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*Celebrating 32 Years of Excellence in
Undergraduate Research*



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The abstracts included in this publication describe research presented at the Minnesota Academy of Science Annual Meeting / Winchell Undergraduate Research Symposium hosted by Century College on April 27, 2019, in White Bear Lake, Minnesota.

BIOCHEMISTRY

ANTIBIOTIC GENE IDENTIFICATION IN *Pseudomonas*

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Antibiotic resistance, the phenomenon in which bacteria gain the ability to survive antibiotics, has become a pervasive problem for human health. It is estimated that by 2050 the death toll due to antibiotic resistance will be 10 million people. As the efficacy of current antibiotics is reduced due to resistance, scientists are searching to find new antibiotics. The purpose of our work was to identify one such antibiotic from an antibiotic producing *Pseudomonas* sample gathered from soil. In order to identify the antibiotic gene, we introduced a transposon capable of interrupting the gene. A selective media was used to screen for colonies which had lost their antibiotic production. Four transposon-containing colonies were chosen and grown. Arbitrary PCR was used to amplify the region where the transposon had inserted and were sent for Sanger Sequencing. A BLASTn search was used to identify the sequence of the gene that was disrupted and could potentially be responsible for antibiotic production.

ATTENUATION OF G-WIRE SELF-ASSEMBLY USING G-QUADRUPLEX LIGANDS

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Guanine-rich DNA and RNA sequences, including guanine-rich oligonucleotides (GROs), readily adopt quadruple helical structures due to the association of guanine bases forming G-quartets. Recent discoveries indicate G-quadruplex structures are significantly involved with information metabolism. G-DNA structures occur in a variety of locations in chromosomes, such as the promoter regions, telomeric regions, and replication origin sequences. Certain GROs resembling G-DNA forming repeat motifs can self-assemble into supramolecular configurations called G-wires. G-wires readily self-assemble in the presence of specific monovalent and divalent cations to produce stable polydisperse linear structures. This work investigates a strategy for limiting the polydispersity of simple G-wire forming GROs as proof of concept for controlling self-assembly. The GROs used in this work were 5'-dGGGGG-3' (GRO7), 5'-dTGGGGG-3' (GRO8a), and 5'-dGGGGGT-3' (GRO8b). The sequence composition of these GROs consequently varied in their G-wire formation. The parallel G-DNA specific fluorescent dye, N-methylmesoporphyrin (NMM) at varying concentrations to attenuate G-wire self-assembly. Analysis of NMM attenuated G-wire assemblies by polyacrylamide gel electrophoresis (PAGE) shows a shortening of G-wire size. The extent of attenuation is dependent on the NMM:GRO ratio and the type of cation used for self-assembly. At saturating concentrations of NMM, the presence of a presumed G-DNA supramolecular repeat monomer and dimer were observed. Based on PAGE attenuation experiments, we hypothesize a 5'-Head to 3'-Tail (HTT) stacking association of supramolecular monomer G-DNAs that NMM competes for 3'-tail binding. The putative dimer may be due to HTH (5'-5') stacking association. We plan to investigate the HTH and HTT stacking hypothesis using mass spectroscopy.

CHARACTERIZATION OF THE TRANSMEMBRANE REGION OF A NOVEL CEFTAZIDIME RESISTANCE GENE

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Antibiotic resistance is a significant threat to infectious disease control. β -lactamases represent some of the most commonly found enzymes that confer antibiotic resistance. β -lactamases are enzymes that confer resistance to β -lactam antibiotics such as ceftazidime. Studying how these enzymes confer resistance to β -lactam antibiotics is a key factor in fighting the battle against resistance. A novel antibiotic resistance gene, *cft2*, from a commercial apple orchard encodes an unusual β -lactamase that provides resistance to the cephalosporin antibiotic ceftazidime. *Cft2* encodes a 607 amino acid residue class A β -lactamase that is nearly 400 residues longer than typical β -lactamases. The goal of this project is to characterize the novel aspects of the *cft2* enzyme. This project focuses on one specific feature, a putative transmembrane helix found in *cft2*. HMMTOP software was used for analysis which identified a transmembrane helix in the *Cft2* enzyme at amino acid residues 290-307. The *Cft2* enzyme was shown to be in the insoluble fraction of lysate from western blot analysis, suggesting this enzyme is embedded in the membrane. Here, we conducted site-directed mutagenesis to remove the suspected transmembrane region, amino acid residues 290-307. Once expressed in *Escherichia coli* BL21 the mutated gene was assayed on media supplemented with ceftazidime (2.5 $\mu\text{g/mL}$) against the non-mutated gene. The deletion mutant lacking the transmembrane helix failed to grow on media supplemented with ceftazidime, whereas the wild type grew. Resistance profile coupled with the bioinformatics analysis suggest the transmembrane domain is essential for conferring resistance to ceftazidime.

