations for the samples were 5-20 mg L-1 and 0.5-4.0 mg L-1 respectively. These results suggested major inputs of carbon and nitrogen at four locations in the watersheds; furthermore, temporal variations were identified with higher TOC content in March than April and May. For EEM analysis, we investigated integration times of 1, 2, and 3 s and wavelength step sizes of 1, 2, and 3 nm. Relative regional volumes corresponding to (i) tyrosine, (ii) tryptophan, (iii) fulvic acid, (iv) soluble microbial product, and (v) humic acid -like fluorescence were calculated to assess impacts on fluorescence response. Smaller wavelength step sizes and longer integration times improved EEM resolution; however, these changes also decreased instrumental throughput. To balance analytical resolution and runtime, an integration time of 2 s and wavelength step size of 3 nm were selected. Future work will involve spatiotemporal analysis of EEMs, TOC, TN, and specific contaminants to identify leaking sewers in Baltimore City.

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POSTER 29

PARTICLE COLLECTION MECHANISM FOR DUSTY PLASMA CHAMBER

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Monodisperse particles generally refer to a sample of microscopic particles that are uniform in shape and size. Monodisperse particles are becoming increasingly important, especially in medical studies. In order to obtain a uniform distribution of particles, a separation processes needs to be carried out. This work is part of a larger effort underway at the Dusty Plasma Laboratory at the University of Maryland Baltimore County, in which new separation methods using a dusty plasma chamber are being investigated. In a plasma chamber, various types of micron-sized particles (called dust) can be added and levitated in layers according to their size. When plasma is turned off, particles fall to a collecting plate approximately preserving the layered structure. The objective of this project is to design, build, and test a particle collection mechanism to extract samples of monodisperse particles from the bottom of a dusty plasma chamber without disturbing the vacuum. Solidworks was used to model the design of the collection mechanism. Details of the design, and progress of the assembly and testing will be presented.

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POSTER 30

OPTIMIZATION OF CONDITIONS FOR EXPRESSION OF THE HIV-1 MATRIX PROTEIN

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The human immunodeficiency virus (HIV) is a retrovirus that infects roughly 40 million people globally and attacks the immune system as it infects CD4+ T-cells. The viral genome frequently mutates which gives rise to evasion of current therapies; thus, new treatments are necessary and can be achieved by better understanding viral replication. One critical process of HIV replication is membrane trafficking of the Gag polyprotein to the plasma membrane via Gag's matrix protein (MA). This prerequisite for virion formation is of interest as it has potential as a target for new therapies. In addition to the role of MA in assembly, recent studies have shown that MA interacts with cellular tRNAs before binding to the plasma membrane; however, the role of tRNA in assembly is poorly understood. The long-term goal of this work is to study the MA:tRNA complex and elucidate its 3D structure to shed light on the influence of tRNA during membrane targeting. In order to achieve this goal, large quantities of MA must be expressed, and conditions in which MA is soluble for extended periods must be identified. Analysis of SDS-PAGE data of samples collected from various stages of protein expression and purification illustrated that salt did not influence protein solubility. Decreased expression temperature from 37 °C to 20 °C appears to increase natural abundance protein expression. Optimization of conditions during protein expression and purification will increase efficiency and, ultimately, help to characterize the MA:tRNA complex interaction.

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POSTER 31

RNA PURIFICATION FOR BIOPHYSICAL STUDIES

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The human immunodeficiency virus (HIV) infects millions of people each year, deteriorating their immune systems and causes the onset of acquired immunodeficiency syndrome. As a retrovirus, HIV carries its genetic material as RNA, whose sequence and structure is important to virus production. Especially the 5′ untranslated region (5′ UTR), most of whose sequence is shared in all viral RNAs, is highly conserved and structured, and its conformation directs and regulates viral life activities such as reverse transcription, splicing, translation and packaging. Therefore, studies on the structure of 5′ UTR helps us to have a better understanding of the HIV infection mechanisms. RNA preparation needs to be done prior to structural studies. Our work describes how to prepare the 5′ UTR of envelop RNA for further structural studies that use nuclear magnetic resonance (NMR). The RNA is made through in vitro transcription. The optimal transcription condition is determined by a small scale trial transcription and a high yield is achieved by large scale transcription. Denaturing gel electrophoresis followed by electro-elution is used for RNA purification and extraction. The RNA is further purified with high salt concentration and then exchanged in water. Once purified, the RNA sample is lyophilized and exchanged in deuterated water for better NMR detection. NMR provides definitive structural information of RNA that can be used to help design better drug therapies for HIV infection.

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POSTER 32

RELATIONSHIP BETWEEN CAPSID AND TAIL LENGTHS FOUND IN MYOVIRUS PHAGES

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Bacteriophages are viruses that target, infect, and replicate within the domain bacteria. The research experiment focuses on the morphology of isolated phages and investigates the possibility of a correlation between phage capsids and uncontracted tails of myovirus phages. The process of isolating phages from soil samples is the priority in the experiment. The isolation is accomplished using direct plating or the use of an enrichment, followed by three days of phage purification. To accomplish this, webbed plates are made from three days of serial dilutions. Webbed plates are then used to create a stock lysates of the phages after the final purification. The lysates are then placed on individual copper grids and a Transmission Electron Microscopy (TEM) is used to produce images of the phages. Once the images are collected, an image measurement software, ADI Java, is implemented to determine the phage dimensions. Data collected at UMBC from 2014-2016 and 2019 was considered for this analysis. Certain characteristics were considered when selecting the phages used such as infecting Bacillus, belonging to the myovirus classification, and having an uncontracted tail. This was done to maintain consistency among the data set. Both enrichment and direct plate samples were considered. Soil samples used for the analysis were not limited by location.
The phage's head lengths ranged from 45-160nm, and its tail lengths ranged from 80-300nm. The average head length was found to be 87.74 (+/-5.71) nm, while the average tail length was 189.35 (+/-189.35) nm. A standard deviation of 16.42 and 28.78 was also found for the head length and tail length respectively. A graph of the ratio between head and tail length produced a Gaussian distribution with an average of 2.21. This means the phages tend to have tail lengths about twice their head lengths.

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POSTER 33

LOSE OF TRNA POST-TRANSCRIPTIONAL MODIFICATIONS AND ITS IMPACT ON TRNA ACCURACY IN SACCHAROMYCES CEREVISIAE

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tRNA, the mediator molecule that helps to convert an mRNA template into a protein product in ribosomes, is a known source of translational errors. Two common forms of tRNA error include misacylation, the charging of tRNA with the wrong amino acid, and misreading, the matching of a tRNA's anti-codon region to the incorrect mRNA codon. We are investigating how the loss of specific post-transcriptional modifications of the tRNA core structure may affect its rate of translational error. While the role post-transcriptional modifications play in tRNA stability is well established, we believe these modifications may serve a more direct role in maintaining translational accuracy, independent of preventing tRNA degradation.

In order to measure the difference in translational error rates we grew up 16 leucine deficient mutant *Saccharomyces cerevisiae* colonies. The 16 colonies had a plasmid inserted into them that contained leucine synthesis genes and a gene that encoded for the production of a his-tagged albumin protein. These mutant colonies each contained glutamic acid tRNA that lacked modifications, lysine tRNA that lacked modifications, or neither. We proceeded to purify the albumin protein product of these colonies using nickel resin affinity chromatography. We used western blotting to analyze the albumin protein product and found that the colonies had produced inconsistent amounts of our desired protein product. We are currently investigating and optimizing our protocol to ensure a more consistent protein yield. We are also exploring the option of a different His-Tagged protein product being utilized.

Future work will include use of mass spectrometry to analyze the amino acid sequences to compare the rates of lysine and glutamic acid misincorporation for the respective mutant colonies.

NAIVE ETHANOL ODOR PREFERENCE IN DROSOPHILA MELANOGASTER

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Addiction is the continued use of a substance despite the consequences, approximately 70,000 Americans died from drug overdoses in 2017. The detrimental effects of addiction is expected to increase annually. It is known that genetics and environment play significant roles with addictive-like behavior. Drosophila melanogaster, or the common fruit fly, have been shown to have an innate preference to ethanol, making them a model organism to study the genetic component of addictive-like behaviors. We were interested to understand the impact of mating status (virgin or mated) and group dynamics (individual or groups of 10) on fruit flies naïve ethanol odor preference (NEOP). To address our question, the NEOP to 23% ethanol dissolved in apple juice for the D. melanogaster DGRP-774 line was tested. Individual and groups of Drosophila were tested in T-maze assays where their sense of smell, olfaction, was isolated to show their preference to ethanol. We hypothesized mated female Drosophila would have a high NEOP. We hypothesized sexually-deprived individual male Drosophila would show a high NEOP because ethanol would satisfy reward centers in the brain. Additionally, we hypothesized isolated Drosophila would exhibit different preferences than a group of Drosophila because there are no environmental or social influences. Our results demonstrated that individual female flies have a repulsion to 23% ethanol compared to male flies. Overall, our data has shown that sexual status does not have a significant effect on individual male and female flies ethanol preference on ages 1 to 4 (23%.) Our results show that group dynamic with virgin male Drosophila had a significant role in NEOP on age 2. While not significant, our results showed varying NEOP patterns depending on the social environment, suggesting that Drosophila exhibit more complex social behavior than believed.

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POSTER 35

CHARACTERIZING THE DYNAMIC CAPSID-SP1 JUNCTION HELIX OF THE HIV-1 GAG POLYPROTEIN AND MATURATION INHIBITOR INTERACTION

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Currently, 36.9 million people worldwide are living with the Human Immunodeficiency Virus (HIV) and new drug targets are in demand due to HIV's ability to rapidly mutate. Research efforts have been directed toward the replication cycle of HIV in order to identify landmarks crucial to the virus' infectivity as targets for inhibitory drugs. During assembly, thousands of the major structural protein for HIV-1, the Gag polyprotein, multimerize at the cell membrane and form a hexagonal lattice. Gag consists of Matrix (MA), Capsid (CA), Nucleocapsid (NC), and P6 domains, as well as two spacer peptides, SP1 and SP2. The transition of the CA-SP1 junction region from a random coil to six helix bundle is critical for Gag assembly. Assembled Gag is cleaved by the viral protease between different domains resulting in a mature infectious virus. The rate determining step of maturation is the cleavage between CA and SP1 with the scissile bond buried inside the six helix bundle. Maturation inhibitors, such as bevirimat, prevent the cleavage at CA-SP1. The CA-SP1 junction helix should have sufficient stability to allow Gag assembly, however, it should also have appropriate flexibility to allow viral protease access to the cleavage site. We hypothesize that the CA-SP1 junction helix is in a dynamic equilibrium between a tight alpha helix and loose random coil in order to mediate assembly and maturation. We aim to use solution Nuclear Magnetic Resonance (NMR) to elucidate the dynamic nature of the junction helix. NMR studies can also allow for the study of whether the cleavage-inhibitory effect of bevirimat is due to stabilizing the CA-SP1 junction helix. A greater understanding of the dynamics of the junction helix and its interaction with bevirimat provides more information to be used for the design of drugs that cease viral infectivity in those affected by HIV-1.

