Rochester Academy of Science
43rd Annual Fall Scientific Paper Session

November 12, 2016

Hosted by:
School of Natural and Social Sciences

ROBERTS
WESLEYAN COLLEGE

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Roberts Wesleyan College

Schedule of Events:

8:30-9:30AM	Registration – Link between Crothers and Smith Hall *Refreshments available; Poster set-up recommended*
9:30-11:15AM	Oral Presentations – Smith Hall *Presenters – arrive at your room 15 minutes prior to start of the session* Session I – General Topics (Smith 360) Session II – Physics + (Smith 359) Session III – Chem and Biochem + (Smith 365) Session IV – Biology – General I (Smith 166) Session V – Biology – General II (Smith 353) Session VI – Biology – Microbiology (Smith 355) Session VII – Biology – Diseases, Cancer, Viruses (Smith 265 – Auditorium)
11:15-12:30PM	Poster Presentations – Crothers and Smith Hall
12:30PM	Luncheon – Garlock Dining Hall
1:15PM	Larry King Memorial Lecture – Garlock Dining Hall "Surviving the Mass Extinction: The Amazing Story of Bird Recovery and Radiation after the End-Cretaceous Catastrophe" Jacob Berv, Cornell University

ORAL PRESENTATIONS

SESSION I: GENERAL TOPICS

SMITH 360 MODERATOR: COURTNEY FANTAUZZO

9:30 ANALYZING SOUNDSCAPE TEMPORAL VARIATION IN WESTERN NEW YORK AS A POTENTIAL ASSESSMENT OF BIOLOGICAL DIVERSITY.
Jeffrey Doser and Kristina Hannam

9:45 THE PARAMETERS OF TARGETED SPITTING IN BELUGA WHALES (*DALPHENACTORUS LUCAS*).
Allison C. Maynard and Michael Noonan

10:00 INDIVIDUAL DIFFERENCES IN THE PLAY BEHAVIOR OF BELUGA WHALES (*DELPHINAPTERUS LEUCAS*).
Mary J. Woodruff and Michael Noonan

10:15-10:30 BREAK

10:30 REPRODUCTIVE TRADE-OFFS ASSOCIATED WITH MOUNTING AN IMMUNE RESPONSE IN FEMALE BROWN ANOLES (*ANOLIS SAGREI*).
Aaron C. Heisey, Racquel Case, and Christina Schmidt Ph.D.

10:45 PRESENCE OF *Agrobacterium vitis* STRAINS ON FINGER-LAKES REGION VINEYARD AND NON-VINEYARD SOIL AND ON CULTIVATED (*Vitis vinifera)* AND WILD VINES (*Vitis riparia*).
Luciana Cursino and Uyen Tran

11:00 BIOLOGY FIGURES MISS THE POINT OF ARROW USAGE.
Jordan J. Cardenas, Dina L. Newman, L. Kate Wright

SESSION II: PHYSICS +

SMITH 359 MODERATOR: MICHAEL SCHILACI

9:30 EXAMINING THE COLLECTIVE BEHAVIOR OF CELLS IN A 3D CO-CULTURE.
Roland Sanford and Moumita Das

9:45 INFLUENCE OF THE WATER LAYERS ADSORBED ONTO STAINLESS STEEL 316 ON TRITIUM MIGRATION.
Matthew Sharpe, Cody Fagan, and Walter T. Shmayda

10:00 CRACK FORMATION AND PROPAGATION IN A SEMIFLEXIBLE NETWORK EMBEDDED IN A GEL.
Andrew Sindermann, Moumita Das

10:15 THE EFFECT OF SURFACE MODIFICATIONS ON TRITIUM ADSORPTION AND ABSORPTION BY STAINLESS STEEL 316.
Cody Fagan, Matthew Sharpe, Walter T. Shmayda, and W. Udo Schröder

10:30-10:45 BREAK

10:45 SPENT COFFEE GROUNDS AS A VIABLE FEEDSTOCK FOR BIOFUELS PRODUCTION AND ITS POTENTIAL COMMERCIAL USES.
Fatima Zara, Saddam Alrobaie, Jeffrey Lodge PhD

11:00 ECONOMIC ANALYSIS OF THE LIFE CYCLE OF SPENT COFFEE GROUND AS VIABLE FEEDSTOCKS FOR HEATING OIL AND BIOFUELS PRODUCTION.
Saddam Alrobaie, Fatima Zara, Jeffrey Lodge PhD

SESSION III: CHEMISTRY AND BIOCHEMISTRY +

SMITH 365 MODERATOR: JASON TAYLOR

9:30 GENOMIC ANALYSIS OF *CAS* GENES ISOLATED FROM *STAPHYLOCOCCI* IN WHITE TAIL DEER POPULATIONS.
Shawn Warner and Mark Gallo, Ph.D.

9:45 ANALYSIS OF THE *PVC*ABCD OPERON.
Christopher S. Campomizzi, William Adams, Collin Edbauer and Mark A. Gallo Ph.D.

10:00 INDICATION OF TRICHLOROMETHANE SEGREGATION IN 1-HEXYL-3-METHYLIMIDAZOLIUM BIS(TRIFLUOROMETHYLSULFONYL)AMIDE – TRICHLOROMETHANE BINARY SYSTEM.
Markus M. Hoffmann

10:15-10:30 BREAK

10:30 SYNTHESIS AND CHARACTERIZATION OF LITHIUM CARBOXYLATES FOR USE IN LIQUID ORGANIC SCINTILLATOR.
Melissa Schmitz, Christopher Bass, and Spencer Stuckey

10:45 EFFECTS OF PRENATAL MUSIC STIMULATION ON EARLY EMBRYONIC DEVELOPMENT OF *Gallus gallus.*
Emma Strujo, Cliff-Simon Vital, and Poongodi Geetha-Loganathan

11:00 QUANTIFYING LACCASE ACTIVITY AND DEGRADATION OF 17α-ETHINYLESTRADIOL USING *LENTINULA EDODES* AND *PHANEROCHAETE CHRYSOSPORIUM.*
Alexander S. Milliken and Corey M. Johnson Ph.D.

BIOLOGY – GENERAL I

SMITH 166 MODERATOR: MICHAEL GRENIER

9:30 MELANIN-CONCENTRATING HORMONE RECEPTOR 1 SIGNALING IS MODIFIED BY CILIARY LOCALIZATION IN FAT CELLS.
Henry Ophardt, Lucas Galbier, Rongkun Shen, and Laurie B. Cook.

9:45 MODELING THE POPULATION DYNAMICS OF MITOCHONDRIA IN MAMMALIAN CELLS.
Kellianne Kornick and Moumita Das

10:00 GENE EXPRESSION AND REGULATION IN FOOD RESTRICTED MICE.
Theodore Nguyen, Preet Sohal, Richard Ruh and Douglas J. Guarnieri

10:15 NOVEL GROWTH BASED LONGEVITY ASSAYS FOR THE DEVELOPMENT OF DRUGS TO TREAT AGING AND AGE RELATED DISEASE.
Jonathan Millen

10:30-10:45 **BREAK**

10:45 FACTORS AFFECTING SUPER-SPREADING OF EPIDEMICS: A STUDY OF INFECTION IN *PEROMYSCUS.*
Anastasia Toumpas

11:00 USE OF FATTY ACID SIGNATURES TO EXPLORE THE RIVER CONTINUUM CONCEPT.
Kinsey Irvin and Jacques Rinchard

BIOLOGY – GENERAL II

SMITH 353 MODERATOR: RACHEL GRAHAM

9:30 DEVELOPMENT OF MICROSATELLITE MARKER FOR *Scaevola plumieri*.
Adriana Morales and Susan Witherup

9:45 DISSOLVED ORGANIC MATTER STRUCTURE AND QUALITY ACROSS A GRADIENT OF NORTH TEMPERATE LAKES.
Meredith Kadjeski

10:00 ARE COEFFICIENTS OF CONSERVATISM ALWAYS ACCURATE IN PREDICTING SPECIES PERSISTENCE? COMPARING COC VALUES WITH COMMUNITY COMPOSITION DATA FROM THE WESTERN AND FINGER LAKES PORTION OF NEW YORK TO DETERMINE ANTHROPOGENIC DISTURBANCE THRESHOLDS FOR THE STATE-RARE VINE AMERICAN BITTERSWEET (*CELASTRUS SCANDENS*).
Scott Ward and Kathryn Amatangelo

10:15-10:30 **BREAK**

10:30 MEASURING CYP1A IN FRESHWATER FISH OF WESTERN NEW YORK AS AN INDICATOR OF POLLUTION LEVELS
T. Koetsier, T. Taggart, S. Johnson, K Miller, R. Williams

10:45 ISOLATION OF BACTERIA FROM LAKE WATERS ASSIOCIATED WITH WASTEWATER EFFLUENTS CAPABLE OF DEGRADING VARIOUS PHARMACEUTICALS.
Noreen Gallagher and Dr. Jeffrey Lodge

11:00 FURTHER CHARACTERIZATION OF HYDROCARBON DEGRADING BACTERIA ISOLATED FROM SEDIMENT SAMPLES OF SLATER CREEK, NEW YORK.
Norathirah Ahmadtarmizi and Dr. Jeffrey Lodge.

BIOLOGY – MICROBIOLOGY AND GENETICS

SMITH 355 MODERATOR: CYNTHIA DAVIS

9:30 ISOLATION AND CHARACTERIZATION OF MUTANT STRAINS OF *ACETOBACTER* DSW_54 WITH ALTERED HYDROGEN PEROXIDE SENSITIVITY PHENOTYPES
Alec Walter and Peter D. Newell

9:45 ISOLATION AND CHARACTERIZATION OF MICROBIAL COLONIZATION IN SNAPPING TURTLE (*CHELYDRA SERPENTINE*) EGGS.
Jessica Gibbons and Poongodi Geetha-Loganathan

10:00 GENOMIC ANALYSIS OF *STAPHYLOCOCCUS* BACTERIOPHAGE.
James P. Lioi, Janelle Fancher and Mark A. Gallo, Ph.D.

10:15 CHARACTERIZATION OF NON-RIBOSOMAL PEPTIDE SYNTHASES FROM *STAPHYLOCOCCI*.
Megan Helf, Samantha Sauer, Adam Siedlecki and Mark Gallo, Ph.D.

10:30-10:45 **BREAK**

10:45 THE EFFECT OF ANTI-BACTERIAL, TRICLOSAN, ON EPILITHIC BIOFILM COMPOSITION, FUNCTION, AND RESISTANCE.
David Kerling and Jonathan O'Brien

11:00 TOWARD THE CHARACTERIZATION OF AEROBACTIN SYNTHETASE IUCC FROM A HYPERVIRULENT PATHOTYPE OF *KLEBSIELLA PNEUMONIAE*.
Matthew Rice, Daniel Bailey, Eric Drake, and Andrew Gulick, Ph.D.

BIOLOGY – DISEASES, CANCERS AND VIRUSES

SMITH 265 MODERATOR: PETER LaCELLE

9:30 EVALUATING THE BINDING POTENTIAL OF CY5.5-DCL AND CY5.5-DCL-DSS-K-NH_2 TARGETED MOLECULAR IMAGING AGENTS (TMIA) TO C4-2 PROSTATE CANCER CELLS.
Aflah Hanafiah, A. Karim Embong, Rebecca Walden, and Dr. Irene Evans

9:45 HUMAN CYTOMEGALOVIRUS REGULATION OF AKT FOR THE INDUCTION OF MONOCYTE TO MACROPHAGE DIFFERENTIATION.
Maia Baskerville, Olesea Cojohari and Gary Chan

10:00 COMPARISON OF COCKSACKIEVIRUS B4 SURFACE PROTEINS TO BETA-ISLET CELLS SURFACE PROTEINS IN *HOMO SAPIENS*.
Aaron Weaver, Mia Byrd, and Mark Gallo, Ph.D.

10:15-10:30 **BREAK**

10:30 VIRAL MODIFICATION OF HLA GENE COMPLEX OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS.*
Mahad Noor and Mark Gallo, Ph.D.

10:45 INVESTIGATING THE EFFECTS OF STRESS ON REOVIRUS TRANSLATION AND REPLICATION.
Michael Lutz and Emily Ledgerwood

11:00 SMALL COLONY VARIANT SWITCHING PHENOMENON IN *STAPHYLOCOCCI*.
Adam Siedlecki, Mahad Noor, Rafay Tariq, and Mark Gallo, Ph.D.

POSTER PRESENTATIONS

ASTRONOMY AND PHYSICS

1. EFFECTS OF FULLERENES ON A FRESHWATER BENTHIC COMMUNITY: TOXICITY AND IMPLICATIONS FOR ENVIRONMENTAL PROCESSES AND FUNCTIONS
   Charles Border, Sarah Ponte Cabral, Callie Babbitt, Christy Tyler, and Elizabeth Wronko

2. HOMOPOLAR MOTOR ACCELERATION AND BRAKING SYSTEM
   Scott Calnan, Ileana Dumitriu, Ph.D., Peter Spacher, Ph.D.

3. UNDERGRADUATE ELECTRONICS COURSE WITHIN THE HWS PHYSICS MAJOR.
   Joseph Carrock, Ileana Dumitriu, Ph.D., Peter Spacher, Ph.D.

4. ENHANCING EFFICIENCY FOR ALL-ORGANICS SOLAR CELLS THROUGH INTERFACE-ENGINEERED MATERIALS
   Julia D'Rozario, Zahra Ahmadi, Jack Rodenburg, Lucie Rutaboul, Dr. Axel Enders, Dr. Peter Dowben and Dr. Carolina C. Ilie

5. PHOTODYNAMIC THERAPY DOSING PROPERTIES OF PROTOPORPHYRIN IX FOR ACNE AND CANCER TREATMENT
   Christopher Demas, Ileana Dumitriu, Ph.D., Peter Spacher, Ph.D.

6. FROM MUSIC TO PHYSICS: A STUDY OF ACOUSTIC THEORY AND ULTRASOUND APPLICATION
   Ian R. Evans and Carolina C. Ilie

7. LEVITATION WITH SUPERCONDUCTING ELECTROMAGNETS
   Tyler Hanzlik, Ileana Dumitriu, Ph.D., Peter Spacher, Ph.D.

8. ELECTRIC TRANSPORT OF ORGANIC THIN FILM SEMICONDUCTORS
   Andres Inga, Ian Evans, Vincent DeBiase, Nicholas Jira, Ildar Sabirianov and Carolina C. Ilie

9. VOLATGE CONTROLLED PERPENDICULAR MAGNETIC ANISOTROPY
   Nicholas Noviasky, Ildar Sabirianov, Shi Cao, Xiaozhe Zhang, Andrei Sokolov, Eugene Kirianov, Peter Dowben, Carolina Ilie

10. HIGH ALTITUDE MEASUREMENTS OF MUON FLUX
    Frank Oplinger, Ileana Dumitru Ph.D., Peter Spacher Ph.D.

11. BAND GAP ENERGY CALCULATIONS FOR THIN FILM ORGANIC SOLAR CELLS
    Stephen J. Porter, Shelby K. Davis, Jerry T. Chamnichanh, Julia R. D'Rozario, Carolina C. Ilie

12. SURFACE ANALYSIS OF MoS_2 AND $MoSe_2$.
    Mayuka Sasaki

13. CHARACTERIZATION OF PHOTOMULTIPLIERS FOR USE IN A FAST NEUTRON SPECTROMETER
    Joshua Sands and Christopher Bass

14. THE EFFECTS OF BACKGROUND OXYGEN ON GRAPHENE GROWTH
    Alexander S. Sidou, Mayuka Sasaki, Zachary R. Robinson

15. THE SEARCH FOR A STANDARD CANDLE EFFECT IN THE SLOAN DIGITAL SKY SURVERY QUASAR DATABASE
    Christopher Wahl

16. GALAXY CLASSIFICATION SCHEMES FOCUSING ON EARLY UNIVERSE GALAXIES
    Samuel Zimmerman

BIOLOGY: GENETICS, CELL BIOLOGY, MICROBIOLOGY

17. MELANIN-CONCENTRATING HORMONE MAY FUEL EXPANSION, ADHESION AND DIFFERENTIATION OF ADIPOSE CELLS IN CULTURE.
    Hiba Y. Abdullah and Laurie B. Cook.

18. CREATING A NEW MODEL FOR PCR INSTRUCTION.
    Ashley Adair, Callie Donahue, and Dina L. Newman

19. PILOTING A PATHOGEN: THE DEVELOPMENT OF AN AMBER SUPPRESSOR STRAIN IN *PSEUDOMONAS AERUGINOSA.*
    Lily Adams and Julie A. Thomas

20. EFFECTS OF DOCETAXEL ON HISTONE MODIFYING ENZYMES IN OVARIAN CANCER CELLS EXPOSED TO ESTROGEN AND BISPHENOL A
    Lanni Aquila, Laura Hayes, and Lisa Morey, PhD.

21. CHARACTERIZING THE EFFECT OF *HSF* MUTATIONS ON BRAIN TUMORS IN *D. MELANOGASTER.*
    Jordan Aronowitz, Michael Welte

22. INFECTION OF A PATHOGEN: STUDYING THE EFFECT OF THE GENOME OF GIANT PHAGE SPN3US ON SALMONELLA.
    Melissa Barton, Martine Bosch, Susan T. Weintraub, and Julie A. Thomas

23. CALCIUM ACTIVITY IN THE NEUROMAST
    C. Brady, T Smith, A. Mahoney, and A. Rich.

24. DEVELOPING A METHOD FOR PURIFYING PRIMARY CILIA FROM DIFFERENTIATING 3T3-L1 PRE-ADIPOCYTES
    Tameciah Browne and Laurie B. Cook

25. COMPARATIVE ANNOTATION OF A REGION OF THE *DROSOPHILA ELEGANS* MULLER D ELEMENT.
    Patrick M. Buckley and Matthew R. Skerritt, PhD

26. ACCURACY OF STUDENT-SUPPLIED BIOCHEMICAL CHARACTERIZATION DATA FOR ANALYSIS OF UNKNOWN STAPHYLOCOCCI.
    Amanda Caruso, Sook-Keng Tung, and Jeremiah J. Davie

27. TOWARDS INVESTIGATION OF SMALL-EYE MUTANT USING CRISPR/CAS9 GENE TARGETING.
    Alexandra R. Dananberg, Hannah Loo, Maria V. Suarez and Travis J. Bailey

28. FUNCTIONAL ANALYSIS OF RAD51 AND RAD54 RELEVANT TO HDR EFFICIENCY.
    Allie Dananberg, Pei Xin Lim, Rohit Prakash, Maria Jasin

29. DELETION OF EITHER GENE ENCODING THE GRP170 CHAPERONE OF *CAENORHABDITIS ELEGANS* FAILED TO ELICIT THE UNFOLDED PROTEIN RESPONSE IN EMBRYONIC, LARVAL OR ADULT TISSUES.
    Sara Dannebrock

30. THE ROLE OF BACTERIOPHAGES IN CHEESE MICROBIAL COMMUNITIES.
    Michael Delmont, Michael McKay, Michael Weiler, and Daniel P. Haeusser

31. GP22: THE MISSING LINK OF PHAGE HEAD MORPHOGENESIS.
    Maxim I. Desmond, Julie A. Thomas

32. TRANSCRIPTIONAL ANALYSIS OF BIPOLAR CANDIDATE GENES IN MODELS OF STRESS SUGGESTS A COMMON ROLE FOR ER STRESS.
    Maria Fernanda, Juarez Anaya and Douglas J. Guarnieri

33. SPERM OR OOCYTE? THE ROLE OF SPECIFICITY IN THE EMERGENCE OF POST-TRANSCRIPTIONAL REGULONS IN GERMLINE DEVELOPMENT.
    Dallas Fonseca, Eric Eichelberger, Vandita Bhat, Te-Wen Lo, Zachary Campbell

34. BUILDING PROFILES FOR MICRORNA TARGET PREDICTION USING MACHINE LEARNING
    Lucas Galbier and Rongkun Shen

35. RNA-SEQ DATA ANALYSIS FOR ADIPOCYTE DIFFERENTIATION
    Lucas Galbier, Laurie B. Cook and Rongkun Shen

36. UNIQUE CLEAVAGE PATTERNS OF CIDAROID SEA URCHINS.
    Danielle Granata, Sorenda Muth, Jannell Nichols, and Hyla Sweet

37. A STUDY OF MCH RECEPTOR LOCALIZATION AND FUNCTIONAL ROLE OF PROLIFERATION IN DIFFERENTIATING FAT CELLS.
    Brett Henderson and Laurie B. Cook.

38. STUDYING THE ROLE OF ANO2 ON NEUROMAST FUNCTION IN ZEBRAFISH USING A RHEOTAXIS ASSAY.
    B Henderson, C. Albano, N. Caster, K. Gray, and A. Rich.

39. ISOLATION AND CHARACTERIZATION OF BACTERIAL AND FUNGAL SPECIES FROM FOLIAR AND SOIL SAMPLES OF ASIAN PEAR TREES.
    Taylere Herrmann, Morgan Pimm, Maryann Herman

40. MITOPHAGY IN YEAST CELLS
    Tyler Hoskins and Eric Cooper

41. VIRULENCE TESTING OF A *PSEUDOMONAS AERUGINOSA* MUTANT USING *CAENORHABDITIS ELEGANS* AS A BACTERIAL PATHOGENESIS MODEL.
    Erin Izydorczak and Johanna Schwingel, PhD

42. INDUCTION OF CELL DEATH IN CAL-27 AND HeLA CANCER CELL LINES USING BERRY EXTRACTS.
    Ashley Jarkowski and Robert S. Greene

43. INVESTIGATION OF CASPOFUNGIN TOLERANCE GENES IN CANDIDA ALBICANS.
    Natalie Jay, Sumanun Suwunnakorn, and Elena Rustchenko-Bulgac

44. AGE-DEPENDENT CHANGE IN TDP-43 REGULATION IN MOUSE MODELS OF ALZHEIMER'S DISEASE
    Liam Kaylor

45. A CUSTOM CRISPR SYSTEM TO INVESTIGATE THE ROLE OF HYPOXIA-INDUCIBLE FACTOR-1α IN THE EPIDERMAL KERATINOCYTE RESPONSE TO UVA IRRADIATION.
    Ben Leahy, Dylan Phelps, Elizabeth Osborne, Elizabeth McNeil, and Peter LaCelle, PhD.

46. BATTLING BIOLFILM DEVELOPMENT: CONSTRUCTION OF NARI MUTANT AND VISUALIZATION OF ASSOCIATED PROTEINS IN *PSUEDOMONAS AERUGINOSA.*
    Haley Majot, Nyshidha Gurijala, Shradha Mamidi, and Johanna Schwingel

47. CHARACTERIZATION OF MUTANTS OF A *SALMONELLA* KILLER
    Mazin Mar and Julie A. Thomas

48. DIRTY VIRIONS: ISOLATION AND CHARACTERIZATION OF PHAGES INFECTIVE FOR *BACILLUS THURINGIENSIS.*
    Mohamed Mohamed, Ei Thinzar Phyo, and Julie A. Thomas

49. RESTORED IN VITRO ASSEMBLY OF TEMPERATURE SENSITIVE E. COLI FTSZ84 BY FTSZ ACCESSORY PROTEINS (ZAPS).
    Christian Montes, Monika Buczek, Anuradha Janakiraman, and Daniel P. Haeusser

50. ANALYZING THE CANINE GENOME USING RFLP'S TO LOCATE CANCER BIOMARKERS.
    Simran Reddy, Samantha Terhaar, Armon Panahi, Eleanor Gerhard, and Douglas J. Guarnieri

51. EFFICIENT QUANTIFICATION OF RXRG ISOFORMS
    Teagan Skotarczak, Erin Karnath, Lydia Monin, Yana Shimanovich, Matthew Petrishin, Daniel Danovskis, Aaron Zelko, andGaia Bistulfi

52. VISUALIZATION OF ACTIVATED NEUROMASTS IN ZEBRAFISH.
    I. Tahir, T. Boswell, O. Pimentel, A. Welch, and A. Rich.

53. EFFECT OF A LOW MAGNESIUM DIET ON THE MOUSE GUT MICROBIAL FLORA.
    Michelle Tartaglia, Bernardo Ortega, and Michel Pelletier.

54. MULTIPLE VARIABLES INFLUENCE DISTRIBUTION OF STAPHYLOCOCCI ISOLATED FROM HEALTHY STUDENT VOLUNTEERS.
    Sook-Keng Tung, and Amanda Caruso, and Jeremiah J. Davie

55. THE EFFECTS OF GASTROINTESTINAL MOTILITY ON THE ENTERIC MICROBIOTA IN ZEBRAFISH.
    Ashley White, Adam Rich, and Michel Pelletier.

BIOLOGY: ANIMAL AND ORGANISMAL

56. DOES AN IMAGE-BASED AGING GUIDE FOR TREE SWALLOW NESTLINGS WORK WELL FOR OTHER SPECIES?
    Tessa Alianell and Bill Brown

57. FORAGING BEHAVIOR OF ALLEGHENY MOUNTAIN DUSKY SALAMANDERS (*DESMOGNATHUS OCHROPHAEUS*) EXPOSED TO KAIROMONES FROM SYNTOPIC AND ALLOTOPIC SNAKE SPECIES.
    Alison M. Apgar, Sarah C. Kopa, Evan R. Stern and Aaron M. Sullivan

58. VARIATIONS IN FATTY ACID SIGNATURES OF BROWN TROUT AND COHO SALMON FROM LAKE MICHIGAN.
    Nathan Barker, Chris Maier, Michelle Edwards, Sergiusz Czesny, and Jacques Rinchard

59. A PILOT STUDY TO ASSESS THE EFFICACY OF THE PACIFIC CREST TRAIL AS A MEGATRANSECT OF AMPHIBIAN AND REPTILE DIVERSITY IN THE KLAMATH MOUNTAINS OF NORTHERN CALIFORNIA.
    Erica I. Barney, Emilia A. R. Gildemeister, Aaron M. Sullivan and Michael C. McGrann

60. THERMAL TOLERANCE OF ANTS IN WESTERN NEW YORK.
    Sonya Bayba and Robert J. Warren

61. ANALYSIS OF *D. MELANOGASTER* VIABILITY ON DIFFERENT DIETARY STEROLS.
    Andrew Beiter, Grace Lindsey, Lisa Nelson, Robert Grebenok, Andrew Stewart

62. THE SURVIVAL OF *Agrobacterium vitis* ON THE FEET OF HOUSE SPARROWS (*Passer domesiticus*) SAMPLED FROM FINGER LAKES VINEYARDS.
    Luciana Cursino and William Brown

63. FATTY ACID SIGNATURES OF LAKE MICHIGAN RAINBOW TROUT.
    Michelle Edwards, Chris Maier, Nathan Barker, Sergiusz Czesny, and Jacques Rinchard

64. THIAMINE CONCENTRATIONS IN PREY FISHES FROM LAKE ONTARIO.
    Nicholas Farese, Matthew Futia, and Jacques Rinchard

65. OCCURRENCE OF MICROPLASTICS IN THE STOMACHS OF LAKE ONTARIO FORAGE FISHES.
    Nina House, Scott Minihkeim, C. Eric Hellquist, and Maureen Walsh

66. INTER- AND INTRA-SPECIES VARIATIONS IN FATTY ACID SIGNATURES OF NEARSHORE FISHES FROM LAKE MICHIGAN.
    Erica Kingdollar, Matt Futia, Nicholas Farese, Sergiusz Czesny, Sara Creque and Jacques Rinchard

67. DETERMINING FEMALE SPECIFIC LOCI IN THE TERRESTRIAL ISOPD *TRACHELIPUS RATHKEI.*
    Joseph Laricchiuta and Dr. Christopher Chandler

68. INCIDENCE OF *WOLBACHIA* INFECTION IN FREE-LIVING, ENSLAVED AND SLAVEMAKING *FORMICA* ANTS.
    Hannah Loo, Jennifer Apple

69. FATTY ACID SIGNATURES OF PREDATORY FISH FROM LAKE MICHIGAN.
    Chris Maier, Nathan Barker, Michelle Edwards, Sergiusz Czesny, and Jacques Rinchard

70. DESIGN AND CONSTRUCTION OF A HYPEROXIC ENVIROMENT TO TEST THE EFFECTS OF HIGH OXYGEN CONCENTRATION ON HOUSE CENTIPEDE (*SCUTIGERA COLEOPTRATA)* BODY SIZE.
    Sachelle Martin, Abdulrehman Rashid, Tyresius Hunter, and David A. Dunn

71. CAN NATIVE AND NON-NATIVE ANTS COEXIST.
    Abby Mathew and Robert J. Warren

72. COMPARISON OF SUGARS AND AMINO ACIDS IN NECTAR FROM *SCAEVOLA TACCADA* AND *SCAEVOLA PLUMIERI*
    Colette Piasecki-Masters and Susan Witherup

73. RELATIVE BODY SIZE SCALING IN DROSOPHILA MELANOGASTER.
    Kyle Samson and Andrew Stewart

74. INFLUENCE OF PHLOEM STEROLS ON THE GROWTH AND DEVELOPMENT OF PHLOEM FEEDING INSECTS.
    Rebecca VanLaeken, Alexis Grebenok, Jake Wojakowski, Robert Grebenok, Todd Ugine and John Losey

PLANT BIOLOGY, ECOLOGY, AND EARTH SCIENCES

75. GENETIC AND ENVIRONMENTAL INFLUENCES ON THE SIZE-FECUNDITY RELATIONSHIP IN THE ASIAN TIGER MOSQUITO, *AEDES ALBOPICTUS*.
    Gabrielle Barthelme, Mary Bridge, Paul Hart, Courtney Kramer, Kaitlyn Taylor, Kira Voyer, Katrina Wagar, AustinWuerch, Kathleen Westby, and Katie Costanzo

76. THE INFLUENCE OF *DIDYMOSPHENIA GEMINATA* ON THE CONSUMPTION PATTERNS OF FISH AND INVERTEBRATES IN FRESHWATER STREAMS.
    Michelle Baskins, Jonathan O'Brien, Natalie Knorp, Justin Murdock

77. THE RELATIONSHIP OF PITCHER PLANT MORPHOLOGY TO BACTERIAL DIVERSITY IN PITCHER LEAF FLUID
    Akwasi Buansi, Sicily Palmeri, Melinda Falcon, and C. E. Hellquist

78. COMPARISON OF HEAVY METAL CONCENTRATIONS IN TERRESTRIAL PLANTS IN VIEQUES, PUERTO RICO.
    Danielle Bucior, Susan Witherup

79. THE INFLUENCE OF LEAF LITTER QUALITY AND STREAM VELOCITIES ON AQUATIC MACROINVERTEBRATE ABUNDANCE AND DIVERSITY IN RICE CREEK (OSWEGO, NY).
    Alyssa Cassar, Robert Jarvis, and C. Eric Hellquist

80. THE LATE SILURIAN, EURYPTERID-BEARING FIDDLERS GREEN FORMATION (BERTIE GROUP) AT LANG'S QUARRY, HERKIMER COUNTY, NEW YORK.
    Samuel J. Ciurca, Jr. and Allan Langheinrich

81. SPECIES COMPOSITION OF NORTHERN HARDWOOD FORESTS DEPENDS ON SITE AND STAND AGE
    Athena Czerwinski Burkard, Braulio A. Quintero, Corrie A. Blodgett, Yang Yang, and Ruth D. Yanai

82. GENERATION OF NOVEL MOTILITY MUTANTS IN *CHLAMYDOMONAS REINHARDTII*.
    Julie Delles and Noveera Ahmed

83. SEASONAL ANALYSIS OF INVASIVE *TYPHA* (CATTAIL) MITIGATION IN SILVER LAKE FEN (OSWEGO COUNTY, NY).
    Stephanie Facchine, Gabrielle Solomon, Sarita Charap, Corey Kane, Faith Page, and C. Eric Hellquist

84. THE IMPACT OF SELECT SIGMA LIGANDS ON THE ACTIVITY OF THE C-8,7 STEROL ISOMERASE IN TOBACCO.
    Joshua Harkins, Alyssa Tzetzo, Ivy Chen, Spencer Behmer, Keyan Salzman and Robert Grebenok

85. BEECH INTERFERENCE WITH MAPLE REGENERATION: FUTURE CHANGE IN FOREST COMPOSITION.
    Daniel S. Hong, Adam D. Wild, and Ruth D. Yanai

86. LEAD CONTAMINATION OF SOIL AND WATER IN DANIEL BOONE NATIONAL FOREST.
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ABSTRACTS

MELANIN-CONCENTRATING HORMONE MAY FUEL EXPANSION, ADHESION AND DIFFERENTIATION OF ADIPOSE CELLS IN CULTURE.