THE EFFECTS OF WINTER STRESS ON THE PHOTOSYNTHETIC RECOVERY OF *Pinus strobus* AND *Picea glauca*

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When put under conditions of extreme stress, such as the cold of winter, plants tend to lose some of their photosynthetic efficiency; conifers are no exception. When spring arrives, conifers recover from the winter stress and regain their photosynthetic efficiency. Research has shown that white spruce is able to recover better and faster than white pine. This experiment aimed to confirm those results, as well as explore reasoning as to why this could be. To that end, the xanthophyll cycle and phosphorylation of the proteins LHC, D1, D2, and CP43 were explored. Needles were recovered early winter's morning in the dark and allowed to recover for a total of 174 hours in the lab. The results confirmed the increased recovery of white spruce compared to white pine. Additionally, the data implied an inverse relationship between photosynthetic efficiency and xanthophyll cycle activity as well as an inverse relationship between photosynthetic efficiency and phosphorylation of LHC and D2 proteins. The decreased activity and phosphorylation could explain the increased recovery of white spruce, but specifics as of why require more research.

INVESTIGATING PLANT BASED MEDIA FORMULATIONS WITH YEAST EXTRACT SUPPLEMENTATION FOR PROPAGATION OF *Bacillus* SPECIES

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The propagation of microbial cell cultures is dramatically influenced by the media in which it is grown. Bacteria require media rich in both carbon and nitrogen in order to produce optimal growth. While animal-based peptone

sources have been traditionally used as a nitrogen source, more recently there have been movements to plant-based peptones to support bacterial propagation. One notable bacterium is the genus *Bacillus* with various applications in agricultural, pharmaceutical and clinical practices. For instance, *Bacilli* cultures have been utilized for their antimicrobial peptides in the production of biopesticides and topical antibiotics. Due to the wide range of applications *Bacillus* cultures possess, there is an increasing need to propagate cultures as efficiently and sustainably as possible. Herein we report the growth characteristics of *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus megaterium*, and *Bacillus pumilus* in plant-based media formulations with yeast extract supplementation. For our investigation five different peptone sources were utilized including pea peptone, soy peptones, pea flour and soy flour each with an increasing supplementation of yeast extract. Bacterial growth was analyzed using a series of viable plate counts (VPC) and spectroscopically measured growth curves. From these analyses, it was determined that pea flour medias did not provide desirable growth conditions, while the remaining media types showed variable growth densities dependent on the *Bacillus* strain used. Furthermore, for some species, media formulations with the largest percent supplementation of YE produced poorer growth, indicating a balance of C, N, and other nutrients provided by YE must be optimized.

LIPIDS IN *Tetrahymena thermophila*, A UNICELLULAR CILIATE

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Our experiments compare lipid accumulation in starved and fed *Tetrahymena thermophila*. Nile red staining detected an increase in lipid droplets, the subcellular compartment for neutral lipid storage, when *T. thermophila* cultures were removed from a nutrient-rich environment. To explore this further, we have developed techniques for extraction and identification of *T. thermophila* lipid species. Moreover, we have successfully isolated lipid droplets from *T. thermophila* and visualized associated proteins by SDS-PAGE and silver staining. We aim to use these techniques to identify the pathways that regulate lipid homeostasis in *T. thermophila*.

NATURAL PRODUCT EXTRACTION AND CHARACTERIZATION OF ANTIMICROBIALS FROM *Pseudomonas*

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Bacterial natural products have been utilized for both medicinal and industrial applications. Recently, interest in these compounds for their antimicrobial properties has become a focus to help deter the spread of antibiotic-resistant bacterial strains. In partnership with the Tiny Earth Network, we have identified environmental *Pseudomonas* bacterial strains that produce secondary metabolites with antimicrobial properties. Natural products from two different environmental *Pseudomonas* strains were extracted using a variety of solvents and assayed for their antibiotic activity. Crude extracts were separated by thin layer chromatography and a bioassay protocol for locating the active inhibitory molecule on the TLC plate was used. In addition to biochemical characterization, we performed random gene knockout mutagenesis in search of the genes responsible for the production of these compounds.