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POSTER 36

STRUCTURAL CHARACTERIZATION OF HUMAN IMMUNODEFICIENCY VIRUS TYPE-1 SPLICED RNA

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During human immunodeficiency virus (HIV) infection, only the full-length genomic RNA (gRNA) is packaged as a dimer, from a large excess of viral spliced RNAs and monomeric gRNA, through the packaging signals located in the 5′ untranslated region (5′ UTR) in the gRNA, whose conformation is crucial to viral life activities. However, most of the 5′ UTR, including most of the packaging signals, are shared in all viral RNAs, leading to the question of why the spliced RNA is not packaged efficiently. Our work aims to provide a structural insight into the inefficient packaging of spliced RNA. The structure of the 5′ UTR in the spliced RNA was characterized by both two-dimensional nuclear magnetic resonance (2D-NMR) and selective 2′ hydroxyl acylation analyzed by primer extension (SHAPE). The formation of the TAR and U5:DIS stem loops in spliced RNA has been confirmed by 2D-NMR with various selective deuteration strategies. Due to the size limitation and peak broadening in NMR, SHAPE will be used to probe the flexibility of the polyA region and help elucidate the structure of larger spliced RNA constructs. Using a combination of NMR and SHAPE will allow us to get a more thorough understanding of the structure and function of the HIV spliced RNAs 5′ UTR.

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POSTER 37

CORRELATION OF MAGNESIUM AND CALCIUM CONCENTRATION TO HOST RANGE OF PHAGES INFECTING B. THURINGIENSIS KURSTAKI

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In this study of bacteriophages that inhabit soil, environmental samples from different locations in the East Coast were used to expand our knowledge of phages that infect Bacillus cereus group species such as B. thuringiensis subsp. kurstaki (Btk). Data collected after isolating and characterizing eight phages were analyzed to investigate the relation of soil composition and host range.

Bacillus phages were characterized by testing the host range of the phages as well as the magnesium and calcium concentrations found in their soil. Phages were plaque purified on Btk lawns at least three times, then plate harvested to produce a crude lysate. This lysate was serially diluted and spot tested onto plates of nine unique Bacillus cereus group species to test the host range of the phages. Using magnesium and calcium standards, five dilutions ranging from 0.5 ppm to 150 ppm were measured using an ion chromatograph. Conductivity detection was used to create calibration curves for the soil samples the phages were harvested from. The soil was prepared using two percent nitric acid buffer and analyzed to determine the concentrations of magnesium and calcium.

The eight soil samples from which phages were isolated contained varying concentrations of magnesium and calcium. Ranges of magnesium and calcium concentration found for the bacteriophages were 0.002-17.5 ppm and 6.63-284 ppm respectively. It was determined that there was no statistical significance between the magnesium concentration and number of hosts lysed ($p=0.54$) or the calcium concentration vs. hosts lysed ($p=0.07$). Additionally, no relationship was found between the magnesium and calcium concentrations for the eight phages ($p=0.05$), demonstrating that elemental concentrations of the soil vary for the phages isolated in this study and have no direct correlation to the hosts they infect.

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POSTER 38

EDGE DETECTION USING RADON TRANSFORMS AND DYNAMIC PROGRAMMING FOR INDOOR ROBOTIC NAVIGATION

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The way computers and humans see differs greatly. Humans can recognize individual objects, like chairs and tables. A computer, however, sees only an assortment of colors arranged as a grid of pixels. It has no concept that these colors have any meaning. Computer vision is the study of algorithms and mathematical techniques that allow machines to comprehend the contents of images. Line detection is an important problem in computer vision where straight lines in images, like walls and door frames, are detected, which robots must use to effectively navigate boundaries and obstacles.

We evaluate the use of an optimal line detection algorithm known as the Approximate Discrete Radon Transform (ADRT). The Radon transform is an essential method used for digital reconstruction of Computed Tomography (CT), but is rarely applied to computer vision or line detection due to the slow processing time of a traditional implementation. Although faster processing times can be achieved by means of the Fourier transform with the projection slice theorem, this approach is subject to loss of quality due to discrete sampling of a continuous function.

The algorithm uses Dynamic Programming (DP) to remove redundant calculations. DP is a technique where complex problems are broken into smaller overlapping subproblems, whose results are stored in memory. This algorithm runs in $O(n^2 \log(n))$, improving processing time and enabling use in a wider variety of applications compared to the traditional technique's time of $O(n^3)$. Furthermore, this method does not suffer from sampling issues of the projection slice techniques.

We present the ADRT algorithm, its implementation, and performance analysis for the identification of linear edges in indoor photography. Finally, we discuss its applicability to robotic navigation as well as the potential benefits and limitations of ADRT as compared to standard line detection algorithms, including the Hough transform.

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POSTER 39

DETERMINING THE VIABILITY OF BROMINATED CARBON NANODOTS AS BACTERIAL INACTIVATORS

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 40

SYNTHETIC HYDROGELS FOR HIDE GLUE REMOVAL FROM PARCHMENT

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Hydrogels are regularly used to clean works of art in the conservation process. Identifying residual gel left on works of art after a cleaning treatment is necessary because it is unknown how residual gel will affect the treated artwork over time. Parchment, a water-sensitive substrate commonly used in old books and manuscripts, can be treated with hydrogels to remove dirt and adhesives for the restoration and conservation of historical works. In this work, physical gels were prepared from high acyl gellan gum (HAGG) in an aqueous solution of calcium acetate. In parallel, pHEMA/PVP chemical gels were synthesized via polymerization of 2-hydroxyethyl methacrylate (HEMA) and cross-linking with polyvinylpyrrolidone (PVP). The performance of high acyl gellan gum (HAGG) and pHEMA/PVP hydrogels for treating hide glue on parchment was evaluated. Hide glue removal efficiency for HAGG gel was determined using gravimetric analysis and by observing parchment modification using scanning electron microscopy/electron dispersive x-ray spectroscopy (SEM-EDS). HAGG gel was found to take up 44.6% to 59.4% of new hide glue from parchment as a function of a 20- to 75-minute contact time. However, infrared spectroscopy (IR) showed evidence of residual HAGG gel left on the parchment. pHEMA/PVP gel liquefied the glue by delivering water to its surface. The efficiency of this process was analyzed at varying gel hydration levels and HEMA concentrations using gravimetric analysis. It was found that decreasing concentration of HEMA in the gel and increasing hydration level increased the efficiency of water delivery to the samples. No residual pHEMA/PVP gel was found on parchment using IR spectroscopy. The combination of chemical and physical gels may offer an effective adhesive removal treatment in the art conservation field.

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POSTER 41

FINANCING PUBLIC HEALTH OUTCOMES: EXPLORING THE RELATIONSHIP AMID HEALTH EXPENDITURES AND MATERNAL MORTALITY IN THE STATE OF MARYLAND

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Abstract not available at time of printing. Please see the poster for more information.

POSTER 42

PHOTODEGRADATION OF TETRACYCLINE ANTIBIOTICS AT UV-254: SPECIES-SPECIFIC REACTION KINETICS

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Tetracyclines are the most frequently prescribed class of antibiotics employed in human and veterinary health. These pharmaceuticals are not completely metabolized by the human body and, consequently, have been detected in wastewater treatment plants at concentrations up to 4 μg L-1. In this study, the direct photolysis degradation kinetics of six tetracycline antibiotics, namely chlortetracycline, doxycycline, meclocycline, methacycline, oxytetracycline, and tetracycline, were investigated at 254 nm using a merry-go-round Rayonet reactor. The tetracycline pharmacophore consists of an octahydrotetracene backbone, and different tetracycline derivatives involve incorporation of various functional groups. At pH 7.2, apparent quantum yields ranged from 3.96×10-3 mol Ein-1 (doxycycline) to 1.20×10-2 mol Ein-1 (oxytetracycline). The complex electronic structure of tetracycline generates up to 18 theoretical protonated/deprotonated species; however, three apparent acid dissociation constants (i.e., approximately 10-3, 10-7, and 10-9) are generally used to describe chemical speciation. To determine the impact of speciation on tetracycline degradation kinetics, experiments were conducted at pH 2-12 by adding 5 mM phosphate buffer to solutions with 5 μM antibiotic. The apparent fluence-based rate constant increased with solution pH due to the increased electron density of deprotonated species. For example, the species-specific, fluence-based rate constants for oxytetracycline were 1.45×10-4 cm2 mJ-1, 1.87×10-4 cm2 mJ-1, 9.59×10-4 cm2 mJ-1, and 2.21×10-3 cm2 mJ-1 for the cation, zwitterion, monovalent anion, and divalent anion, respectively. To identify other kinetic impacts from real wastewater matrices, the influence of divalent cations on phototransformation kinetics of tetracyclines was investigated by dosing 5 mM Ca2+ and 2 mM Mg2+ to experimental solutions containing 5 μM of individual tetracyclines. These cations can bridge or complex tetracycline molecules, which may result in higher apparent degradation kinetics. Despite the relatively fast phototransformation kinetics and high quantum yields reported in this study, advanced treatment processes are needed to effectively transform tetracyclines in wastewater treatment plants.

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POSTER 43

DEVELOPING 3D SCREEN BIOPRINTING TECHNIQUES FOR TISSUE ENGINEERING APPLICATIONS

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3D bioprinting constructs better in vitro structures than the 2D monolayers which are currently being used in tissue engineering. The 3D bioprinted structures are able to guide the growth of cells of functionally engineered tissues and are able to better mimic in vivo conditions.[1] The high efficiency, precision, and accuracy of 3D bioprinting made it gain popularity throughout the world.[2] However, the cost to printing these 3D structures is very high, due to the requirement of specialized equipment, which is why we are investigating technique inspired by screen printing process to create an inexpensive way to print 3D structures. In this project we will explore the most cost-effective way to create 3D prints using hydrogel scaffolds for tissue engineering. A bioink made of hydrogels, extracellular matrix proteins and cells will be used to print the different patterns using the screen-printing process. With this new technique of bioprinting, more researchers will have access to inexpensive bioprinting and thus this will open the door for more scientists to have an opportunity to study models which are more similar to in vivo conditions. This study presents the construction of the screens for the bioprinting process, along with the reproducibility and resolution of the prints. When testing the resolution of the prints, different patterns were used, such as, lines, dots and curves, with different sizes ranging from 300 micrometers to 1000 micrometers. The preliminary data demonstrates the reproducibility and reliability of the screen-printing process and also gives an estimate of the resolution of the prints. In the future, more patterns will be developed such as a circular grid to mimic crypt patterns which are found in the gastrointestinal tract.

[1]Pina, Sandra, et al. "Scaffolding Strategies for Tissue Engineering and Regenerative Medicine Applications." Materials 12.11 (2019): 1824.
[2] He, Yong, et al. "Research on the printability of hydrogels in 3D bioprinting." Scientific reports 6 (2016): 29977.

POSTER 44

TESTING THE EFFICACY OF A DOPAMINE 1 RECEPTOR IN VITRO

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Melanopsin, a visual pigment expressed in intrinsically photoreceptive retinal ganglion cells (ipRGCs) contributes to circadian photoentrainment and other image forming and non-image forming visual process. It is hypothesized that Protein Kinase A (PKA) has a role in attenuating the signaling of melanopsin. Because PKA activation is part of the dopamine cascade, we are also interested in studying the effect of dopamine on melanopsin signaling. In my work, we are testing the efficacy of a dopamine 1 receptor antibody in HEK cells, as many dopamine receptors are expressed in HEK cells. To test the efficacy of our antibody, we used Immunohistochemistry to determine the localization of the antibody reactivity in the cells. The results suggest that the antibody is effective in labeling D1 receptors, as the localization of the antibody is in the plasma membrane of the HEK cells, which is where we hypothesized the receptor would be localized. In the future, we will use this antibody in vivo, to look at dopamine 1 receptor expression in ipRGC in the retinas of dopamine 1 receptor knockout mice and wild type mice. By determining the efficacy of this antibody, it can be used as a control to determine the quantity of D1 receptors, enabling further experimentation on the role of dopamine and PKA on melanopsin signaling.