Hiba Y. Abdullah and Laurie B. Cook.

Melanin-concentrating hormone (MCH) is a neuropeptide that is expressed in the central nervous system and periphery with a highly conserved amino acid sequence that is found in a variety of species. MCH plays critical roles in feeding behavior, sleep-wake cycle, mood, and metabolism regulation in mammals. 3T3-L1 pre- and post-adipocytes express MCH receptors on the plasma membrane. Previous studies in our lab suggest that MCH signaling in 3T3-L1 pre-adipocytes promotes mitotic expansion, increases cell adherence to the culture dish, and protects from apoptosis. Furthermore, our preliminary studies have also found MCH signaling promotes lipid accumulation in adipocytes, which may facilitate the development of adipose tissue. The goal of this study was to further explore these MCH-mediated effects on 3T3-L1 cells by conducting a variety of assays varying MCH dose and time. 3T3-L1 pre-adipocytes were cultured in 12-well dishes in complete media with MCH concentrations of up to 1mM and incubated for either 1 hr (short-term) or 6 days (long-term). For the cell adhesion assay, floating cells and adhered cells (dislodged via trypsin) were counted either using a hemocytometer or an automatic cell counter. Viable and nonviable cells were distinguished using 0.4% Trypan Blue. Preliminary data supports a role for MCH in facilitating cell proliferation, perhaps protecting against apoptosis. In an assay used to detect glycerol synthesis and secretion from differentiated adipocytes we found a measurable MCH effect, suggesting that MCH does indeed positively influence fatty acid synthesis and metabolism in 3T3-L1 adipocytes. Together, these results indicate a novel role for MCH in regulating pre- and post-adipocytes, potentially influencing adipose tissue development and expansion.

CREATING A NEW MODEL FOR PCR INSTRUCTION.

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The Polymerase Chain Reaction (PCR) is a fundamental laboratory technique that allows for the production of many copies of a desired DNA fragment and subsequently the analysis of genes, DNA, and genomes. This study focuses on identifying the misconceptions that students had pertaining to the process of PCR and developing a new model that would address these issues. We initially collected statistics from the AP Scholars Introduction to Biology course at the Rochester Institute of Technology via a pilot assessment that students had taken and consequently performed poorly on. We used this data as our primary motivation for the creation of our new model. By doing so, we were able to successfully develop an interactive activity and worksheet that aimed to reverse the popular misconceptions that our students had with PCR. The results indicate that, while there were minimal flaws in our design which may have slightly hindered the students' ability to retain the important aspects of PCR, the modeling activity as a whole significantly transformed the ways in which students were able to understand and grasp the concepts of PCR and how it related to the field of biology. We are currently working on improving both the model and the assessment.

PILOTING A PATHOGEN: THE DEVELOPMENT OF AN AMBER SUPPRESSOR STRAIN IN *PSEUDOMONAS AERUGINOSA*.

Lily Adams and Julie A. Thomas
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Giant phages are bacterial viruses of extreme interest due to their highly unusual properties and potential for biotechnological and clinical applications. We have developed a novel model genetic system to assign function

to unknown proteins of *Salmonella* phage SPN3US. This system utilizes a suppressor strain of bacteria - one that supports the growth of conditional lethal genetic mutations - and a non-suppressor - normal - strain of the same species. To date, our studies have been limited to *Salmonella*, as no host counterpart exists to study giant phages that infect the pathogen *Pseudomonas aeruginosa*, such as ϕKZ. The goal of this study was to create *Pseudomonas* suppressor strains using gene manipulation techniques. These strains are being utilized in the isolation and examination of mutant phage candidates. These studies will illuminate interactions between giant phages and their pathogenic hosts, and provide foundation for the exploitation of phage products to fight multi-drug resistant bacterial infections.

FURTHER CHARACTERIZATION OF HYDROCARBON DEGRADING BACTERIA ISOLATED FROM SEDIMENT SAMPLES OF SLATER CREEK, NEW YORK.

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Oil pollution has been a serious environmental problem worldwide. It is known that microorganisms have the ability to detoxify polluted environments, a process termed bioremediation. However, different microbes have different hydrocarbon degrading properties, which is influenced by many factors. The purpose of this research is to isolate and characterize hydrocarbon-degrading bacteria from Slater Creek, which was contaminated with oil leaked from the Russell RGE substation. This is important to ensure that bioremediation is ongoing in Slater Creek in the effort to remove oil that has contaminated the area by natural attenuation. This area of Slater Creek is a DEC approved fishing area for local residents and Slater Creek also flows into Lake Ontario, which could lead to more widespread shoreline contamination. Several bacterial isolates were found by enriching sediment samples from two areas of Slater Creek with short chain and medium chain alkanes. The isolates, A3, B3, B7, and D4 degraded medium chain alkanes with consistent degradation over a range of pH values from 6 to 8, but slower degradation activity for short chain alkanes over the same range of pH values. All isolates can also degrade other hydrocarbons such as a motor oil mix and kerosene, B7 degrades mix motor oil the best compared to other isolates. When given different source of nitrogen, A3, B3 and D4 show good activity for short chain alkane degradation with ammonium nitrate, while B7 had a better degradation activity with ammonium chloride. As for medium chain alkanes, A3 and D4 degraded medium chain alkanes well using ammonium nitrate, B3 in ammonium chloride and B7 in ammonium chloride. The isolates were also able to degrade both types of alkanes using different concentration of nitrogen, with the highest activity for short chain by B7 (702 ppm / NH_4Cl) and medium chain by D4 (700 ppm / NH_4NO_3). The data suggests that there are indigenous microbes that are able to remediate Slater Creek area, helping to degrade the oil remaining and reduce the risk to the environment.

THE ELUSIVE TITER: DETERMINATION OF LONG TERM PRESERVATION OF GIANT PHAGE SPN3US.

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SPN3US is a bacterial virus or phage that infects the food pathogen *Salmonella enterica*. SPN3US is referred to as a "giant phage" as it has an unusually long genome of 240kb. We are studying it as a model for an expanding group of giant phages that infect human and plant pathogens. About 96% of phages that have been isolated are tailed, meaning their virions consist of a head or capsid, which contains the double-stranded DNA genome, and a tail. Phage SPN3US and related phages belong to the *Myoviridae* family which is a family of tailed phages with contractile tails. These giant phages are ancient and diverse, and knowledge about their phage life-cycle and host-interactions are limited. To address this problem, we have successfully isolated the first collection of amber mutants of a giant phage for SPN3US.

Many phages store well at 4 °C for many years, even decades. However, SPN3US loses its viability over time, for instance high titer stocks have been observed that almost completely lose titer when stored at 4 °C for just two years. This decrease in viability could be a major problem, leading to the loss of mutants or the entire collection. Therefore, the goal of this research was to develop a preservation method to preserve amber mutants at -80 °C. To do this we tested several different cryoprotectants for their effect on viability over periods of time. These studies have shown SPN3US can be successfully preserved at -80 °C in different cryoprotectants.

DOES AN IMAGE-BASED AGING GUIDE FOR TREE SWALLOW NESTLINGS WORK WELL FOR OTHER SPECIES?

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Aging guides based on digital images were previously developed for nestling Eastern Bluebirds (*Sialia sialis*), House Wrens (*Troglodytes aedon*), and Tree Swallows (*Tachycineta bicolor*). Age estimates produced by the bluebird and wren guides were equally accurate: ~90% of estimates were within one day of actual nestling age. If nestlings of different species share developmental patterns, even if timing of development differs, it may be possible to produce age estimates for all such species based on one generalized aging guide. In order to assess this possibility, the Tree Swallow guide was used to produce age estimates of nestling bluebirds and wrens. Age estimates of bluebird nestlings were generally underestimated and estimates of wrens were generally overestimated. Errors were corrected with regression analyses, however, indicating that a general aging guide could be developed to produce nestling age estimates for species with similar patterns of development.

ECONOMIC ANALYSIS OF THE LIFE CYCLE OF SPENT COFFEE GROUND AS VIABLE FEEDSTOCKS FOR HEATING OIL AND BIOFUELS PRODUCTION

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The economic potential for using spent coffee grounds (SCG) as a feedstock for heating oil is being investigated. The goal of this study is to assess the environmental and economic potential of alternate use of SCG. SCG oil extract can range between 8-15% using 1.83ml hexane/1g SCG, with 60-80% hexane recovery. The recovered hexane can be used for additional extractions for a cost savings in the process. Hexane recovery and oil extraction cost $38.91/350 kg of SCG. The energy content of the oil extracted from SCG is 38.45 MJ/L which is nearly identical to 38.5 MJ/L of residential heating oil. The transesterification of oil will produce biodiesel and crude glycerol for $6.55/350kg SCG. Acid hydrolysis was used for carbohydrate extraction, these carbohydrates were then used for ethanol fermentation. The cost for ethanol production is $82.62/350 kg SCG. The major cost of this process is the sulfuric acid used for hydrolysis. The potential reduction in cost of this reagent may lie in the collaboration with power plants facilities which are producing sulfur dioxide as a byproduct which may be converted to sulfuric acid and represent an inexpensive alternative for generating sulfuric acid. Alternative uses of SCG also show reduced global warming potential.

EXPOSURE TO LEAD ALTERS MOTOR ACTIVITY OF INVERTEBRATES.

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Lead is a metal which interferes with a variety of body processes and is toxic to many organs in humans and other animals. Recently, in Flint, Michigan the water has been an issue and high concentrations of lead have been found in several homes. This can have a harmful effect on humans, especially children. To learn more about the effects lead can have on organisms, we examined how lead affects motor activity of *C. elegans*, a nematode model commonly used to understand questions in neurobiology. *C. elegans* nematodes were dosed with two different concentrations of lead based on the "allowed" amount in municipal water systems and the highest concentration found in the Flint, Michigan household water. *C. elegans* exposed to the higher dose of lead experienced a nearly ~50% decline in motor activity in comparison to those not exposed to lead at all. This work provides a better understanding of potential neurological effects of lead in humans.

THE DEVELOPMENT OF IMPROVED TUMOR MODELS FOR EVALUATION OF TARGETING MOLECULAR IMAGING AGENTS (TMIAs).

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The recent discovery that imaging and therapeutic agents can be targeted to cancer cells via specific markers opens a new therapeutic window to identify, treat, and potentially eradicate various carcinomas. The goal of this research stands to evaluate targeted molecular imaging agents (TMIAs) that bind to cancer cells carrying a specific biomarker. The focus of our research has been the development of TMIA-conjugated near-infrared fluorescent peptide inhibitors which bind to prostate-specific membrane antigen (PSMA). Desirable agents will bind to the PSMA receptor and be internalized via endocytosis, increasing the TMIA signal within the cells. We have developed two- and three-dimensional models to aid in the identification of agents that bind to cells and penetrate the malignant biomass. An ever increasing body of literature indicates significant differences in cell morphology, gene expression, proliferation, and migration between 2D and 3D cultured cells. Cells cultured in 3D matrices more accurately represent live animal models and human tumors. TMIA penetrates 3D cancer models and stains cells buried inside the spheroid tumor bodies, demonstrating enhanced penetrability characteristics. We conclude that such use of 3D cancer models more closely mimic *in vivo* conditions and should facilitate development of TMIAs. This will result in molecules which target metastatic tumors; illuminating their presence, size, and structure thus allowing better clinical treatment and therefore patient survival.

FORAGING BEHAVIOR OF ALLEGHENY MOUNTAIN DUSKY SALAMANDERS (*DESMOGNATHUS OCHROPHAEUS*) EXPOSED TO KAIROMONES FROM SYNTOPIC AND ALLOTOPIC SNAKE SPECIES.

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Many prey species reduce the likelihood of injury or death by engaging in defensive behavior but often incur costs related to decreased foraging success or efficiency. In some cases these defensive responses are mediated through the use of chemical stimuli from predators deposited within their environment. In the current study we examined the foraging behavior of Allegheny Mountain Dusky Salamanders (*Desmognathus ochrophaeus*) exposed to kairomones from three different species of snake. We attempted to evaluate the generalized nature of the snake

kairomones by exposing salamanders to a syntopic predatory snake (*Thamnophis sirtalis*), a syntopic non-predatory snake (*Opheodrys vernalis*), and an allotopic predatory snake (*Thamnophis brachystoma*). We hypothesized that in the presence of kairomones from predatory snakes (e.g., *Thamnophis* spp), salamanders would exhibit a reduction in foraging behavior and success. Conversely, in the presence of kairomones from a primarily insectivorous snake (e.g., *O. vernalis*), salamander foraging would not differ significantly from a control (water) stimulus. To evaluate our hypothesis, we observed salamander behavior in four different chemical treatment conditions: 1) *T. sirtalis*, 2) *O. vernalis*, 3) *T. brachystoma*, and 4) water. To each treatment condition we added five *Drosophila* prey and observed salamander foraging behavior for 10 minutes. Our results indicate no significant differences related to the source of the predator kairomone with regards to the number of strikes ($p = 0.055$), number of *Drosophila* consumed ($p = 0.061$), or latency to strike ($p = 0.104$). Our results suggest that exposure to the predator stimuli suppressed foraging activity versus a control and furthermore the effect is unrelated to syntopy or predator diet but that additional experimental evaluation is required.

EFFECTS OF DOCETAXEL ON HISTONE MODIFYING ENZYMES IN OVARIAN CANCER CELLS EXPOSED TO ESTROGEN AND BISPHENOL A

Lanni Aquila, Laura Hayes, and Lisa Morey, PhD.

Ovarian cancer is the ninth most common cancer but the fifth leading cause of cancer death for women. While estrogenic compounds are not mutagenic, it has been shown that they are able to alter gene expression. A previous study demonstrated that the epigenome of two ovarian cancer cell lines, SKOV-3 and OVCAR-3, were altered when exposed to estrogen and BPA. Specifically, Set8, a histone methyltransferase, and Sirt1, a histone deacetylase were two genes found to be altered. The current study built off of these results, and focused on the expression of these histone modifying enzymes when cells were exposed to the same physiological doses of estrogen or BPA with a therapeutic agent, Docetaxel. After analysis, it was found that no significant changes in either gene occurred in the SKOV-3 line. In the OVCAR-3 cell line, changes in gene expression were noted, with Set8 being more susceptible.

CHARACTERIZING THE EFFECT OF *HSF* MUTATIONS ON BRAIN TUMORS IN *D. MELANOGASTER*.

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Previous research in mammals has shown that by knocking out Heat Shock Factor, a transcription factor, tumor growth can be suppressed (Dia, 2007). We are interested in figuring out if the same is true in *D. melanogaster*. To do so, we induce brain tumor development using mutations in the gene *lgl* (lethal giant larvae). These mutations cause neuroblasts to divide symmetrically instead of asymmetrically, leading to over proliferation. By using genetic recombination, we created stocks with both *lgl* and *HSF* mutations. These stocks were then placed over a balancer chromosome with a Tubby mutation, allowing for selection of skinny larvae with two copies of an *lgl* mutation and varying levels of *HSF* knock down. In order to study the brain tumors we used the antibody Deadpan, which binds specifically to neuroblasts. Currently we are working with two *HSF* mutations, HSF^{1} and HSF^{4}. The first mutation is a null allele and the latter is a proposed hypomorph. So far we have looked at brain samples from *HSF* wild type larvae, larvae with one copy of HSF^{1}, and larvae with one copy of HSF^{1} together with one copy of HSF^{4}, all in an *lgl* mutant background. The HSF^{1} mutation by itself reduced the size of the brain tumors as compared to wild type, but when combined with HSF^{4} the tumors returned almost to the size of the wild type tumors. This went against our simple model saying the more we reduced *HSF* function the more antagonized tumor development would be. Future studies will aim to understand why this occurs.

VARIATIONS IN FATTY ACID SIGNATURES OF BROWN TROUT AND COHO SALMON FROM LAKE MICHIGAN.

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Non-native species introduced through human activities have altered the food web of Lake Michigan. To better understand these changes, diets of several salmonid species were studied using fatty acid signatures (FAS) as these predators appeared to rely more on nearshore species compared to historic accounts. Specifically, inter and intra-species (spatial) FAS variations were assessed in brown trout (*Salmo trutta*) and coho salmon (*Oncorhynchus kisutch*). Fish were collected by federal, state and tribal agencies throughout the lake and assigned to one of the four quadrats of the lake: southwest, southeast, northwest and northeast. Belly flaps were sampled and analyzed for lipid and fatty acid composition. Our preliminary results indicated that lipid content was higher in brown trout than in coho salmon (29.9% vs. 11.2%). Ongoing statistical analysis will reveal potential inter- and intra-species (spatial) FAS variations and provide a better understanding of the prey-predator interactions in Lake Michigan as well as the ability of these salmonid species to utilize alternative energy resources.

A PILOT STUDY TO ASSESS THE EFFICACY OF THE PACIFIC CREST TRAIL AS A MEGATRANSECT OF AMPHIBIAN AND REPTILE DIVERSITY IN THE KLAMATH MOUNTAINS OF NORTHERN CALIFORNIA.

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The Pacific Crest Trail is a National Scenic Trail that extends from Mexico to Canada through the states of California, Oregon and Washington. Over the course of its approximately 4,265 km it passes through a number of distinct ecoregions within the Pacific cordillera. The PCT as a 'megatransect' is an attempt to provide baseline data on the occurrence and distributions of species and an assessment mechanism regarding biodiversity responses to projected changes in climate. To date, data have been collected related to avian biodiversity, including breeding behavior and phenology, with the ultimate goal of facilitating long-term assessment of species distributions as well as possible altitudinal and latitudinal shifts. With the current pilot study, we hoped to evaluate the efficacy of the megatransect as a low-impact and efficient mechanism to document, predict, and explain patterns in the biological diversity of amphibian and reptile species. To that end, we backpacked a 322-km section of the PCT from Dunsmuir, CA to Ashland, OR through several wilderness areas (e.g., Castle Crags, Trinity Alps, Russian and Marble Mountain wildernesses) of the Klamath Mountains. During trail surveys, we made an effort identify every individual amphibian or reptile detected within the trail boundary as well as any that could be seen from the trail. For each sighting, we recorded the time detected, GPS coordinates, California Wildlife Habitat Relationship habitat type, distance from the trail margin (if applicable), temperature, cloud cover, wind velocity, and other useful or relevant information regarding an individual's disposition (e.g., behavior). Although the bulk of the analysis is pending, we are able to report the detection of 144 total sightings with individuals from 12 different species (four amphibian and eight reptile species). The most common species was the Sagebrush Lizard (*Sceloporus graciosus*) with 110 occurrences whereas the Mountain Garter Snake (*Thamnophis elegans*), Northern Rubber Boa (*Charina bottae*) and Southern Alligator Lizard (*Elgaria multicarinata*) were each represented by a single individual.

GENETIC AND ENVIRONMENTAL INFLUENCES ON THE SIZE-FECUNDITY RELATIONSHIP IN THE ASIAN TIGER MOSQUITO, *AEDES ALBOPICTUS*.

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The Asian tiger mosquito, *Aedes albopictus* is an important vector of several arboviruses around the world. Disease transmission models that predict transmission rates include several parameters such as the population growth of the mosquito vector. Population growth estimates often rely on size-fecundity relationships that have been established for a particular species, but are from a limited number of studies. We wish to determine if there are genetic and environmental factors that may shift the size-fecundity relationship for *Ae. albopictus*. In this study, we test the hypothesis that different populations of *Ae. albopictus* raised in different temperature environments will cause variation in the size-fecundity relationship. In a laboratory experiment, we reared *Ae. albopictus* from four different populations in the United States across five different temperatures. For each population, cohorts of mosquitoes were reared from hatched larvae through adulthood across one of the following five temperature treatments: 18^{o}C, 21^{o}C, 25^{o}C, 28^{o}C, or 31^{o}C. Following emergence, adult females were given the opportunity to mate and provided a bloodmeal. For each bloodfed female, the ovaries were dissected and eggs were counted as a measure of fecundity, while wings were dissected and measured as a proxy of size. The size-fecundity relationships are compared across populations and temperature treatments and the implications on estimates of disease transmission rates are discussed.

INFECTION OF A PATHOGEN: STUDYING THE EFFECT OF THE GENOME OF GIANT PHAGE SPN3US ON SALMONELLA

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Bacterial viruses (phages) are the most abundant group of organisms on the planet. Many of the proteins encoded by giant phages, with genomes over 200 kb, are currently of unknown function. *Salmonella* phage SPN3US acts as a model system for related phages, as many of the genes in its genome are well-conserved in other giant phage genomes. An unusual feature of SPN3US and its relatives is that they all have two multi-subunit RNA polymerases coded for by the genome, one a virion RNAP and the other a non-virion RNAP. It is expected that the vRNAP is ejected into the host cell with the DNA, for early gene transcription, while the nvRNAP is produced later for mid and late gene transcription. It is expected these RNAPs allow for the phage to have control of its gene expression; however, very little of this process is understood at the molecular level.

These experiments look to study the gene expression of the *Salmonella* host against that of the host infected with wild-type SPN3US to observe the differences in the transcriptome and the proteome. Our preliminary proteomics data, from mass spectrometry experiments, suggests that *Salmonella* gene expression during infection is intricately manipulated by the phage, with some gene products being upregulated and others downregulated.

Planned future work includes liquid infections of the *Salmonella* host with SPN3US mutants. Samples would be taken at time points during infection for qRT-PCR, proteomic analysis, and RNA sequencing. This would allow us to observe how the loss of function of phage genes affect the upregulation and downregulation of different host gene products, which ultimately provides information on phage gene function. These studies will have broader impacts on our understanding of SPN3US and giant phages in general and will increase the potential for these phages to be used in phage therapy and other novel biotechnological applications.

HUMAN CYTOMEGALOVIRUS REGULATION OF AKT FOR THE INDUCTION OF MONOCYTE TO MACROPHAGE DIFFERENTIATION.

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Human cytomegalovirus (HCMV), a member of the betaherpesviridae family, asymptomatically infects a majority of humans worldwide by adulthood; the virus is responsible for widespread fatalities among immunocompromised and newborn patients. HCMV establishes quiescent infection in monocytes, prolonging monocyte survival and forcing differentiation into macrophages, where it is capable of viral gene expression and replication and spread into tissues. During HCMV infection of monocytes, activity of phosphorylated Akt (p-Akt), a monocyte apoptosis suppressor, is required at high levels for monocyte survival early in their lifespan, prior to the 48-hour monocyte viability gate. After 48 hours, HCMV downregulates p-Akt, which we hypothesize drives differentiation of monocytes into pro-inflammatory M1 macrophages, as low p-Akt expression is required for monocyte-to M1-macrophage differentiation. Here we show an HCMV microRNA, miR-US25-2-5p, is expressed at both 24 hours post-HCMV infection and after the monocyte viability gate, at 48 and 72 hours post-infection. Additionally, we concluded that miR-US25-2-5p is a regulatory factor of p-Akt, resulting in its downstream downregulation. Overall, deciphering how HCMV manipulates the p-Akt signaling pathway has potential for the development of HCMV-specific antiviral drugs targeting its monocyte-to-M1 macrophage differentiation and widespread proliferation through tissues.

THE INFLUENCE OF *DIDYMOSPHENIA GEMINATA* ON THE CONSUMPTION PATTERNS OF FISH AND INVERTEBRATES IN FRESHWATER STREAMS.

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Didymosphenia geminata, commonly known as Didymo, is an nuisance freshwater diatom that, when introduced into aquatic environments, produces a thick matt material that will overlie all flat surfaces. Didymo has been shown to affect fish and invertebrate communities and is likely to alter the resource use and food web dynamics in affected rivers. We used fatty acid methyl ester signatures to investigate changes in resource use of invertebrates and fish in rivers impacted by Didymo mats. Invertebrates samples were collected in tail water sections (below dams) from three rivers in eastern Tennessee. At each river, samples were collected from sites of high Didymo concentration, upstream near dam outflow, and low Didymo concentration, further downstream. We performed a lipid analysis of macroinvertebrate taxa (*Gammarus, Baetis,* Chironomidae and Simuliidae) common in both stream locations and compared their fatty acid profiles to determine shifts in their food source. Within each taxa, we found consistent decreases in the ratio of omega-3:omega-6 fatty acids, suggesting a shift in diet away from algal resources. We additionally found reductions in fatty acids biomarkers associated with diatoms, similarly suggesting reduced reliance on biofilms. Stable isotope data conducted on invertebrates from both concentration sites suggests an increased reliance on macrophytes within their diets. Collectively, our results indicate that Didymo mats alter basal resource use and that invertebrates are not heavily relying on Didymo as a food source. Lipid profiles of Brown trout (*Salmo trutta*) and rainbow trout (*Oncorhynchus mykiss*) showed a similar pattern to that of invertebrates, resulting in an increase in omega-6 fatty acids in the presence of Didymo. Brown trout also showed an increase in DHA in the presence of Didymo, suggesting a possible accumulation of some resources through direct Didymo consumption. Overall, the presence of Didymo within these rivers may both directly and indirectly alter the energy flow through the food web.

THERMAL TOLERANCE OF ANTS IN WESTERN NEW YORK.

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Temperature radically influences the physiological functioning of all organisms, ultimately impacting biota survival. As such, species distributions often are determined by their thermal tolerance. At continental scales, species disperse by their thermal tolerances due to thermoclines caused by latitude and landform barriers. However, thermoclines also exist at smaller scales, such as the effect of large water bodies and urban environments ("urban heat islands"). Two closely related ant species, *Aphaenogaster picea* and *A. rudis*, sort out by elevation thermal gradients, with *A. picea* being more tolerant of the cold. In this study, we investigated whether similar thermal tolerance gradients occur with distance from the Great Lakes and the greater Buffalo metropolitan area (Western New York). Individuals from sample sites were collected from locations that varied in proximity to Lake Erie, Lake Ontario and Buffalo. Live ants from the sample sites were subjected to thermal tolerance testing in order to determine their maximum and minimum temperature tolerance. Given the temperature moderating effects of large water bodies and urban areas, we expected that the *Aphaenogaster* spp. located nearer these would have higher minimum and lower maximum thermal tolerances. Unexpectedly, we found not discernable patterning with distance to urban areas, but minimum temperature tolerance was lowest with closer proximity to the Great Lakes. The terrestrial lake thermocline reverses seasonally with relatively colder temperatures near water in the Spring and relatively warmer temperatures in the Fall. Our results suggest that the cold spring temperatures are more selective on ant physiology than mean annual temperatures.

ANALYSIS OF *D. MELANOGASTER* VIABILITY ON DIFFERENT DIETARY STEROLS.

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Dietary sterols play a critical role in hormone production and insect development. Prior work has indicated that cholesterol is the primary base for the molting hormone ecdysone, which is required for larval pupation in many insects. Subsequent studies have also suggested that ecdysone specifically plays a role in the developmental timing of *Drosophila* species. Recent work suggests that not only is cholesterol is the most efficient sterol for *Drosophila* utilization, but they also lack the ability to functionally utilize any other sterol for ecdysone synthesis. Puzzlingly, *D. melanogaster* has a diet that typically consists of items rich in β–sitosterol and campesterol, but lacking in cholesterol. The question of where the *Drosophila* are obtaining cholesterol for ecdysone synthesis becomes a fascinating question, since neither their natural diet (i.e. fruit), nor any standard laboratory diet appears to contain cholesterol in utilizable quantities. Therefore, it would appear that *Drosophila* must be, at least initially, utilizing some sterol other than cholesterol for its developmental processes. In order to do this, *Drosophila* is likely using one (or more) of three strategies: 1) converting other dietary sterols into cholesterol, 2) utilizing a lipid sparing strategy in which cholesterol from the plasma membrane is used to synthesize ecdysone and is replaced with another sterol, and/or 3) converting another sterols directly into ecdysone. In order to determine which of these strategies are used, our lab has developed a chemically defined, or "synthetic", diet containing only β–sitosterol, campesterol, stigmasterol, and ergosterol, the sterols that we have determined are present in natural and laboratory diets. By rearing multiple generations of *Drosophila* on this diet, and, thus, removing any maternal contributions from the stock population, we can directly test the sparing hypothesis. Given our success in maintaining multiple generations in this synthetic media, we provide evidence that *D. melanogaster* may not, in fact, require dietary cholesterol, and rather may be converting other sterols to cholesterol or using the other dietary sterols to directly synthesize ecdysone, something which has never been previously documented. Through further analysis of egg-to-adult viability across multiple generations on these synthetic diets, we hope to gain more insight into how and with what these organisms are using to synthesize ecdysone.

AN ALTERNATIVE SYNTHETIC PATHWAY FOR A CYTOTOXIC COMPOUND FOR LYMPHOCYTIC LEUKEMIA.

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(−)-Communesin F is a naturally occurring compound isolated from marine and terrestrial Penicillium fungi. This compound sparked interest in the scientific community due to its significant cytotoxicity against lymphocytic leukemia cells in humans. (−)-Communesin F also has minimal effects on other cells making it highly selective against leukemia, however, extracting even trace amounts from natural sources is extremely costly, difficult, and time-consuming. Research on this compound has revealed that it can be biosynthesized from another natural product, (–)-aurantioclavine. Our goal is to efficiently synthesize (–)-aurantioclavine at a minimal cost, to be able to produce the final material in appropriate quantities. We are currently comparing two potential starting materials, tryptamine and 3-indolepropionic acid, which give us an inexpensive platform to start the synthesis. Our key synthetic steps include a Schmidt reaction and a Meier chiral formamidine-based alkylation, to install two important structural features found in aurantioclavine: a seven-membered ring and a benzylic chirality center. Our progress in these efforts will be presented.

EFFECTS OF FULLERENES ON A FRESHWATER BENTHIC COMMUNITY: TOXICITY AND IMPLICATIONS FOR ENVIRONMENTAL PROCESSES AND FUNCTIONS

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Fullerenes are a class of carbon allotropes with unique properties that make them useful in different applications. Due to their high strength, electrical conductivity, electron affinity, structure and versatility, fullerenes are being increasingly used as nanomaterials in cosmetics, medicine, optics and electronics. This diverse array of applications and derivatives might make the potential environmental impacts of fullerenes equally variable. Thus, it is important to understand how fullerenes, which are incorporated into products and industrial processes, affects toxicity on benthic macroinvertebrates caused by particle settling in aquatic systems and, consequently, their potential implications on ecosystem processes and functions. The purpose of this experiment is to quantify the effects that carbon fullerenes, specifically C60, PCBM, and C70, on the health of *Lumbriculus variegatus*, a benthic oligochaete that plays a key ecological role in freshwater ecosystems as organic matter feeders and water pollution indicators. Additionally, this project will investigate fullerene impacts on the microbiotic communities and ecosystem function in lake sediments using a microcosm experiment able to measure oxygen and nutrient changes over time at acute (2 day) and chronic (22 day) intervals, and daily water samples will be used to calculate the change in fullerene concentration in the water over time. Pilot studies suggest that C60 added to the water column may have a positive effect on the oxygen fluxes of these microcosms, potentially due to increased metabolism, changes on denitrification rates and no significant lethal or sub-lethal effects effects on *L. variegatus*. The ultimate goal of this project is to enhance our understanding of engineered nanomaterials and their potential risks in aquatic systems, support development of guidelines and policies regarding environmental safety of engineered nanomaterials and contribute to a safe and sustainable nanotechnology industry. Further research will focus on the effects of fullerenes on benthic microalgae, the synergistic effects of fullerenes with heavy metals and their toxic implications on benthic organisms.