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POSTER 45

ASSESSING THE FUNCTION OF HUMAN AMYLOID PRECURSOR PROTEIN AND ITS FLY HOMOLOG APP-LIKE IN DROSOPHILA

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Alzheimer's disease (AD) is a type of dementia that is progressive over time and eventually leads to a loss of basic human brain function. Currently this neurodegenerative disease affects 5.8 million of Americans and it is the 6th leading cause of death according to the Alzheimer's association. AD manifests itself by the destruction of nerve cells which in turn causes loss of brain function. The amyloid beta fragment (Aβ42) that results from the cleavage of the amyloid precursor protein (APP), forms plaques in the brain which causes cell death. The fruit fly Drosophila melanogaster has a protein APP-like (APPL) that shares a high degree of conservation to human APP. Therefore, we use powerful genetic tools and tractable neuroanatomy available in Drosophila to study human APP and its homolog APPL. We tested appl mutants, as well as flies expressing transgenes of different variants of APPL and human APP. We used flight behavioral assays to analyze the effects of the expression of the different transgenes in flies that are 2 days (2d), 10 days (10d), and 30 days old (30d). To test the flies, a drop test was conducted which consists of dropping flies in a graduated cylinder and recording their landing distance. The measured flight performance is a reading of the function of the motor network including identified flight motoneurons. Large falling distances indicate poor network performance. We observed a decline in flight performance in 30d flies expressing APPL with mutated intracellular domain as well as the human Aβ42 fragments when compared to the performance of 2d flies, suggesting aging-dependent neurodegeneration. Moving forward, we plan to perform anatomical analyses of the motor network to explain the observed behavioral deficits in transgenic flies in order to better understand the role of APP in network function.

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POSTER 46

METAL TOXICITY IN DROSOPHILA MELANOGASTER

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Metal biology and homeostasis are essential mechanisms for the maintenance of human health, which are part of a quickly expanding research field. Transition metals such as Copper, Zinc, Iron, and Aluminum play various roles in cellular function including cell metabolism, signaling, and cell differentiation. However, accumulation, deficiency, or prolonged exposure of these metals can lead to cell dysfunction or even cell death. In fact, previous studies have shown that alteration of metal homeostasis has been linked to neurodegeneration; in particular Alzheimer's disease. To further explore the role and impact these metals have in neurodegenerative diseases, we are using Drosophila melanogaster, a model organism that shares many core genes in cell metabolism with mammals.

The objective of this study is to explore the influence of metals in neuronal function of wild-type male flies by testing their flight performance. Our results show that exposure to high concentrations of Zinc caused an immediate lethality after 5 days of exposure, whereas prolonged exposure to medium and low concentrations showed a delayed, but still lethal outcome after 10 days. We also observed that high concentrations of Aluminum decreased flight performance, as well as lethality after 5 days. To further investigate the role of metals in neurodegeneration, we will examine the anatomy of the nervous system, paying special attention to neurons in the flight motor network. Anatomical abnormalities found in metal exposed Drosophila will be compared to pathological symptoms observed in Alzheimer's disease to identify shared mechanisms and possible common regulators. These findings would increase our understanding of how metal regulation affects neurodegeneration and brain function to promote the development of future genetic or pharmacological treatments.

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POSTER 47

TRANSCRIPTION AND PURIFICATION OF ΔPBS_U1A FOR STRUCTURAL ANALYSIS

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Human Immunodeficiency Virus (HIV) is a global pandemic that has infected 36.9 million individuals worldwide. It is most prevalent in Sub-Saharan Africa, where 71% of all individuals are infected. This retrovirus specifically targets CD4 T-cells found within the immune system and must reverse transcribe viral RNA to viral DNA to facilitate its integration within the nucleus of the host cell. Existing therapies target mutation prone regions of HIV-1, leading to the necessity of using a cocktail of drugs to combat HIV-1 losing its effectiveness over time. As a result, this study aims to elucidate the secondary structure of the 5' Untranslated Region (UTR) of the viral RNA, in the hopes of discovering breakthrough therapies in the future.

Large RNA – greater than 60 nucleotides— have historically been difficult to study structurally due to both their size and flexibility. To bypass the typical problems that arise from studying such RNA in hopes of elucidating the secondary structure of the 5' UTR, a novel technique was proposed. Specifically, the PBS region within the 5' UTR was cleaved and replaced with a U1A binding loop to which the U1A reporter protein paired with a paramagnetic metal ion tag would bind. However, before the latter work could be completed, a 5' UTR construct, in this case, dPBS_U1A, must first be procured and extensively synthesized .

To begin, template DNA of dPBS_U1A must undergo PCR amplification to obtain large quantities of template dPBS_U1A RNA. Next, a trial transcription is done to determine optimal conditions, followed by a large scale transcription reaction of the RNA template with the optimal conditions. In order to rescue and purify the RNA, it is placed in an elutrap, where an electrical current runs through the gel pieces containing the RNA and drives them toward a filter that catches the RNA, thus purifying the RNA. Purification of the RNA continues by putting it through a series of different solutions including NaCl solution, MgCl solution, and RNA Water that got rid of unwanted nucleotides and waste products when centrifuged. Finally, the RNA is rescued from the filter and ready for use in structural studies that will pave the way for novel therapies in the future.

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POSTER 48

THE DEVELOPMENTAL ROLE OF APPL IN DROSOPHILA MELANOGASTER

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Alzheimer's Disease (AD) is a progressive brain disorder that deteriorates memory, decision-making, and thinking skills, and is often accompanied by smaller brain size. In 2018, AD was named the sixth leading cause of death in the United States, thus research in understanding the molecular mechanisms underlying AD is essential for therapeutic purposes. The fruit fly Drosophila melanogaster can be used as a genetic model to study human diseases because 75% of the genes associated with neurological diseases are present in the fly genome. One of the genes associated with AD, the Amyloid Precursor Protein (APP), is evolutionary conserved and has a Drosophila homolog, called App-like (APPL), making it a relevant gene to our study.

In my project, I focus on the developmental role of APPL in Drosophila. In order to do so, we mated APPL flies to produce an F1 generation with mutations in the APPL gene. In collecting data, I monitored the reproduction rate, fertility, and gender of the flies in order to observe developmental effects of mutations in APPL. In the future, I would like to use larvae to study not only APPL but also different versions of human APP and I would like to also conduct dissection to see where else they may be a difference.

This project was supported by the NSF USM LSAMP Program and the UMBC Natural Sciences Pre-Professoriate Fellowship to Fernando Vonhoff.

POSTER 49

ESTABLISHING ZEBRAFISH AS A MODEL TO STUDY GENETIC COMPONENTS UNDERLYING NEURAL TUBE DEFECTS USING CONSERVATION OF MOLECULAR AND GENETIC COMPONENTS.

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Primary neurulation is the process via which the neural plate bends and folds around medial and lateral hingepoints to promote the fusion of the neural folds (the lateral edges of the neural plate) to form the neural tube, the precursor of the brain and spinal cord. Neurulation is frequently disrupted in human populations, causing neural tube defects (NTDs). While the underlying causes are not well understood, mutations in genes encoding Planar Cell Polarity (PCP) pathway components are associated with severe NTDs. In mice mutant for PCP genes, it has been demonstrated that the neural plate fails to narrow due to abnormal cell polarization. Furthermore, the medial hingepoint does not form properly in these mutants. These combined defects result in an open neural tube. The goal of my research project is to investigate whether the PCP pathway plays a conserved role in the zebrafish embryo, in an effort to develop this organism as a model to study neurulation. Indeed, our laboratory has recently found that hallmarks of primary neurulation, hinge points and neural folds, are present in the presumptive forebrain. Furthermore, a mutation in the PCP core component vangl2 resulted in a failure of the hinge point to form. To test whether this defect prevents proper convergence of the neural folds, I carried out in situ hybridization on WT embryos and PCP vangl2 mutants, using emx3 (a neural fold marker) as a riboprobe. My data reveal delayed convergence of emx3-positive cells in vangl2 mutants at the 5 somite stage, which was less obvious at 7 somites. Furthermore, the shape of the neural folds in the mutants appeared abnormal, suggesting that neural folds fusion was not properly established in these embryos. These data are consistent with a conserved role for PCP in hingepoint formation and convergence of the neural folds.

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POSTER 50

DUAL RELEASE POLYURETHANE NANOCAPSULES: A NEW APPROACH TO DRUG DELIVERY

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Drug delivery systems are becoming increasingly important in targeted transport and controlled release of various therapeutic agents. While there is a multitude of cases wherein a single drug delivery system would have therapeutic effects, certain circumstances warrant the creation of a multi-drug delivery system to address challenges such as drug resistance. Despite some two-part drug delivery systems already being in clinical use, there is currently no way to deliver two different drugs in a manner that allows for sustained and targeted drug release while simultaneously releasing the drugs at two different desorption rates. We propose the production of polyurethane nanocapsules via a two-phase poly-condensation system through mini-emulsions using isophorone diisocyanate (IPDI) and 1,6-hexanediol (HDOH). These nanocapsules will contain both hydrophobic and hydrophilic fluorophores: the hydrophobic fluorophores occupying the core of the capsule and hydrophilic compounds in the capsule matrix. Hydrophobic fluorophores, like rhodamine 6G and 4-chloro-7-nitrobenzofurazan, and hydrophilic fluorophores, such as fluorescein, are used for proof of concept in encapsulation procedures. Polyurethane is the polymer of choice because it is thermally stable, biocompatible, and biodegradable. The synthesized capsules are characterized using dynamic light scattering (DLS) to determine the size and zeta potential and Fourier-transform infrared spectroscopy (FT-IR) to determine the chemical composition. Release studies are being performed at bodily equilibrium in a 37°C oven in phosphate-buffered saline (PBS) to determine duration of release. We found polyurethane capsules containing rhodamine 6G can release an average of 1.28 µg over a five-week period, proving its ability for long term release. We also found the loading (mg) of fluorescein per mass (mg) of capsules to be 0.1.38E-09 mg/mg. The capsules are being optimized to ensure effective loading efficiency and release of both hydrophobic and hydrophilic fluorophores, which would provide a novel method for the simultaneous delivery of two different drugs.

EVALUATION OF METHODS FOR THE QUANTITATION OF NITRATE IN AQUATIC SYSTEMS

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Nitrogen is an important element that comes in many different forms, such as ammonia which is used to make fertilizers, nitrite; which when used with sodium fights harmful bacteria in meats and nitrate, a major source of nitrogen for aquatic plants. Even though nitrate helps aquatic plants grow, high concentrations of nitrate can be detrimental. Excess nitrogen in a body of water could cause algal blooms, which prevents sunlight from penetrating deeper waters and depletes the area of oxygen, causing aquatic life to suffer from a lack of vital resources. The importance of nitrate necessitates monitoring its concentration across the environment. A multitude of nitrate water testing methods are used, varying in difficulty, accessibility, and cost. Three common methods are test strips, titration kits, and ion chromatography (IC). The goal of this project is to evaluate these methods for accuracy and precision and application to various samples. Test strips, which are cost effective and easily accessible, indicate concentration by color gradients and provide general estimates of nitrate levels. Titration kits also work by color change and provide more specific values but are more difficult and time consuming. IC is analytical instrumentation typically only found in a laboratory, making it largely inaccessible and costly. Chromatography separates nitrate from a mixture and a UV detector provides a measurement of nitrate present. A standard of known concentration will be analyzed by all three methods and used to statistically determine accuracy and precision. Accuracy is determined by how close the data is to the known value; precision measures how repeatable the data is. To determine precision, samples will be analyzed in triplicate. The three quantitation methods will also be used on samples collected from fresh water and saltwater environments to assess how successful the methods are for various environments and applications.