CALCIUM ACTIVITY IN THE NEUROMAST

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Background: Neuromasts are the functional unit of the lateral-line system in aquatic vertebrate, a sensory organ that detects movements in the surrounding water. Shearing forces open non-specific ion channels in hair cells

of the neuromast, depolarizing the cell and releasing neurotransmitters, which stimulate afferent sensory neurons. Anoctamin 2 (Ano2), a calcium-activated chloride channel (CaCC), has been shown to be expressed in hair cells of 5 days post fertilization (dpf) zebrafish, suggesting Ano2 has a functional role in neuromast mechanotransduction. Characterization of calcium activity within the neuromast is necessary to elucidate Ano2 function.

Aims: (1) Confirm neuromast stimulation results in increased intracellular calcium and (2) determine the relationship between calcium, Ano2, and neuromast function.

Methods: Intracellular calcium concentration in hair cells will be measured in unstimulated and stimulated Neuromasts hair cells. A potential role for Ano2 function will be determined using Ano2 antagonists. Neuromasts will be ablated using neomycin or EDTA. Neuromast function will be confirmed using a rheotaxis assay.

Results: Incubation of 5-dpf zebrafish in 10µM cal-520-AM resulted in non-specific fluorescence. Adjusting loading times and concentrations were in-effective. An alternative approach using a transgenic GCaMP fish line that expresses a calcium-sensitive form of green fluorescent protein will be used to measure calcium oscillations in hair cells.

Conclusion: Non-specific fluorescence after incubation in cal-520 indicates a need for a new method for cal-520 loading in hair cells.

DEVELOPING A METHOD FOR PURIFYING PRIMARY CILIA FROM DIFFERENTIATING 3T3-L1 PRE-ADIPOCYTES

Tameciah Browne and Laurie B. Cook

Obesity has become a leading health crisis in Western society. An understanding of the development of fat cell precursors can lead to intentional pharmaceutical design that will combat obesity by inhibiting the accumulation of excess fat tissue. The melanin-concentrating hormone receptor 1 (MCHR1) is a G protein-coupled receptor found in the plasma membrane. MCH is a key appetite signaling hormone. Our lab has recently identified this signaling pathway as a potential regulator of adipose tissue development. 3T3-L1 cells are a useful cell culture model for studying the development of adipose tissue. Interestingly, during differentiation, 3T3-L1 pre adipocytes produce a primary cilium, to which MCHR1 migrates, but only transiently before returning to the plasma membrane. We hypothesize that MCH signaling is altered during ciliary localization. Our overall experimental goal is to determine the proteins that MCHR1 interacts with in the primary cilium. We ultimately want to perform mass spectroscopy analyses as an identification method. The Aim of this project was to develop a procedure to isolate purified primary cilia from 3T3-L1 cells on Day 2 of a 10-Day differentiation protocol. First, a calcium shock method was attempted, but we were unable to replicate the published protocol despite multiple attempts to keep a critical calcium salt in solution. We attempted to modify the protocol in a variety of ways: adjusting the salt concentration, pH level and centrifugation speed, with unsuccessful results. Next, we tried a shear force procedure to strip the primary cilia from the surface of these cells. For both procedures, Western blot and fluorescence microscopy for acetylated tubulin, an important ciliary protein, were used to verify that the cilia were purified. In future experiments we will try two additional versions of the calcium shock protocol and a slide/peel method.

THE RELATIONSHIP OF PITCHER PLANT MORPHOLOGY TO BACTERIAL DIVERSITY IN PITCHER LEAF FLUID

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Carnivorous plants have generated a large amount of interest due to their use of invertebrates and small vertebrates to supplement their nutritional requirements. Usually plants acquire nitrogen and phosphate through nutrient rich soil. Pitcher plants (*Sarracenia purpurea;* Sarraceniaceae) are primarily found in nutrient-poor peatland (bog-like) ecosystems throughout North America. Pitcher plants compensate for lack of nutrients in the soil by obtaining nutrients from the insects they capture in their fluid-filled leaves. Pitcher plant leaves act as pitfall traps that commonly attract flies, moths, butterflies, beetles, and ants via nectar secretion and UV reflection patterns on

leaves. When trapped, insects drown, and their bodies are broken down by inquiline communities, and pitcher plant enzymes. The processing of insects allows the pitcher plant to absorb the digested nutrients as a supplement for photosynthesis. We predicted that pitcher plants leaves that are larger would have more captured insects, and greater bacterial diversity in the pitcher fluid. To examine this hypothesis we measured environmental characteristics (pH and light), pitcher characteristics (approximate plant age, width of opening, length, volume and photosynthetic efficiency). In addition, the bacterial metabolic richness and organic content of the pitcher fluid will be analyzed using BioLog Ecoplates. Initial results indicate that pitcher plants with larger leaf sizes collect more rain water and contain more organic matter within the pitcher fluid.

COMPARISON OF HEAVY METAL CONCENTRATIONS IN TERRESTRIAL PLANTS IN VIEQUES, PUERTO RICO.

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According to recent studies (Mattina et al., 2003), plants have been found to be reliable biological indicators for detecting toxins and heavy metals in their immediate and surrounding environments. Upon root contact, both terrestrial and aquatic plants can take up and bio-accumulate heavy metals. The Atlantic Fleet Weapons Training Facility is south east of the main island of Puerto Rico on the island of Vieques. The training range encompasses about half the area of the island and was used for artillery missile training from 1941 until 2003. This area has since been converted to a National Wildlife Refuge. We collected plant samples from four sites located on public beaches in Vieques National Wildlife Refuge. On these beaches we collected the leaves, roots and shoots of two species of coastal dune dwelling plants: *Scaevola taccada*, and *Scaevola plumieri*. Using an X-Ray Fluorescent spectrometer and an Inductively Coupled Plasma Optical Emission Spectrometer, we tested for the presence and quantity of heavy metal in dried tissue samples. We compared metal uptake in each of the plant species and also considered the effect of pH on the uptake of heavy metals. Using these plants as primary indicators, we will generate information regarding health, toxicity and contamination of the ecosystem, allowing us to provide remediation recommendations and assess the impacts these metal levels may have on other flora and fauna present.

COMPARATIVE ANNOTATION OF A REGION OF THE *DROSOPHILA ELEGANS* MULLER D ELEMENT.

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The *Drosophila melanogaster* Muller F element (fourth chromosome) is a small, mostly heterochromatic region of the genome containing genes that, unexpectedly, are expressed at or near euchromatic levels. To better understand the regulation of genes operating in this environment, we have annotated a euchromatic region near the base of the *D. elegans* Muller D element (positions 1,050,501 to 1,115,000). This information will be used to compare and contrast the types and distributions of conserved regulatory motifs near the transcription start site of F and D element genes. Annotation was carried out using a *Drosophila*-specific mirror of the University of California, Santa Cruz Genome Browser supported by the Genomics Education Partnership (GEP) at Washington University in St. Louis. The browser displayed evidence tracts for BLASTX alignments to *D. melanogaster* orthologous proteins, gene predictions, RNA-Seq read alignments, and TopHat splice-site junction predictions. Using these lines of evidence, the best-supported gene model for each predicted gene was generated, including translation start site, intron splice sites, and translation termination site. In total, three genes were annotated: *eg*, *CycH*, and *CG7407*. For genes with multiple isoforms due to alternative splicing events, each unique isoform was also annotated. All gene models were assessed for accuracy and completeness, and have been independently verified. This work supports and extends the overall goal of the GEP project, which is to better understand the regulation and expression of genes on the *Drosophila* F element.

DEVELOPMENT OF A BIARYL OXIDATIVE COUPLING-BASED ROUTE TO THE ANTI-TUMOR NATURAL PRODUCTS TMC-95.

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First isolated from the fermentation broth of *Apiospora montagnei* Sacc. TC 1093, the natural products TMC-95 A–D are of great interest because of their biological activity against the 20S proteasome. This distinctive activity makes them promising candidates as agents for the treatment of cancer. However, constructing such complex molecular structures requires many synthetic steps, which hinders their potential medical use. These active compounds feature a peptide-based structure composed of tyrosine, asparagine, a highly oxidized tryptophan, (*Z*)-1-propenylamine, and 3-methyl-2-oxopentanoic units. A particularly unusual bond is found in these natural products: a biaryl connection between the tryptophan and tyrosine residues and, as a result of this strange C–C linkage, axial chirality is observed around this bond. Our primary interest in this project is to develop chemical conditions to form this important biaryl linkage via oxidative coupling of suitable tripeptide-based building blocks. Such an oxidative coupling can make the synthetic production of TMC-95 significantly easier, by starting with the inexpensive and widely available natural amino acid units. With an easier synthetic route, TMC-95-based compounds could become viable anti-tumor drug candidates.

HOMOPOLAR MOTOR ACCELERATION AND BRAKING SYSTEM.

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Homopolar motors are simple electric motors that use direct current and two magnetic poles to produce rotational movement. The rotational movement of these motors can be described by the Lorentz force. In many demonstrations of a simple homopolar motor, the driving magnets stay stationary and the wire rotates. For this project, the same principle is used but the helical wire is stationary and the magnets move through the coil. From this design, a small "pod" containing a current source and two magnets can accelerate and brake through an enclosed track. The small "pod" and limiting factor on its maximum velocity will be presented in the poster/talk.

ANALYSIS OF THE *PVC*ABCD OPERON.

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Pseudomonas aeruginosa is a Gram-negative pathogen that may cause infections in immunocompromised patients. This organism produces the peptide siderophore pyoverdine, which is a component of one of its virulence factors and is synthesized by the activity of at least 15 proteins including four non-ribosomal peptide synthetases. The *pvc*ABCD operon was identified and originally believed to have a role in the synthesis of pyoverdine, but it is now shown to regulate the expression of pyoverdine associated proteins via the production of another secondary metabolite, paerucumarin. Within the *pvc*ABCD operon a protein of interest is PvcA, which belongs to a family of enzymes that produce isocyano derivatives of amino acids, in this case tyrosine. Of note is that this enzyme is involved in the production of a carbon-nitrogen triple bond. This study involves the elucidation of *pvcA* homologs in the *Pseudomonadaceae* and *Enterobacteriaceae* families, investigating the prevalence of the operon and its associated genes throughout proteobacteria in an attempt to purify these proteins for structural analysis.

BIOLOGY FIGURES MISS THE POINT OF ARROW USAGE.

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Figures in biology textbooks are essential to communicating biology concepts to students, but representations used by experts are often unclear to novices. We find that the use of arrows in these figures often contributes to their ambiguity, as they are used liberally with no consistent style for a particular meaning. This observation was quantified by selecting figures from introductory biology

textbooks and coding the arrows for style and concept they meant to convey. Analysis of a subset of 47 figures reveals that there is little consistency in the usage of arrow styles to convey any meaning. Of the 11 conceptual categories determined, each was depicted by an average of 3.6 styles. Using data obtained from preliminary interviews, an online survey designed to elicit students' ideas about meanings of arrows in various representations was created. The data from 201 participating undergraduate students agreed with our initial findings; for most arrow styles there is no agreed upon biological or scientific meaning. To determine whether arrow usage creates confusion for students, 14 additional individual interviews were conducted with students with varying background levels of biology experience. During these interviews, subjects were asked to describe all arrows contained within seven different figures selected from various introductory biology figures. The results showed that students often found the representations confusing or misleading, especially when common preconceptions about style meanings were not met. We propose that a set of guiding principles for arrow usage would improve instruction and allow biologists to communicate more effectively with each other and with biology learners.

UNDERGRADUATE ELECTRONICS COURSE WITHIN THE HWS PHYSICS MAJOR.

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Modern "black box" electronics have caused many students to stray away from their natural sense of curiosity and desire to explore the unknown. The secrecy incites hesitance, their warning labels kinder fear. With a desire to create a "safe space" for tinkerers, hobbyists, and physicists alike we strive on. The PHY 240 Electronics course at Hobart and William Smith Colleges in Geneva, NY stands out against the rest of the physics curriculum. The course combines lab and lecture periods into a 90-minute seminar that meets three times per week. This unique course structure holds students' attention and genuine interest through each meeting, while preparing them to live in an increasingly electronic world. Upon completing one semester of Electronics, students will have gained skills soldering, using oscilloscopes, reading electrical diagrams, troubleshooting circuit failures, and point to point wiring. Additionally and concurrently, students find themselves solidifying conventional theory of both AC and DC circuit structure. This fall semester the author is the Teaching Assistant (TA) for the PHY 240 Electronics class. The poster will present projects completed in the Electronics course.

ACCURACY OF STUDENT-SUPPLIED BIOCHEMICAL CHARACTERIZATION DATA FOR ANALYSIS OF UNKNOWN STAPHYLOCOCCI.

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Background: Undergraduate students preparing for careers in healthcare or healthcare-associated fields frequently complete clinical rotations as part of their education while remaining members of the general college community. This positions them as possible source of both community-acquired and healthcare-acquired MRSA.

Methods: From Fall 2012 to Fall 2013, 153 healthy individuals enrolled in Biology or Allied Health majors consented to the sampling and characterization of bacterial isolates from the anterior nasal nares or skin. Staphylococci were selected for by sequential culture in mStaph broth and mannitol salt agar. Each isolate was assayed for mannitol fermentation and β-hemolysis to provide presumptive species identification and the results were interpreted by the student volunteer prior to strain submission. Each isolate in the collection was subjected to repeated hemolysis testing and assayed for coagulase production.

Results: From a total pool of 153 subjects, 27 putative *S. aureus* (beta-hemolytic, mannitol fermentation positive; 18.0%), 107 putative *S. epidermidis* (gamma-hemolytic, mannitol fermentation negative; 70.0%), and 17 putative *S. saprophyticus* (gamma-hemolytic, mannitol fermentation positive; 11.0%) isolates were recovered. The student supplied data for these isolates were compared to the authors' testing regimen to determine the accuracy rate of testing. Of note, hemolysis assay results differed for 24% (36 of 153) of the submitted sample and dataset pairs.

Conclusion: Approximately one-quarter of hemolysis assays were misinterpreted by the student volunteer, suggesting that additional instructional time on this topic is warranted in undergraduate laboratories. Additionally, the lack of accuracy in interpreting hemolysis assays by students may be the result of imperfect technique elsewhere in the laboratory (i.e. poor streak plate or aseptic technique).

THE INFLUENCE OF LEAF LITTER QUALITY AND STREAM VELOCITIES ON AQUATIC MACROINVERTEBRATE ABUNDANCE AND DIVERSITY IN RICE CREEK (OSWEGO, NY).

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Evaluating macroinvertebrate communities in streams is an inexpensive and simple method that can assess water quality. We measured the percentage of ephemeroptera, plecoptera, and/or trichoptera (EPT) at Rice Creek in Oswego County, NY. We hypothesized higher quality water will have a higher %EPT and also there will be a greater abundance of other macroinvertebrates. In addition to water quality, the leaf litter present in a stream bed influences the abundance of macroinvertebrates found in the water. We chose maple (*Acer rubrum* and *A. saccharum*) and oak (*Quercus rubra*) to contrast leaf tissue nutrient levels. The breakdown of nutrients within the maple and oak leaf litter play an important role in colonization and energy within the trophic levels. We hypothesized that maple litter would have a larger macroinvertebrate colonization rate in comparison to the oak litter. We chose three study sites along Rice Creek with varying velocity; high, intermediate, and low. There were six replicates for each treatment (litter submersion time and litter identity) at the three sites. Leaf litter bags were submerged for 7 and 14 days. The leaf litter bags contained either a majority (>90%) of maple or oak leaves weighed to 7 ± 0.2 g. After collection, the leaf litter bags and leaf litter were gently rinsed under cold tap water to acquire the macroinvertebrates that were settled on the outside of the bag as well as the leaves themselves. Following the gentle rinse, the macroinvertebrates were collected, stored, and later counted. Preliminary results indicate that the low water velocity site had the highest abundance of EPT. Amphipods have been the dominant macroinvertebrate recovered. The majority of our the maple leaf litter replicates had a greater abundance of macroinvertebrates, specifically amphipods. The abundance of amphipods is a good indication that Fallbrook has high water quality with low inputs of pollution.

THE LATE SILURIAN, EURYPTERID-BEARING FIDDLERS GREEN FORMATION (BERTIE GROUP) AT LANG'S QUARRY, HERKIMER COUNTY, NEW YORK.

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A quarry excavating the Phelps Member of the Fiddlers Green Formation was begun in 1980 by Allan Langheinrich and is known as Lang's Quarry. The purpose of the quarry is to access the eurypterid-bearing waterlime that constitutes much of the Phelps Member. At this fossil site, the Phelps is about 76 cm plus 30 cm of overlying mudcracked waterlime. Recently, excavation revealed more of the overlying and underlying strata than has been observed in the past and this is described below.

One section, for the first time, revealed about 4 meters of the Forge Hollow Formation resting upon uppermost Phelps Waterlime. The waterlime itself is the repository of the extensive eurypterid fauna that is so well-known in this region of New York. Excavation of the waterlime here over many years has, importantly, allowed for the distribution of many fine specimens to museums and universities all over the world.

One relatively small area in the quarry had been excavated into layers below the eurypterid beds, i.e. uppermost Victor Member. The beds encountered were finely-crystalline, brown dolostone replete with trace fossils (mostly burrows) not seen in the overlying eurypterid-bearing waterlime. Two samples were retained for further study as was another piece showing a grouping of crystal molds (probably originally gypsum). Such crystal molds have been observed as far west as Phelps, N.Y.

To summarize, Lang's Quarry reveals a portion of the Fiddlers Green Fm., including a unit well known from other sites to the west, which contributes to our understanding of the lithology and distribution of this important eurypterid-bearing sequence across New York State. A much closer examination of the units mentioned above is planned for the months ahead.

PRESENCE OF *Agrobacterium vitis* STRAINS ON FINGER-LAKES REGION VINEYARD AND NON-VINEYARD SOIL AND ON CULTIVATED (*Vitis vinifera)* AND WILD VINES (*Vitis riparia*).

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Agrobacterium vitis is the causative agent of the crown gall of grapevines and have caused extensive losses in the past 30 years in New York, in particular in the Finger Lakes region vineyards. This work aimed to evaluate the presence of the *A.vitis* in vineyard and non-vineyard soils (apple orchard soils) as well the presence of the bacteria in roots, shoots and petioles of cultivated (*Vitis vinifera L* cv. White Reisling) and wild vines (*Vitis riparia*) from 12 and 15 different sampling sites, respectively. Our results show that 85% of the bacteria recovered in RS media from soil around the grapevines was *A. vitis* . None of the apple orchard soil sampling sites had the bacteria present. In the same way, we found that *A. vitis* was present in 90% of roots and ~70% of shots and petioles isolated from cultivated grapevines, while no *A. vitis* was isolated from *V. riparia* plants. Our data suggested that in the past 30 years the level of *A. vitis* in the vineyards soil has not increased. We can propose that the bacteria are highly dependent on its host *V. vinifera* and its surrounding soil.

THE SURVIVAL OF *Agrobacterium vitis* ON THE FEET OF HOUSE SPARROWS (*Passer domesiticus*) SAMPLED FROM FINGER LAKES VINEYARDS.

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We investigated the hypothesis that *Agrobacterium vitis,* the causing agent of crown gall of grapevines, was able to survive for an extended period on the feet and nails of House Sparrows (*Passer domesticus*) foraging in vineyards of the Finger Lakes region of New York State. The feet of sparrows were surface sterilized (30s 2% sodium hypochlorite, 30s 70% ethanol, 2x 60s water). Feet of birds in the treatment group were immersed in a buffer solution of *A. vitis* ($1x10^9$ CFU/ml) for 2 min (n=4), while feet of birds in the control group were immersed in buffer solution for 2 min (n=3). Treatment and control groups were caged separately and swabbed for the presence of the bacteria in RS media at 0, 2, 4, 8 and 16 days post inoculation (dpi). All RS media plates (selective to *A. vitis)* were incubated for 4 weeks at 28°C. End point- PCR was used to confirm the presence of *A. vitis*. The experiment was repeated twice. At 0 dpi we were able to recover $1x10^9$ CFU/ml and the amount of bacteria decreased over time to 10^7 CFU/ml (2 dpi); 10^4 CFU/ml (4 dpi); 10^3 CFU/ml (8 dpi), 10^2 CFU/ml (16 dpi). Our results show that the *A. vitis* can survive in the feet and nails of House Sparrows and therefore these birds might function as a vector of crown gall disease of grapevines.

SPECIES COMPOSITION OF NORTHERN HARDWOOD FORESTS DEPENDS ON SITE AND STAND AGE

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Northern hardwood forests have a diversity of tree species that vary with forest age and site characteristics. We collected leaf litter in thirteen stands of different ages at three sites in the White Mountain National Forest in New Hampshire in fall 2009 and 2010. Each stand contains four plots, usually 0.25 ha in size, and each plot contains five litter baskets. Leaves were sorted by species, oven dried, and weighed. Species composition varied as a function of stand age. Young stands (aged 26 to 28 years) included *Prunus pensylvanica* (pin cherry), *Betula papyrifera* (white birch), and *Acer rubrum* (red maple). Old stands (aged 106 to 133 years) had mostly *A. saccharum* (sugar

maple), *B. alleghaniensis* (yellow birch), and *Fagus grandifolia* (American Beech). The mid-aged stands (aged 40 to 31 years) were the most diverse, containing species representative of both young and old stands. Species composition also varied by site. The stands at Jeffers Brook had more sugar maple, and Hubbard Brook had more yellow birch. At Bartlett, where we have three stands of each age class, there is also variation among stands of the same age class. Finally, in some stands, species composition was very similar across the plots, but in others, in spite of our best efforts to select stands with four replicate plots, species composition was inconsistent. This information has been useful in selecting stands for further study

TOWARDS INVESTIGATION OF SMALL-EYE MUTANT USING CRISPR/CAS9 GENE TARGETING.

Alexandra R. Dananberg, Hannah Loo, Maria V. Suarez and Travis J. Bailey

A genetic screen to identify alleles affecting eye development uncovered the good effort (gef) mutant. The gef mutants are characterized by smaller eyes relative to wild-type fish. Although gef mutants exhibit smaller retinas, the lens appears unaffected, suggesting the gef phenotype is a result of retinal-specific degeneration. Meiotic mapping linked gef near the chaf1b gene, which is required for assembly of histone onto newly replicated DNA. Loss of chaf1b function results in inability to attach DNA to new histones, ultimately resulting in DNA damage. This damage activates tp53, which may trigger apoptosis if damage is irreparable. This model of cellular death is consistent with the activation of apoptosis seen in the gef mutants. Sequencing of chaf1b in gef mutant embryos has shown that the gef phenotype correlated with a three-base-pair deletion in intron 3. To determine whether the deletion causes the gef phenotype, we are targeting chaf1b using CRISPR/Cas9 knockout technology. We generated a vector to create double transgenic fish. One transgene drives expression of Cas9 endonuclease and the other a guide RNA specific to chaf1b intron 3 that should result in small DNA deletions only at the same location.

FUNCTIONAL ANALYSIS OF RAD51 AND RAD54 RELEVANT TO HDR EFFICIENCY.

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Double strand breaks (DSB), if not repaired properly can lead to tumorigenesis. Homology-directed repair (HDR) uses homologous DNA as a template to correct DSB in an error-free way. In order to understand the factors that influence HDR efficiency, two components of the pathway, RAD51 and RAD54, were investigated. RAD51 forms nucleoprotein filaments with resected DNA and initiates ATP-dependent strand exchange to allow for completion of repair synthesis. RAD51 mutations identified from two cancer databases and one Fanconi anemia patient have been used to investigate the functional implications of RAD51 on HDR. Previously established DR-GFP assay was used to measure HDR efficiency and protein expression was examined via western blot. Out of 18 novel RAD51 mutants examined, 10 displayed decreased HDR efficiency compared to wild type. Protein expression of RAD51 must be taken into account before concluding. While some of these mutations lie in important domains, others are undefined. Nevertheless, these mutations can be used as biomarkers for HDR efficiency and to identify novel interactions of RAD51. RAD54 promotes sister chromatid exchange in HDR. Unpublished studies from Jasin lab suggest a synergistic effect on HDR efficiency in BRCA2/RAD54 double mutant mice compared to BRCA2 mutant mice. In order to emulate the BRCA2/RAD54 mouse model in human cells, CRISPR/Cas9 technology was used. Guide RNA were designed in exon 5 and 7 in RAD54 locus and were transfected in BRCA2 conditional MCF10A cells to obtain RAD54 knockouts. Once the RAD54 knockout cells have been generated, they will be studied for phenotype in regards to HDR proficiency. The functional analysis of RAD51 and RAD54 is critical as readouts for HDR efficiency, which impacts personalized chemotherapeutic choices. The result of this study will hopefully expand the benefits of using PARP inhibitors not just on BRCA1/2-deficienct tumors but also on somatic tumors with RAD51 or RAD54 mutations.

DELETION OF EITHER GENE ENCODING THE GRP170 CHAPERONE OF *CAENORHABDITIS ELEGANS* FAILED TO ELICIT THE UNFOLDED PROTEIN RESPONSE IN EMBRYONIC, LARVAL OR ADULT TISSUES.

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Animal growth and development requires folding of cellular proteins into functional active conformations. Protein folding is facilitated by cellular machinery called chaperones. The function of the largest ER chaperone in animal cells, GRP170, is not fully understood. The round worm *Caenorhabditis elegans* has two genes encoding GRP170, the grp170a and the grp170b genes. The loss of grp170a is known to slow larval development of the worm while the loss of grp170b does not affect the rate of development. To further characterize the function of these genes, worms lacking grp170a or grp170b were analyzed for defects in protein folding during development. Defective protein folding was assayed by monitoring the expression of an Unfolded Protein Response inducible transgene. This transgene expresses the green fluorescent protein (GFP) when unfolded proteins accumulate in the ER. The transgene was introduced into worm strains lacking functional grp170a or functional grp170b. When these strains were examined by fluorescence microscopy, there was not any apparent induction of GFP in any of the tissues in embryos, larva and adult worms. This demonstrates that neither gene was by itself critical to general protein folding. Further, it suggest the slow rate of development observed in grp170a deficient worms was not caused by a defect in general protein folding.

GENERATION OF NOVEL MOTILITY MUTANTS IN *CHLAMYDOMONAS REINHARDTII.*

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The cellular organelles, cilia and flagella, play critical motor and sensory roles in eukaryotes. In humans, motile cilia or flagella are found in the respiratory, nervous, and reproductive systems. Disruptions in ciliary or flagellar assembly have been shown to cause several diseases or disorders, collectively termed ciliopathies. Ciliary and flagellar assembly is a complex processed involving an estimated 250 proteins, for which less than half have been identified. We propose to identify and characterize novel proteins needed for ciliary or flagellar assembly using the model organism *Chlamydomonas reinhardtii*. Mutants will be generated using insertional mutagenesis and screened for those displaying a disruption in flagellar assembly. Phenotype analysis will include quantification of swimming velocity and Western blots of flagella proteins. The mutants will be genotyped using TAIL PCR to identify the insertion site. Identification of new proteins needed for flagellar and ciliary assembly will help in the diagnosis and treatment of human ciliopathies

THE ROLE OF BACTERIOPHAGES IN CHEESE MICROBIAL COMMUNITIES.

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Microbes are essential in the cheese-making process. Bacteria and fungi have been found to form complex communities in cheese rinds with widespread positive and negative interactions [1]. These microbial interactions can have significant effects on the resulting cheese end product. Bacteriophages are viruses that infect bacteria. Phages interact with bacteria throughout the environment, including within cheese rind communities. However, characterization of cheese-associated phages and the role they play in rind community development has not been much addressed. Here we present methods for isolating novel phage from cheese rinds, and their preliminary characterization, as a prelude to better understanding the role of phages in cheese microbial communities.

PHOTODYNAMIC THERAPY DOSING PROPERTIES OF PROTOPORPHYRIN IX FOR ACNE AND CANCER TREATMENT

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There are a number of treatment options available for people who have acne and one of those options is called Photodynamic Therapy (PDT). This technique is used both for cancer treatment in addition to treating acne. This treatment option makes use of photosensitive compounds. When these chemicals are exposed to light of a certain wavelength, they induce the formation of oxygen radicals, which are very reactive and will kill damaged or cancerous cells. PDT is preferable to other types of treatment options since the photosensitive chemicals tend to linger in damaged cells more than healthy cells, so when they are irradiated, the chemicals kill the unhealthy tissue and leave healthy tissue unaffected. In this project, we have been testing Protoporphyrin IX (PpIX) the chemical of choice for acne and cancer treatments to determine the dosing of light required to activate PpIX to produce Photoprotoporphyrin (Ppp), which ultimately kills damaged cells. There has been little to no research done specifically on the dosing of light required to activate these compounds.

GP22: THE MISSING LINK OF PHAGE HEAD MORPHOGENESIS.

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The virions of tailed bacterial viruses, or phages, consist of two main structures, a head and a tail. The head comprises a protein shell which houses the double-stranded DNA genome and the tail, an apparatus used to adsorb to the bacterial host cell. Phages with unusually long genomes encoding hundreds of genes have in recent years been found to abound in the environment and are referred to as giant phages. Little is known about the complex virions of giant phages and how they are assembled. We are studying the giant *Salmonella* phage SPN3US as a model phage for an expanding family of related phages that infect human and plant pathogens.

This research project was based on the purification and characterization of the SPN3US protein gp22. Gp22 has recently been indicated as having an important function during phage head morphogenesis. Previous studies have revealed that cleavage of proteins in the virion is an essential step in morphogenesis. In SPN3US gp245 is the protease enzyme responsible for these detected cleavages. Recent studies have shown that gp22 is highly abundant in the immature virion but not in the mature phage particle indicating it may be an excellent candidate for the long missing "scaffold" protein.

Scaffold proteins help determine phage head shape and fill the interior of the capsid prior to DNA being packaged into it. Our hypothesis is that gp22 will be cleaved at sequence motifs by the SPN3US gp245 prohead protease, proving that it is the intermediate scaffold protein in morphogenesis. To test this hypothesis we have cloned, expressed and purified gp22 and gp245 and performed assays of them *in vitro*. Our results indicate that there is partial cleavage of recombinant gp22 by gp245. Further studies to support these findings are underway. Determining if gp22 is the missing scaffold protein could have a large importance in our understanding of viral morphogenesis both for phage work and for pathogenic viruses. Additionally we may be able to use this information to further understand and combat pathogenic viruses, as tailed phages share a common ancestry to the Herpesvirus group.

DIADENOSINE POLYPHOSPHATASES OF THE NUDIX HYDROLASE SUPERFAMILY IN *M. TUBERCULOSIS*

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M. tuberculosis contains 11 potential Nudix hydrolases, and we are characterizing these enzymes as potential novel antibiotic targets. The diadenosine polyphosphatases (Ap_nAases) / mRNA decapping enzymes are a family of enzymes within the Nudix hydrolase superfamily. In *M. tuberculosis* there is the primary Nudix Ap_nAase and the secondary Nudix Ap_nAase. The diadenosine polyphosphatases from *Legionella pneumophilia* and *Bartonella bacilliformis* have been found to be important in each pathogen's ability to invade its host cells. It is of interest to know whether these enzymes act in the same way in *M. tuberculosis.* If they are all found to be involved in invasiveness and thus in virulence, then these enzymes could be novel antibiotic targets. We have cloned and overexpressed each protein and have subcloned each into a HisTag vector to optimize purification. We have purified the secondary Nudix Ap_nAase from *M. tuberculosis* so that we can complete its characterization. Thus far we have determined its substrate specificity, Ap_nAase activity, optimal pH, divalent metal ion requirements. This research has been supported by an NIH AREA grant.