I would like to thank Mrs. Johnson for giving me the opportunity to be a part of the Summer Biomedical Training Program funded by the College of Natural and Mathematical Sciences. Also, I would like to thank the MCAC team for helping me with my research.

POSTER 52

EFFECT OF AUTISM SPECTRUM DISORDER ON MORPHOLOGY OF NEURONS IN FRUIT FLY LARVAE

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Drosophila melanogaster, or more commonly known as the fruit fly, is apart of the genus of flies from the Drosophilidae family. They are excellent for biological studies because of their genetic mechanisms as well as basic neurological development are conserved in humans. In our study, we are investigating the genetic basis of autism disorder using the fly larva from a physiological perspective. For this, we analyzed fly larvae that have genetic manipulations affecting different genes associated with autism, as well as control larvae that have "normal" or unaffected genes in order to compare their behavioral and anatomical properties to identify developmental defects. In order to do this, we do different lab techniques such as "rolling" and dissections to study them. Rolling is a lab technique where larvae are placed on a flat surface and poked with a sharp laboratory device in order to test their sensitivity and response to pain stimuli. When the larva has a high sensitivity to the device, it tends to curl and roll, hence the name. We also dissect these same larva leaving only their brains after dissection in order to analyze their neurons under the microscope. The neurons involved in this response are nociceptive sensory neurons located in the larval epidermis. Due to this information, we are also studying the epidermis of the flies in order to look at their thickness. To accurately measure the epidermis properties, we will use a Transmission Electron Microscope (TEM) or confocal microscopy. We have a slight modification of our focus on male and female larvae to only females because of the lack of male crosses produced. For further studies, we are testing the hypothesis that secreted factors may regulate the interactions between the nociceptive sensory neurons and the larval epidermis.

ANALYSIS OF GLUCOSOME FORMATION IN HUMAN IMMUNE CELLS AND MOUSE CANCER CELLS

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Multienzyme complexes have been observed to form in cancer cells in response to metabolic stress. These complexes, termed "glucosomes," spatially cluster enzymes involved in glycolysis, increasing the metabolism of glucose in cells and promoting the growth and spread of tumor cells. Here, we examined whether the formation of glucosomes is conserved in human immune cells (promonocyte cell line U937) and mouse cancer cells (4T1 mammary carcinoma cell line) to understand how glucosomes affect tumor-immune cell interactions.

We focused on generating stable cell lines by transfecting plasmid DNAs encoding liver-type phosphofructokinase (PFKL), a key protein found in glucosomes. We used the human and mouse homologs of PFKL fused to a fluorophore, denoted hPFKL-mCherry and mPFKL-mCherry respectively. These were expanded by bacterial transformation and purified using a modified MiraPrep protocol. Plasmid sequences for mPFKL-mCherry matched reference sequences >96%. Transfection of hPFKL-mCherry into U937 cells was attempted by chemical transfection, using PEI and lipofectamine. However, confocal microscopy did not show significant mCherry signal after 24 hours. The high viability also suggested transfection was unsuccessful. Ongoing studies will focus on electroporation. Successful transfection will be followed by selection of stable cells using the antibiotic G418. We determined the minimum concentration of antibiotic required by a kill curve, testing U937 viability at G418 concentrations from 100 to 500 ug/mL. These viability data followed the expected trend, which was a decrease in viability over time. Ongoing studies are focused on replicating these results. Once both desired cell lines are successfully generated, glucosome formation can be studied in vitro and in vivo in mice to determine the effects of glucosomes on tumor growth.

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POSTER 54

INVESTIGATING THE THERAPEUTIC POTENTIAL OF A GAL3 INHIBITOR AGAINST PROSTATE CANCER PROGRESSION

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 55

CREATING A SERIES OF NIR DYE-DOPED POLYMER DOTS

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The goal of this research is to produce a series of near-Infrared (NIR) dye-doped polymer dots. Polymer dots are nanoparticles consisting of pi-conjugated polymers and are useful for a wide range of applications when exhibiting small particle size and high brightness. Doped polymer dots are made by mixing dyes with the polymer during dot-synthesis. Steps that contribute to series production include optimizing the doping ratio, controlling the size and zeta potential of the nanoparticles. NIR dyes have been explored in recent years, however, successes are limited due to availability and poor performance of the NIR fluorescent markers.

The polymer PFBT was used to synthesize polymer dots because of its high photostability. Photostability is vital regarding long-term imaging and tracking applications. Doping polymer dots with the NIR dyes, including 4,4-difluoro-3,5-bis[(E)-2-(furan-2-yl)vinyl]-1,7-dimethyl-8-(4-methoxycarbonylphenyl)-4-bora-3a,4a-diaza-s-indacene (SA247) and 4,4-difluoro-3,5-bis[(E)-2-(1H-pyrrol-2-yl)vinyl]-1,7-dimethyl-8-(4-methoxycarbonylphenyl)-4-bora-3a,4a-diaza-s-indacene (SA248), has the ability to control the fluorescence properties of the dots and ultimately shift the emissions towards the NIR region, which leads to the stabilization and improved brightness of the dye. The initial doping ratio tested for each dye was 20% and was raised or lowered based on the resulting data. So far, it has been determined that the optimal doping ratio for SA247 dye is ~5% while maintaining an acceptable particle size and negative zeta potential. Regarding controlling the size of the nanoparticles, a size of ~20 nm was ideal because the particles need to be small though large enough to maintain a steady fluorescence and good photostability. The next step of this research is to assess the photoblinking and photobleaching properties of these polymer dots.

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POSTER 56

COMPARING STOCHASTIC AND DETERMINISTIC MODELS OF ENZYME CLUSTERING IN GLUCOSE METABOLISM

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Human glucose metabolism involves processes that break down, transform, and produce glucose. While glycolysis is a catabolic process that transforms glucose into pyruvate, gluconeogenesis generates glucose from gluconeogenic substrates. The glycolysis and gluconeogenesis reactions are connected to other pathways to produce various metabolic outcomes, such as the pentose phosphate pathway, serine biosynthesis, and downstream oxidative phosphorylation. The regulatory enzymes involved in these pathways associate into three different sizes of glucosome clusters. Previous work in Jeon et al. (2018) introduced a mathematical model for enzyme clustering in glucose metabolism to study this phenomenon. The study demonstrated that the size of glucosome clusters influences the direction of glucose flux between energy production and biosynthetic pathways, such as the pentose phosphate pathway and serine biosynthesis. In this work, we derive a reduced system using the model in Jeon et al. (2018) and investigate two mathematical models of enzyme clustering: a deterministic model of ordinary differential equations and a stochastic model simulated by Gillespie's algorithm. Stochastic modeling can be utilized for biological systems that have small populations of molecular species especially when stochastic fluctuations play an important role in the system dynamics. In contrast, deterministic models can be applied to systems with large populations of chemical species. We compare the stochastic and deterministic models to examine the role of inherent fluctuations in the reduced system for enzyme clustering in glucose metabolism. Future research will be focused on conducting a sensitivity analysis to examine the relationship between input parameters and metabolic outcome concentrations. Finally, this work has broader applications to understanding the role of stochasticity in biological systems.

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POSTER 57

ROLE OF N-MYC DOWNSTREAM REGULATED GENE 3 (NDRG3) IN CELLULAR ARREST UNDER ANOXIA

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 58

USING NUCLEAR MAGNETIC RESONANCE (NMR) SPECTROSCOPY TO EXPLORE THE STRUCTURE OF THE U5-PRIMER BINDING SITE (PBS) OF THE HIV-1 GENOME

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The human immunodeficiency virus type 1 (HIV-1) affects over thirty million people worldwide and is the causative agent for acquired immunodeficiency syndrome (AIDS). HIV-1 is a retrovirus that has a viral RNA genome which needs to be reverse transcribed into DNA before it can be integrated into the host cell's genome. The integrated viral genome is transcribed back to viral RNA, and these viral RNA transcripts exist in an equilibrium between a monomer and dimer conformation with each conformation having its own unique function. The monomer conformation is translated into the gag-polyprotein while the dimer conformation is packaged into new virions. Once the dimer is packaged into new virions and infects a new cell, the viral RNA needs to be reverse transcribed from RNA into DNA. In order to do this, the reverse transcriptase enzyme needs a primer to initiate reverse transcription. HIV-1 uses tRNALys3 as the primer, and it binds to the primer binding site (PBS) of the 5' leader to initiate reverse transcription. It is hypothesized that the dimer conformation promotes tRNALys3 binding to PBS. To better understand the structure of the PBS region, we use nuclear magnetic resonance (NMR) spectroscopy to structurally analyze this region. Currently we are working on assigning the dimer conformation of the PBS region. The full dimer conformation is too large to be seen clearly on NMR; therefore, we transcribe small RNA oligos of the PBS region into fragments that can be observed by NMR. By assigning the structure of PBS, we can better understand the mechanisms by which tRNALys3 binds.

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POSTER 59

IDENTIFICATION OF ABL AS A POTENTIAL BTK SUBSTRATE: IMPLICATING NEW TREATMENT OF CHRONIC LYMPHOCYTIC LEUKEMIA

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 60

EVALUATING POTENTIAL ISOLATION BIASES IN COMMON PHAGE ISOLATION PROCEDURES

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Bacteriophages are the most abundant entities on the planet. They are viruses that exclusively infect and kill bacteria. With the decreasing effectiveness of antibiotics, it is essential that we find another way to combat bacterial infections, and phages are becoming a more likely solution. The purpose of this research is to not only discover and characterize phages, but to determine whether or not there is a correlation between the isolation method used and the capsid dimension of the phage.

Sixteen soil samples were initially collected from across the east coast and were brought into the lab for isolation. The samples were either direct plated onto lawns of Bacillus thuringiensis subsp. kurstaki and then incubated overnight at 30°C, or placed into an enrichment broth with B.t. kurstaki and incubated overnight. The resulting enrichments were plated on B.t. kurstaki and incubated overnight. Of the sixteen samples, fourteen yielded phage, five from direct isolation and nine from enrichment. Phages were imaged by transmission electron microscope. The program Analyzing Digital Images was used to measure phage particle sizes from the resulting micrographs.

An analysis of the phages head length and width via a 95% confidence interval was performed. This analysis revealed there was no statistically significant difference in the length or width of the heads of the phages found using either isolation method. This was important to know that there is no bias of the isolation methods toward phages of any specific size, and thus shows that the phages discovered in our lab are not preferentially isolated based on capsid size.

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POSTER 61

CONTROLLING ZETA POTENTIAL OF HEMOSTATIC NANOPARTICLES TO REDUCE COMPLEMENT ACTIVATION RELATED PSEUDO ALLERGY

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According to the Center of Disease Control (CDC), trauma is the leading cause of death in individuals between the ages of 1 to 44, with excessive blood loss making up a large portion. The goal of this project is to reduce the internal bleeding in trauma patients using hemostatic nanoparticles. Nanoparticles with a peptide that binds to activated platelets were studied on small and large animal models. In the small animal model, the nanoparticles had successfully reduced bleeding time by 50%. In the large animal model, increased bleeding and a stress response was observed, caused by the Complement Activation Related Pseudo Allergy (CARPA). This is part of an immune response to activation of the complement pathway. One possible explanation for CARPA is the zeta potential (surface charge) of the nanoparticles. The nanoparticles are composed of Poly (d-lactic acid) (PDLA), Poly (L-lactic acid)-Poly (ethylene glycol) (PLLA-PEG), and the amino acid sequence Gly-Arg-Gly-Asp-Ser (GRGDS). There are carboxylic acids on the end of PEG that reside on the surface of the nanoparticles. Once deprotonated by the aqueous phase, the zeta potential becomes negative due the negative charge of the carboxylate. However, it was seen in the Naïve study on the porcine model that highly positive and negative nanoparticles caused CARPA, while neutral ones did not. Therefore, this project investigates the use of cationic surfactants and a positively charged coating to create neutral nanoparticles. The surfactants and coating have a positively charged amine group that should counteract the negative charge of the carboxylate. The cationic surfactants used are Didodecylmethylammonium bromide (DMAB) and Cetyl pyridinium chloride (CPC) and the coating used is Chitosan. Currently, Chitosan holds the most promise controlling the zeta potential and the only material studied that has a trend to help pinpoint the amount of surfactant needed to create neutral nanoparticles.

POSTER 62

DOMAIN BASED ANALYSIS OF YEAST LYSINE METHYLTRANSFERASE IN SET5

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Set5 is a protein found in budding yeast with a split SET domain that belongs to the SET and MYND domain containing family of lysine methyltransferases. Set5 is known to methylate histone H4 lysine residues 5, 8, and 12 and has a mammalian ortholog called SMYD3, an enzyme that methylates histone H4 at lysine 5. SMYD3 is over-expressed in several different types of cancers. By studying Set5 and discovering its function within the cell, we may be able to correlate our findings to SYMD3, leading us to find future chemotherapeutic targets for cancers showing over-expression of SMYD3. Our overall goal in this project is to functionally analyze the methyltransferase activity of Set5 through a series of domain deletions, specifically the N-terminal domain and the N-terminal plus the first SET domain. We aim to express and purify N-terminally truncated versions of Set5 and test the role of the N-terminus in Set5 methylation activity. To synthesize our domain deleted inserts, we began by designing primers to amplify our insert via PCR, using a SET5 containing template vector. We then carried out a restriction enzyme digest to create complementary overhangs on our PCR products and a vector that encodes a GST tag sequence for creating an N-terminal fusion protein. Once ligated, we transformed chemically competent E.coli and grew our colonies on LB+ampicillin agar plates. Currently we are working on refining the cloning protocol to improve the ligation efficiency. Once our construct is obtained, we plan to express and purify the deleted versions of Set5 using glutathione sepharose affinity resin and perform in vitro methylation assays to determine the contribution of the N-terminal regions to Set5 methyltransferase activity.

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POSTER 63

INVESTIGATING THE GENETIC CONTROL OF BORDER CELL MIGRATION IN D. MELANOGASTER

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The process in which groups of cells coordinate their movements as a cohort is known as collective cell migration. This mechanism is essential to the formation of our tissues during development and can also contribute to disease, such as cancer metastasis. To better understand the genetic basis of coordinated cell migration, we used Drosophila melanogaster, the fruit fly, as a model organism to identify conserved processes. A border cell cluster is formed from a group of epithelial follicle cells in an egg chamber (located in Drosophila ovary). In response to several signals, border cells detach from the epithelium and begin migration to the oocyte, a process necessary for the formation of a viable egg. Here, we investigated the roles that the genes effete (which encodes a ubiquitin conjugating enzyme), Spase22-23 (which encodes a peptidase in the signal peptidase complex), and wunen and wunen2 (both of which encode lipid phosphatases) play in border cell migration. We first determined the expression patterns of these genes in egg chambers. We used RNA interference to knock down expression of these genes in subsets of cells to determine their function. We have been investigating the effects of loss of function of the four genes by using antibody staining procedures and immunofluorescence imaging in egg chambers observing if border cell migration is impaired when compared to a wild type control. The results we obtained were that effete and wunen gene knockdown in the follicle cells did not have a mutant phenotype in border cell migration. However, the knockdown of Spase22-23 in the follicle cells displayed delayed migration of the border cells. wunen2 loss of function egg chambers also showed a defect in cell migration. The knockdown of wun2 in polar cells resulted in the border cell cluster to arriving to the oocyte at an early stage.

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POSTER 64

LIGHT-DEPENDENT ENDOCYTOSIS OF MOUSE MELANOPSIN

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Melanopsin is a unique vertebrate visual pigment expressed in intrinsically photosensitive retinal ganglion cells (ipRGCs) of the mammalian retina. It plays a role in non-image forming vision by signaling to the suprachiasmatic nucleus (SCN) and olivary pretectal nucleus (OPN) of the brain and regulating functions such as circadian photoentrainment and pupillary light response. It initiates a Gq signaling cascade that results in ipRGCs depolarization. The majority of the work in the field has focused on how melanopsin activates and deactivates but little is known about how it resensitizes and how this might contribute to sustaining light responses. We hypothesized that light activated melanopsin bound to arrestin will be endocytosed through clathrin mediated vesicular transport. To test our hypothesis, we transfected (cell culture) HEK 293 cells with the mouse melanopsin gene. Then, we performed immunocytochemistry of transfected cells. The antibody we used specifically labeled melanopsin, and we observed that it labeled melanopsin expressed in HEK cells. A clathrin specific antibody was used to analyze localization of both proteins (clathrin and melanopsin) in both dark and light conditions. Confocal microscopy was used to visualize the cells. We have preliminary data suggesting that melanopsin is endocytosed after light exposure. Specifically, melanopsin fluorescence was observed in the cytoplasm and this labeling overlaps with the clathrin fluorescence. In conclusion, our data suggests that melanopsin undergoes a light-dependent endocytosis process which can contribute to sustain light responses and unique to the retina.

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POSTER 65

MODIFICATION OF SURFACE OF HEMOSTATIC NANOPARTICLES USING CATIONIC SURFACTANTS

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To combat trauma, the leading cause of death of humans from ages 1 through 44, hemostatic nanoparticles have been created and modified to resolve the trauma of bleeding. Hemostatic nanoparticles are made from poly (l-lactic acid)-b-poly (ethylene glycol) block copolymer and poly (D-lactic acid). These nanoparticles work via the intravenous route, traveling to the site of injury, and binding with activated platelets to assist in faster blood clotting. Within the rodent model, specifically the femoral artery and liver injury model, these nanoparticles improved the survival rates as well as reduced the clot formation time by 50%. When tested on the porcine model, it resulted in hypersensitivity reactions as a result of complement activation. Essentially, complement protein fragments are generated, some of which are anaphylatoxins that cause hypersensitivity reactions which clear the nanoparticles from the system. Based on the naïve injury model, highly negative and highly positive zeta potential lead to complement activation whereas neutral nanoparticles within range of -3 to 3 mV did not. The nanoparticles are inherently in negatively charged due to deprotonation of the carboxyl group of the polymer. To combat this, we are working on surface modification utilizing cationic surfactants and positive coatings. In the case of cationic surfactants, it is expected that the cationic surfactant will lead to an ionic core within the nanoparticles, that will help in getting the shift in zeta potential towards the neutral zone. The focus of our research has been determining optimum conditions to reproducibly produce neutral nanoparticles. For that, we have been working with a range of concentrations of cationic surfactant. Future direction would be towards utilizing these nanoparticles for in vitro complement assays to determine whether the neutral charge can overcome CARPA and eventually apply it in a large animal trauma model.

This work is funded by Accelerating Innovation in Military Medicine (AIMM) Research award (DOD) (Award Number: W81XWH1820061)
Title of project: Intravenously infusible nanoparticles to stop bleeding and increase survival following traumas

POSTER 66

DISCOVERING CAUSAL RELATIONSHIPS FOR ATMOSPHERIC TELECONNECTIONS USING BAYESIAN NETWORK

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For years, fluctuations in global climate patterns has been influenced by atmospheric teleconnection patterns. These atmospheric teleconnections are related to one another at large geographical distances. Although climate variabilities have been confirmed to be related to atmospheric teleconnections, what still remains to be discovered is the causal relationships between atmospheric variables.

Thus, this study seeks to discover the causal relationships between these variables and how they can be used to identify teleconnection patterns. For this study, the Dynamic Bayesian Network (DBN) based approach was applied, where each node represents a variable and location while their arcs represents a relationship. Using this probabilistic graphical model focused on dynamic systems allows for making inferences on the causal relationships between variables.

To begin, data retrieved from ERA-Interim global atmospheric reanalysis data set between 1979 and 2018 was used and recomposed within an empirical orthogonal function (EOF). To discover the DBN, a time lag of a fixed amount was imposed on each variable. Then, the K2 algorithm was implemented for score-based structure learning on the lagged data set. Next, the structure was used to estimate the parameters of the learned model which can be used to make inferences.

After running the data through the K2 algorithm and scoring the connections with the Bayesian Information Criterion (BIC) scoring function, it was concluded, from the structure of the network, that there exist several causal connections between variables at different locations with varying time lags. What remains to be studied is comparing this causal approach to other graphical models and their techniques to rate their accuracy and efficiency between one another. The findings present causal relationships between atmospheric variables which domain experts can utilize to make general predictions on teleconnection patterns.

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POSTER 67

THE EFFECTS OF HYPERGLYCEMIA ON NEURULATION

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Neurulation is the process via which the neural tube, the tissue that develops into the brain and spinal cord, is formed during early embryogenesis. A flat sheet of cells, called the neural plate, bends, folds and closes to form this tube. Impaired neurulation leads to the formation of neural tube defects (NTDs), such as spina bifida or anencephaly, found in about 3,000 pregnancies each year in the United States. NTDs are caused by both genetic and environmental factors. In recent years, a significant correlation between diabetic mothers and babies born with NTDs has led to the conclusion that hyperglycemia is an environmental risk factor that increases the incidence of these birth defects. Furthermore, a mouse model of diabetes has confirmed that high glucose prevents neural tube closure and revealed that elevated levels of reactive oxygen species and apoptosis are likely to underlie this defect.

This study aims to establish the zebrafish as a model to study environmental factors causative of NTDs and more specifically focuses on the effects of hyperglycemia. We hypothesize that if mechanisms underlying neurulation are conserved in zebrafish, neural folds would fail to fuse in hyperglycemia. To test this, zebrafish embryos were placed in solutions of varying glucose concentrations at dome stage and removed at 5 and 7 somites stages, the time period when the lateral edges of the neural plate, the neural folds, come together and fuse. The embryos were fixed at their respective stages and processed for in situ hybridization, using the neural fold marker emx3 as a riboprobe.We will present our data measuring the distance between the neural folds across treatment groups and expect to observe an increased distance in the hyperglycemic groups if our hypothesis is correct.

This investigation was supported by the Howard Hughes Medical Institute's Precollege and Undergraduate Science Education Program at UMBC.

POSTER 68

DETERMINING THE MOLECULAR MECHANISM OF THE INHIBITORY EFFECT OF THE NSC COMPOUND IN HIV-1 GENOME PACKAGING

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There are more than 1 million total cases of diagnosed HIV-1 in the United States. Mutations can cause the virus to become resistant to specific drugs, therefore there is still a need to find alternative mechanisms to prevent viral replication. Focusing on research of the replication cycle of HIV-1 would assist in the discovery of new and more efficient treatment. The goal of this project is to focus on the genome recognition step of HIV-1 replication cycle. The 5'-untranslated region (UTR) of HIV-1 genome is recognized by the NC domain of Gag polyprotein for the selective packaging of a dimeric RNA genome. NSC260594 (NSC) is a quinolinium derivative exhibiting potent antiviral activity, which is due to its interference with HIV-1 selective genome packaging. However, the working mechanism of the compound remains largely unknown. We aim to gain a better understanding of the function of NSC. Gel shift results showed that NSC does not inhibit the dimerization process of 5'-UTR. Gel shift and Isothermal Titration Calorimetry (ITC) experiments suggest a marginal effect on the Gag binding to the packaging signal in 5'-UTR. Our NMR titration experiments revealed that the binding site of NSC in the 5'-UTR is in the bottom junction of the core packaging signal (CES), instead of the SL3 loop proposed in literature. We are currently studying whether NSC will stabilize the packaging signal upon its binding to the junction bottom, which is deleterious for genome packaging. This work will contribute to the understanding of the working mechanism of NSC, which will potentially benefit the development of new therapeutics for HIV-1 infection.