ANALYZING SOUNDSCAPE TEMPORAL VARIATION IN WESTERN NEW YORK AS A POTENTIAL ASSESSMENT OF BIOLOGICAL DIVERSITY.

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Analysis of soundscapes may provide a way to quantify the biodiversity and examine the impact of anthropogenic noise on an area. Because many organisms use vocalizations as a primary channel of communication, biological diversity assessments can now be done, in part, through the use of soundscape recordings. The effectiveness of using soundscape recordings in this way will be dependent on the proportion of biophony, anthropophony, and geophony in the soundscape. To begin to understand this, we were interested in examining two factors: how time of day influences acoustic diversity measures, and how these measures change from the center of a forest plot to the edge of a forest plot. We present analyses of the daily temporal variation in soundscapes in western New York, specifically looking at how the proportions of anthropophony, biophony, and geophony change throughout a given day and from the center of a habitat to the edge of that same habitat. We recorded soundscapes in 9 different forest patches across western New York in 2016, at three different time periods each recording day (6am-8am, 11am-2pm, and 6pm-9pm). We used Raven Pro software from the Cornell Lab of Ornithology, and the R statistical software package to determine the proportions of biophony, geophony, and anthropophony, how their contributions to the soundscapes differed across the three time periods, and how the proportions of the three times of sound varied from center to edge habitat. We computed three measures of acoustic diversity (NDSI, ACI, and ADI) and looked at how these values changed across the time periods, how they were associated with the proportions of sound, and how they varied from center habitat to edge habitat. We will present our findings to provide insight into how soundscapes can be used to assess the biodiversity of an area, and how anthropogenic sound is impacting these soundscapes and measurements of acoustic diversity.

ENHANCING EFFICIENCY FOR ALL-ORGANICS SOLAR CELLS THROUGH INTERFACE-ENGINEERED MATERIALS.

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Creating flexible and bendable solar cell arrays would be very valuable for fast implementation or temporary renewable energy generation. An investigation of robust, large area, lost cost and efficient organic solar cells shows the need to identify the better solar cell materials and the many different combinations between the organic materials. The addition of a molecular dipole layer from p-benzoquinone monoimine zwitterions in the active layer can enhance solar cell efficiency. By developing techniques to explore the many different organic semiconductors combined with dopants and specialized organic additives will distinguish the most promising molecular combinations.

FATTY ACID SIGNATURES OF LAKE MICHIGAN RAINBOW TROUT.

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The objective of this study was to evaluate spatial variations in fatty acid signatures (FAS) of rainbow trout (*Oncorhynchus mykiss*) from Lake Michigan. Fish were collected by federal, state and tribal agencies throughout the lake during their annual predator assessments and assigned to one of the four quadrats of the lake: southwest, southeast, northwest and northeast. Belly flaps were sampled and analyzed for lipid and fatty acid composition (n =144). Total lipid content averaged 13.4%. Ongoing statistical analysis will reveal potential spatial FAS variations and with our prey FAS database will provide a better understanding of the feeding habits of rainbow trout in Lake Michigan.

FROM MUSIC TO PHYSICS: A STUDY OF ACOUSTIC THEORY AND ULTRASOUND APPLICATION.

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With a general interest in both physics and music, a general study of acoustics was pursued. A solid foundation of acoustical and ultrasonic wave propagation was established with the purchase of basic ultrasound equipment, including transducers and receivers for both gaseous and liquid states. Theoretical calculations for the speed of sound in different mediums were made and then compared to experimental results obtained from the equipment. Accuracy in measurement was found to be less than 1 percent difference from the theoretical calculation of sound in air at room temperature. With applications ranging from materials science to medical physics, the fundamental knowledge established within experimentation is essential for further work as both a Physicist, as well as a musician.

SEASONAL ANALYSIS OF INVASIVE *TYPHA* (CATTAIL) MITIGATION IN SILVER LAKE FEN (OSWEGO COUNTY, NY).

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Silver Lake is an intermediate fen located on the Lake Ontario coastal plain in Oswego County. This peatland is a critical site for the New York State endangered Bog Buckmoth (*Hemileuca* sp 1) whose primary larval

food source is *Menyanthes trifoliata* (Bog Buckbean). Habitat occupied by *Menyanthes* has been encroached upon by invasive cattails (*Typha angustifolia* and *T. x glauca*). Dead *Typha* biomass decomposes slowly and accumulates on the peatland mat creating a mulch that inhibits growth of native flora. Due to the invasive nature of cattails, land managers decided *Typha* should be controlled to help preserve habitat for the Bog Buckmoth. Our objective was to determine the most effective time of year to mitigate invasive *Typha* by manual removal. Living and dead *Typha* biomass was collected and dried to determine the initial density of cattail on the peatland mat. Sample plots (n=12) that contain *Typha* were cut in both Spring and Fall 2016. In Spring, the average living stem count per $5m^2$ plot was 41 and biomass was 40 $g/5m^2$ plot. The dead *Typha* stem count was 126 and biomass was 476 $g/5m^2$. In the Fall, we resampled plots to determine the effectiveness of Spring cutting and also cut twelve new plots as a Fall removal treatment. Data from Fall sampling will help us determine the most advantageous time to depress *Typha* growth in an effort to help prevent *Typha* from homogenizing the Silver Lake Fen ecosystem.

THE EFFECT OF SURFACE MODIFICATIONS ON TRITIUM ADSORPTION AND ABSORPTION BY STAINLESS STEEL 316

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Previous studies have shown that when a metal is exposed to a deuterium–tritium gas environment, a significant quantity (20% or more) of the absorbed tritium remains on or near the surface.[1] This has important implications for fusion-reactor materials, which are exposed to a tritium environment.
The interaction of tritium with the metal surface is a key step in the overall process of absorption by the metal. Therefore, one may expect that changing surface characteristics of metal samples, such as topological roughness or chemical composition, may significantly affect their absorption of tritium.

In the present study, sets of stainless-steel samples were prepared by first mechanically skimming their surfaces to eliminate any manufactured surface inclusions. Samples were then treated with chemical or physical methods intended to alter surface roughness or composition. Finally, all samples were degreased with acetone, washed with water and, finally, dried with isopropyl alcohol. The room-temperature samples were then exposed to 1 atm of an ~50/50 deuterium–tritium gas mix for 24 h and stored under dry helium.

The effects of surface roughness and chemical composition on the total tritium uptake by metal samples were measured using linear thermal desorption. This robust technique involves heating the sample to an elevated temperature for extended periods of time. Extended exposure at high temperature allows for total extraction of tritium from the metal sample, making it possible to measure its total tritium inventory.

The results obtained thus far indicate that some surface modifications of the stainless-steel samples have strong effects on their total tritium content; however, no correlations between surface roughness and tritium inventory were found. These observations suggest that tritium absorption by metal samples depends crucially on the surface chemistry, i.e., reactions of tritium or tritium compounds with surface atoms.

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CONCENTRATIONS IN PREY FISHES FROM LAKE ONTARIO.

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Early mortality syndrome, resulting from thiamine (vitamin B1) deficiency, is prevalent in salmonid species from the Great Lakes. Thiamine plays major roles in growth, reproduction, and neurological development of fish and can only be obtained through diet. Thiamine deficiency is a direct consequence of consumption of diets

consisting largely of alewife or other forage fish species with elevated amounts of thiaminase, a thiamine-degrading enzyme. In the present study, we investigated the whole body thiamine concentrations in three prey fishes (n=58); alewife, round goby, and rainbow smelt; from Lake Ontario. Samples were collected using trawling nets during the annual assessment surveys conducted by the US Geological Survey – Lake Ontario Biological Station and NYS Department of Environmental Conservation. Thiamine concentrations were measured using high-performance liquid chromatography. Preliminary results showed that alewife had the lowest total thiamine concentration (3.3 ± 2.3 nmol/g), while the highest concentration was found in round goby (7.4 ± 2.4 nmol/g). Thiamine pyrophosphate was the dominant vitamer in rainbow smelt and round goby (67%), whereas free thiamine was prevailing in alewife (57%). These results suggest that predators that consume alewife will have less thiamine available to them than those that feed on either rainbow smelt or round goby, possibly increasing likelihood of thiamine deficiency.

TRANSCRIPTIONAL ANALYSIS OF BIPOLAR CANDIDATE GENES IN MODELS OF STRESS SUGGESTS A COMMON ROLE FOR ER STRESS.

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Bipolar disorder, also known as manic depression, is known to be a polygenetic disease. However, replicable risk alleles have not yet been identified by linkage analysis. Since 2006, multiple Genome Wide Association Studies (GWAS) have focused on finding novel risk alleles, but their findings have not been validated. This poses a problem in terms of understanding this disorder. Without relevant genes to analyze, how will we know why some people develop bipolar disorder or why some treatments are effective for some people but not others. From previous GWAS studies, we developed a list of strong candidate genes. These genes include: *Ankyrin 3* (*Ank3*), *Diacyclglycerol kinase* (*Dgk*), a calcium channel subunit (*Cacna1c*), *Synapsin like1 (Syne1*), *FK-506 binding protein* (*Fkbp5*) and *Teneurin transmembrane protein 4* (*Tenm4*). Using these genes, we designed qPCR primers in the mouse genome that would capture most or all of the known transcripts. By analyzing various models of stress, we hope to find common gene expression patterns that may suggest a common biological pathway underlying this disorder. Our results show that there is not a common pathway in cellular or animal models of physiological stress mediated by glucocorticoids. However, all genes showed an upregulation in a rodent model of depression and downregulation in cellular models of oxidative stress. Specifically, it seems like endoplasmic reticulum (ER) stress is responsible for the observed changes. For future studies, we are continuing to test these genes, as well as two more recent candidate genes, *Tetratricopeptide repeat and ankyrin repeat containing 1* (*TRANK1*) and *Neurocan* (*NCAN*). This analysis suggests a common biological process that may be defective in patients with bipolar disorder and we hope this information can lead to a better understanding of the disease as well as potential novel treatment options for the future.

SPERM OR OOCYTE? THE ROLE OF SPECIFICITY IN THE EMERGENCE OF POST-TRANSCRIPTIONAL REGULONS IN GERMLINE DEVELOPMENT.

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During the early development of complex organisms, their cells must undergo differentiation from pluripotent stem cells into either somatic or germ cells. Germ cells are then faced with another critical decision, to become sperm or oocytes. This process is highly regulated by a series of molecules in order to ensure proper differentiation, such as proteins and mRNA. We are using the model organism, *C. elegans* to study the role of PUF domain proteins in cell differentiation. Two PUF domain proteins, PUF-8 and FBF play a critical role in the germline development of *C. elegans*. (Bachorik, 2005) Both proteins contain RNA binding domains but the RNA sequences preferred by each protein is different. Previous research has shown that alterations in the RNA binding domain of FBF can greatly alter FBF signaling specificity (Bachorik, 2005). Our hypothesis is that changes in the RNA binding domain of FBF-2 will alter its specificity to match that of PUF-8.

We used a yeast three-hybrid assay to test if specific changes in the RNA recognition domain of PUF proteins alter the protein's ability to recognize and bind RNA, and as a result, alter germline development. All screen positives will be introduced *in vivo* using the genome-editing technology, CRISPR/Cas9 to verify their role in germline development. Our data will not only further our understanding of how RNA:protein interaction regulate sperm/oocyte decisions in the germline, but also how protein specificity can change over evolutionary time to enable cell fate decisions.

PREPARATION OF L- AND D-VINYLGLYCINE-BASED BUILDING BLOCKS FOR THE SYNTHESIS OF MEDICALLY RELEVANT COMPLEX MOLECULES.

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The unusual amino acid vinylglycine and a number of related compounds have been studied throughout the years for their involvement in certain biological processes and special reactivity. Given the presence of an alkene moiety, the structure of vinylglycine could be manipulated through a variety of chemical reactions, leading to larger and more valuable amino acid-like structures. Exploiting late-stage transformations on vinylglycine-containing peptide-like molecules could be of great use in the medicinal field.

While the preparation of vinylglycine has been extensively investigated in the past, its production is still problematical due to its sensitivity to racemization and isomerization, which renders key steps irreproducible during its synthesis. This project aims at developing an inexpensive approach to synthesize L- and D-vinylglycine derivatives as single enantiomers, using D- and L-serine respectively as starting materials. Additionally, we expect to find a means to protect this structure from racemization and isomerization via an appropriate derivatization. Our progress in these endeavors will be presented.

BIOCHEMICAL ANALYSIS OF THE EFFECTS OF T450 PHOSPHORYLATION OF LGN PROTEIN FUNCTION.

Justin Galardi, Ryan Elnicki, Laurie B. Cook, and Brandy M. Sreenilayam

Breast cancer is a relatively common disease, developing in 1 in 8 women in the U.S. statistically. Currently, no cure is available.The basis of this study centers around LGN protein, named specifically for its characterized repetition of leucine (L), glycine (G), and asparagine (N) residues in the N-terminal half. The protein holds an important role in mammalian cell division and has been determined to have notable effects, including in both mitotic spindle alignment and cell polarity. LGN has a high concentration in most breast cancer cells and it has been determined that the 450th threonine residue (T450) is phosphorylated. The goal of this project was to explore the biochemistry of both wild-type LGN and two T450 mutants of LGN to gain insights as to how LGN phosphorylation results in proliferation of breast cancer cells. PCR is being utilized to generate the T450A T450D mutants, which mimic the unphosphorylated and phosphorylated T450 residues of LGN. Immunofluorescence and confocal microscopy techniques will be used to determine LGN's localization within baby hamster kidney (BHK)-570 cells. Characterization of LGN function relative to phosphorylation status of T450 could lead to development of novel treatments for breast cancer.

BUILDING PROFILES FOR MICRORNA TARGET PREDICTION USING MACHINE LEARNING

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MicroRNAs (miRNAs) are about 21-22 nucleotide long, single-strand, non-coding RNA molecules that are naturally expressed and play important roles in posttranscriptional regulation. MiRNAs down-regulate the translation of their targeting messenger RNAs (mRNAs) by binding to mRNAs leading to the silencing or degradation. Each miRNA might bind to hundreds of mRNA targets and each mRNA target might have multiple

miRNA recognition elements (MREs). Due to the high cost of experimental methods to identify miRNA targets, computer algorithms have been developed to predict miRNA target. Machine learning is a specialized artificial intelligence approach that guides the model to learn critical information from the training data and then predict the unknown data. In this project, we generated profiles for miRNA target prediction for both training and testing. With the availability of our unique high quality datasets of miRNA direct targets from RISCtrap that published from this lab, we utilize them as the training dataset to build the profiles. The profile contained features of energy thresholds assessment for complementary matches between miRNA and MRE, conservation assessment and structural accessibility estimation. We developed and implemented an algorithm to find the MREs on the 3' untranslated region (3'UTR) of mRNAs (human hg19 RefSeq Genes) based on the human miRNA extended seed sequences (miRBase v20). The matching of MRE and miRNA seed sequences could have some flexibility to allow some minimal mismatches, G:U wobble pairs, or bulge. The matched MRE and miRNA extended seed sequences were used to calculate the free binding energy using RNAhybrid. After filtering out the sites of the low binding energy, the remaining MRE will be incorporated into the profiles. We calculated the conservation scores of the MREs across 46 vertebrate genomes since the studies show that the MREs are conserved among various species. All those three features will be combined and further fed into the machine learning model for both training and prediction. This machine learning model will be developed via Pylearn2, using our custom dataset, a softmax regression model, and a stochastic gradient descent algorithm.

RNA-SEQ DATA ANALYSIS FOR ADIPOCYTE DIFFERENTIATION

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During the cell differentiation, the expression of different genes within the cell experience various changes. Using next-generation sequencing, RNA-Seq is an approach to measure the transcriptional profiles on an unbiased way in a whole-genome scale. Due to huge amount of data, the RNA-Seq data analysis usually requires biology knowledge but also bioinformatics expertise. Traditionally, the process started with aligning all the sequencing reads to the genome and the unmapped reads were aligned to splice junctions of annotated transcripts. Then all the reads mapped either to genome or splice junctions were counted and assigned to each gene (the isoforms of each gene are merged). It usually takes half a day to days to finish. In this study, we used a totally new alignment algorithm, which is called kallisto. It builds up the index for all the annotated transcripts (mm10 RefSeq annotation in this study) but doesn't take the genome into account. Although it seemed to be missing some information, it's proven valid. Aligning RNA-Seq reads is much faster, which completes within an hour. Meanwhile, due to sequencing technology limitation, we trimmed the bases with low quality scores both in the beginning and the end of all sequencing reads, namely keeping bases from position 7 to 106. Another program *sleuth*, was then employed to discover more than 100 significantly changed genes during cell differentiation. We are working on functional analysis to decipher the biological meaning of those genes.

ISOLATION OF BACTERIA FROM LAKE WATERS ASSIOCIATED WITH WASTEWATER EFFLUENTS CAPABLE OF DEGRADING VARIOUS PHARMACEUTICALS.

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Many wastewater treatment plants (WWTPs) are not properly equipped for the removal of non-steroidal anti-inflammatory drugs (NSAIDs) such as ibuprofen and naproxen, analgesics such as acetaminophen, and hormones such as 17β-estradiol. These compounds are continually discharged into surface waters and, although in very low concentrations, their presence is becoming an emerging issue for the environment as well as public health. Microorganisms in the natural environment may play a key role in ecosystem self-purification processes such as contaminant degradation. The aim of this research was to determine if there were microorganisms from water and

sediment samples located near wastewater effluent outfalls in Central and Western New York that could degrade ibuprofen, naproxen, acetaminophen, and 17β-estradiol, and if the degradation capability of microorganisms varied seasonally. An isolation approach was developed using serial enrichment in mineral medium containing 7.5 mg of each individual pharmaceutical as the sole carbon source available to heterotrophs. After four weeks of enrichment, bacteria were isolated and the growth of each isolate on its selected pharmaceutical source was measured. Biodegradation capability of pharmaceuticals as measured by carbon dioxide evolution was then examined with the isolates that showed the best growth. Results from the various enrichment experiments have led to the isolation of several heterotrophic bacteria capable of growing on ibuprofen, naproxen, acetaminophen, and 17β-estradiol as their sole carbon sources. One isolate cultured from Payne Beach (Rochester area) during the fall had the ability to remove up to 80.2% $\pm$ 7.7% of acetaminophen, 46.4% $\pm$ 11.3% of ibuprofen, and 37.2% $\pm$ 10.5% of 17β-estradiol and another isolate cultured from Charlotte Beach (Rochester area) during the winter had the ability to remove up to 46.7% $\pm$ 6.9% of ibuprofen, 64.4% $\pm$ 5.0% of naproxen, and 58.1% $\pm$ 3.8% of 17β-estradiol. The data suggests that there are endogenous heterotrophs located near wastewater outfalls that can degrade various pharmaceuticals, and that the degradation capability of microorganisms on some compounds varies seasonally.

CHARACTERIZATION OF NOVEL RENEWABLE ALPHATIC-AROMATIC POLYESTERS

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The use of conventional plastics is not sustainable because they are based on petroleum or natural gas, and plastic waste ends up in landfills or in the ocean. In our research group we have synthesized and characterized several aliphatic-aromatic polyesters based on renewable monomers, including lignin derivatives. We will report the composition of the polymers as determined by ^{1}H and ^{13}C Nuclear Magnetic Resonance (NMR) spectroscopy, glass and melting transition temperatures as determined by Differential Scanning Calorimetry (DSC), the purity and heat stability of the polyesters determined by Thermal Gravimetric Analysis (TGA), molecular weight properties measured by Solution Viscometry and Gel Permeation Chromatography (GPC).

THE INFLUENCE OF THE CELLULAR ENVIORNMENT ON THE STABILITY AND STRUCTURE OF Z-FORM NUCLEIC ACIDS.

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In the cell, nearly 40% of the volume is occupied by macromolecules and smaller, chemically diverse solutes known as osmolytes, which accumulate in the cell in response to environmental stresses. To add to the understanding of how the cellular environment affects nucleic acid structure and stability, our research investigates the influence of osmolytes and crowders on the transition from A-form RNA to Z-form RNA. In contrast to the familiar, right-handed nucleic acid helical forms, Z-form is a left-handed double helical structure with its phosphodiester backbone arranged in a pronounced zig-zag pattern. We monitor the formation of Z-form nucleic acids using circular dichroism (CD) spectroscopy as the Z-form spectrum is distinct from that for A and B-form helices. We proposed that both osmolytes and crowders will promote the formation of Z-form nucleic acids and decrease the *in vitro* salt concentration required for Z-form stabilization. Thus far we have observed that for DNA and RNA duplexes containing CG repeats the presence of PEG 200, a model osmolyte, decreases the salt concentration required to adopt the Z-conformation, but this effect is much larger for Z-DNA. This difference in response to the cosolute could suggest one mechanism by which Z-form DNA is stabilized *in vivo*, and provide a chemical basis for why Z-RNA has not been readily observed *in vivo*.

ISOLATION AND CHARACTERIZATION OF MICROBIAL COLONIZATION IN SNAPPING TURTLE (*CHELYDRA SERPENTINE*) EGGS.

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Microbial infections are one of the main causes for loss and extinction of animal wildlife posing a serious threat to ecosystem and biodiversity. Here, we report the pathogenic fungal and bacterial species infecting *Chelydra serpentina* eggs inhibiting embryo development. We isolated fungal and bacterial species from the yolk and albumin of infected snapping turtle eggs collected from Rice Creek (RC) Field Station, Oswego, NY. All the embryos from an infected clutch are killed at some stage of development during incubation and we found that since 2014, four of seven clutches (57%) collected from RC were infected that might contribute major threat to snapping turtle population in near future. Our major findings are 1) direct culturing of fungi from inside of the egg, morphological analysis of established cultures using toluidine blue O (TBO) staining and Scanning Electron Microscope (SEM) imaging showed fungal structures similar to members of the group Ascomycetes. 2) PCR amplification of fungal ITS gene regions from DNA extracted from infected egg samples and sequencing of the amplicons showed almost 95% match with the fungus species *Fusarium solani* and *Fusarium keratoplasticum.* 3) Two bacterial clones were also isolated from the infected samples and molecular characterization by colony PCR using standard 16S primers revealed the presence of four bacterial species *Bacillus pumilus, Bacillus safensis, Pseudomonas aeruginosa* and *Pseudomonas alcaligens* in association with fungi. Further studies will be initiated to identify the source of infection (soil or transmitted from mother or both) and also to check if the infections are wide spread in snapping turtles from other regions in New York.

UNIQUE CLEAVAGE PATTERNS OF CIDAROID SEA URCHINS.

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Sea urchins are model organisms for developmental biology. Research has focused more on the derived Euechinoids when compared to the primitive Cidaroid sea urchins. Despite this, Cidaroids prove to be an interesting subject in terms of development. The Cidaroid species *Eucidaris tribuloides* has been previously shown to develop one, two, or three micromeres at the vegetal pole. In comparison, the well-studied Euechinoids consistently have four micromeres. The objective of this project is to document the unique cleavages of live *E. tribuloides* embryos up to the 16-cell stage with time-lapse microscopy. The jelly canal of the sea urchin egg, visualized with sumi ink, is a marker for the animal pole. One finding was that the first cleavage is not always in line with the animal-vegetal axis, resulting in the designation of first cleavages as parallel or oblique. The first cleavage pattern is correlated to the number of micromeres that form at the 16-cell stage. Oblique first cleavages are correlated with the formation of one or three micromeres. Another finding was that the second cleavage plane has three possible patterns relative to the first cleavage plane (parallel, perpendicular, or mixed). The results suggest that the potential mechanism of variable micromere numbers may be related to the unique cleavage pattern at the first and second embryonic divisions.

EVALUATING THE BINDING POTENTIAL OF CY5.5-DCL AND CY5.5-DCL-DSS-K-NH_2 TARGETED MOLECULAR IMAGING AGENTS (TMIA) TO C4-2 PROSTATE CANCER CELLS.

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Prostate cancers (PrCa) would have a higher cure rate if they were detected earlier especially during the initiation stage. However, well-characterized and non-invasive diagnosis methods are not quite yet available to allow for early detection. The goal of our research group is to develop and evaluate targeted molecular imaging

agents (TMIAs) that zero in on prostate tumors overexpressing the prostate-specific membrane antigen (PSMA). To fulfill this objective, two TMIAs were synthesized that preferentially target prostate cancer cell lines overexpressing the PSMA. The PSMA-positive cell line that is used in this research is C4-2 while A549 is used as the negative control. TMIAs essentially consist of a targeting and a fluorescent group whereby the groups can be changed based on the type of cancer cells to be targeted as well as the diagnostic purpose. The Cy5.5-DCL-DSS-K-NH_2 (B1) TMIA has a fluorophore (Cy5.5) conjugated to a urea moiety (DCL) bridged by a linker group (DSS) while Cy5.5-DCL (A1) TMIA does not have a linker. Molecules that bind to PSMA have been shown to be taken up by receptor-mediated endocytosis via clathrin-coated pits, which normally reside deeper in the cell membrane hence the reason for synthesizing a TMIA with a linker. C4-2 and A549 cells were stained with both TMIAs in a T-25 flask overnight. The stained cells were spun down before being seeded in a 96-well plate. The TMIAs' fluorescence was quantified in relative fluorescent units (RFU) using the Varioskan® Flash microplate reader. It was found that generally, both A1 and B1 showed excellent binding but there was more fluorescence in C4-2 cells than in A549. Molecular dynamics of receptor-ligand coupling might facilitate the more efficient binding of A1 compared to B1. The detected fluorescence in A549 cells can be due to the cells' peptidase activity. The development of new and improved prostate-specific TMIAs should facilitate the diagnosis, treatment, and possibly cure for PrCa.

LEVITATION WITH SUPERCONDUCTING ELECTROMAGNETS.

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The purpose of this study is to critically analyze the properties of Second Generation High Temperature Super Conducting wire (2G HTS). The wire is used to build an electromagnet capable to levitate on an aluminum plate. The levitation is the product of induced eddy currents from alternating current in the electromagnet. The eddy currents induced in the aluminum plate produce a second magnetic field which opposes the initial magnetic field from the electromagnet. The study requires in depth analysis of the criteria of electromagnets such as wire type, wire diameter, coil diameter, number of turns, accompanied by others in order to produce the optimal magnetic field to mass ratio. Aluminum plate stacking, permeable magnetic metal and foam cores will be implemented and investigated in the experiments as well. Ultimately the research will be directed towards producing an efficient super conducting electromagnet levitation system design with minimal friction and low energy consumption for real world applications

THE IMPACT OF SELECT SIGMA LIGANDS ON THE ACTIVITY OF THE C-8,7 STEROL ISOMERASE IN TOBACCO.

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Insects lack the ability to synthesize sterols de novo and therefore must acquire sterols from their diet to meet basic developmental needs. Cholesterol is the chief sterol found in most insects, but in plant vegetative tissue cholesterol (usable sterol) makes up only a small fraction of the sterol profile. All herbivorous insects must convert dietary phytosterols into useable forms (chiefly cholesterol) to support their growth and development. In recent studies we have genetically knocked down the expression of the C-8,7 sterol isomerase in *Arabidopsis thaliana* and thus modified the chemical structure of the plant sterol by causing the retention of the C-8,9 double bond in much of the accumulated phytosterol. These modified plants resist insect herbivory and decrease sucking insect's fecundity. Previous work in our lab has demonstrated that various sigma ligands will biochemically inhibit the C-8,7 sterol isomerase. Tobacco was exposed to Verapamil and Haloperidol at varying concentrations to demonstrate the replication of the transgenic phenotype to validate the genetic silencing phenotype of the enzyme. The impact of sigma ligands on the activity of the C-8,7 sterol isomerase is discussed.

REPRODUCTIVE TRADE-OFFS ASSOCIATED WITH MOUNTING AN IMMUNE RESPONSE IN FEMALE BROWN ANOLES (*ANOLIS SAGREI*)

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Trade-offs between the reproductive system and self-maintenance show the allocation of energy in an organism's life history. An organism must allocate recourses appropriately in order to support self-maintenance and optimize reproduction. We hypothesised that would be at trade-off between the immune response and the reproductive output. We tested this by analysing the degree of swelling associated with an immune response in relation to the reproductive output. Over a ten-week span, we kept 16 female brown anoles (*Anolis sagrei*) in captivity. We collected and measured the eggs on a daily basis and at the end of the ten-week period; we administered an immune challenge via subcutaneous injection of the novel antigen phytohaemagglutinin (PHA) and measured the swelling response. The results showed a negative correlation between egg density and the magnitude of the immune response. This suggests that there is a trade-off in the immune response for reproductive output.

CHARACTERIZATION OF NON-RIBOSOMAL PEPTIDE SYNTHASES FROM *STAPHYLOCOCCI*.

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Antibiotic resistance is an ever-growing problem with certain *Staphylococcus* strains exhibiting pathogenic properties such as methicillin resistant *Staphylococcus aureus*. A recent study has isolated a bioactive compound - lugdunin - from *Staphylococcus lugdunensis*, that is able to inhibit colonization of *Staphylococcus aureus* on humans. This discovery has shown great promise of a field of discovery whereby the human microbiome could harbor new antibiotics. The compound lugdunin belongs to a class of compounds known as non-ribosomal derived peptides and this research will use the following approaches to find novel ones. One strategy is to pinpoint highly conserved areas of peptide synthases that are responsible for compounds like lugdunin and then attempt to discover related genes through a bioinformatics approach. A second strategy will involve the direct analysis of strains of *Staphylococcus* isolated from white-tailed deer for any antibiotic activity through competition assays against pathogenic strains of *S. aureus.*

STUDYING THE ROLE OF ANO2 ON NEUROMAST FUNCTION IN ZEBRAFISH USING A RHEOTAXIS ASSAY.

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Background: Zebrafish neuromasts are a sensory system on the surface of their skin enabling detection of changes in water displacement and vibration. Each neuromast contains hair cells that are mechanotransducers that send afferent electrical signals to the central nervous system informing the zebrafish of changes in water movement. Rheotaxis, the tendency for fish to orient into an oncoming current, requires functional neuromasts in zebrafish.

Aims: To determine a possible role for Ano2 in neuromast function.

Methods: A flow apparatus was made using a 2 inch PVC pipe and gravity pump. A group of ~10 larvae were added to the apparatus and flow as started. Larvae behavior was recorded using a digital camera and analyzed using ImageJ. Body angles of the larvae on a 180° scale in relation to the flow of the water will be collected and analyzed using a macro from ImageJ. It is hypothesized that functional Ano2 is required for rheotaxis. The role of Ano2 will be tested using Ano2 antagonists. Neomycin destroys neuromasts, and EDTA which destroy the tip-links of neuromast hair cells, will be used to confirm the role of neuromasts in rheotaxis.

Results: Preliminary experiments showed that flow in our apparatus is laminar, and flow rates was optimized. Zebrafish exhibited positive rheotaxis and have an average body angle between 0-30° of the direction of

the current. Our next step is to examine larvae treated with an Ano2 antagonist, and with disrupted neuromasts in separate experiments.

Conclusion: If results display negative rheotaxis after Ano2 inhibition we would conclude that Ano2 has an important functional role in neuromasts. Alternatively, it is possible that separate Anoctamin channels are expressed and that the system has built-in redundancy. This can be examined using non-specific chloride channel antagonists.

A STUDY OF MCH RECEPTOR LOCALIZATION AND FUNCTIONAL ROLE OF PROLIFERATION IN DIFFERENTIATING FAT CELLS.

Brett Henderson and Laurie B. Cook.

3T3-L1 cells are used to study adipocyte development. 3T3-L1 pre-adipocytes are induced to differentiate by growing to confluency and transitioning them into DMEM media containing fetal bovine serum, dexamethasone, insulin and/or isobutyl-methyl-xanthine over a period of 10 days. Differentiated adipocytes upregulate expression of caveolin-1, a key component of caveolae membranes, suggesting that melanin-concentrating hormone receptors (MCHRs) are more likely to reside in these regions in an adipocyte when compared to a pre-adipocyte. Therefore, MCHR signaling may be altered. Many signaling complexes localize to lipid rafts, particularly caveolae, acting as structural anchors for signaling, and MCHR1 has been found to reside in caveolae when overexpressed in CHO-K1 cells. MCH plays a crucial role in controlling circadian sleep/wake cycles, appetite, and mood, and is also hypothesized to affect adipogenesis and cell adhesion. Aim 1 investigated the potential influence of caveolae on MCH signaling during adipogenesis. Caveolae membranes were isolated from both pre- and post-adipocytes by sucrose gradient ultracentrifugation and furthermore localization of MCHR1 to caveolin-containing fractions were to be verified by Western blot. Visual inspection of the gradients indicates that we were able to successfully separate caveolae in both cell types, however further experiments via Western blot are needed to verify co-localization. Aim 2 was an extension of previous work showing that 1 nM MCH facilitated cell adhesion and mitotic expansion over that of 1 μM. We explored the effect of low nanomolar MCH on number of cells adhered and number of cells in the supernatant following a time course of 0 to 72 hours, and our results support previous preliminary conclusions. Taken together, this work highlights the potential interplay between MCH signaling and adipose cell development.

ISOLATION AND CHARACTERIZATION OF BACTERIAL AND FUNGAL SPECIES FROM FOLIAR AND SOIL SAMPLES OF ASIAN PEAR TREES.

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Little is known about microbes that live on and around Asian pear trees (*Pyrus pyrifolia*) and potential symbioses that exist among these species. The purpose of this project was to isolate and identify bacteria and fungi from leaves, fruit, and soil of Asian pear trees located on a farm in Ontario, NY. Random samples were taken from the cultivar 'Olympic' at six different locations across the field at three time points. Bacteria and fungi were isolated via filtration, subcultured until pure, and stored at -80°C. Universal 16s ribosomal DNA primers were used to amplify and sequence bacterial isolates. Research is ongoing to complete fungal and bacterial identification. The microbe library will be used to investigate potential biological controls for diseases and insect pests that could be used by Asian pear farmers.

INDICATION OF TRICHLOROMETHANE SEGREGATION IN 1-HEXYL-3-METHYLIMIDAZOLIUM BIS(TRIFLUOROMETHYLSULFONYL)AMIDE – TRICHLOROMETHANE BINARY SYSTEM.

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There is much research interest in Ionic liquids (ILs), which are salts that are liquid below 100^{o}C. ILs come in contact with molecular solvents in many chemical applications, but a general understanding on the solution structure and dynamics of ILs in particular with molecular solvents of low polarity is presently absent. A study of transport properties for the binary system 1-hexyl-3-methylimidazolium bis(trifluoromethylsulfonyl)amide – trichloromethane ($[C_6mim][NTf_2] - CHCl_3$) is presented as a function of composition and temperature. Self-diffusion coefficients of cation and anion are identical for ionic liquid mole fractions $x_{IL} < 0.95$. The self-diffusion coefficient of $CHCl_3$ is consistently larger than that of the ions by a factor of 4. A double logarithmic plot for the ratio of self-diffusion coefficient and temperature versus viscosity is linear for ionic liquid mole fractions $0.1 < x_{IL} < 0.9$ indicating a) a fractional Stokes-Einstein applies where self-diffusion is inverse proportional to some power b of viscosity ($D \sim \eta^{-b}$), and b) single average length scales are associated with the mass transport of $[C_6mim][NTf_2]$ and $CHCl_3$. However, the obtained length scale for $CHCl_3$ is unreasonably small, which is indicative of $CHCl_3$ segregation. The molar conductivity displays a maximum near $x_{IL} = 0.2$. Evaluation of the ionicity from molar conductivity and self-diffusion coefficients indicates a gradual speciation change from charged species to neutral species for $x_{IL} < 0.5$. The temperature dependencies of self-diffusion and molar conductivity follow Arrhenius behavior. The obtained x_{IL}-dependent activation energies are found to be linear for molar conductivity and largest for the cation and anion self-diffusion coefficients. The activation energies for the self-diffusion of $CHCl_3$ appear to be identical with those obtained from fluidity data.

SYNTHESIS OF NOVEL RENEWABLE ALIPHATIC-AROMATIC POLYESTERS.

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Most commercial plastics and polymers are synthesized from monomers derived from fossil fuels. To reduce environmental impact and preserve the limited supply of fossil fuels, research into polymers synthesized from renewable starting materials has seen an increase in interest. In this work we have used mostly renewable monomers to synthesize copolyesters, including lignin derivatives. Polymerizations used a two stage process, argon was used to form oligomers, then high vacuum was applied to form longer polymer chains and increase molecular weight. The resulting conversions exceeded 90 %. The type of monomers varied on type and stoichiometric ratio to study the thermal and mechanical properties of each polymer.

BEECH INTERFERENCE WITH MAPLE REGENERATION: FUTURE CHANGE IN FOREST COMPOSITION.

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Beech bark disease is a pathogenic complex that causes morbidity and mortality of American Beech (*Fagus grandifolia*) in northern hardwood ecosystems. Under stress, American beech produces root sprouts. As a result, aftermath stands have a dense population of small beech in the understory, which interferes with regeneration of more valuable species, such as sugar maple (*Acer saccharum*). The purpose of this study was to investigate beech interference with maple regeneration in 26 forest stands in the White Mountain National Forest, New Hampshire. Beech and sugar maple juveniles <2 cm in diameter at breast height and >50 cm tall were inventoried in 1994, 2003, and 2012 in 13 of the stands and in 2004, 2010, 2011, and 2015 in the other 13 stands. We compared the

density of beech saplings to those of other species as a function of stand age and soil characteristics. Phosphorus and nitrogen have been shown to affect the development of beech bark disease, and base cations, aluminum and manganese have been shown to be important in the health of sugar maple. Understanding these influences could lead to better management of beech and the species that compete with it in the context of the continuing spread of the invasive disease complex.

MITOPHAGY IN YEAST CELLS

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Families have been identified in which individuals develop Parkinson's disease at very early ages (~ 21-40 years old). Genetic studies determined that these patients possess defective versions of a gene named Parkin, which encodes an enzyme that targets damaged mitochondria for degradation via a process termed mitophagy. Specifically, Parkin assembles a polymer, or chain, of a protein called ubiquitin on specific proteins lining the surface of mitochondria, which then "flags" it to be engulfed into a vacuole and digested. Ubiquitin can be assembled into seven different types of polymers, and we are using yeast, a simple and commonly used laboratory organism, to determine which one(s) are necessary for mitophagy induction. To do so, we are adapting an established yeast mitophagy assay (), which requires us to introduce a fluorescent version of the mitochondrial gene OM45 into yeast strains incapable of assembling each different type of ubiquitin polymer. We are monitoring mitophagy in the yeast cells using a common analytical technique called Western Blotting, and anticipate that if we can determine the ubiquitin polymer responsible for mitophagy in yeast, we can extrapolate our results to mitophagy induction in human cells.

OCCURRENCE OF MICROPLASTICS IN THE STOMACHS OF LAKE ONTARIO FORAGE FISHES.

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Plastic debris has become a pervasive pollutant in both marine and freshwater ecosystems. When plastics degrade, they break down into increasingly smaller pieces that can be ingested by organisms. In addition to fragmentary plastics, microbeads and fibers from fleece clothing are commonly found within aquatic organisms. Microplastics can transport harmful organic chemicals (e.g. PCBs) and heavy metals throughout the ecosystem. These chemicals can bioaccumulate in a system and become concentrated in apex predators. We sampled three fish from 15 locations in Lake Ontario at water depths 55-125m: Round Goby, Deep Water Sculpin, and Alewife. The Round Goby and Deepwater Sculpin are benthic feeders, while the Alewives are pelagic feeders. By studying fish that use different habitats and have different feeding habits, we can gain a better understanding of the distribution of microplastics in the environment. Fish were weighed and digestive tracts were removed and then dissolved in KOH to isolate microplastics. To date we have analyzed the stomach contents of digestive tracts from Alewife (37), Round Goby (14), and Deepwater Sculpin (14). The most abundant type of plastic found were fibers (approx. 75%), followed by fragments (approx. 23%). The remaining 2% consisted of unidentified spheres that were too large to be considered microbead pollution. On average, we found 4.26 fibers and 0.80 fragments per Round Goby, 2.43 fibers per Alewife, 1.14 fragments per Alewife, and 1.89 fibers, 0.07 fragments, and 2.80 spheres per Deepwater Sculpin. Based on our sampling to date, approximately 56% of the total plastics discovered were found in Alewives (51.4% of all fibers, and 77.8% of all fragments). Round Gobies contained 29.9% of the total plastics discovered (33.7% of all fibers, and 20.4% of all fragments). Lastly, 13.7% of the total plastics discovered were found in Deepwater Sculpins (14.9% of all fibers found, 1.8% of all fragments found, and 100% of spheres of unknown composition). Our work indicates that microplastics are being ingested by multiple forage fish species throughout Lake Ontario.

EXPRESSION AND PURIFICATION OF LGN PROTEIN FOR SOLVING A CRYSTAL STRUCTURE.

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LGN protein, also known as G-protein signaling modulator-2 (GPSM-2), is a protein present during the division of mammalian cells whose function is to maintain cell polarity and alignment of mitotic spindles. It is known that high levels of LGN are present in breast cancer cells and T450 is phosphorylated. Furthermore, overexpression of the LGN T450A mutant in breast cancer cells suppresses their growth. The purpose of this research is to understand the structural aspects of how LGN regulates the growth of breast cancer cells using protein crystallography. Two mutants, T450A and T450D, will be utilized to mimic the un-phosphorylated and phosphorylated versions of LGN. LGN was expressed using mammalian baby hamster kidney (BHK)-570 cells and transfected using Lipo-D reagent. LGN was then isolated by immunoprecipitation using rabbit LGN polyclonal antibodies and protein A/G Plus-Agarose beads. Purification has been attempted by adding LGN peptide to compete and remove LGN from the antibody, but is currently being optimized to maximize the amount of free LGN present. The T450A and T450D mutants are being generated by PCR and will be submitted for sequence analysis. Western Blot analysis determined the presence of the LGN protein in the supernatant, and thus was released from the antibody. SDS-PAGE will determine the purity of LGN. Crystallization conditions to grow LGN protein crystals will be set up after reaching a 95% purity level so that a 3D structure can be determined. Upon solving the crystal structure, it is likely that drugs can be designed to slow or inhibit breast cancer proliferation.

ENCAPSULATION AND DELIVERY OF TRASTUZUMAB INTO HUMAN BREAST CANCER CELLS USING CHOLESTOSOMES ™.

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According to the American Cancer Society, 1 in 8 (12%) of women in the United States develop invasive breast cancer. Among those individuals, approximately 25 to 30% of breast cancer cells exhibited elevated HER2 levels.[1] HER2 positive breast cancers identified by a pathologist typically exhibit amplification of the HER2 gene resulting in an overexpression of HER2 receptors.[2] The HER2 receptor (Human Epidermal Growth Factor Receptor 2) is a member of the epidermal growth factor family important for the intracellular signaling and regulation of cell growth. Trastuzumab (Herceptin®) is an IgG1 monoclonal antibody that has been proven to be effective in HER2 positive patients. Trastuzumab binding to HER2 interferes both directly and indirectly with downstream intracellular signaling pathways.[3,4] Unfortunately, less than about 35% of patients benefit from treatment with Trastuzumab while the remainder exhibit initial or acquired resistance to treatment.[4,5] Importantly, brain metastasis frequently occurs in trastuzumab treated patients.[6] This population of resistant patients inspires efforts towards a more effective delivery system for trastuzumab, including those that can cross the blood-brain barrier. This laboratory has developed a neutral lipid based vesicle (the Cholestosome™), that uses naturally occurring lipids for the delivery of a wide variety of therapeutics, including small molecules, antibiotics, peptides, and proteins. Previous work has shown Cholestosome™ -mediated delivery of FITC-labelled peptides into various mouse tissues (including brain) after oral administration. The Cholestosome™ can therefore potentially be used to orally deliver compounds for which intravenous administration is the only effective dosing route. The present studies describe the initial efforts at Cholestosome™ encapsulation of trastuzumab.

ELECTRIC TRANSPORT OF ORGANIC THIN FILM SEMICONDUCTORS.

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We discuss herein the nanocomposite organic thin film diodes for the use of solar cells. The goal of this study is to create and test organic thin films semiconductors for use in plasmonic solar cells. Organic semiconductors are created using thin films of polymers deposited on a substrate. When doped with certain nanoparticles, some polymers exhibit the properties of a semiconductor. The samples were fabricated using organic thin films made from Poly(1-vinylpyrrolidone-co-2-dimethylaminoethyl methacrylate) copolymer and doped with $MnFe_2O_4$, silver and gold nanoparticles. The samples were fabricated using a spin coating method. The transport properties are obtained by analyzing the I-V curves and band gap calculations using HyperChem.

USE OF FATTY ACID SIGNATURES TO EXPLORE THE RIVER CONTINUUM CONCEPT.

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The objective of this study was to evaluate if fatty acid signatures (FAS) of aquatic organisms could be used to assess the river continuum concept, which predicts biological community responses to physical changes from headwaters to the mouth of any river. Thus, four species (e.g., round goby, northern clearwater crayfish, rock bass, and striped shiner) were collected using backpack electrofishing at twelve sites throughout Sandy Creek located in western New York. Gas chromatography/mass spectrometry were used to assess whole body fatty acid signatures of each species. Our results showed that FAS of each species differed throughout Sandy Creek (ANOSIM; R = 0.587, 0.43, 0.336, 0.518 for round goby, crayfish, rock bass, and striped shiner, respectively).The organisms from the headwaters of the creek showed higher concentrations of 22:4n-6, 18:2n-6, and 18:1n-9, whereas fish sampled at the mouth of the creek showed higher concentrations of 18:3n-3, 22:6n-3, 20:3n-3, and 20:4n-3. These results indicate that the organism's diets shifted from terrestrial sources (high in n-6) and microbial/detritus sources (high in n-9) in the headwaters to instream production (high in n-3) in the mouth of the creek.

VIRULENCE TESTING OF A *PSEUDOMONAS AERUGINOSA* MUTANT USING *CAENORHABDITIS ELEGANS* AS A BACTERIAL PATHOGENESIS MODEL.

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Pseudomonas aeruginosa is a ubiquitous gram negative bacterium that is best known to affect immunocompromised individuals. Observations of bacterial virulence can be done by infecting the nematode *Caenorhabditis elegans. C. elegans* feeding on *P. aeruginosa* will accumulate bacteria within the digestive tract which results in an infectious process. Specifically a slow-kill assay was performed to demonstrate the bacterial virulence effects on the model organism over a span of three days. Juvenile, wild type nematodes at the fourth larval stage were placed onto NG plates containing two strains of *P. aeruginosa*, PA14 and PA14 Δ*moaE*, and an *E. coli* (OP50) *C. elegans* maintenance strain. The wild-type (PA14) and the mutant Δ*moaE* strains showed significantly different survival rates than the OP50 maintenance strain, while the same significant difference in survival was not observed between the *P. aeruginosa* strains. This finding suggests that the loss of MoaE does not affect the bacterial virulence measured in a *C. elegans* slow-kill model of infection.

INDUCTION OF CELL DEATH IN CAL-27 AND HeLA CANCER CELL LINES USING BERRY EXTRACTS.

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Oral epithelial cancer is one of the most prominent types of cancer, being the sixth most common worldwide[4]. Cervical epithelial cancer used to be the leading cause of death in women in the United States. However, advances in diagnosis and treatment of cervical cancer have improved survival outcomes to 70-73% [2], while oral cancer has not improved and remains at 50-55% [4]. In the current research, HeLa and CAL-27 cell lines are compared for their induction of apoptosis following treatment with eleven different fruits, all combined in a compound known as Berry Balance™. The active element of these fruit extracts is reported to be Anthocyanins; it is the conjugated bond structure that is responsible for the bright colors of the fruits. Anthocyanins are flavonoids found in many fruits that have antioxidant and anti-carcinogenic properties. They have been shown to induce apoptosis in cancerous cells by triggering the intrinsic mitochondrial pathway and extrinsic FAS ligand pathway. Treatment of CAL-27 oral cancer and HeLa cervical cancer cells with varying concentrations of berry extracts demonstrated induction of apoptosis. Apoptosis/ cell death was quantified by hemocytometer, fluorescence microscopy, flow cytometry, and DNA agarose gel electrophoresis. Results showed positive correlation between increasing concentration and incidence of apoptosis and cell death. HeLa cell and CAL-27 cell results showed comparable responses to treatment with berry extracts. These results suggest that berry extracts may induce cell death in CAL-27 cells in a similar fashion as in HeLa cells, potentially implying improved therapeutic effect in oral cancer.

INVESTIGATION OF CASPOFUNGIN TOLERANCE GENES IN CANDIDA ALBICANS.

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Candida albicans, a yeast species, lives in the mouth, gastrointestinal tract, and genitourinary tract of humans. In healthy individuals *C. albicans* causes superficial infections, but immunocompromised patients get severe infections that reach the blood stream and can exponentially reduce survival rates. Caspofungin is one of the most recent antifungal treatments for *C. albicans* infections and targets the 1,3-β-glucans in the cell wall. Some strains of *C. albicans* are resistant to caspofungin. The mechanism of tolerance is unknown, but genes implicated in caspofungin tolerance include *HST3*, *FKS1*, *FKS2*, *NBN1* and *PGA4*. To directly test the connection of these genes to caspofungin susceptibility, each gene is being individually deleted from the genome using a homologous recombination based method. Yeast without the genes in question are being tested with caspofungin to determine their role in tolerance.

DISSOLVED ORGANIC MATTER STRUCTURE AND QUALITY ACROSS A GRADIENT OF NORTH TEMPERATE LAKES.

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The concentration of dissolved organic matter (DOM) in lakes is influenced by climatic and topographic characteristics as well as by catchment area and internal lake properties. Variations in any of these potentially affect the quantity and quality of DOM input into lakes. While the properties of DOM are diverse and source-dependent, its origins, bioavailability, and chemical composition are poorly understood. Ultraviolet-visible spectroscopy allows detection of organic substances. These spectra also contain information on whether the organic matter is produced in the lake or its catchment. In this study, two spectral slope regions (275-295 nm and 350-400 nm) within log-transformed absorption spectra were used to identify the temporal and spatial variability of DOM from ten north

temperate lakes. The slope of the 275-295 nm region and the ratio of these slopes (S_R: 275-295 nm slope : 350-400 nm slope) are related to DOM molecular weight. The lakes were characterized by different concentrations of DOM, forming a gradient ranging from clear-water to brown-water lakes. The results indicated the DOM in all lakes had low molecular weight and low aromaticity. Spectral slope regions were significantly correlated with chlorophyll-*a*, light attenuation, pH, and a_{440}, an indicator of terrestrial carbon input, indicating strong connections between DOM absorption and molecular weight. A_{440} was found to provide the highest correlation with measured DOM absorption. Despite the small set of lakes included in the present study, these analyses highlight their interactions with the catchment, allowing better understanding of the trophic condition of these lakes as indicated by their spectral properties. As the condition of lakes fluctuate with their surroundings, sustained environmental assessments may accurately track the impacts of climate and anthropogenic changes on the landscape.

AGE-DEPENDENT CHANGE IN TDP-43 REGULATION IN MOUSE MODELS OF ALZHEIMER'S DISEASE

Liam Kaylor

The transactive response DNA-binding protein 43 (TDP 43) has been reported as a potential contributor to the severity of Alzheimer's Disease (AD). TDP-43 is a neurofilament light (NF-L) messenger RNA (mRNA)-binding protein, and its implication in AD has been suggested in studies whose patients had amyotrophic lateral sclerosis and down-regulation of NF-L mRNA. Pathological TDP-43 mislocalizes from the nucleus, accumulating in the cytoplasm and forming insoluble plaques that contribute to the loss of synaptic function observed in AD. Direct links between TDP-43 and AD, however, are still limited. In this study, we investigated the expression of molecular TDP-43 through western blotting of cerebral protein extracts and quantitative analysis with normalization. Additionally, we examined the localization of TDP-43 through immunohistochemistry and qualitative analysis of transverse coronal sections of the mice brains. We concluded that there were no significant differences (p values <0.05) in the expression of TDP-43 between wild-type (WT) and amyloid precursor protein (APP)/presenelin 1 (PS1) mutant mice, at either nine months or eighteen months of age. Immunohistochemistry revealed that TDP-43 did not mislocalize from the nucleus in either WT or APP/PS1 mice at nine months or eighteen months of age. Our results indicate that while TDP-43 does not hold direct links to AD, it may be a contributor to a pathology that includes much more complicated pathways and cellular interactions.

THE EFFECT OF ANTI-BACTERIAL, TRICLOSAN, ON EPILITHIC BIOFILM COMPOSITION, FUNCTION, AND RESISTANCE.

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Triclosan is the active ingredient in antibacterial hand soaps and can reach detectable levels in many waterways. Because of its antimicrobial nature, triclosan is expected to have an impact on microbial-mediated ecosystem processes. We assessed the effect of triclosan on epilithic biofilms collected from Cattaraugus Creek in western New York. Biofilms were incubated for 3 weeks at four concentrations of triclosan (0.0, 0.1, 1.0 and 10 µg/L), representing the full range of concentrations observed in rivers and streams. Biofilm condition (chlorophyll a and AFDM) and function (including photosynthesis, respiration, nitrate and phosphate uptake, and extracellular enzyme activities) were measured at the end of the incubation. Triclosan significantly reduced the chlorophyll content and autotrophic index of the biofilms relative to control, but did not appear to affect measured biofilm function. Interestingly, bacteria from the biofilms did not show triclosan resistance regardless of the treatment level (i.e. most bacteria in the biofilm are still susceptible to the antimicrobial effects). Subsequent assays indicate that culturable bacteria from the biofilms did not show reduced growth until triclosan concentrations reached 100 µg/L. Our data indicate that triclosan concentrations observed in the field may not be sufficient to reduce biofilm growth and function in rivers and streams.

LEAD CONTAMINATION OF SOIL AND WATER IN DANIEL BOONE NATIONAL FOREST.

Selina Kernen, Jonathon Malzone, and David T.R. Stewart

Lead is a heavy metal that can have many harmful effects on the environment and the organisms living in it. The recent incident of lead contaminated water in Flint, Michigan has raised awareness of the prevalence of lead that can be found in the environment. In collaboration with the Eastern Kentucky University, water and soil samples from wetlands in the Daniel Boone National Forest were tested for levels of lead.

The sites were either natural or constructed ephemeral wetlands at higher elevations where no obvious source of water is present besides rain. These sites have been being studies for approximately 10 years for amphibian populations. Dr. Malzone is beginning to measure the water budget and soil conditions to understand factors that influence the amount of surface water available for spawning and development.

Our part of the project is to measure the amounts of lead in the soil and water to see if lead may be contributing to population dynamics as well. We expect atmospheric deposition to be the primary source of lead. To test this hypothesis the soil samples were collected as soil cores to at least 15cm depth in order to do a depth profile. The water samples were just taken as surface samples or ground water collected from the wells used to determine the water budget.

INTER- AND INTRA-SPECIES VARIATIONS IN FATTY ACID SIGNATURES OF NEARSHORE FISHES FROM LAKE MICHIGAN.

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The objectives of this study were to assess inter- and intra-species (spatial, seasonal, and annual) variations in fatty acid signatures (FAS) of four fishes (round goby, alewife, spottail shiner and yellow perch) from Lake Michigan during 2013-2015. Fish were collected in spring, summer and fall at three sites with different habitat complexity; their substrates were characterized as fine sand (DR), rocky gravel and boulder (M2), and coarse and intermittent gravel and cobble (S2). Significant inter-species FAS variations were found among the four species (ANOSIM, overall R = 0.641): 22:6n-3 concentration was highest in alewife and yellow perch; 18:1n-9 concentration was highest in spottail shiner; and 20:5n-3 concentration was highest in round goby. Intra-species FAS variations were found in three species: seasonal in round goby (fall vs. spring), spatial in spottail shiner (DR vs. S2), and annual in yellow perch. However, these variations were smaller than the ones observed among species. The results could potentially be used to assess diets of nearshore fishes in Lake Michigan.

MICROWAVE SYNTHESIS OF IRIDIUM COORDINATION COMPLEX AND METAL-ORGANIC FRAMEWORK.

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Microwave irradiation has proved to be an efficient synthetic tool for organic, inorganic, and organometallic compounds as well as solid-state and inorganic nanomaterials. The irradiation and thereby direct heating of the sample often leads to shorter reactions times and higher yields making microwave synthesis a green synthetic pathway.[1,2]

Tetrakis(2-phenylpyridine-C^2,N')(μ-dichloro)diiridium, [$Ir_2(ppy)_4Cl_2$], was rapidly synthesized using microwave irradiation. The synthesis of a zinc metal-organic framework containing an iridium coordination complex derived from [$Ir_2(ppy)_4Cl_2$] was explored via microwave irradiation. The reaction conditions, including solvent and temperature, with be presented. Elemental analysis, infrared spectroscopy, ^{1}H NMR, and powder x-ray

diffraction results will be used to determine the structure and bonding in the complexes and metal-organic framework.

MEASURING CYP1A IN FRESHWATER FISH OF WESTERN NEW YORK AS AN INDICATOR OF POLLUTION LEVELS

T. Koetsier, T. Taggart, S. Johnson, K Miller, R. Williams

Freshwater fish can reveal information concerning levels of aqueous contamination through regulation of the CYP1A protein. Fish that inhabit the sediment of water systems are more likely to indicate contamination levels than fish that feed along surface because toxins often reside in the sediment of freshwater bodies due to their low aqueous solubility (Andrade, 2004). Previous research suggests that bottom-dwelling fish with a higher tolerance for contamination will be more fit to survive and produce offspring that also have a higher tolerance for similar environments. Over time, this causes a genetic shift towards populations that are resistant to pollution (Nacci et al., 1999). If the trait is genetically linked, then adaptation of the population will follow as the trait is passed onto future generations. In this study we explored the effect of contaminants on CYP1A expression in freshwater fish of clean and contaminated bodies of water across western New York as a measure of adaptation. Sites visited include Moss Lake, Tifft Nature Preserve, Rushford Lake, Love Canal, Genesee River, the Hanging Bog and Cuba Lake. Using protein extraction, western blotting and densitometry, levels of CYP1A were measured for individual fish and used to estimate pollution levels in each of the bodies of water. Certain contaminated bodies of water contained lower levels of CYP1A expression, indicating that the fish populations in those bodies of water may have adapted over time to their contaminated environments.

MODELING THE POPULATION DYNAMICS OF MITOCHONDRIA IN MAMMALIAN CELLS.

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Mitochondria are organelles located inside eukaryotic cells that play several key cellular roles, including providing energy (i.e., ATP), participating in cell signaling, triggering cell differentiation, and initiating apoptosis. All organisms are believed to have low levels of variation in mitochondrial DNA (mtDNA), and repeated mitotic segregation and clonal expansion can enable a mitochondrion to eventually dominate the mtDNA pool. Alterations in mtDNA are connected to a range of human health conditions, including: epilepsy, heart failure, Parkinson's disease, diabetes, and multiple sclerosis. Therefore, understanding how changes in mtDNA accumulate over time and are correlated to changes in mitochondrial function and cell properties can have a profound impact on our understanding of fundamental mammalian cell biology and the origins of some human diseases.

Motivated by this and drawing from population dynamics models, we develop and study a mathematical model to determine which cellular parameters have the largest impact on mtDNA population dynamics. The model consists of coupled ODEs to describe subpopulations of healthy and dysfunctional mitochondria subject to mitochondrial fission, fusion, autophagy, mutation, and varying levels of cellular ATP, which depend on fusion-based ATP generation advantages and energy dissipation by fission and other cellular mechanisms. We study the time evolution of each sub-population under specific selection biases and pressures by tuning specific terms in our model, and study the stability of population in the parameter space of the ratio of fusion rates and the mutation rate of the healthy populations. Our results may provide insights into how sub-populations of mitochondria survive and evolve under different selection pressures and with time.

EVIDENCE OF A POSSIBLE BIOCONTROL METHOD OF INVASIVE PURPLE LOOSESTRIFE (*LYTHRUM SALICARIA*) WITH THE USE OF *GALERUCELLA* BEETLE HERBIVORY.

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Purple loosestrife (*Lythrum salicaria*) is an invasive wetland plant in North America that is native to Europe. Purple loosestrife has spread extensively throughout North America and can displace native wetland plant species. Purple

loosestrife is known to reduce native plant coverage and lower the overall plant diversity. In addition, extensive *Lythrum* growth can reduce open water in shallow wetlands and alters habitat structure. In the United States, there are no native herbivores that control purple loosestrife populations. At the SUNY Oswego Rice Creek Field Station (RCFS) purple loosestrife is abundant. In 2001, managers released *Galerucella pusilla* to help control the spread of *Lythrum*. To investigate whether the biocontrol beetles are still having an impact on *Lythrum*, we established research plots at a known Galerucella release area as well as in an area distant from release sites. At each site we measured the species richness, ground cover and total number of purple loosestrife. At each sampling location, we established five one-meter squared quadrats. In each quadrat, we collected the five largest purple loosestrife plants and 20 leaves were collected from both low and high branches of the plant. Using ImageJ image analysis software we are quantifying the amount of herbivory on *Lythrum* leaves. To date, we have found that areas closer to *Galerucella* release sites have experienced more herbivory. Using plant community and herbivory data we hope to be able to assess relationships between *Lythrum* colonization and biocontrol at RCFS.

DETERMINING FEMALE SPECIFIC LOCI IN THE TERRESTRIAL ISOPD *TRACHELIPUS RATHKEI.*

Joseph Laricchiuta and Dr. Christopher Chandler

In many species, sex chromosomes influence the morphological and behavioral differences between the sexes. The most known sex chromosome such as the mammalian X and Y, or the avian Z and W are heterogametic. In the case of X/Y species males have on copy of the Y chromosome and one copy of the X chromosome, while females have two X chromosomes. On the other hand, in the Z/W system, males have two copies of the Z chromosome, where females have one copy each of the Z and W chromosomes. In the terrestrial isopod *Trachelipus rathkei* it is hypothesized that they have the ZW system. Terrestrial isopods are particularly interesting because their sex determination mechanisms are often influenced by bacteria (*Wolbachia*), which often skews the sex ratio by producing more females. Using this non-model organism, we look to find the female specific regions on the presumed W chromosome. With determining these regions, we can test the gene expression in the future of these regions to see if the gene regions influence morphological and behavioral development.

EFFECTS OF NITROGEN, PHOOSPHORUS, AND CALCIUM ON FOLIAR CHARACTERISTICS OF PIN CHERRY AND AMERICAN BEECH.