The project is supported by the National Science Foundation Research Experience for Undergraduate (REU) Research Award CHE1460653 and the Howard Hughes Medical Institute.

POSTER 69

SYNTHESIS OF GADOLINIUM CHELATES FOR MAGNETIC RESONANCE IMAGING OF NANOCARRIERS

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Cancer is one of the most prevalent diseases in our society. With the aggressive nature and evasive properties of cancer cells, we need novel methods in order to overcome this issue. Nanotechnology has shown extreme potential in cancer therapy by optimizing drug delivery and reducing systemic toxicity. The Daniel lab aims to develop multifunctional nanocarriers carrying MRI contrast agents, chemotherapeutic drugs, and targeting antibodies altogether. This project focuses on the design and synthesis of very stable Gadolinium (Gd) chelates that afford the nanocarriers with imaging properties. Multiple steps taken allow for the transformation of L-Phenylalanine to a p-Nitro-Bn-DOTA complex. All reactions were monitored closely through Mass Spectrometry and 1H NMR Spectroscopy in order to characterize and ensure the purity of each product. Upon completion of this synthetic scheme, the Gd complex will subsequently be coupled with a carboxylate-terminated Dendron (TA-TEG-G3COOH). The final Dendron-chelate compound obtained will act as a contrast agent allowing for the nanocarriers to be tracked in a non-invasive manner by MRI scans.

This investigation was sponsored by NIH/NIGMS MARC U*STAR T34 HHS 00026 National Research Service Award to UMBC

POSTER 70

USING CHITOSAN TO IMPROVE SEPARATION OF NUTRIENT-DEFICIENT POULTRY LITTER SOLIDS AND NUTRIENT-ENRICHED WATER IN THE PHOSPHORUS EXTRACTION AND RECOVERY SYSTEM

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Millions of tons of agricultural waste are generated in the Chesapeake Bay watershed from poultry operations. We developed the Phosphorus Extraction and Recovery System (PEARS) to recover phosphorus from poultry litter. PEARS extracts nutrients and, thereby, produces nutrient-deficient poultry litter solids that can be applied as a soil amendment without contributing to eutrophication. The extracted phosphorus and other nutrients are recovered in the form of slow-release struvite fertilizers. The pilot-scale PEARS reactor recovered about 75% of phosphorus; however, some nutrient-deficient poultry litter solids are co-recovered with struvite. The objective of the current work is to investigate improved solid-liquid separation using chitosan, a biodegradable natural coagulant. Batch reactors containing 200 mL of water and 8 g of poultry litter (i.e., 40 g L-1 poultry litter slurries) were acidified, mixed for 15 min, dosed with 0, 200, 350, 500, 650, and 800 mg L-1 of chitosan, mixed for 5 min, and allowed to settle. Samples were taken from the overlying water after 0, 0.5, 1, 2, 3, 4, 6, 8, 10, 15, 20, and 25 min of settling. Particles in the samples were analyzed by laser diffraction to obtain the volume density, volume concentration, and particle size distribution. Experimental results indicated that the particle volume concentration plateaued after 10-15 min of settling, corresponding to the optimal settling time for chitosan-dosed poultry litter. The higher chitosan doses shifted the particle size distribution to smaller particles, and the 800 mg L-1 chitosan dose provided the most benefit to solid-liquid separation. The effect of pH on settling efficiency was also investigated using slurries acidified to pH 2, 4, and 6 for each chitosan dose. These results will be used to improve solid-liquid separation of poultry litter in PEARS operations and produce a cleaner, purer struvite product.

This work was supported by an REU supplement to National Science Foundation project CBET-1511667.

POSTER 71

ROLE OF N-MYC DOWNSTREAM REGULATED GENE 1 (NDRG1) IN THE ADAPTATION OF THE KIDNEY TO ANOXIA

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 72

MOLECULAR LEVEL STUDIES OF THE IMPACT OF POLY (OXONORBORNENES) ON D. RERIO. EMBRYOS

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Poly (oxonorbornenes) (PONs) are amphiphilic cationic polymers that possess antimicrobial properties. The two side chains of PONs, a hydrophobic alkyl and a charged amine, are responsible for these properties. Cationic polymers are proposed as an alternative to antimicrobial peptides and it is important to assess their impact on various organisms in addition to bacterial cells. In this study, we investigated how changing the amine/alkyl ratio and polymer length affects the activity of PONs on the model vertebrate organism, D. rerio. (zebrafish). Zebrafish embryo toxicity tests were used to elucidate the LC50 of PONs. Whole-mount immunofluorescence with caspase-3 was used to analyze apoptotic cells. We hypothesize that PONs would interact with the cell membranes of embryos to induce toxicity and the level of toxicity would depend on the molecular structure of PONs. Our results indicate that increasing the hydrophobicity and polymer length decreases the viability and increases the number of apoptotic cells in the embryos in a relevant PONs concentration range used to inhibit bacterial growth.

The project is supported by the National Science Foundation Research Experience for Undergraduate (REU) Research Award CHE1460653.

POSTER 73

MODELING OF MIGRATORY BORDER CELLS IN THE EGG CHAMBER OF A DROSOPHILA

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During the egg making process of a Drosophila (Fruit Fly) a cluster of cells moves from one end of the egg chamber to the oocyte, developing egg. When considering movement and path of this cell cluster as it moves through the egg chamber. One factor is causing the range of motion seen during the cell migration is thought to be receptor cycling. We looked at the inactive and active receptors with respect to three different variables. The first variable we looked at was with respect to time. We used a set of differential equations to and then graphed the solutions in MATLAB. Next, we took a set of steady state equations and made a plot of the inactive and active receptors with respect to the concentration of the signal molecule. Lastly, we are using the concentration as our independent variable, but instead of it being in a given range we used two functions, a linear and an exponential function, to determine the concentration at different points in space, to then plot the active and inactive receptors as the cluster migrates along the central axis of the egg chamber.

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POSTER 74

DISCOVERING AND CHARACTERIZING PHAGES IN ORDER TO ANALYZE THE CORRELATION BETWEEN HOST RANGE AND PHAGE LOCATION

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Bacteriophages, or phages, are viruses that infect bacteria. The estimated population of phages is 1031, but many of their characteristics remain unknown. This experiment expands the scientific knowledge of phages through discovering and characterizing a new phage and by researching if there is a correlation between location and bacteria host range.

Phages were isolated from soil samples that were collected from three different cities around Maryland. Tested phages underwent a purification process that included a diluted infection of Bacillus thuringiensis that incubated overnight. The plates formed from this procedure were used to create a lysate that would then be combined with different species of bacteria to test the host range that the phages could infect. The host range of the phages was then compared to the origin location to test correlation. Additionally, many phages were collected from a single location to analyze the host range variability of that location.

Host range testing analysis shows that certain sub-species of Bacillus thuringiensis are more likely to be infected by the tested phages, and that location may have an effect on host range. 81% of the phages sampled infected B.t. kustaki, and B. t. DSM-350, while only 19% infected B. t. Al Hakam. When comparing the host ranges between locations, the phages from Ellicott City, MD had significantly different host ranges from Catonsville, MD ($p= 0.03$) and Rockville, MD ($p= 0.015$). However, Catonsville, MD and Rockville, MD did not have significantly different host ranges. Additionally, there is no apparent correlation between the three groups from UMBC. In conclusion, the data supporting a correlation between origin location and host range is inconclusive. Further research with a larger sample size is necessary in order to make a more accurate conclusion.

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POSTER 75

PHOSPHORUS RECOVERY FROM WASTEWATER BY DONNAN DIALYSIS WITH REVERSE OSMOSIS CONCENTRATE DRAW SOLUTIONS

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Nutrients, such as nitrogen and phosphorus, that contribute to eutrophication of the Chesapeake Bay are present in municipal wastewater. This work explored application of Donnan dialysis, which exploits the equilibrium chemistry of ions across cation- and anion-exchange membranes, to remove and recover nutrients from wastewater to produce fertilizers. For example, orthophosphate ions (e.g., $H_2PO_4^-$, HPO_4^{2-}, PO_4^{3-}) from wastewater can be exchanged with chloride (Cl^-) from a draw solution containing salt. The two main objectives of the present work were as follows: (1) determine the orthophosphate removal efficiency for single- (i.e., NaCl) and multi- (i.e., synthetic reverse osmosis (RO) concentrate) ion draw solutions; and, (2) verify the ability of ethylenediaminetetraacetic acid (EDTA) to prevent precipitation of calcium phosphate particles in the RO concentrate and drive formation of struvite ($NH_4MgPO_4 \cdot 6H_2O$). To address the first objective, a 10 mM PO_4^{3-} waste solution was treated by Donnan dialysis with 100 and 500 mM Cl^- draw solutions, which provided 69% and 87% phosphate removal, respectively, after 30 h. With the RO concentrate draw solution, 99.3% and 84% removal efficiencies were achieved for 1 and 10 mM phosphate waste solutions after 54 h. To address the second objective, the chemistry of cations (e.g., ammonium (NH_4^+), calcium (Ca^{2+}), magnesium (Mg^{2+}), and potassium (K^+)) in the RO concentrate was carefully investigated. These cations can precipitate to form different phosphate minerals. The relatively high calcium concentration in the RO concentrate favors formation of calcium phosphate particles that are not effective fertilizers. To prevent formation of calcium-based minerals, EDTA was dosed to complex the free Ca^{2+} in the RO concentrate and enable struvite precipitation. Overall, the experimental results suggested the feasible use of RO concentrate waste streams to recover phosphorus from municipal wastewater through Donnan dialysis.

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POSTER 76

TESTING DRUG DELIVERY ENDURANCE USING MICROSPHERES IN RELATION TO THE TREATMENT OF MACULAR DEGENERATION

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Age related macular degeneration (AMD) is the leading cause of vision loss in individuals over the age of 60. AMD comes in two forms: dry and wet. The dry form is characterized by the formation of yellow deposits in an area under the retina called the macula while the wet form affects around 10% of individuals AMD and involves the leakage of fluid from newly formed blood vessels1. Hypoxia, or the lack of oxygen in certain areas, induces the formation of new blood vessels, angiogenesis2. Many drugs, such as Avastin, Lucentis, and Ranibizumab, have been developed to inhibit blood vessel growth, but unfortunately, these drugs are administered every two to four weeks. The complicacies that surface from frequent injections of medication include a higher risk of infection, lack of patient compliance, tissue loss and irritation, and overall inconvenience. To resolve these drawbacks, we propose to encapsulate drugs for macular degeneration in polylactic-co-glycolic acids (PLGA) microspheres to extend the drug release length to six to nine months.