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Nitrogen additions to forests in the northeastern USA have increased at least 5- to 10-fold due to industrialization, vehicular exhaust, and agricultural fertilizers. Increased chemical deposition to forests disturbs forest ecosystems and may affect levels of elements leading to a potential decrease in tree species productivity. Nitrogen (N) and phosphorous (P) play important roles in nutrient cycling in forest ecosystems and are readily measured in leaves. This study focused on pin cherry (*Prunus pensylvanica*), a common pioneer species throughout the northeastern USA, and American beech *(Fagus grandifolia)* a climax species currently threatened by beech bark disease. Samples were collected in the White Mountain National Forest in New Hampshire in four stands that naturally regenerated following clearcutting 36 to 41 years ago. Beginning in 2011, plots in each stand received no treatment or N (30 kg N/ha/yr as NH_4NO_3), P (10 kg P/ha/yr as NaH_2PO_4), N&P, or Ca (1150 kg Ca/ha in the form of $CaSiO_3$ as a one-time addition). Sun-exposed leaves were collected with a 20-gauge shotgun from three trees of each species in each plot in August, 2016. The leaves have been analyzed for mass, area, and moisture content, and will be processed for nutrient concentration. These properties of tree leaves can be used to indicate forest health, to predict nutrient fluxes in leaf litter and subsequent nutrient mineralization, and to determine the effects of nutrient limitation on forest productivity.

A CUSTOM CRISPR SYSTEM TO INVESTIGATE THE ROLE OF HYPOXIA-INDUCIBLE FACTOR-1α IN THE EPIDERMAL KERATINOCYTE RESPONSE TO UVA IRRADIATION.

Ben Leahy, Dylan Phelps, Elizabeth Osborne, Elizabeth McNeil, and Peter LaCelle, PhD.

Ultraviolet light (UVA) induces stress responses, DNA damage, and even cell death in epidermal keratinocytes, the cells that form the protective outer layers of the skin. UVA is also the primary carcinogen in epidermal skin cancers, the most prevalent of all human cancers. The hallmarks of transformed cells typically include resistance to apoptosis (programmed cell death, a process by which damaged cells are eliminated), and uncontrolled growth. Interestingly, normal keratinocytes exposed to UVA also exhibit an initial increase in resistance to cell death. HIF-1 is a dimeric transcription factor important in the survival of cells under hypoxic stress. We found previously that the levels of HIF-1α, the regulated subunit of HIF-1, increase in UVA exposed skin, in UVA-irradiated keratinocytes in culture, as well as in tumorigenic keratinocytes. We hypothesize that elevated HIF-1 α functions in UVA-exposed keratinocytes to promote cell survival, and that it contributes to UVA-induced keratinocyte transformation. In support of this hypothesis, we have also observed that a chemical HIF-1 inhibitor, YC-1, renders the keratinocyte cell line HaCaT more susceptible to UVA-induced cell death. To investigate the function of HIF-1 in more detail, this study focuses on the production of lentivirus particles to target the HIF-1 α gene using CRISPR recombinant DNA technology. A series of ten guide RNAs with homology to the HIF-1 α upstream untranslated region will be expressed in keratinocytes, along with the bacterial dCAS9 protein, linked to either a transcriptional activator (VP64) or inhibitor (KRAB). Guide RNAs yielding the greatest degree of inhibition and transactivation of HIF-1 α will be selected for evaluation of the effects of HIF-1 modulation on the human keratinocyte response to UVA irradiation, and on maintenance of the transformed phenotype in epidermal carcinoma cells.

GENOMIC ANALYSIS OF *STAPHYLOCOCCUS* BACTERIOPHAGE.

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Staphylococcus is a normal inhabitant of humans. Certain strains of *Staphylococcus* exhibit pathogenic characteristics with Methicillin-resistant *Staphylococcus aureus* (MRSA) being the most prevalent. There are numerous strategies, including antibiotics, that are failing due to the increased resistance of many *Staphylococcus* strains. New methods are constantly being explored in order to combat this ever-growing problem; one involves the use of bacteriophage to kill the target bacteria. An analysis of known *Staph* prophages was performed and primers to shared genes within the three large families of phage were designed to characterize virulent human associated *Staphylococcus* and non-human associated *Staphylococcus*.

INCIDENCE OF *WOLBACHIA* INFECTION IN FREE-LIVING, ENSLAVED AND SLAVEMAKING *FORMICA* ANTS.

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Wolbachia are a group of maternally inherited bacteria commonly found in arthropods and are one of the world's most abundant intracellular symbionts. Although the bacteria is commonly transmitted vertically, from mother to offspring, recent research has suggested that horizontal transmission, which occurs between members of different species, may be a means of transmission as well. Here, my work seeks to identify whether *Wolbachia* is being horizontally transmitted between slavemaking ants and their slaves. Slavemakers and corresponding slaves from the same colony were assessed for *Wolbachia* infection through use of polymerase chain reaction (PCR) to amplify *Wolbachia*-specific genes. PCR results point to differing rates of infection between slavemakers and slaves, with higher incidence of *Wolbachia* infection among slavemakers. Subsequent sequencing of positive samples show homology to *Wolbachia* strains of other ant species; however, the appearance of a single consistent polymorphism

between slavemaking and enslaved ants suggests that they may be harboring different *Wolbachia* strains and thus transmitting the infection vertically rather than horizontally. In addition, the existence of another *Wolbachia* sequence in a slave that differs by 5.4% suggests there are multiple strains in the *Formica glacialis* population, suggesting the possibility of multiple infections.

INVESTIGATING THE EFFECTS OF STRESS ON REOVIRUS TRANSLATION AND REPLICATION.

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Infection with Mammalian Orthoreovirus induces the formation of structures known as viral factories (VF) throughout the host cell cytoplasm. VF are the sites of virus replication, translation and assembly. Following viral infection the host cell stress response is initiated resulting in the sequestration of vital host translational machinery, including ribosomal subunits and translation initiation factors, as a mechanism to limit viral protein synthesis. Many of the cellular proteins found in stress granules are also found in VF. Therefore, because stress granules and VF share similar contents, we hypothesized that stress granules may act as a precursor during VF formation. To test this, we first examines the localization of stress granules proteins during infection. We found that stress granule proteins co-localize to VF at both early and late time points. We next examined viral protein expression in the absence and presence of stress. The induction of stress granules in cells prior to infection resulted in increased viral protein expression starting as early as 10 hours post infection. Additionally pre-treatment of cells with sodium arsenite resulted in an increase in viral replication compared to cells not treated with sodium arsenite. Together these findings are consistent with our hypothesis that reovirus may benefit from the host stress response. Current work in the laboratory is focused on understanding the role of key stress granule proteins in viral replication.

FATTY ACID SIGNATURES OF PREDATORY FISH FROM LAKE MICHIGAN.

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Understanding energy flow pathways in Lake Michigan food web is prerequisite to making wise stocking and management decisions. The declines in abundance of plankton and pelagic forage fish appear to have reduced the lake's overall carrying capacity, but it is unlikely that all fish species are equally affected. The goal of this project was identify current trophic pathways using fatty acid signatures (FAS). This approach is based on the concept that fatty acids are conservatively transferred from prey to predator and therefore infer diet in accordance to the principle you are what you eat. In this study, we focused on two salmonid species, lake trout (n = 192) and Chinook salmon (n = 264), which were collected by federal, state and tribal agencies throughout the lake. Upon capture, each fish was assigned to one of the four quadrats of the lake: southwest, southeast, northwest and northeast. Belly flaps were sampled and analyzed for lipid and fatty acid composition. Our preliminary results indicated that lipid content was higher in lake trout than in Chinook salmon (30.7% vs. 14.0%). Ongoing statistical analysis will reveal potential inter- and intra-species (spatial) FAS variations and provide a better understanding of the prey-predator interactions in Lake Michigan as well as the ability of these salmonid species to utilize alternative energy resources.

BATTLING BIOLFILM DEVELOPMENT: CONSTRUCTION OF NARI MUTANT AND VISUALIZATION OF ASSOCIATED PROTEINS IN *PSUEDOMONAS AERUGINOSA*.

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Pseudomonas aeruginosa causes opportunistic infections, especially during cystic fibrosis. Its' biofilm forming ability maintains virulence while exploiting nitrate reductase (integral membrane NarI, membrane associated NarGH, and a molybdenum cofactor [MoCo]) for anaerobic respiration. In prior studies, MoCo biosynthesis maybe membrane localized and may associate with proteins like NarI. To investigate this possible interaction, a previously constructed *narI* mutant construct was introduced into *P. aeruginosa* via conjugation from *E. coli*. Resulting mutants were counterselected on sucrose and confirmed by PCR. GFP complementation constructs were elctroporated into the *narI* mutant, confirmed by PCR, and protein interactions were confirmed by fluorescence.

CHARACTERIZATION OF MUTANTS OF A *SALMONELLA* KILLER

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A giant bacterial virus or phage is one with an unusually long genome relative to other phages, typically greater than 200 kilobase pairs (kb). Giant phages were thought to be rare but in about the last decade it has been shown that they abound in the environment and were previously not isolated due to the methods used for isolation. There is currently great interest in giant phages for their potential to control human and plant pathogenic bacteria as an alternate solution to the problem of multi-drug resistance. However, giant phages are generally poorly understood as a large percentage of their genes encode proteins that cannot be assigned functions using bioinformatics. To overcome this problem, we are using the giant *Salmonella enterica* phage SPN3US as a model genetic system to study giant phage gene function. To do this we treat the phage with a mutagen and isolate amber mutant phages which have an amber stop codon interrupting an essential gene that disrupts the production of its protein product. These mutants can be identified by plating characteristics; they are able to grow on suppressor strains which have a specialized transfer RNA (tRNA) to insert an amino acid at the mutated amber stop codon but unable to grow on the normal non-suppressor strain. In order to identify the mutated SPN3US genes, we then sequence the mutant phage genomes. Prior to sequencing, it is crucial for each mutant candidate to be confirmed as true amber mutant phenotypically. Equally important is to ensure that each mutant is not genetically identical to other mutant so they will not be sequenced twice. In this study, we show that nearly all isolated SPN3US mutant phages hold true to expected phenotype and are mostly genetically different to one another. Future studies will include sequencing of these mutants and studies to characterize the effect of gene knockouts on SPN3US. Our studies are relevant to an increasing group of related giant phages that infect pathogens, such as *Pseudomonas aeruginosa* and *Cronobacter sakazakii*, which share homologous genes with SPN3US.

ARAL PHOSPHATASE FROM *BACILLUS SUBTILIS*, A MEMBER OF THE HAD SUPERFAMILY

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The HAD (Haloacid Dehalogenase) superfamily is a diverse superfamily with a majority of the enzymes being phosphatases. One family of the HAD superfamily is the nitrophenyl phosphatase family, so named because the first family members were yeast enzymes found only to hydrolyze p-nitrophenyl phosphate. Since that time, a number of enzymes with a variety of activities have been identified, including an enzyme from *B. subtilis*, AraL, originally designated as a sugar phosphatase. The AraL gene has been subcloned to incorporate a HisTag for nickel

affinity chromatography, and the enzyme has been expressed, purified and characterized. Interestingly, it was found that although AraL does cleave phosphate from some sugar phosphates (ribose 5-phosphate, ribulose 5-phosphate, and arabinose 5-phosphate), intermediates of glycolysis (glyceraldehyde 3-phosphate, phosphoenolpyruvate, and dihydroxyacetone-phosphate) are much better substrates for the enzyme. Since glycolytic intermediates are better substrates, AraL's role may be to regulate glycolysis when arabinose is the carbon source. Arabinose is metabolized into intermediates that enter in the middle of the glycolysis pathway. The fact that intermediates after the arabinose point of entry are substrates, and intermediates before the arabinose point of entry are not substrates, suggests that AraL may inhibit glycolysis and activate gluconeogenesis.

DESIGN AND CONSTRUCTION OF A HYPEROXIC ENVIROMENT TO TEST THE EFFECTS OF HIGH OXYGEN CONCENTRATION ON HOUSE CENTIPEDE (*SCUTIGERA COLEOPTRATA)* BODY SIZE.

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Carboniferous fossils (~300 million years ago) show arthropods that had a relatively larger body size than similar contemporary animals. Respiration in many groups of air-breathing arthropods is carried out through simple diffusion in which gas exchange occurs in internal tissues via a tracheal system. It is commonly hypothesized that high atmospheric oxygen levels allowed the evolution of large body size due to the ability of concentrated oxygen to diffuse more deeply into tissues. Here, we describe the use of house centipedes, *Scutigera coleoptrata,* to test this hypothesis. Centipedes will be bred and reared in hyperoxic and normoxic environments over several generations, selecting for large body size. Methods for measuring house centipedes are described as well as design and construction of a hyperoxic growth chamber. Image processing software Image J is used to measure the body length and growth rates in centipedes. The Arduino UNO microcontroller platform was used in the centipede habitat to control light, heat, and oxygen concentration.

ASSESSMENT OF ACID DIGESTION FOR MEASUREMENT OF SUGARS FROM THE BREAKDOWN OF WOOD.

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Second generation biofuels, whose feedstock includes wood chips and cornhusks, can be a new source of energy. Degradation of wood into sugars is an important step in this process. Previous work in our lab attempted to produce sugars from birch and spruce using cellulase and other enzymes. Sugar production was detected by the 3,5-dinitrosalicylic acid (DNS) assay, but this assay is not specific. Analysis of glucose and xylose species can be done with Liquid Chromatography-Electrospray Ionization-Mass Spectrometry (LC-ESI-MS). However, the concentrations of glucose and xylose monomers were much lower with LC-MS than expected from the DNS assay, indicating that the signal from the DNS assay may have arisen from soluble oligomers of the sugars. Furthermore, it was discovered that there were sugars in the proteins, which were assumed to have been added as stabilizers. The current work assesses a modified acid digestion procedure for the conversion of the oligomers in the supernatants of wood digestions. Cellulose and xylan standards were acid-digested and analyzed using DNS and LC-MS. Furthermore, sugar standards of glucose and xylose were tested to ensure that acid digestion did not degrade the original sugars. Future work will be to apply a successful digestion method to both extracted and unextracted birch and spruce supernatants to see which enzyme combinations most effectively produce sugars, which can eventually be used as fuel.

POSITIVE INTERACTION BETWEEN *Curtobacterium* SPECIES AND FOUR DIFFERENT CULTIVARS OF *Phaseolus vulgaris.*

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Bacteria association with plants can result in three different types of interactions, namely negative, neutral, and positive. They can infect plants and cause disease and are referred to as phytopathogenic (negative interaction). Bacteria that can also live inside of plants without causing any harm, and are intimately associated with the plant, the so-called endophytes (neutral interaction). Lastly, many plant growth-promoting bacteria (PGPB) are endophytic bacteria that can enhance plant growth or protect plants from disease and abiotic stress (positive interaction).

In order to test the effect of *Curtobacterium sp.* strain ER2/2 (an endophytic strain of oranges) on 10-day-old healthy bean plants (n=10 per cultivar), we inoculated five different cultivars (cv.) of *Phaseolus vulgaris* (Brown, Pinto, Black Turtle, Red and Great Northern) with $1x10^6$ CFU/ml. For 15 days while in a growth chamber plants were observed and recorded for presence of disease or growth-promotion compared to the control buffer inoculated (n=10).

In four out of five cultivars the bacteria-inoculated plants grew similar to or better than the buffer inoculated plants. One out of the four cultivars reacted negatively to the bacterium; the cv. Brown bean plants showed signs of disease indicated by wilting and browning leaves.

To investigate whether the negative interaction was due to the bacteria inoculated into the bean plants, or to some other pathogen we isolated the bacteria from all the cultivars. In all four cultivars, except cv. Brown most of the colonies isolated appeared to be *Curtobacterium sp.* strain ER2/2 –like on TSA plates, while bacteria isolated from cv. Brown plants were more diverse in appearance. It could indicate that other bacteria could have contaminated the plant during the inoculation process, so we are presently repeating this work. To confirm the presence of *Curtobacterium sp.* strain ER2/2 end point-PCR reactions are currently underway. Based on our data we can say that for four bean cultivars *Curtobacterium sp.* strain ER2/2 is a good candidate as a PGPB. Our future goal is to use this strain as a biocontrol against pathogenic strains of *Curtobacterium* in beans.

CAN NATIVE AND NON-NATIVE ANTS COEXIST.

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Niche theory assumes that species coexist because each has unique niche requirements, which lessens competition between species. My objective was to investigate species invasion from a niche theory perspective. First, I conducted field studies of two ant species, the native Aphaenogaster rudis and the invasive 'fire ant' Myrmica rubra, as both species occupy similar habitats in eastern deciduous forests. Aphaenogaster rudis generally dominates forest habitat, but it appears displaced by the invasive European ant at Tifft. I measured the density of foraging ants and collected food they retrieved at Tifft Nature Preserve (Buffalo, NY). To determine whether the ants occupy similar trophic levels (i.e., eat the same things), I collected and processed workers for stable isotope analysis. I then surveyed bellow dead logs and stones to determine the invasive ant impact on arthropod communities. Finally, I collected workers from the native A. rudis colonies and the invasive M. rubra colonies and conducted ant aggression assays to observe levels of competition. The food retrieval and log/stone surveys showed that the invasive A. rudis ants are both scavengers and predators. The stable isotope analysis indicated that M. rubra and the native A. rudis eat similar foods, and the aggression assays showed that the two species of ant vigorously fight with one another. Surprisingly, the native ant is more aggressive, and sometimes kills, the invasive ant. I observed very little aggression among ants from different M. rubra colonies whereas ants from different A. rudis colonies fought vigorously. These results suggest that the overwhelming success of the invasive ant is not because it occupied a unique niche in the invaded habitat, but because it was not hindered by intraspecific competition whereas the native ant fights with itself as much as it fights with the invader. As a result, the thousands of M. rubra colonies at Tifft may act as one supercolony that monopolizes food resources.

THE PARAMETERS OF TARGETED SPITTING IN BELUGA WHALES (*DALPHENACTORUS LUCAS*)

Allison C. Maynard and Michael Noonan

Beluga whales inhabit shallow waters in the high Arctic, where they are thought to use jets of water to dislodge their prey from the sea floor. The goal of the present study was to document the speed and volume of mouth jets of water in this species. The subjects of this investigation were housed at Marineland of Canada (Niagara Falls, Ontario). The animals were trained to squirt mouth jets of water at targets positioned on a large calibrated panel. Frame-by-frame analyses of video recordings allowed precise measurements of the water movements against the target panel. The water jets produced by the whales were comprised by as much as four litters in volume, and they left the whales' mouths at a maximum rate of three meters per second. Not surprisingly, lesser volumes and speeds were produced by juveniles. These results confirm that beluga whales are able to produce very forceful jets of water form their mouths. In future studies the degree to which these whales can selectively target (aim) their water jets will be investigated.

MICROALGAE TREATMENT OF ANAEROBIC DIGESTER EFFLUENTS FROM A FOOD WASTE TO ENERGY DIGESTOR IN WYOMING COUNTY, NY.

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CH4 Biogas runs an anaerobic digester in Wyoming County, NY that is used to digest Greek yogurt and cheese whey with dairy manure to produce methane for the generation of electricity and heat. After digestion is complete the effluent is treated with a screw press to remove solids and the subsequent effluent is released to a storage lagoon. Over time the effluent is moved to several more lagoons before the effluent is used as a fertilizer for crops (mostly corn). The problem is that the effluent contains as much as 1700 to 2000 ppm of NH_3 , 200-300 ppm of PO_4, 40-50 ppm of iron, and 20,000 ppm of potassium. These high levels make it more difficult to utilize as a fertilizer. When used the fertilizer cannot be surface applied, it must be injected in selected areas and at limited amounts. This raises the cost of using it as a fertilizer. In our lab we are working on using microalgae to reduce the level of ammonia, phosphate, and iron to allow for the surface application of this waste effluent, thus making it more usable and reducing cost. One problem is the color of the effluent which is a dark brown to black such that we have found that a 1:50 or 1:100 dilution of the effluent with pond water is required to allow sunlight to penetrate the waste in a test lagoon for microalgae growth. Chlorella sp was used in early laboratory experiments and it has showed significant growth on the diluted effluent and the reduction of nutrients by as much as 90%. During the summer of 2016, a 1000 gallon algae tank was set up at CH4 Biogas and used to treat effluent waste from lagoon 3. The first trial run showed significant ammonia and phosphate reduction over 2 weeks. A second run was initiated and once again there was significant reduction in ammonia and phosphate over a 3 week period. Microalgae biomass isolated from the second run was extracted for lipids and was found to have a triglyceride fraction which can be used for biodiesel production. More studies are ongoing this fall on site and in the lab to optimize nutrient reduction in digester effluents.

NOVEL GROWTH BASED LONGEVITY ASSAYS FOR THE DEVELOPMENT OF DRUGS TO TREAT AGING AND AGE RELATED DISEASE.

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Aging is the number one cause of death in the world today. Up to this point the medical community has focused on the treatment of age related diseases while largely ignoring the underlying cause, aging itself. With a large portion of our population entering retirement age it is imperative that new drugs are developed that can treat

the common aging components of most if not all age related diseases. A major constrain of the development of drugs to fight aging is the process is the inherently slow and laborious process of aging research that stems from the length of natural lifespans of even short lived organism. To speed up the process of drug discovery for the treatment of aging and age related disease we have established 3 novel assays for the detection of compounds that alter the lifespan of the model organism *S. cerevisiae*. Unlike traditional lifespan assays that measure replication or survival over time, these new procedures rely on growth as a proxy for lifespan. The growth based metric of these assays allows for high through put screening of both chemical and genetic libraries in short periods of time. We have already used these assay to identify many potential drug candidates as well as a novel longevity pathway. In this presentation I will provide an overview of each of the growth based longevity assays and showcase the results from several high throughput studies.

QUANTIFYING LACCASE ACTIVITY AND DEGRADATION OF 17α-ETHINYLESTRADIOL USING *LENTINULA EDODES* AND *PHANEROCHAETE CHRYSOSPORIUM*.

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Synthetic estrogen (17α-ethinylestradiol / EE2) is not being properly eliminated in current wastewater treatment facilities, but instead is leaking into the environment. Laccase is one of three lignolytic enzymes produced by white-rot fungi being explored for use in bioremediation of EE2 and similar phenolic pollutants. Laccase is a multi-copper oxidase that catalyzes the oxidation of phenolic compounds (including EE2), while reducing molecular oxygen to water. No clear consensus for the best source of the enzyme has been reached. To determine a good source of laccase and the extent to which it participates in EE2 oxidation, we carried out *in-vitro* experiments using two fungal cultures *Letinula edodes (L. edodes)* and *Phanerochaete chrysosporium (P. chrysosporium)* from Oak Mountain State Park. For each culture, the efficiency of EE2 removal was determined using enzyme assays that measure the rate of oxygen depletion. Our results show higher levels of EE2 degradation by *L. edodes* than by *P. chrysosporium* after one week of exposure. The data correlated well with increased laccase activity in *L. edodes*, as measured by two different assays (product formation and oxygen depletion). While the Km for EE2 is high (0.412), it is apparent that shiitake laccase is a safe, available and efficient enzyme for EE2 removal. These results will enable the design of an improved, enzymatic process for the removal of EE2 in wastewater.

DIRTY VIRIONS: ISOLATION AND CHARACTERIZATION OF PHAGES INFECTIVE FOR *BACILLUS THURINGIENSIS*.

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Bacteriophages or phages are viruses that infect and replicate within a host bacterium. It has long been known that bacteria are abundant in nature, but it has only been determined in the last couple of decades that phages are also highly abundant in the environment – there have been estimates of 10 phages to each bacterial cell. With this realization, and the fact that phages are present everywhere their hosts reside, phage research has recently gained increased popularity. However, limited genetic information is available on the innumerable phage in the environment, particularly in soil environments. Given this, our objective was to isolate and further characterize phages from soils collected from different regions. The goal was accomplished as we were able to isolate three phages infective for the host bacterium *Bacillus thuringiensis*; M&M from a sample from Buffalo, NY, Onix from a sample from Dominican Republic and Emrys from a sample from Chicago, IL. Phages were propagated to high titer stocks from single plaque stocks and DNA extracted. Restriction enzyme digests were performed to verify the

phages are different. Digestion by the restriction enzyme, XbaI, clearly illustrates the diversity between each phage and their respective sequences. Future work will be to characterize each phage based on its genome sequence and virion structure, and toward this goal DNA samples are currently undergoing genome sequencing.

RESTORED IN VITRO ASSEMBLY OF TEMPERATURE SENSITIVE E. COLI FTSZ84 BY FTSZ ACCESSORY PROTEINS (ZAPS).

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Bacterial cell division is a highly regulated process that centers around regulating the activity and localization of the FtsZ protein with a wide array of accessory proteins. FtsZ is a prokaryotic tubulin homolog that assembles *in vitro* into protofilaments and bundles in the presence of GTP. Accessory proteins help control FtsZ assembly *in vivo*, and assembled FtsZ recruits other cell division proteins to the division site, permitting membrane constriction and cell wall growth.

A long-utilized temperature sensitive *E. coli* FtsZ mutant, FtsZ84, is known to function at permissive temperatures *in vivo*, but when studied *in vitro* shows no ability to assemble at any temperature. Previous work identified intragenic suppressors that restored division to *ftsZ84* cells at restrictive high temperature. Yet, the purified proteins encoded by these suppressors still demonstrate no ability for *in vitro* assembly.

Our goal is to understand why the FtsZ84 mutant and its suppressors still fail to assemble comparably to wild type FtsZ *in vitro*, despite working adequately *in vivo*. We hypothesize that these mutants function in vivo due to support from accessory proteins that were absent in previously tested *in vitro* conditions. To test this, we have purified *E. coli* wild type FtsZ, FtsZ84, and the FtsZ84 suppressor mutants, as well as *E. coli* accessory proteins ZapC and ZapD. We then assayed FtsZ assembly in the presence and absence of the accessory proteins using 90-degree angle light scattering. Our preliminary results suggest that interaction between the FtsZ variants and accessory proteins ZapC or ZapD permits assembly of the FtsZ mutants *in vitro*.

DEVELOPMENT OF MICROSATELLITE MARKER FOR *Scaevola plumieri*.

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Scaevola plumieri is a Caribbean native species, occupying coastal dune habitats in the Greater and Lesser Antilles. We are interested in documenting the occurrence of populations in the islands of Puerto Rico and exploring the possible impact of an invasive congener, *Scaevola taccada*, on the number, range, and genetic diversity of the native populations. As part of this research project, we have used microsatellites for estimating the levels of genetic diversity within the *S. plumieri*. Microsatellites, also called short tandem repeats (STRs) are short repetitive sequences that are susceptible to rapid mutations. These polymorphic regions contain 1 to 6 nucleotide repeats, and the number of repeat units at a locus may be different, resulting in alleles of numerous lengths. This variation can be used to quantify genetic variation among individuals in a population. Four primer pairs were selected for amplification trials in 82 *S. plumieri* individuals and 14 *S. taccada* individuals. All four of the primer pairs produced a PCR product but only two pairs revealed polymorphic amplification products among the individuals. Using the polymorphic regions, we present a preliminary analysis of the population genetic diversity of *S. plumieri* in Vieques including assessments of gene flow among populations, inbreeding coefficients, and tests for Hardy-Weinberg equilibrium.

SNAPCHAT FOR SCIENCE: COMPARING LEAF RETENTION ON NITROGEN- AND PHOSPHORUS-FERTILIZED BIRCH AND MAPLE TREES.

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The scientific community has potential to exploit the use of hand-held internet devices to improve data collection, for example, capturing images to quantify whether nutrient additions change the timing of leaf fall in autumn. There are plots in the White Mountains of New Hampshire which have received nitrogen, phosphorous, and nitrogen-phosphorous treatments since 2011. On October 24th and 25th, 2015, photos were taken of four randomly selected maple (*Acer rubrum* and *Acer saccharum*) and four birch (*Betula papyrifera* and *Betula alleghaniensis*) trees in each treatment plot from five stands using the social media app, Snapchat. Thirteen impartial observers were asked to rank the photos by the extent of leaf loss. The average ranking for each tree was used to test the effects of treatment on leaf loss using a randomized complete-block analysis of variance. Birch trees had lost more leaves in the nitrogen-treated plots, while they retained more leaves in the control and phosphorus-treated plots. For maple, there was no significant difference in leaf retention across the treatments. Results from this study demonstrate that the popular social media app, Snapchat, is a practical tool for scientific research as it allows photos to be labeled immediately after capturing the image

GENE EXPRESSION AND REGULATION IN FOOD RESTRICTED MICE.

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While it has been widely recognized that food restriction enhances learning and motivation, the molecular mechanisms underlying these adaptations are not well understood. We suspect that these adaptations are a result of changes in gene expression. Our lab previously performed a microarray analysis on male mice that were food restricted (75% of caloric intake) over 5 days. Differential expression of stress-responsive and nutrient-regulated genes was observed across various brain regions, including the medial pre-frontal cortex (mPFC). The purpose of our experiments is to expand our study of the expression of these previously identified genes by looking at changes in expression in the peripheral organs such as kidneys, as well as in female mice to better characterize any gender differences we observe in response to stress. We hypothesized that the molecular mechanisms that underlie mammalian adaptation to stress is conserved across multiple organs, and we show that there is minimal difference in gene expression between the mPFC and the kidneys for male mice. We have seen that there is little overlap in expression of these select genes between male and female mPFC, indicating that there are differences in the molecular mechanisms that lead to adaptation between the two sexes. These studies will better characterize the transcriptional response to mild food restriction and allow us to characterize the response across stress models, tissue types and in males compared to females. Ultimately, we anticipate that these studies will allow us to address the role of these molecular responses in mediating long-term behavioral changes after mild food restriction.

VIRAL MODIFICATION OF HLA GENE COMPLEX OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS.*

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Methicillin resistant *Staphylococcus aureus* (MRSA) is responsible for numerous bacterial infections in hospitals and costs thousands of dollars in healthcare spending. Furthermore, antibiotic resistance is a growing

concern in the global community. The MRSA Alpha Toxin (Hla) is chiefly responsible of the necrosis and hemolysis of the host's cells. In the presence of methicillin, the *hla* gene complex is dramatically up-regulated. Keeping this Hla up regulation in mind, another method to eliminate pathogenic microbes like MRSA without the use of antibiotics would be to use an attenuated viral vector containing genetic material to latch on to the *hla* gene complex and create a self-destruct mechanism. This added viral vector is a promising method to eliminate MRSA infections and similar methods could prove useful against a host of other pathogenic bacteria. Various methods will be used such as PCR to amplify the gene of interest to induce destruction of MRSA and will indicate incorporation of the gene into the MRSA genome. Identification of the presence of Hla will be shown using primarily the western blotting technique. Successful elimination of Hla will also be visualized by blood plates.

VOLATGE CONTROLLED PERPENDICULAR MAGNETIC ANISOTROPY

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The purpose of this project is to analyze the effects of a voltage applied across a particular sample in respect to the Magneto Optical Kerr Effect, or MOKE. The main principle behind the MOKE is that when light, an electro-magnetic wave, is polarized and incident upon a sample within a magnetic field, it may be affected by the interaction with the surface of that sample. If the sample has magnetic properties, the reflected light will obtain a shift in polarization angle which can be measured by a change in intensity as a function of external magnetic field. This allows us to determine the orientation of the sample's magnetic moment. The particular samples we are using contain a layer of gadolinium oxide (Gd2O3) followed by a layer of cobalt (Co). When a voltage is applied to the sample, an electric field will produce a change in oxidation state of the Gd2O3 which will in turn affect the oxidation state of the cobalt. Cobalt has strong, in-plane magnetic properties whereas cobalt oxide does not. This implies that as the voltage is increased across the sample we should be able to detect a change of the magnetic moment within the sample. A practical application could involve integrating this technology into a magnetic tunneling junction (MTJ) device or spin wave device. Memory storage could be obtained without the use of external magnetic fields which may lead to higher areal densities.

COMPUTATIONAL STUDIES OF THE NUDIX HYDROLASE SUPERFAMILY AND NITROPHENYL PHOSPHATASE SUBFAMILY OF THE HAD SUPERFAMILY.

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The Protein Structure Initiative (PSI) was an effort by consortiums to solve as many unique protein structures as possible; the Protein Data Bank contains a number of enzymes whose structures have been solved, but for which no enzymatic activity has been determined. The Enzyme Function Initiative (EFI) is an effort to determine as many unique enzyme functions as possible. There are a number of putative NUDIX Hydrolase and Haloacid Dehydrogenase (HAD) superfamily members whose structures have been solved, but for which no enzymatic activity has been determined. We have catalogued the structurally determined enzymes within the NUDIX Hydrolase superfamily and the nitrophenyl phosphatase subfamily of the HAD superfamily using BLAST, Dali, and SCOP; we are beginning to characterize these enzymes now.

Computational programs, such as ProMOL, aid in annotating uncharacterized enzymes. ProMOL works by aligning the relative spatial arrangement of the catalytic residues of a reference enzyme with query searches. We have used ProMOL to design catalytic motifs for the NUDIX hydrolase superfamily and the nitrophenyl phosphatase subfamily of the HAD superfamily, which we have then used to uncover family members whose structures have been solved. Likewise, we have used the docking program PyRx to predict substrate specificity.

Through this process, we discovered the strengths and limitations of these programs. Bioinformatics tools, including databases and computational programs, are good starting points for determining protein function; however, the only way to definitively determine protein function is through experimentally determining activity.

THE RELATIONSHIP OF MICROBIAL DIVERSITY TO WATER QUALITY AT FOUR LOCATIONS ALONG THE OSWEGO SHORELINE OF LAKE ONTARIO.

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Microbial communities are important indicators of environmental health. Microbes react quickly to change by increased metabolism of specific compounds that results in population growth. Water chemistry characteristics will influence what microbial groups can exist in certain conditions. For example, nutrient-rich eutrophic water is likely to have different microbial communities than nutrient-poor oligotrophic water. Similarly, the presence of pollutants also may impact bacterial abundance. The SUNY Oswego campus is located on the shore of Lake Ontario. Changes in water quality are visually evident along the Lake Ontario shoreline from the SUNY Oswego campus to Oswego Harbor based on proximity to runoff sources and to development. We collected samples from a campus drainage pipe emptying into Lake Ontario, a stream feeding into the lake, a marina in the city of Oswego and water from the lake itself in three consecutive weeks during September and October 2016. Samples from these four areas are being tested using Biolog Ecoplates. These ecoplates provide thirty unique substrates for bacterial growth. A plate reader will be used simultaneously record the absorbance values of each of the thirty substrates. Higher absorbance values will be indicative of higher bacterial growth on a given substrate. Since different bacteria are capable of metabolising different compounds, differences in water quality will likely correlate to differences in bacterial growth on the thirty substrates. Data analysis is ongoing and we hypothesize that the campus drainage pipe, the stream, and marina samples will have distinct bacterial communities compared to the open water of the lake.

MELANIN-CONCENTRATING HORMONE RECEPTOR 1 SIGNALING IS MODIFIED BY CILIARY LOCALIZATION IN FAT CELLS.

Henry Ophardt, Lucas Galbier, Rongkun Shen, and Laurie B. Cook.

Most biological processes that occur within a cell are directed by molecular signals received from the surrounding environment. Integral membrane proteins such as G-protein coupled receptors (GPCRs) are critically important to signal transduction. A GPCR, melanin-concentrating hormone (MCH) receptor 1, is expressed in neurons and pre- and post-adipocytes. MCH exerts its effects on diverse bodily functions including regulation of the sleep/wake cycle, metabolism, and feeding behavior. 3T3-L1 pre- and post-adipocytes express MCH receptor 1 on the plasma membrane. However, on the second day of the ten-day differentiation process, MCH receptor 1 localizes to the primary cilium on the cell surface transiently. We hypothesize that the sequestration of MCH receptor 1 to the primary cilium influences the signaling of this GPCR. To examine this idea, pre-adipocytes and Day 2 differentiating adipocytes were treated with or without 100 nM MCH, and total RNA was extracted. RNASeq was employed to elucidate the transcriptional changes between the differing conditions, and differential gene expression was observed. Expression of selected genes was verified by qPCR. The expression of genes involved in GPCR signaling, cytokines, and inflammatory responses were influenced by MCH receptor 1 localization to the primary cilium. In conclusion, MCH receptor localization to primary cilia causes differential gene expression patterns that may influence adipose tissue development. Future experiments are aimed at further verifying MCH-mediated changes in gene expression through cell-based assays and qPCR.

HIGH ALTITUDE MEASUREMENTS OF MUON FLUX

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Muons are elementary particles similar to electrons. Muons have a charge equal to that of an electron and a mass which is 207 times the mass of an electron. There is limited data describing the flux of muons in the upper atmosphere. We designed/built/tested a dual Geiger Mueller muon detector and measured the muon flux in the upper atmosphere. The muon detector was integrated into an Orion sounding rocket which was launched in June 2016 at the NASA Wallops Flight Facility in Virginia. We collected data during flight. Our data showed similar trends as were seen in the data collected during 2015 HWS RockSat-C flight. There was a noticeable increase in muon count as the rocket ascended. In order to interpret data collected during flight we tested the dual Geiger Muller detector in lab exploring how various parameters (temperature and tilt angle of detector) influence the muon flux. Also we try to correlate the muon flux with atmospheric parameters (solar activity, atmospheric pressure, humidity, etc) In Spring 2017 we plan to suspend our dual Geiger Mueller muon detector on a weather balloon and take measurements of muon flux at different altitudes, for longer periods of time.

CYSTEINE-CAPPED QUANTUM DOTS SYNTHESIS AND FLUORESCENCE

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CdSe quantum dots have potential applications in biological imaging, solar cells and light emitting diodes. An inspection into the synthesis of quantum dots that absorb and fluoresce within precise wavelengths is important for these applications. The quantum dots were prepared by adding an aqueous solution of sodium sulfate with selenium powder at the appropriate temperature to an aqueous solution of cadmium sulfate and cysteine, again at the appropriate temperature. Using a UV-Vis spectrophotometer absorbance of diluted samples of quantum dots were taken every 5 minutes. The observed absorbance peaks of quantum dots grown for 30 minutes at 20, 50, 80 and 100°C are 393, 414, 414, and 417 nm respectively. A shoulder towards the red end of the spectrum is observed in quantum dots grown at 100°C indicating larger quantum dots. Shifting absorbance to the red end of the spectrum is desirable for metal enhanced fluorescence of quantum dots using gold nanoparticles, which exhibit an absorption band at about 524 nm. A mixture of these quantum dots and gold nanoparticles show significant increase in fluorescence when compared to fluorescence of just quantum dots. Further research direction includes covalently attaching the quantum dots and gold nanoparticles at different lengths to determine the effects of proximity on enhanced fluorescence.

A DERIVATIZATION METHOD FOR THE SYNTHESIS OF PROSPECTIVE AGENTS AGAINST AMERICAN TRYPANOSOMIASIS (CHAGAS DISEASE).

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Chagas disease (American trypanosomiasis)—a neglected tropical disease that affects millions of people mainly in rural areas in Latin America—is caused by the parasitic protozoan *Trypanosoma cruzi*. Trypanothione reductase (TryR), a NADPH-dependent flavoenzyme, essential in the antioxidant metabolism of the parasite, has been recognized in the past decades as a target for the development of novel drugs. TryR performs a function equivalent to that of glutathione reductase (*h*GR) in humans, but because of the structural differences in the substrate-binding sites of the two enzymes, selective inhibition of TryR has emerged as a promising choice for rational design of agents for treatment of *Trypanosoma cruzi* infections.

Consistent with the fact that at the binding site of TryR is large, hydrophobic, and has an overall negative charge, recently reported computational studies have revealed that natural steroidal alkaloids such as tomatidine,

solanidine, and solasodine can serve as scaffolds for the design of selective inhibitors. Our *in silico* studies suggest that derivative structures containing a 2-(methylamino)ethylamino pendant chain at the steroidal 3-position could inhibit TryR with enhanced selectivity and potency. Currently, we are developing an efficient synthetic route to alter the naturally occurring compounds and install this structural feature without affecting other sensitive functionalities present in steroidal alkaloids. Our progress toward the synthesis of these derivatives will be presented.

OCEAN ACIDIFICATION INDIRECTLY AFFECTS MICROZOOPLANKTON GRAZERS VIA INDUCED ALTERATIONS TO PREY STATE

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Increases in anthropogenic CO_2 outputs have resulted in an increase in CO_2 levels in the ocean, currently around 400 ppmv and projected to increase to between 800-1200 ppmv by the year 2100. This process, termed ocean acidification (OA), increases dissolved inorganic carbon (DIC) and decreases pH and has been shown to have significant effects on marine ecosystems. Specifically, high DIC content can increase the carbon ratio in primary producers. Primary consumers ingest these high C food sources and as a result may experience metabolic shifts. We investigated the effects of OA on the copepod *Calanus pacificus* by maintaining them under OA conditions and feeding them the dinoflagellate *Prorocentrum micans* maintained under the same OA conditions of 400 ppmv, 800 ppmv, and 1200 ppmv at 12°C. We measured respiration and ingestion rates in *C. pacificus* and cell size in *P. micans*. Copepods were acclimated to treatments for 10d. There was an effect of treatment on ingestion rate, with copepods in elevated pCO_2 treatments consuming fewer cells. Ingestion rate results may have been due to increased stress or inhibition of chemotaxis. No effect of treatment was observed on respiration or cell size, possibly due to a large carbon drawdown observed in *P. micans* cultures, decreasing culture pCO_2.

COMPARISON OF SUGARS AND AMINO ACIDS IN NECTAR FROM *SCAEVOLA TACCADA* AND *SCAEVOLA PLUMIERI.*

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Scaevola plumieri (Goodeniaceae), a species of coastal shrub, is native to the Caribbean Islands, Florida, and South Africa. *Scaevola taccada*, a congener native to the Indopacific, was introduced to the Caribbean in the 1970s as a dune stabilizer and was first recorded in Vieques, Puerto Rico in 2002. *S. taccada* has been reported to encroach upon and displace S. *plumieri* and other native species in the Bahamas and the Cayman Islands. *S. plumieri* is now listed as critically endangered in many Caribbean locations, like the Cayman Islands, and considered threatened in other locations. Since these species compete for similar resources in coastal habitats on the Puerto Rican islands, we are interested in exploring the possible impact the invasive *S. taccada* has on the pollination biology of the native species.

Scaevola attracts many pollinators including wasps, ants, birds and bees. Bees are believed to be *Scaevola*'s primary pollinators. Both *Scaevola plumieri* and *Scaevola taccada* produce nectar from nectaries located within small, white flowers. We are interested in noting the differences in these plants' nectar constituents and what effect this difference has on the pollinator preferences of both species. This plant-pollinator relationship plays a vital role in the overall reproductive success of both plants. Thus, we present preliminary data on the nectar constituents, specifically sugar concentrations and amino acid content, of these two species from Vieques Island, Puerto Rico.

Although there have been no previous studies on *Scaevola*, both sugar and amino acids are found within the majority of plant nectars. Pollinators use sugars as their primary energy source—a high concentration of sugar is thought to correlate with better pollinator fitness. Although the primary functions of amino acids in nectar is unknown, their common and diverse presence suggests varying functions, such as an important nitrogen source, microbial defense, or contributing to the nectars taste. Thus, the study of both these constituents should provide insight into possibly essential differences between the two species.

Nectar samples were collected on Vieques in 2015 and 2016 and from Ithaca College's greenhouse using micropipettes or glass microcapillary tubes. The nectar volume was measured from individual flowers, then pooled for sucrose and amino acid analysis. The sucrose percentage was analyzed using a digital refractometer and the amino acids, specifically proline, arginine, and threonine, were analyzed using reverse-phase high performance

liquid chromatography. We will present a comparison of nectar volume, sucrose concentration and amino acid content for both species. Using this data, we will comparatively analyze and assess the impact these differences or similarities have on the success and competition between *Scaevola taccada* and *Scaevola plumieri.*

HPLC-ESI-MS ANALYSIS OF SUGARS IN BIOFUEL-RELATED PROTEINS.

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Second generation biofuels using plant tissues have the potential to be a powerful fuel source. Using enzymes to break down the hemicellulose and cellulose of plant tissue into simple sugars could be an efficient way to generate these biofuels. The sugars released (xylose and glucose) from plant matter (such as wood) can be measured by High Performance Liquid Chromatography-Electrospray Ionization-Mass Spectrometry (HPLC-ESI-MS). The main goal of this research is to develop a robust HPLC-ESI-MS method to validate that enzymatic degradation of wood causes the release of sugars that will be used in the production of biofuels. In previous work, it was anticipated that the presence of protein in the supernatants of the wood digestions might cause matrix effects. Therefore, matrix-matched calibration curves were prepared using sugar standards with high and low cellulase protein. However, the low end of the calibration curve was limited. Thus, all of the proteins used (cellulase, xylanase and laccase) were prepared in distilled water and analyzed without added sugar. It was concluded that there were sugars present in all of the protein stocks, likely added as a stabilizer. The present goal is to develop reliable calibration curves of sugars in the presence of the cellulase, xylanase, and laccase proteins that are used in the treated wood samples. The calibration curves were generated using sugar concentrations between 0.1mg/mL and 1.0mg/mL with and without the mediator molecule (ABTS). The matrix matching for the curves will be further discussed. Once the influence of the proteins on the detection limits and sensitivity are understood, accurate measurements in wood supernatants should be possible.

BAND GAP ENERGY CALCULATIONS FOR THIN FILM ORGANIC SOLAR CELLS

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Solar cells are an efficient way to harness the sun's light energy and utilize it for energy purposes. We analyze here different organic thin films with potential use for solar cells. We calculate the molecular orbitals and we obtain the band gap. We notice that the added zwitterions diminish the band gap of the film, making better solar cells. The two solar cells are obtain by depositing on the substrate of choice two different polymers, polyaniline and poly(3-hexylthiophene-2,5-diyl), and the zwitterion: p-benzoquinone monoamine. These orbital energies were found using HyperChem and then graphically displayed using Mathematica. The I-V curves show that these films have great potential as efficient solar cells.

ANALYZING THE CANINE GENOME USING RFLP'S TO LOCATE CANCER BIOMARKERS.

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Annually, millions of canines are diagnosed with various types of cancer within the United States of America. Cancer is fundamentally a genetic disease due to many distinct mutations in genes primarily involved in mitosis. In prior studies, the canine genome has been analyzed and used to pinpoint mutations which lead to specific types of cancer. However, the process of genotyping canines and identifying biomarkers requires sophisticated and expensive molecular biology facilities. Therefore, our project involves using existing genomic information and polymerase chain reaction (PCR) to allow genotyping at a much more economical scale. This will be valuable for veterinary oncologists in rural areas. We are using bioinformatics tools, as well as writing our own software, to identify Restriction Fragment Length Polymorphism (RFLP's) in the canine genome in order to create a PCR based approach to genotyping canines. Our eventual goal is to perform multiplex PCR within a single test tube. Using the current canine single nucleotide polymorphism (SNP) array, we focused on those alleles to create our novel assay.

These ongoing studies will allow us to create a more cost effective way to diagnose canines that are predisposed to cancer.

TOWARD THE CHARACTERIZATION OF AEROBACTIN SYNTHETASE IUCC FROM A HYPERVIRULENT PATHOTYPE OF *KLEBSIELLA PNEUMONIAE*.

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Iron is an essential mineral for nearly all lifeforms. Despite being a relatively abundant element within earth's crust, it is often poorly bioavailable in aerobic, aqueous environments. For bacteria looking to establish an infection within a human host, usable iron is often even scarcer. Certain pathogens, such as *Klebsiella pneumoniae* (KP), produce iron chelating molecules known as siderophores to scavenge extracellular iron from the host.

The importance of siderophore systems as virulence factors has recently been demonstrated in a relatively newly recognized pathotype of KP known as hypervirulent *Klebsiella pneumoniae* (hvKP). In contrast to the opportunistic pathogenicity of classical strains of KP, hvKP has been documented to cause life-threatening infections in healthy, ambulatory individuals. Recent findings by the Russo and Gulick research groups at UB have attributed the enhanced virulence of hvKP to the overproduction of the siderophore aerobactin. To better understand this key virulence factor, we aim to study the fundamental enzymology of aerobactin biosynthesis. In the current study, we worked toward the structural characterization of the aerobactin synthetase IucC, an enzyme required to biosynthesize aerobactin. In order to determine the atomic structure of IucC by X-ray diffraction, high-quality protein crystals must be grown. Previous attempts to crystallize wild-type IucC yielded poorly-diffracting crystals. Herein, we report the expression and purification of a number of IucC surface mutants that were used in crystal growth screening trials. Several crystallization conditions were identified and will be further optimized toward growing high-quality crystals of IucC for structural elucidation by X-ray diffraction.

ELEMENTS OF THE FINGER LAKES: BUILDING A BRIDGE BETWEEN THE COMMUNITY AND CHEMISTRY

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This project was my attempt to answer the question: Can I find every element on the periodic table of elements in the local area? More importantly it was also an attempt to bring people, local businesses and scientists together and connect our worlds.

The periodic table can be hard to relate to. It is a grid packed with letters and numbers with very little explanation. The table assumes you know what you are looking at. It is, however in its simplest sense a list of the essence of every material that we can touch, see or interact with in our day-to-day lives. These elements are everywhere, from a simple piece of aluminum foil to complex mixtures of carbon, hydrogen, oxygen, nitrogen, sulfur, phosphorous and more working in unison to create you and I.

So I recruited photographer and Keuka College Biology graduate Phil Longyear and we set out to find as many as we could. We want to show people where these elements exist, how they drive local businesses, how you can use them to create art and just how many of them people likely have in their house. We took photographs of elements and compounds where we could find them, used them to tell a story about the element or location and put them up all over main street in Penn Yan, NY for everyone to see.

THE GREEN SYNTHESIS OF P-BROMO SAL IMINE AND THE STUDY OF ITS PHOTOCHROMISM USING KINETIC.

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Due to Sal Imine's interesting electronic properties, a reversible change of color occurs upon its exposure to a light source with a particular wavelength, known as Sal imine's photochromic property. The study focused on para bromosalicylidene imine (pBrSal), which is a crystalline yellow compound that changes color to red when exposed to 400 nm Ultra-Violet (UV) light. The goal is to conduct an integrated laboratory consisting of green synthesis of pBrSal, as well as a determination of the reaction order and activation energy of the photochromic process using simple instrument set-ups and technique.The experimental melting point of the product is 111.3 ° C. The experimental results supports that the reaction order of pBrSal photochromic process is a 1st order reaction. The activation energy of this reaction is 19.05 ±1.1 kJ/mol. Considering that simple glassware, a rapid work-up technique, and general instruments were used, we were able to perform this laboratory. This study could be done in an advanced integrated laboratory course.

RELATIVE BODY SIZE SCALING IN DROSOPHILA MELANOGASTER.

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In any organism, body-size is a fundamental trait, affecting the outcomes of both sexual and natural selection. Moreover, body size is a trait likely controlled by hundreds, if not thousands, of independently assorting gene loci. While body size is often studied in an evolutionary context, it is largely unknown, however, whether all components of body size change at the same rate (i.e. scale), when under uniform selection pressure. In *Drosophila melanogaster* main body components include: head, thorax, abdomen, wings, and legs. Currently in the lab, a long term (>10 years) selection experiment has been running, where lines of flies have been concordantly selected to be smaller, larger, or disruptively selected (i.e. large males and small females). After 280 generations of selection, the body size of flies in these experimental treatments all changed in predicted directions, relative to control flies. This study utilized these lines to address the question of body size scaling. By comparing the wing length/area and thorax lengths of both males and females from each of eight selected populations (2 large, 2 small, 2 disruptive, & 2 control) we were able to determine whether or not these body size components scaled as they changed in response to their selection regime. Generally, there is a strong linear relationship between thorax and wing size, indicating changes in size is largely scalar. Additionally, there is are strong differences in both thorax size and wing size between sexes. However, these relationships were substantially weakened in the disruptively selected lines, indicating a reduction in body size dimorphism. These results suggest that scalar body changes are not always consistent under different selection pressures or between sexes.

CHARACTERIZATION OF PHOTOMULTIPLIERS FOR USE IN A FAST NEUTRON SPECTROMETER.

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We are developing a fast neutron spectrometer based on lithium-loaded liquid scintillator. The design of our prototype detector requires 2.5 liters of scintillator fluid, which necessitates the use of eight photomultipliers that have good light collection, linearity, and low noise. They also need to be gain-matched. For this project, we acquired a batch of 40 surplus Phillips XP-2262 12-stage photomultipliers from a previous nuclear physics experiment and eight ET Enterprises 9266KB48 10-stage photomultipliers. The goal of my research was to characterize these photomultipliers using measured energy spectra from gamma ray sources.

EXAMINING THE COLLECTIVE BEHAVIOR OF CELLS IN A 3D CO-CULTURE.

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During tissue morphogenesis, cells often live and migrate in a heterogeneous environment consisting of many types of cells. Studying how differences in the cells' biophysical properties affect the cellular organization of the developing tissue is vital to understanding the development of complex biological systems, such as embryos and tumors. Motivated by this, we examine the physical properties of a binary system of breast cancer and healthy breast epithelial cells in order to emulate laboratory co-culture models of tumorigenesis. To this end, we construct and study a mathematical model that incorporates equilibrium and non-equilibrium characteristics of the cellular populations. Individual cell mechanics, cell-cell interactions, cell division, and active Langevin dynamics of self-propelled systems are considered. The significance of cellular properties are explored by investigating how differences between the elasticity, adhesivity, activity, and division rates of the two cell types govern collective properties of the binary cell population, such as self-assembly and dynamic migration. The predictions of the model are compared to experimental results from our collaborating labs.

SURFACE ANALYSIS OF MoS_2 AND $MoSe_2$.

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In this research project, growth of two-dimensional (2D) materials MoS_2, $MoSe_2$ and graphene was studied. Together, these materials are attracting attention due to their unique electrical and optical properties. Semiconductor materials with a finite band gap, such as monolayer MoS_2 can be used in devices which need to switch on and off (such as transistors, photodetectors, solar cells, etc.). Graphene is a 2D semiconductor material without a bandgap and has potential applications in electrical, mechanical, and other technology-related fields due to its unique properties. Since MoS_2 and graphene both have different properties, incorporating MoS2 in graphene-based devices or combining them could result in devices that make use of each material's properties.

We performed atomic force microscopy (AFM) on MoS_2 and $MoSe_2$ grown on top of graphene on SiC, and bare Si. Samples show some interesting features such as grains aligned with steps in the underlying SiC substrate, grains formed by coalescence of many small particles or uniform coverage films, depending on their growth conditions. We also performed low energy electron microscopy (LEEM) on the MoS_2 on graphene on SiC sample. The diffraction patterns from graphene and MoS_2 are aligned, which indicates that MoS_2 grew rotationally aligned to the orientation of the graphene. Also, the lattice constant of MoS_2 was found to be 26.1% larger than the graphene, compared to an accepted value of 26.9%.

In order to measure the crystal structure of the remaining samples using low energy electron diffraction (LEED), we built an ultra-high vacuum (UHV) chamber. The UHV chamber allows us to measure the sample crystallography without interference from ambient gas molecules.

SYNTHESIS AND CHARACTERIZATION OF LITHIUM CARBOXYLATES FOR USE IN LIQUID ORGANIC SCINTILLATOR.

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Aqueous solutions of enriched lithium salts emulsified within liquid organic scintillators have been used for fast neutron spectrometry. However, these emulsions can undergo phase instabilities at loading fractions above a few percent of lithium by mass, which gives rise to poor optical performance. We propose an alternative loading method that directly dissolves long-chain lithium carboxylates into liquid organic scintillator which could potentially avoid the deleterious effects of emulsification. We discuss the synthesis of lithium dodecanoate, lithium octanoate,

and lithium hexanoate. We further characterize the loading of a these carboxylates within the liquid scintillator cocktail Ultima Gold AB and a comparable scintillator formulation lacking surfactants in terms of solubility and light transmittance properties.

PATTERNS OF WATER CHEMISTRY IN RELATION TO GEOLOGIC CONTEXT IN GRAND TETON NATIONAL PARK, WY.

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Grand Teton National Park (GRTE) has a rich geologic history as part of the Greater Yellowstone Geoecosystem formed by the Yellowstone hotspot. The landscape of GRTE is dominated by the Grand Teton mountain range and the Snake River plain. Glaciation during the last ice age has also played a central role in the formation of landscape features throughout GRTE. In addition, other areas in GRTE or in the adjoining John D. Rockefeller Memorial Parkway (JDRMP) are influenced by hydrothermal formations. Our objective was to sample a variety of lakes, ponds, wetlands, and rivers throughout GRTE to examine how water chemistry patterns may differ based on geological setting. Eventually this data will be correlated to patterns of aquatic plant distribution that are being documented as part of a large study of the aquatic plant diversity of the Greater Yellowstone Geoecosystem. Water samples were collected from four separate regions of GRTE; The Snake River plain (SR), the glacial moraine (GM), John D Rockefeller Memorial Parkway (JDRMP), and Geothermal areas (GT). Water chemistry from each region was analyzed, which included pH, conductivity, alkalinity, and presence of trace metals. In general there were no differences in pH found between the four regions; pH ranged from 7.1-7.9. Conductivity was highly variable across the four regions. Lakes and wetlands located on GM sites had low conductivity, with an average value of 72 uS/cm. GT areas had high conductivity at 478 uS/cm. Similarly, moraine sites had the lowest alkalinity (28 Mg/L) and GT areas had high alkalinity (135 Mg/L). Analysis of trace metals are ongoing and will further contribute to our understanding of water chemistry in this geoecosystem.

INFLUENCE OF THE WATER LAYERS ADSORBED ONTO STAINLESS STEEL 316 ON TRITIUM MIGRATION.

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Tritium adsorption on the surfaces of stainless steel represents a key step in the overall migration of the isotope through the substrate metal. Understanding the nature of tritium adsorption, and the subsequent transport from the surface into the substrate metal, is vital for the development of surfaces that hinder the migration of tritium through stainless steel.

In the present study, we draw on previous works in the literature to show the structure in the first 20 nm of the surface, and how this structure relates to tritium adsorption. Previous studies have shown that the near-surface region of stainless steel consists of three regions: a region of mixed chromium(III) and iron(III) oxides bound to the substrate metal, one or two layers of hydroxyls bound to the metal oxides, and, finally, a multilayer structure of water molecules, which are adsorbed onto the hydroxyls.[1–3] We show that this multilayer water structure contains a sufficient number of potential binding locations for tritium to indicate the observed[4] high concentrations of tritium on stainless steel surfaces. Additionally, a chemical method has been adopted to remove adsorbed water layers[5] to determine the quantity of adsorbed tritium on stainless-steel surfaces. The results show ~17% of the total tritium inventory resides on the surface after storing the sample for more than 80 days.

The present study also outlines a quantitative tritium migration model (QTRIMM), which allows for the calculation of the tritium concentrations throughout a stainless-steel specimen. QTRIMM is a novel approach to calculating tritium migration, since it includes a condition to relate the high surface concentrations of tritium to the

concentrations within the substrate metal. This model successfully describes the data collected from a plasma-induced, ion-sputtering experiment.

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THE EFFECTS OF BACKGROUND OXYGEN ON GRAPHENE GROWTH

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Graphene was first isolated by two professors at The University of Manchester, Andre Geim and Kostya Novoselov, in 2004 using Scotch tape and graphite. Since then, there have been many attempts to grow graphene films on silicon carbide substrates. Graphene is an appealing material to produce, not only for its high tensile strength but also for its electrical properties. One widely used technique for growing graphene is sublimation of Si from SiC. However, production of high crystal quality, low defect density graphene films can be difficult in conventional tube-furnace style growth reactors due to trace impurities present during the growth. In this work, we are studying the effects of trace amounts of oxygen gas during growth. Additional factors that may affect the growth of graphene on silicon carbide is the crystal face on which the graphene is grown (carbon or silicon) and the polymorph of silicon carbide, commonly 4H and 6H. The effects of these conditions must all be understood for production of high quality graphene films for technological applications.

SMALL COLONY VARIANT SWITCHING PHENOMENON IN *STAPHYLOCOCCI*.

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Staphylococcus aureus, a gram-positive bacterium that can be isolated from individuals suffering from respiratory complications like cystic fibrosis (CF), possesses certain traits that confer antibiotic resistance and thus difficulty in treatment. One of these characteristics is that *S. aureus* can exist in multiple phenotypic subpopulations induced by environmental conditions or genetic changes. One of these morphological subgroups is a slow-growing, non-virulent, non-pathogenic form aptly named “small-colony variants” for its conspicuously smaller size compared to a wild-type, “normal-colony variant.” An interesting finding is the same strain of *S. aureus* can revert between the two colony sizes however it is unclear what factors or cues induce the transition between normal and small colony variants. A long term, multi-generational quantitative analysis of the switching phenomenon has not been performed. By counting the number of small and normal colonies produced in each generation and noting the frequency of reversion, one could describe this observed switching phenomenon with appropriate statistical models that would be useful in predicting the future behavior of each strain. Such a model would have great clinical significance in the treatment of not just *S. aureus* infections, but other microbial pathogens with similar characteristics.

IMPACTS OF PRECIPITATION AND STREAM DISCHARGE ON PHOSPHATE LOADING TO AND CONCENTRATIONS IN OWASCO LAKE.

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Yearly precipitation totals in the Finger Lakes region fluctuate over time and space. Precipitation in the region over the past five years (2011-2015) has varied from 31.78 to 45.83 inches per year, on average, between three adjacent weather stations; Syracuse, Ithaca, and Penn Yan, the closest meteorological stations to Owasco Lake in central New York. Precipitation has a direct correlation to both total phosphate loading and discharge at Dutch

Hollow Brook in the Owasco Lake watershed (Halfman et al., 2016). This study investigates how annual changes in precipitation influence the concentration of total phosphate in Owasco Lake.

Total phosphate concentrations and stream discharge were measured daily (or more frequently) between the months of April and October during 2011-2015 and provided mean daily total phosphate loads from the Dutch Hollow watershed. Total phosphate concentrations were also measured from surface and bottom water samples collected at two mid-lake sites each month during May through October in Owasco Lake.

Even though 2011 had the largest precipitation/discharge ($1.44x10^5$ m^3/day) and phosphate loading (4.38 kg/day), total phosphate in Owasco Lake did not peak until 2012, a year later, when yearly precipitation was significantly lower than all other years. Subsequent years also revealed an apparent, one year, delayed response between total phosphate loads to and total phosphate concentrations in the lake. For example, Owasco Lake experienced a spike in total phosphate loading from Dutch Hollow Brook in 2013. Yet, Owasco Lake total phosphate concentrations were significantly lower in 2013, and more importantly, lake concentrations in 2013 reflected the lower total phosphate load from Dutch Hollow Brook in 2012. In 2014, total phosphate concentrations in Owasco Lake were larger, most likely due to the spike in total phosphate loading from 2013.

The reasons for the delay are unclear. Perhaps the particulate form of the phosphate delivered by the watershed required a summer stratified season for bacterial decomposition and release of soluble reactive phosphate to the hypolimnion of the lake. Subsequently, the soluble reactive form was mixed with the entire lake and made available to algal productivity after the following spring overturn.

CRACK FORMATION AND PROPAGATION IN A SEMIFLEXIBLE NETWORK EMBEDDED IN A GEL.