Our goal is to determine which synthesis methods create the optimal microsphere, one with both a high loading efficiency and a long, steady release of drug. Acriflavine is being utilized as a model drug because it fluoresces and closely replicates the structure of other ARMD drugs. To determine the duration of release from the microspheres, release studies are being performed at bodily equilibrium in a 37°C oven in phosphate-buffered saline (PBS). The loading efficiency in the microspheres thus far has ranged from 3.01% to 14.09%. We have found that a combination of homogenization and sonication when synthesizing the microspheres results in the highest loading efficiency. This, among other variables, will be analyzed to improve current drug-delivery of AMD drugs to not only increase patient compliance but to also lessen the effects of AMD.

CHARACTERIZATION OF THE INTERACTION BETWEEN THE HIV-1 REV RESPONSE ELEMENT AND THE VIRAL GAG POLYPROTEIN

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The Human Immunodeficiency Virus type 1 (HIV-1) is a retrovirus that infects helper T cells and suppresses activity of the human immune system. During the late phase of replication, the HIV-1 RNA genome undergoes different splicing events. However, unspliced and singly spliced RNAs are too large to be exported out of the nucleus. To circumvent this problem, the virus utilizes the Rev Response Element (RRE), a landmark in the unspliced and singly spliced genome. Rev, a viral protein, binds and multimerizes along the RRE forming a complex that is recognized by the host-cell nuclear export machinery. Upon exiting the nucleus, the unspliced RNA is translated into Gag, a polyprotein that facilitates HIV-1 genome packaging. Published crosslinking immunoprecipitation (CLIP) data suggests Gag localizes and binds to the RRE on the untranslated HIV-1 RNA genome. This research will investigate the interaction between the RRE and Gag in vitro.

The wild-type RRE exists as both a four-stemloop (4SL) and five-stemloop (5SL) RNA in solution. Mutations were made to lock-in these conformers: MutA for the RRE 5SL and MutB for the RRE 4SL. Electrophoretic mobility shift assays (EMSA) and isothermal titration calorimetry (ITC) were utilized to identify binding characteristics between Gag mimetics and each RRE mutant. EMSA data suggests hexameric Gag constructs have a binding preference for RRE MutA over RRE MutB, and ITC experiments are underway to analyze the stoichiometry and binding affinity of these interactions. In the future, nuclear magnetic resonance spectroscopy will be used to determine the structural characteristics of RRE and Gag binding. Since HIV-1 has a high mutation rate, current therapies have the potential to become ineffective. Thus, characterizing RRE-Gag interactions will be significant toward developing new HIV-1 therapeutics.

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POSTER 78

PLANARIAN FISSION BEHAVIOR IS MODULATED BY POPULATION DENSITY AND BODY LENGTH

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Planarians are freshwater flatworms with an extraordinary regenerative capacity, able to regenerate body parts and organs from almost any amputation. Planarians can reproduce asexually by fissioning transversally, resulting in each fragment regenerating a complete worm. Fission can occur multiple times consecutively and it is inhibited in dense populations. However, a mechanistic model of fission signaling is still lacking.

Here we investigated the hypotheses that fission behavior is affected by population density, pheromones and body length. First, we tested the effect of individual isolation on latency to fission. Thirty large worms were individually placed in well plates and the number of body fragments recorded for nine days. The results showed that worms underwent fission after 1.8 days, on average. Next, we tested whether pheromones, secreted cues in the water environment, inhibit fission. We recorded the number of body fragments of 36 isolated worms for five days, half in water from the high-density colony and half in fresh water. The difference in fission frequency in fresh versus colony water was not significant (4.2 and 3.6 fragments on average, respectively). Finally, we examined the relationship between body length and frequency of fission. Images of 30 worms from a range of sizes (3.2-14.1 mm) were taken on a dissecting microscope, their lengths computed, and the worms isolated for six days. The results showed a positive relationship between body length and fission frequency, and that worms required minimum body length of 5.2 mm to undergo fission.

In summary, this work validated the hypotheses that the population density and body length modulates fission behavior in planaria. However, our data did not support the hypothesis that an inhibitory cue is secreted in the water environment; therefore, a different type of cue must be involved in the suppression of fission behavior when worms are living in dense populations.

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POSTER 79

ECONOMIC IMPACTS OF PUBLIC SECTOR CORRUPTION

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Public sector corruption is prevalent across the different parts of the world. In this study, I examine the effects of public sector corruption on economic performances and quality of institutions. Using cross-country data for 129 countries, I show that the increase in corruption in the public sector reduces the quality of living, measured by income per capita, and reduces the degree of competitiveness in the economy. These results hold even after controlling for other potential determinants of economic growth such as workforce skills and trade openness. My work, thus, points to the importance of paying attention to corruption in the public sector and drafting policies to reduce its prevalence, both in developing and developed countries alike.

POSTER 80

SYNTHESIS OF IMMUNOSUPPRESSIVE NANOPARTICLES FOR THE TREATMENT OF SYSTEMIC LUPUS ERYTHEMATOSUS

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Systemic lupus erythematosus (SLE) is a chronic autoimmune disease that attacks healthy tissues and organs, such as the kidneys, heart, and lungs. SLE changes over time so that it affects each individual differently throughout their life, thus warranting various therapeutic techniques. Less severe cases are treated with low-dose steroids, pain medications, and antimalarial drugs, while more severe cases require high-dose immunosuppressives and corticosteroids. Disadvantages of such medications include toxicity to non-diseased tissues, opening the door for innovative SLE treatment techniques.

Poly(lactic-co-glycolic acid) (PLGA) is a biodegradable polymer that is often used to form nanoparticles: small particles that are used in several biological applications, particularly to target specific tissues, organs, or cells. Azathioprine and methylprednisolone are immunosuppressive and steroidal drugs, respectfully, both of which have therapeutic potential for the treatment of SLE. Corticosteroids are prescribed as anti-inflammatory medications, while immunosuppressives are given to slow the inflammatory immune response. A nanoparticle approach will allow for tissue-specific distribution of these drugs in order to decrease their toxicity.

Azathioprine and methylprednisolone nanoparticles were synthesized using an oil/water emulsion technique, followed by size and distribution testing via dynamic light scattering. Sizes ranged from 170-2000 nm with polydispersity of 0.1-0.2 depending on the drug identity and the ratio of drug to polymer. The methylprednisolone nanoparticles had a loading capacity of 10% and encapsulation efficiency of 20%, indicating that the drug was successfully incorporated into the nanoparticles. Finally, these particles will be used in both a cell-line study and a mouse model. The results of the in vitro and in vivo studies will provide a holistic understanding of how immunosuppressive drugs can be used to treat lupus, and how nanoparticle innovation can play a role in cutting-edge therapeutics.

This investigation was sponsored by NIH/NIGMS MARC U*STAR T34 HHS 00026 National Research Service Award to UMBC, Undergraduate Research Award from the UMBC Division of Undergraduate Academic Affairs, and the Lupus Foundation of America Gina M Finzi Memorial Fellowship.

POSTER 81

EXTENDING HEALTH ENGAGEMENT TO THOSE WITH DEVELOPMENTAL AND INTELLECTUAL IMPAIRMENTS THROUGH THE REMOVAL OF SOCIAL, PHYSICAL, AND PSYCHOLOGICAL BARRIERS.

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As our healthcare systems continues to advance in terms of medicine and assistive technologies, research continually shows less than ideal statistics in the decrease in treatable conditions among those with intellectual or developmental impairments. According to current literature, the phenomenon of health engagement may serve as a tool to change these outcomes by facilitating healthcare interactions, increasing patient participation and fostering decision-making. In order to integrate this approach, we must reduce the barriers surrounding healthcare services which inhibit health engaging behaviors to further understand the implication of this new perspective. Through indicating the barriers which decrease health engaging behaviors, targeted solutions can be implemented state-wide based on the findings.

Utilizing a literature review to systematically curate current research, this research explores health engagement and promotion behaviors of those with intellectual or developmental impairments and how those behaviors are reinforced by their caregivers and health professionals. For the literature that will be reviewed, certain criteria regarding if the study focuses on healthcare interactions of people with intellectual or developmental impairments, the conceptualization of health engagement and/or research done to compile specific barriers must be met in order to be used within my research parameters. The purpose of this literature review is to promote additional research to address gaps in the literature currently available with the hope of improving health services and outcomes.

I would like to acknowledge the McNair Scholars program, my McNair mentor Dr. Jasmine Lee Ph.D. and my faculty research mentor Dr. Carolyn Tice DSW for providing me with guidance and/or funding to engage in this research opportunity.

POSTER 82

PRESSURIZED CARBON DIOXIDE REACTOR FOR NUTRIENT EXTRACTION FROM POULTRY LITTER

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For decades, industrial poultry farmers have applied poultry litter to their fields as a soil amendment. The high phosphorus content of poultry litter increases its value as a natural fertilizer, but overapplication has led to nutrient runoff and water quality impairments in the Chesapeake Bay. To simultaneously address nutrient pollution and generate alternative fertilizer markets for Maryland farmers, we previously developed a technology to recover phosphorus from poultry litter in the form of slow-release struvite fertilizers. The Phosphorous Extraction and Recovery System uses carbon dioxide (CO2) gas (at atmospheric conditions) and strong acid to lower the pH of poultry litter slurries and release nutrients into the water phase. The objective of the present work was to extract nutrients from poultry litter using only pressurized CO2. Phosphorus extraction efficiency was quantified by the stannous chloride colorimetric assay. At higher pressure, CO2 solubility linearly increases according to Henry's law, lowering the slurry pH and removing the need for expensive strong acid. Based on chemical equilibrium modeling, a CO2 partial pressure of approximately 50 atm was required to achieve the pH setpoint of 4.5. Preliminary work was completed with batch reactors rated at 7.5 atm. The experimental results indicated that higher CO2 pressures provided significant improvement in phosphorus extraction compared to atmospheric conditions. For example, 1, 2, 4, and 7.5 atm of CO2 in batch reactors containing 40 g L-1 poultry litter slurries resulted in phosphorus concentrations of 390, 400, 410, and 450 mg L-1, respectively. Future work will focus on separating the nutrient-rich extract from the poultry litter solids, aerating the extract to release the dissolved CO2, and precipitating slow-release struvite fertilizers that can be sold to farmers in phosphorus-deficient parts of the United States.

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POSTER 83

EFFECT OF METAL CATIONS ON ABSORPTION AND EMISSION PROPERTIES OF COLORANTS OF CULTURAL HERITAGE IMPORTANCE

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In antiquity, paint was created by mixing together a colorant (or dye) and a mordant which contained various metal cations to give a final pigment. The cations form complexes with the colorant and cause a change in the color of the pigment. The goal of the project was to determine whether absorption and emission spectroscopy could be used to identify the colorant-mordant combinations and whether the mordants were intentionally used to achieve color changes. Three specific dyes used in historical art objects were examined: alizarin, purpurin, and quinizarin. Using an understanding of the various paint recipes used in workshops around the world, these spectra may be used to positively identify the geographical and temporal areas in which a painting of interest was created. Fifteen different metal cations and a select few combinations of said cations were examined, and the effect of the metals on the absorption and emission spectra of the resulting complexes were determined.

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POSTER 84

THE GENETIC CORRELATION BETWEEN SLEEP AND IMMUNITY

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Drosophila melanogaster share approximately 75% of their genetic makeup with humans and so can serve as a useful model organism for the study of human genetics. Previous studies have shown that a correlation exists between sleep and immune response, but little is known about the genetic association between these traits. We have tested and compared the immune response of two different populations of flies that have been artificially selected for long and short sleep patterns. We then infected replicate inbred lines of flies that were derived from both long and short sleeping flies with the common bacteria Enterococcus faecalis, a natural pathogen of both flies and humans. We compared the survivorship of the flies chosen for longer sleep durations to those with shorter sleep regimens.