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The mechanical response of a disordered semiflexible fiber network embedded in a gel and subject to shear and tensile strains is studied, motivated by the fracture resistance of articular cartilage. Applied strains range from small deformations and deformations large enough to induce fracture. A combination of rigidity percolation theory and computational energy minimization is used to quantitatively characterize the system, and calculate the effective elastic moduli as well as network-wide heat maps of local strains and energy. Notches are then introduced in the network to study crack formation and propagation under shear and extension strains for various applied loads. Results show that while for small strains the network responds almost identically under shear and compression, for large strains the network stiffens under shear and softens under compression. It is also demonstrated that for a given notch size and fiber density, there exists a critical loading above which the network will undergo catastrophic failure by fracture. Our results, therefore, suggest the existence of a Griffith-like criterion for crack propagation in biopolymer networks. Ongoing work consists of implementing a secondary flexible network weakly interconnected to the primary semiflexible network, and calculating and contrasting the crack propagation in the resulting double network with the above single network. This will help connect microscale structure and composition of polymer double networks, such as in articular cartilage and similar tissues, to their fracture mechanics, thus leading to quantitative predictions.

CRYOPRESERVATION OF *CHLAMYDOMONAS REINHARDTII* USING N,N-DIMETHYLACETAMIDE.

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Cryopreservation is the process by which living tissue and cells are genetically preserved by storing an organism at very low temperatures. This two-step technique is effective for storing genetic data for a variety of prokaryotic cyanobacteria, marine diatoms, and eukaryotic micro algae. *Chlamydomonas reinhardtii* is a single-celled green algae that is approximately 10 micrometers in length, that swims with two flagella. It is a model organism used to study photosynthesis, cell division, phototaxis, and flagellar assembly. The current method for

cryopreservation requires storage in the vapor phase of liquid nitrogen (LN_2) and a cyroprotective agent (CPA) such as dimethyl sulfoxide (Me_2SO) or methanol (MeOH) for freezing. The use of these CPA makes this protocol expensive and results in low yields. There has been success in finding alternative CPAs such as N, N-dimethylformamide (DMF), hydroxyacetone (HA), N-methylformamide (NF), and N,N-dimethylacetamide (DMA), however, these CPAs have only been tested when the organism was stored in liquid nitrogen. We propose to test the effectiveness of DMA as a CPA when the organism is stored long-term at -80˚C. The proposed method is much more cost efficient and would allow for a more accessible technique in storing *Chlamydomonas reinhardtii* and potentially other organisms for an indefinite period of time.

EFFICIENT QUANTIFICATION OF RXRG ISOFORMS

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Many genes are transcribed as multiple variants known as isoforms. Isoforms are transcripts from the same locus with either a different transcription start site or alternative splicing. Isoforms might be characterized by different functions and/or stability. Different isoforms of the same gene can vary in length from a few bases to several kilobases. In some cases, there is no region of the transcript specific to only one isoform, making quantification problematic. We compared the isoforms' sequences using bioinformatic tools freely available online5. We utilized a one-step real-time RT-PCR protocol, using primers specific to one or more isoforms, which included a T7 promoter and terminator sequences. After confirming amplicon identity by DNA sequencing, we built RNA standard curves. Analysis of the data shows acceptable specificity and efficiency for RXRG3 primers as well as primers picking up all three isoforms. We are currently in the process of assessing primers for RXRG1 and RXRG3.

DEVELOPMENT OF A LOW-COST PLATFORM FOR 3D BIOPRINTING APPLICATIONS.

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Three-dimensional (3D) printing using a variety of metals and polymers is a driving force in revolutionizing engineering, art, education and medicine. Accordingly, new adaptations of conventional 3D printing approaches allow for the use of biocompatible materials to build functional tissues and organs. This process, which maintains cell function and viability, is called 3D bioprinting. This nascent technology is transforming the study of regenerative medicine and organ transplantation. An entry barrier for those looking to take advantage of this approach is that commercially manufactured 3D bioprinters can be costly and out of reach for the average undergraduate researcher. Here, we describe the development of a cost-effective approach to bioprinting. The approach involves the use of a low-cost and slightly modified consumer-grade 3D printer and a syringe pump. The aim of the project is to allow the user to build customized scaffolds for cells using materials such as agarose, alginate and collagen. By incorporating simple cooling and heating systems our platform is able to build structures made of agarose gel. Ongoing refinement of the bioprinting platform is currently directed towards the building of 3-dimensional constructs using "bioink", a cell-laden hydrogel. Bioprinting platforms similar to the one described here may offer students at primarily undergraduate institutions the opportunity to work with state of the art approaches in cell biology and bioengineering.

STUDIES TOWARD THE SYNTHESIS OF *ENT*-ARTEMISININ, A POTENTIAL ANTI-MALARIAL COMPOUND.

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Artemisinin is a natural product isolated from the plant *Artemisia annua* that is currently the fastest-acting treatment available against *Plasmodium falciparum*—the protozoan parasite that causes the deadliest form of malaria. The low bioavailability of this compound and its short half-life, however, make the cost of artemisinin therapies very high. Anti-malarial *combination* therapies involving artemisinin are employed to avoid the development of resistance to the drug by the parasite, as recommended by the World Health Organization.

Artemisinin's structure contains a unique peroxide bridge that is believed to be responsible for the drug's mechanism of action. Recent reports show that artemisinin binds covalently to a large number of proteins after being "activated" most likely by heme, which builds up in the parasite cells given its 'blood-eating' nature. We gather that the exceptional biological activity of this compound may originate in the fine-tuned chemical reactivity of its peroxide bridge, rather than the topology of the structure itself. Consequently, we hypothesize that its enantiomer (*ent*-artemisinin)—a yet unreported compound, to the best of our knowledge—could exhibit comparable anti-malarial properties. Seeking an affordable synthetic route, our current goal is to develop a reaction sequence to produce *ent*-artemisinin from zingiberene, a compound found in ginger oil. If successful, we believe that the low cost and high availability of ginger oil would allow for the large-scale production of *ent*-artemisinin.

EFFECTS OF PRENATAL MUSIC STIMULATION ON EARLY EMBRYONIC DEVELOPMENT OF *Gallus gallus.*

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It is believed that listening to classical music such as Beethoven or Mozart will promote fetal brain development, although there has been no solid scientific evidence. Earlier studies on chick embryos and rat pups have shown increased size of brain cells when exposed to classical music such as Mozart, thus focused on the effect of music on growth phase during late embryonic development past the patterning and organogenesis. Here we investigate the effect of different genre music (classical/rock) on early embryonic development in chicken embryos as pregnant women are constantly exposed to music even during early pregnancy. Incubation of fertilized chicken eggs were carried out at 37°C and a relative humidity of 80. We tested two different types and decibel levels of classical and rock music on embryo development. To provide music impulse an iPod with a playlist connected to speaker was set inside the incubator and the music played for every 15 min with a 45 min of recorded silence in between. Control eggs were incubated at the same condition but received no sound impulse. Following incubation the embryos were fixed at two different stages, day 9 and 16, to analyze the phenotypes causes by sound exposure. Also the morphological parameter such as height, weight, forelimb/hind limb length, beak size, and eye diameter were measured. We found that high decibel music (HDM) irrespective of the genre increased mortality rate in chicken embryos. Further HDM resulted in severe morphological defects due to delayed development. We presently investigate the effect of different levels of music on early embryo development.

EXPLORATORY DRONE RESEARCH ON WATER QUALITY OF THE FINGER LAKES.

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Water quality issues, in particular blue green algae, has negatively affected the Finger Lakes region. Monitoring algal blooms using photos and dockside water samples taken by local residents is very helpful to identify where blooms occur but it does not capture the full aerial extent of the bloom. Here we explore the use of drones to

monitor the aerial extent of algal blooms and nearshore macrophytes. This past summer's effort has been a learning experience.

We used two drones: DJI's Matrice 100 with a gimbaled Zenmuse Z3 camera and DJI's less expensive Phantom 3 Advanced with a Sony EXMOR gimbaled camera. Both drones captured 12 megapixel digital photos that were spatially georeferenced in ArcGIS to 2015 satellite digital orthoimagery (NYS Clearinghouse data). Each vertical image spanned an area of ~200 by 300 meters. The cameras separately record the red, blue, and green bands of the color spectrum. We focused on the green band, the color of algae and other biota, and the blue band, the color of scattered light from a clear lake, to determine if they could differentiate the presence and concentration of algae.

Qualitatively, the ability to detect algae was tested by comparing aerial photographs of the eight easternmost Finger Lakes. These lakes span the oligotrophic to eutrophic spectrum of algal productivity (oligotrophic Skaneateles, Keuka & Canandaigua, to mesotrophic Seneca, Cayuga & Owasco, to eutrophic Honeoye). The photos revealed differences in the intensity of green light that paralleled the trophic status of these lakes. It also proved useful to map the distribution and aerial extent of encrusting algae and other macrophytes.

Quantifying the amount of algae in the water was more difficult. Multiple numerical methods were tested focusing on the green band of light, e.g., contouring the green band, calculating the average green intensity on each scene, etc., and each method faced its own problems. Our preliminary analysis of the Green/Blue ratio indicated a proportional relationship to chlorophyll-a abundance and inversely proportional relationship to the log of the Secchi disk depth. We focused on open water photographs of the aforementioned Finger Lakes, calculating the mean G/B ratio from up to 5 different regions in each photo with the least amount of glare. The result have been promising and will continue to be researched to assess the impact of, e.g., glare, camera tilt angle, cloudiness, and extent of wind driven waves on the G/B ratios.

VISUALIZATION OF ACTIVATED NEUROMASTS IN ZEBRAFISH.

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Background: The neuromast is an external mechanosensory structure found in zebrafish that is homologous with human cochlear hair cells. Anoctamin 2 (Ano2) is a calcium-activated chloride channel that is hypothesized to be involved in neuromast function, possibly acting in signal amplification. The fluorescent dye FM1-43 enters and marks activated neuromast primarily via the mechanotransduction (MET) channel, allowing for the individual components of the neuromast to be visualized via fluorescence microscopy.

Aims: We implemented an assay to determine the ideal FM1-43 load times that would detect activated neuromasts, produce the highest quality images of its individual components and thus allow us to test the hypothesis that Ano2 is required for neuromast function.

Methods: FM1-43 enters activated neuromasts via MET channels that open during flow detection. Loading efficacy is influenced by load time, FM1-43 concentration, stimulation and when we image the preparation. Several dye concentrations and loading times were optimized.

Results: FM1-43 load times of <5 minutes were inadequate in complete uptake of dye and the neuromast components were not completely distinguishable. FM1-43 load times of >5 minutes took up excessive amounts of dye resulting in an increased brightness in fluorescence making the individual components of the neuromast difficult to distinguish. This load time also caused labelling that is nonspecific to neuromasts. FM1-43 load time of 5 minutes clearly identified the neuromast, its individual components and produced the highest quality images, therefore it was the optimal load time. Now that we have established the neuromast activation assay, the role of Ano2 in neuromast activation can be evaluated using Ano2 inhibitors.

Conclusion: Loading the neuromast for 5 minutes using 1µM FM1-43 produced the highest quality images of the individual components of the neuromast.

EFFECT OF A LOW MAGNESIUM DIET ON THE MOUSE GUT MICROBIAL FLORA.

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Mammalian epithelial surfaces, especially the large intestine, are colonized by large numbers of microorganisms (more than 99% being bacteria) collectively known as the microbiota. In the large intestine, bacteria have various functions, including the production of essential nutrients and co-metabolization of food. In addition, they prevent bacterial overgrowth and infection through the formation of an ecological barrier for colonization and by inducing the host's production of IgA and anti-microbial proteins. Finally, intestinal bacteria influence central physiological functions such as the development of lymphatic tissue, the induction of mucosal tolerance, angiogenesis, and fat storage. Alterations of the gut microbiota composition have been associated with complex diseases, including inflammatory bowel disease (IBD), diabetes mellitus, and asthma. Although in some particular cases complex diseases have been linked with the presence of specific bacteria, evidences have shown that bacterial communities and not specific bacteria determine susceptibility towards complex diseases.

Magnesium is the third more abundant cation in the human body. Magnesium deficiency is known to induce a pro-inflammatory state that contributes to the development of endothelial dysfunction, hypertension and type 2 diabetes. As magnesium is also an important cofactor for a multitude of enzymatic reactions, we hypothesized that magnesium deficiency is likely to affect the gut microbiota, which in turn, may affect several host biological functions. Mice were either fed a normal diet or a diet low in magnesium for 6 days. The number of bacteria and variety of the gut microbiota were then analyzed by resuspending the fecal matter in sterile saline, and growing the bacteria on non-selective as well as media selective for Gram-negative bacteria. Bacteria were identified by standard techniques used in microbiology (Gram stain, biochemical tests). In addition, the identity and diversity of the gut microbiota from mice fed a normal diet versus a diet low in magnesium is being compared by DNA sequencing.

FACTORS AFFECTING SUPER-SPREADING OF EPIDEMICS: A STUDY OF INFECTION IN *PEROMYSCUS.*

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The idea that all individuals do not carry and transmit infections in the same way is a fundamental aspect of epidemiology. It is estimated that only about 20% of infected individuals in a given population carry the majority of the total pathogen burden and therefore are responsible for a large proportion of disease transmission. Such individuals are often referred to as super-spreaders. The factors that determine whether or not an individual is a super-spreader are largely unknown, however they can be evaluated using either an individual-based or event-based approach. The goal of this study was to identify what factors might determine if an individual becomes a super-spreader. This was done using a wild population of *Peromyscus* mice infected with coccidia, an intestinal microparasite. We used a mark-recapture approach to evaluate host characteristics and parasite burden. We identified potential super-spreaders using home range overlap between individuals as an indicator of parasite transmission and correlated super-spreader status with host characteristics, disease tolerance and population density. No super-spreaders were identified within the 2016 (low density) population, but were found in the 2011 (high density) population. Only population density showed a relationship with super-spreading, with proportion of super-spreaders decreasing as density increased ($p=0.01801$, $chisq=5.594$, $df=1$). Because all of the individual-level host factors examined in this study showed no relationship with super-spreading individuals, we concluded that the dynamics of super-spreading favor the event-based model over the individual-based. Determining how super-spreading fits into these models can change approaches to disease control and potentially improve its success and efficiency.

MULTIPLE VARIABLES INFLUENCE DISTRIBUTION OF STAPHYLOCOCCI ISOLATED FROM HEALTHY STUDENT VOLUNTEERS.

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Background: Undergraduate students preparing for careers in healthcare or healthcare-associated fields frequently complete clinical rotations as part of their education while remaining members of the general college community. This positions them as possible source of both community-acquired and healthcare-acquired MRSA.

Methods: From Fall 2012 to Fall 2013, 153 healthy individuals enrolled in Biology or Allied Health majors consented to the sampling and characterization of bacterial isolates from the anterior nasal nares or skin. Staphylococci were selected for by sequential culture in mStaph broth and mannitol salt agar. Each isolate was assayed for mannitol fermentation and β-hemolysis to provide presumptive species identification and the results were interpreted by the student volunteer prior to strain submission. Each isolate in the collection was subjected to repeated hemolysis testing and assayed for coagulase production.

Results: From a total pool of 153 subjects, 27 putative *S. aureus* (beta-hemolytic, mannitol fermentation positive; 18.0%), 107 putative *S. epidermidis* (gamma-hemolytic, mannitol fermentation negative; 70.0%), and 17 putative *S. saprophyticus* (gamma-hemolytic, mannitol fermentation positive; 11.0%) isolates were recovered. These isolates were then analyzed for patterns in isolation frequency. Recovery of putative *S. aureus* isolates was consistent in Fall and Spring, but considerably lower during the Summer semester. Women represented 69% of the total volunteer pool, limiting the power of sex-based comparisons. Isolation of putative *S. aureus* isolates was most common from the nasal passages than from the skin during the Spring and Summer semesters, but no anatomical location-dependent bias was seen during the Fall semesters.

Conclusion: Among Staphylococci isolated from healthy student volunteers, there exists both a seasonal (semester) and anatomical bias for the isolation of beta-hemolytic Staphylococci. These data are anticipated to be useful for analyzing Staphylococcal colonization patterns of the larger community and in comparison to collections of Staphylococci comprised of clinical specimens.

THERMODYNAMICS AND INTERACTIONS OF THE GAMMA B CRYSTALLIN PROTEIN.

Katharine Umphred-Wilson, Aaron Fadden, Dr. Lea Vacca Michel, Dr. George M. Thurston and Dr. Jeffrey Mills

Gamma B Crystallin proteins are soluble proteins found in the eye lens which help maintain its transparency; however, over time their structure may mutate due to UV radiation and other environmental stresses causing the proteins to aggregate and develop into cataracts. Using light scattering, nuclear magnetic resonance (NMR) spectroscopy and other protein modeling techniques, our team is attempting to understand the intermolecular interactions of gamma B crystallin proteins that are responsible for this aggregation. We expect to learn the structural and chemical properties that dictate how the proteins interact, as well as the effect of the thermodynamic properties in the fluid mixtures of the eye lens on the crystallin interactions. We expressed the gamma B crystallins in *Escherichia coli* and isolated them using size exclusion and ion exchange chromatography. The protein was analyzed using various types of NMR experiments, including T1/T2 experiments and HSQC titrations. Our preliminary results suggest that colder temperatures increase aggregation levels and higher concentrations of our protein increase the number of attractive intermolecular interactions.

INFLUENCE OF PHLOEM STEROLS ON THE GROWTH AND DEVELOPMENT OF PHLOEM FEEDING INSECTS.

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Insects lack the ability to synthesize sterols *de novo* and therefore must acquire sterols from their diet to meet basic developmental needs. Cholesterol is the chief sterol found in most insects, but in plant vegetative tissue cholesterol (usable sterol) makes up only a small fraction of the sterol profile. All herbivorous insects must convert dietary phytosterols into useable forms (chiefly cholesterol) to support their growth and development. Not all phytosterols are readily converted to useable forms, and some structures are deleterious when ingested above a certain level. Carnivorous insects, such as lady beetles, consume herbivorous insects such as pea aphids, *Acyrthosiphon pisum*, and when those aphids lack the necessary sterols for development and reproduction, the lady beetles can be adversely affected. We have noted that lady beetles will actively supplement their diets with fava bean leaves, corn pollen or germ oils in order to restore their fitness. Considering that lady beetles prey mainly on aphids, which feed on plants, we examined the contents of the phloem obtained from several lines of transgenic plants. We also examined the steroid profile of aphids reared on specific transgenic plants. We discuss the imp act of individual plant sterols on lady beetle development by determining how sterol chemical structure affects lady beetle reproduction.

THE SEARCH FOR A STANDARD CANDLE EFFECT IN THE SLOAN DIGITAL SKY SURVERY QUASAR DATABASE.

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Data Release 7 of the Sloan Digital Sky Survey includes over 100,000 quasar spectra. This project seeks to determine the presence of a standard candle effect among quasars in that catalog.

The SDSS was queried for known quasar objects over the redshift range of [0.46, 0.82], selecting for green-filter magnitudes ≥ 19. Known erroneous data points were masked and the individual spectra were shifted to rest frame using Hewett Wild corrected redshifts. Flux densities were binned into wavelength bins of width 1 Å. Spectra were organized into redshift selected bins of $\Delta z = 0.01$ and their AB magnitudes determined. Composite spectra were generated for each redshift bin. A scaling and χ^2 matching system was used to compare bin composites to their respective spectra locate well-defined spectra. The matching range was over both the central portion of the continuum and bright emission lines (MgII and Hβ). Poorly matched spectra were visually inspected and low quality spectra were removed. Each well-defined spectrum was matched against the remaining members of successive redshift bins. The best fits for each bin were indexed and AB magnitude v. Redshift plots were generated. An expected magnitude evolution of the initial well-defined spectrum was generated using the Flat Cosmological Development Model with standard values $H_0 = 70$ km s^{-1} Mpc^{-1} and $\Omega_M=0.3$ to which the matching spectra were compared.

While an effect was not directly detected, indications of a standard candle effect were found. Further investigation is currently being undertaken, including corrective techniques, generalized spectral evolution with redshift, and application of cataloged featured filters such as virial black hole masses.

ISOLATION AND CHARACTERIZATION OF MUTANT STRAINS OF *ACETOBACTER* DSW_54 WITH ALTERED HYDROGEN PEROXIDE SENSITIVITY PHENOTYPES

Alec Walter and Peter D. Newell

The gut microbiota is a major area of study due to its association with nutrition and certain diseases. The fruit fly can be used as a model organism to study the effects that gut microbes may have on a host organism, including interactions with the host immune system. One major component of the *Drosophila* immune system is its ability to produce reactive oxygen species (ROS). The gut microbiota of this fly consists of many different species

of bacteria that some of which are known to impact nutrition and development. An important question about gut microbes is how increased sensitivity to hydrogen peroxide can possibly impact their ability to colonize the fly gut. We initiated a study on the *Drosophila* gut bacterium *Acetobacter* DsW_54 to learn more about the genetic basis for ROS resistance. A mutant library of these bacteria was created using transposon mutagenesis and then screened for hydrogen peroxide sensitivity. This screen was done using a control with no H_2O_2 and a treatment with a H_2O_2 concentration that slowed but did not block growth of the wild type. Mutants that did not grow on the treated plates were then retested for H_2O_2 sensitivity. Of the 3000 mutants screened, 30 were initially identified that show increased hydrogen peroxide sensitivity. During repeated testing, 3 were confirmed to show increased H_2O_2 sensitivity. From this screen, we successfully characterized and isolated 3 mutants that show H_2O_2 sensitivity. Future tests with these mutants will show how much more sensitive the mutants are to hydrogen peroxide than the wild type. We can also perform tests within the fly. The mutants can be tested to investigate if increased sensitivity to H_2O_2 shows a decreased ability to colonize the fly gut compared to the wild type.

ARE COEFFICIENTS OF CONSERVATISM ALWAYS ACCURATE IN PREDICTING SPECIES PERSISTENCE? COMPARING COC VALUES WITH COMMUNITY COMPOSITION DATA FROM THE WESTERN AND FINGER LAKES PORTION OF NEW YORK TO DETERMINE ANTHROPOGENIC DISTURBANCE THRESHOLDS FOR THE STATE-RARE VINE AMERICAN BITTERSWEET (*CELASTRUS SCANDENS*).

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Vascular flora have been assigned coefficients of conservatism (CoC) by regional botanists in an attempt to develop disturbance thresholds for individual species and thus provide implications for management and species conservation. While this method has an inherent level of bias, and can vary substantially from state to state, it is an important foundation in conservation for the Northeast's diverse floral assemblages. In the summer of 2016, we assessed community composition of four sites in the Western and Finger Lakes portion of New York State that support populations of the state-rare vine American bittersweet (*Celastrus scandens*) in an attempt to see if the species' CoC value of 6 was an appropriate rating (meaning its ecological range is narrow and its community is stable). Study plots ranged in size from 100 m^2 to 150 m^2, in which a modification of the Forest Inventory Analysis (FIA) method was performed for the community. This method evaluated community composition ranging in scales from 1-m^2 quadrats, 2.82-m diameter shrub-plots and 100-150-m^2 tree plots. Assigning all associated species with its given CoC value, we then calculated the average score per site. Preliminary results indicate that a CoC value of 6 may underestimate the vine's disturbance threshold, considering one site exhibited a mean CoC value of 1.85, and no site exceeded a rating of 4.04. These results suggest that anthropogenic disturbance may not be the only factor contributing to species rarity within New York State, and that other environmental and biological factors must be considered.

GENOMIC ANALYSIS OF *CAS* GENES ISOLATED FROM *STAPHYLOCOCCI* IN WHITE TAIL DEER POPULATIONS

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Bacterial and archaeal domains of life use horizontal gene transfer as one of their most evolutionary advantages. The DNA that is obtained through this transfer can be very advantageous but also very harmful. But, recently discovered is that bacteria have a mechanism of defense against these harmful gene transfers. There are two mechanisms and they are called clustered regularly interspersed short palindromic repeat loci, or CRISPR, and the associated *cas* genes. This studies goal is to characterized the CRISPR-*cas* elements in a collection of *Staphylococci* that was isolated from local white tail deer in the Western New York area. Our research has used PCR with custom primers, to identify *cas* genes in some of the strains. Since our strains have not been in contact with other clinical strains, their resistance patterns and their mechanisms of defense can provide an understanding to the evolution of

this mechanism. The CRISPR-*cas* loci can provide a mechanism to prevent the development of antibiotic resistance through the horizontal gene transfer pathways, which could provide a possible pathway for bacterial sensitization, and the prevention of the transmission of antibiotic resistance genes in bacterial populations.

COMPARISON OF COCKSACKIEVIRUS B4 SURFACE PROTEINS TO BETA-ISLET CELLS SURFACE PROTEINS IN *HOMO SAPIENS*.

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Type I diabetes is an ever present disease, especially affecting younger persons in the population, producing the term juvenile diabetes. Recent research has shown that type I diabetes may have an autoimmune factor stemming from a viral infection. This infection is now thought to be caused by a strain of the coxsackievirus, with the most likely factor being from the B4 strain. The common thought is that a protein on the surface of the virus is very similar to one of the epitopes on the beta-islet cells and once an immune response takes place, the antibodies attack both the virus and the insulin producing cells, ceasing insulin production resulting in type I diabetes. The protein structure of the coxsackievirus B4 will be compared to other phylogenetically related strains to determine their degree of similarity. Then using a bioinformatics approach, relevant epitopes of the beta-islet cells will be compared to the coxsackievirus proteins to see if the epitopes causing the immune response can be found.

THE EFFECTS OF GASTROINTESTINAL MOTILITY ON THE ENTERIC MICROBIOTA IN ZEBRAFISH.

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This research is a collaborative effort between the laboratories of Dr. Michel Pelletier and Dr. Adam Rich. It utilizes the Zebrafish as a model organism for human gastrointestinal (GI) motility. This model organism is advantages due to their embryos being transparent allowing for direct observation of organ development. The kit genes within the Zebrafish are orthologues of the kit gene present within humans. This gene codes for the Kit receptor tyrosine kinase, which contributes to the development and maintenance of Interstitial cells of Cajal (ICC), which are required for coordinated motility patterns within the GI tract. Kit mutations result in loss of function and the loss of ICC and coordinated motility patterns in both humans and mice. The results of this research could potentially allow for development of new treatments for GI motility disorders in humans.

This research involves a comparison of microbiota present within two strains of Zebrafish, a wild type and sparse mutant strain. The wild type strain is heterozygous for kit genes a and b whereas the sparse mutant lacks a copy of kita. Previous research has shown that the kit genes are involved in GI motility and that the sparse mutant exhibits a disruption in normal motility patterns. The purpose of this research is to identify and compare the microbiota in each strain and decipher whether it may contribute either negatively or positively to the pattern of motility. We hypothesize that the sparse mutant may contain different microbiota then that of the wildtype due to the uncoordinated pattern of motility.

Isolation of the intestinal contents of six fish samples, three of which were wildtype and three sparse mutants was performed. A solution of each of the contents were plated and grown on Brain-Heart Infusion solid medium (BHI), as well as medium selective for enteric bacteria (EMB), and observed for the quantity and characteristics of colonies. Identification of each unique colony was then conducted through numerous biochemical tests and amplification and sequencing of 16s rDNA from isolated genomic DNA.

Through initial observation of colony growth, it was found that there was a significantly greater amount of growth seen on the sparse plates in comparison to the wild type, which could ultimately support our hypothesis. After further completion of biochemical testing, five of the twelve microbiota species sampled were identified. These species are as follows, *Sphyngomonas paucimobilis, Vibrio ichthyoenteri, Providencia sp.,* and two of which

are *Providencia stuartii*. All of which are confirmed to be associated with fish. For those species not yet identified, further testing, including sequencing of the 16S rDNA are being carried out.

CHLORIDE LEVELS IN LAKES AND WETLANDS OF NORTHERN ALLEGANY COUNTY, N.Y.

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In midwinter and early spring 2016, we followed up on a 2014 study of pollution from road salt on various water bodies in northern Allegany County with its low population density (48/square mile), using a Seal AQ2 multichannel analyzer. Data collected in 2016 showed low levels of chloride ranging from exhibited a wide range of concentrations, ranging from a low of 1.5 mg/L from Moss Lake (a Nature Conservancy protected bog) to a high of 14.1 for Keeney Swamp. Concentrations of chloride measured in 2016 were generally lower than those found in winter 2014 and may reflect a decrease in road salt application during the milder winter of 2016.

INDIVIDUAL DIFFERENCES IN THE PLAY BEHAVIOR OF BELUGA WHALES (*DELPHINAPTERUS LEUCAS*).

Mary J. Woodruff and Michael Noonan

Play behavior is a ubiquitous mammalian trait, particularly for large brain species. The goal of the present study was to characterize the play behavior of beluga whales (*Delphinapterus leucas*), and examine the degree to which such behaviors vary from individual to individual. Observations were made in two separate, two-million-liter pools, at Marineland of Canada (Niagara Falls, Ontario). Using an ad hoc, all-occurrences observational paradigm, every instance of play behavior was recorded by twenty-four whales, half of which were juveniles. The playful behaviors observed included instances of solitary play (e.g., corkscrew swim and inverted pec aerial), object play (e.g., mouthing pebble/leaf, and bubbling), social play (e.g., chase, mouthing, and keep-away), and human directed play (e.g., head shake, spit-at, and pec wave). Regarding sex and age, play was most common in juvenile females and least common in adult males. In addition, even within age-sex categories, marked individual differences were recorded in both style and frequency of play. Both the high frequency and the large variety of play behaviors observed place beluga whales among the most playful of animal species. This is compatible with their large brain and highly social natures. The reliable individual differences that were observed are suggestive of consistent personality types, a topic which will be explored in future studies.

SPENT COFFEE GROUNDS AS A VIABLE FEEDSTOCK FOR BIOFUELS PRODUCTION AND ITS POTENTIAL COMMERCIAL USES.

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The potential for using spent coffee grounds (SCG) as a feedstock for biofuels and other commercial uses is being investigated. The model being tested is for processing 25Kg SCG/day. Oil from SCG was extracted using hexane, analyzed by TLC and acid value was determined. Hexane was then recovered using IKA RV8 rotary evaporator and the recovered hexane was used for additional extractions. The extracted oil was used for the production of biodiesel and can potentially be used as heating oil or lubricant oil. Oil extracted grounds, were then treated with 2% H_2SO_4 to isolate the carbohydrates. The extracted sugars contained 80% reducing sugars, most of which was glucose, mannose and galactose, with 20% non-reducing sugars. The extracted carbohydrates were used as media for yeast fermentation to produce ethanol using Kluyveromyces and Sacchromyces. Leftover coffee grounds were tested as fertilizer and compared to Miracle Growth. SCG were also tested for potential antibacterial

properties. Preliminary results show that spent coffee grounds may be a viable feedstock for production of biodiesel and other commercial uses.

GALAXY CLASSIFICATION SCHEMES FOCUSING ON EARLY UNIVERSE GALAXIES

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Galaxy mergers in the early universe may provide explanations for why galaxies take on their well known current morphologies. The majority of existing galaxy classification methods perform poorly when attempting to detect mergers in early universe galaxies. Current best practice is to use extensive visual classification to classify galaxies based on morphology, color, proximity to other galaxies, and other similar parameters. While visual classification is the most robust system currently available, visual methods of galaxy classifications are impractical for extremely large data sets due to the required human effort. This poster outlines the results of and ongoing efforts to test existing parametric and non-parametric classification statistics as they apply to young galaxies. Previous works have indicated that multiple non-parametric statistics are required to properly classify individual galaxies. Future efforts will work toward determining the most effective combinations of parameters to determine classifications and to potentially develop a new classification scheme specifically tailored to these early-universe galaxies.

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