The purpose of this research was to determine whether there is a genetically based correlation between sleep and immune response in the artificially selected lines of fruit flies. In this study, roughly 870 female virgin fruit flies were collected from 10 short and 9 long sleep lines. Using a septic prick, the female virgin fruit flies from each line were injected with E. faecalis that was grown in LB broth suspension. The fruit files were then monitored for 4 days after injection and the survival rate was recorded. We found that flies selected for longer sleep had a higher survivorship (89%) than those selected for short sleep (78%), however these differences were not statistically significant. We found significant differences among genotypes in their ability to survive infection within each selected population ($P < 0.005$), and this could have led to the non-significant overall results between populations.

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POSTER 85

N-MYC DOWNSTREAM REGULATED GENE 1 (NDRG1) PROTECTS THE KIDNEY FROM HYPOXIC DAMAGE

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 86

DEACTIVATION KINETICS OF THE PHOTOPIGMENT MELANOPSIN IN ROD MONOCHROMATS

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Due to adaptations to their light environments, mammals can be characterized by the photoreceptor architecture of their retina (i.e. rod monochromats, cone dichromats, and cone trichromats). Intrinsically photosensitive retinal ganglion cells (ipRGCs), which express the photopigment melanopsin, mediate image-forming and non-image forming visual processes. Melanopsin signaling kinetics is well understood in mice, but not in rod monochromat mammals. In a subtype of ipRGCs, melanopsin activates a Gq protein signaling cascade and it is deactivated by the phosphorylation of melanopsin's carboxy tail with subsequent binding of β-arrestin protein. The deactivation kinetics of melanopsin are dependent on the phosphorylation of serine and threonine residues in the carboxy-tail. Sequence analysis of the melanopsin gene OPN4 has revealed that mammals with different retina architecture have substitutions in important serines and threonines in melanopsin's carboxy-tail. Previous experiments demonstrated characteristic activation and deactivation kinetics linked to these substitutions. In order to isolate the deactivation kinetics of melanopsin in rod monochromats, we created chimeric melanopsin constructs using mouse melanopsin transmembrane region and the carboxy-tail of our mammal of interest. This way, each construct will activate in the same manner due to the interaction of the third intracellular loop with the cognant G-protein, and deactivate according to the phosphorylation sites present in the carboxy-tail. Due to the substitutions in melanopsin's carboxy-tail, we hypothesize that rod monochromat mammals will have slower deactivation kinetics than wildtype mouse melanopsin. To test this hypothesis, chimeras were first cloned into expression vectors, then expressed into HEK293 cells. A calcium signaling assay was used to measure the change in fluorescent calcium as an indicator of melanopsin deactivation kinetics. Our results indicate that melanopsin from rod monochromats deactivates slower than mouse melanopsin. These results suggest that mammals with slow deactivation kinetics have a prolonged pupil constriction response, thus protecting the photoreceptors from photobleaching.

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POSTER 87

DEACTIVATION KINETICS OF MELANOPSIN EXPRESSED IN THE RETINA OF THE DIURNAL RODENT, THE DEGU

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In addition to rod and cone photoreceptors, there is a less studied third class of photoreceptors in the mammalian retina called intrinsically photosensitive retinal ganglion cells (ipRGCs). Their role in both image and non-image forming vision is an area of active research and is the focus of this study. What is known about these photoreceptors is that ipRGCs are critical for mediation of circadian photoentrainment and the pupillary light reflex (PLR). Melanopsin is the photopigment expressed in these ipRGCs. Previous work has demonstrated that melanopsin deactivates via phosphorylation of serine and threonine residues in melanopsin's carboxy tail (C-tail) by G-protein coupled receptor kinases (GRKs) and subsequent binding of the molecule arrestin. Substitution of these residues on melanopsin's C-tail with alanine causes a significant delay in mouse melanopsin deactivation kinetics and a prolonged pupil constriction response due to melanopsin's role in the PLR.

The deactivation kinetics of melanopsin in diurnal rodents such as the degu have yet to be explored, however, amino acid sequence analysis of the carboxy tail serines and threonines demonstrated a single alanine substitution in degu melanopsin on site residue S394A in comparison to mouse melanopsin. Therefore, we hypothesize that melanopsin from diurnal degu will deactivate slower in comparison to wild type nocturnal mouse melanopsin. To address this hypothesis, we have cloned the melanopsin gene Opn4 from degu, expressed it in human embryonic kidney culture cells (HEK293), and tested melanopsin deactivation in these cells using a fluorescent calcium signaling assay. Preliminary results indicate that degu melanopsin deactivates slightly slower than mouse melanopsin. This supports the hypothesis and suggests that degu pupils dilate slower than mouse pupils after a light stimulus. The long-term goal is to characterize the different signaling mechanisms behind melanopsin deactivation and melanopsin-associated behavior in a variety of mammals.

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POSTER 88

MICROWAVE-ACCELERATED PLAMONIC ELECTRICITY

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 89

LONG-RANGE RNA STRUCTURAL INFORMATION FROM PARAMAGNETIC NUCLEAR MAGNETIC RESONANCE

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The human immunodeficiency virus (HIV-1) is a global pandemic that has infected approximately 37 million individuals. The high mutation rate in the HIV-1 genome renders current treatments that target regions of the replication cycle often insufficient. Thus, structural elucidation of the 5' leader within the HIV-1 RNA is pertinent due to the high conservation of this packaging signal, making it paramount to viral replication and a promising target for antiretroviral therapy.

Structural analysis of RNA constructs below 60 nucleotides has been effective by Nuclear Magnetic Resonance (NMR) spectroscopy. However, the size of the 5' leader – approximately 300 nucleotides – has stifled structural studies by NMR due to excessive signal broadening and long instrument acquisition times.

To circumvent the latter complication, site-specific lanthanide labelling of a reporter protein with a high binding affinity to a cognate RNA loop is proposed. It is well-known that paramagnetic lanthanide ions induce measurable pseudocontact shifts (PCS) in NMR spectra. However, binding the metal tag directly to the RNA is deleterious. Consequently, the spiceosomal U1A protein is utilized as an intermediary between the metal tag and RNA. Prior to applying the technique to the 5' leader, a 46 nucleotide MMLV derived construct was used as a model for PCS observation and NMR experiment optimization. Through the use Heteronuclear Multiple-Quantum Correlation experiments, PCS data was obtained in conjunction with residual dipolar coupling, resolving the quaternary structure of U1A:MMLV. Furthermore, the experiment illustrated an increase in distance measurements from 5 Ångstroms (Å) to 30Å in the presence of paramagnetic lanthanides. Subsequently, the technique was validated and applied to elucidating the secondary structure of the 5' leader to enhance our understanding of HIV-1 biology and facilitate the design of novel therapeutics in the future.

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POSTER 90

FOREST FIRES, HABITAT LOSS, AND THE BAHAMA ORIOLE: RECORDING ISLAND BURN HISTORY WITHIN CARIBBEAN PINE FORESTS

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The Bahama Oriole (Icterus northropi) is a critically endangered bird now found exclusively on Andros Island, The Bahamas. This species nests in many of the habitats which cover the island, including the extensive forests of Caribbean Pine (Pinus caribaea). Thus, these forests represent a vital habitat for a critically endangered species, and documenting the island's land cover change remains an important task in the research and conservation of this oriole species. To track such change across the island and discover any patterns or correlations applicable to conservation efforts, we gathered fire ignition and burned area data from two NASA remote sensing satellites. These data were tested for accuracy using data gathered in the field on Andros and were then analyzed using statistical programs and geographic information systems. With them, we created a record of forest fires occurring on the island over time. This allowed us to compare fluctuations in burn frequency and intensity to changes in the various global climate systems, including the North Atlantic Oscillation and El Niño/La Niña Cycles.

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POSTER 91

USING MACHINE LEARNING TO MINE MEDICAL NOTES AND TRANSCRIPTS

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Machine learning allows for scientists to understand what is known as big data comparatively quickly. Our lab utilizes this powerful tool to understand medical notes. This is imperative because we can elucidate information about the quality of care, mortality, doctor bias, among other things from these notes. My work utilized such methods to predict the medical specialty of Medical Transcripts. The process began by using de-identified medical transcripts. These were pre-processed to reduce noise and disorganization for clarity. After this, three separate word vectorization methods; Word2Vec, Doc2Vec, and TF-IDF were utilized to represent the words in a way the computer could understand. After that the word vector representations are put through three different statistical classification models; Logistic Regression, Support Vector Machine, and Random Forest. These models were utilized to make predictions on the topic of each document with varying accuracy. Models and processing such as the one aforementioned can be used to provide information about Medical Documents to the medical community. Ultimately, this information can be used in the medical community to heighten levels of care.

TEMPERATURE DEPENDENCE OF FLUOROPHORE-INDUCED PLASMONIC CURRENT

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The body of the abstract was withheld at the request of the research mentor. For more information, please visit the poster.

POSTER 93

MATHEMATICAL MODEL OF PI3K DEPENDENT AND INDEPENDENT PATHWAYS IN SKELETAL MUSCLE ATROPHY

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Muscle atrophy can be a devastating symptom of aging and disease. The phosphorylation state and nuclear localization of the transcription factor Foxo1 have been identified as critical factors in muscle degradation. Chemical pathways which manipulate Foxo1 have revealed that dephosphorylated Foxo1 enters the nucleus while phosphorylated Foxo1 leaves the nucleus. Stimulus-induced pathways have also been identified. However, with such complicated stimulus pathways, a mathematical model of the Foxo1 nuclear translocation process under varied stimuli is needed.

We aimed to better understand the process by which muscle degrades using mathematical models of the Foxo1 nuclear localization pathway and comparing the results to experimental data. Phosphorylation of Foxo1 traditionally follows a pathway from insulin or insulin-like growth factor (IGF) through PI3K to Akt. However, recent experiments have shown that PI3K inhibitors may not prevent Akt activation of Foxo1 suggesting an alternative pathway. In previous work we have shown how a balance between the PI3K-dependent and PI3K-independent pathways may occur, but this involved a basic mathematical model. Here we reduce a sophisticated dynamical model of Akt activation via IGF through PI3K to steady state and append equations for PI3K inhibition to compare the effectiveness of our basic model in capturing the balance. Ultimately, an accurate model of the Foxo1 translocation pathway may have the predictive capacity to suggest mechanisms for controlling the effects of muscle degradation within at-risk patients.

This work is supported in part by a 2019-20 Undergraduate Research Award (URA) to Catherine Chonai.

POSTER 94

A STUDY ON PEAK PARTICULATE MATTER 2.5 LEVELS IN THE BALTIMORE-WASHINGTON AREA

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This research examined PM2.5 data observed over the last decade (2008-2018) in the Baltimore-Washington Area narrowly focusing on cities around Howard University Beltsville Campus including Baltimore, Washington D.C, Rockville, Bowie, Annapolis. Using wind direction data collected at HUBV, trajectory models were developed to show from where or to where the winds were traveling and then determine PM2.5 levels in these cities. Furthermore, more plots were designed to show peculiar cases of when extreme PM2.5 amounts were observed during a day and during a year. The intended end result of this poster was to show the correlation between the amount of PM2.5 present in the atmosphere and the time of the day/year. This research is relevant to NOAA's mission because it studies aerosols in extreme detail which long term serves to control and possibly curtail pollution to the barest minimum.

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POSTER 95

IRONIC COMEDY, MEMES, AND THE ALT-RIGHT

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Abstract unavailable at time of printing. Please see poster for more information.

POSTER 96

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