REDUCED FUNCTION OF *Citrullus lanatus* (WATERMELON) GLYOXYSOMAL MALATE DEHYDROGENASE DUE TO A MUTATION AT AMINO ACID 269

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Malate Dehydrogenase (MDH) is a widely-found enzyme responsible for catalyzing the oxidation of malate to oxaloacetate with an NAD⁺ cofactor. The wild-type structure of *Citrullus lanatus* (watermelon) glyoxysome MDH was examined using Pymol software. The amino acid 269 forms part of the dimer interface and it was mutated from Leucine to Alanine. This change in the enzyme's primary structure can cause the bond between the two monomers to be weakened or possibly broken. According to Bjork et al., disrupting the subunit interactions of tetrameric MDH from thermophilic bacterium *Chloroflexus aurantiacus* dramatically decreases MDH activity (2003). Therefore, we hypothesized that disruption of the dimer interface will cause the mutated enzyme's turnover number to decrease. We purified both wild type MDH and L269A mutant MDH enzymes, then performed kinetic assays and calculated specific activity and turnover number for each. The mutation reduced the enzyme activity by 96%. Alanine and Leucine are both non-polar amino acids, whose R groups are similar size. When the amino acid 269 was replaced with Alanine, the interface between the two monomers might have been disrupted, but not completely broken. With looser contact between two subunits of the dimers, MDH enzyme's activity may have been reduced.

STUDYING *Staphylococcus aureus*, A GOLDEN (BEARS) OPPORTUNITY

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A team of 65 students has studied the nasal carriage rate of *Staphylococcus aureus* on the Concordia University, St. Paul campus during the past three years. Samples have been obtained from the anterior nares of 1079 on-campus and 330 Minnesota-State-Fair-going consenting adults. Mannitol salt agar (MSA), colistin-nalidixic acid blood agar (CNA), DNase, coagulase, catalase, and Gram stain tests have indicated the presence of *S. aureus* in 250 of the 1021 tested samples, a carriage rate of 24.5%. All *S. aureus* isolates undergo further characterization for methicillin resistance (MRSA) via Kirby-Bauer assay, and production of the following proteins involved in pathogenesis: alpha toxin and superantigens TSST-1, SEA, SEB, and SEC. The prevalence of these genes is also correlated to currently understood carriage and infection risk factors to determine if genetic distributions differ between carrier and clinical isolate populations.

USE OF N-METHYL MESOPORPHYRIN AS A PARALLEL G-DNA STRUCTURE PROBE FOR G-WIRE ASSEMBLY INTERMEDIATES

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Guanine Rich Oligonucleotides (GRO) are strands of DNA sequences that have a high propensity to form quadruple helical G-quartet structures known as G-DNA. Four guanine bases associate in a planar structure via using Hoogsten H-bonding which can then stack upon each other to form a G-quadruplex DNA. The stacking of G-quartets and stability of the G-DNA is greatly enhanced by coordinating cations (K⁺, Na⁺, Sr²⁺, and NH₄⁺) as well as have impact on the formation of antiparallel or parallel strands. Certain GROs can self-assemble in presence of cations to create supramolecular structures named G-wires. In the work presented here, G-wires were produced using the GRO, 5'-dGGGGTTGGGG-3', with and without various functional modifications. Self-

assembly of GRO16 G-wires in the presence of N-methyl mesoporphyrin (NMM) was also investigated and resulted in attenuation of G-wire length distribution. Using polyacrylamide Gel Electrophoresis (PAGE) with differential staining by NMM and the non-specific DNA dye SYBR Green we observe parallel G-DNA and anti-parallel structure intermediates that vary with the type of modifications to GRO16 that varied with the cations used for self-assembly. Furthermore, a comparison of attenuated and non-attenuated self-assemblies of G-wire suggest certain intermediates are favored by the presence of NMM. The result of this work helps us to understand the topologies as well as the self-assembly process of G-wires for use as a potential molecular scaffold in bio/nanomaterial applications.

CELLULAR AND MOLECULAR BIOLOGY

ANALYSIS OF CYCLIN E IN FIBROLAMELLAR HEPATOCELLULAR CARCINOMA

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Fibrolamellar Hepatocellular Carcinoma (FL-HCC) is a rare hepatic malignancy that has an early age onset and is distinct from hepatocellular carcinoma because it is not associated with chronic liver diseases, such as cirrhosis or hepatitis infection. Our collaborator at the Mayo Clinic conducted a proteomic screening and found the proline biosynthetic pathway to be dysregulated in FL-HCC patient samples. Proline plays a major role in the formation of the distinctive collagen banding that is present in FL-HCC patients. The goal of this project is to understand how dysregulation of proline can lead to tumorigenesis in FL-HCC. Previous study has shown addition of proline to primary hepatocyte culture can upregulate full-length cyclin E (FL-E) via the mTOR pathway. In addition, FL-E can be partially cleaved by an enzyme called serine protease neutrophil elastase (NE) to create a low molecular weight cyclin E (LMW-E) that has been linked to tumorigenesis in breast cancer. We hypothesize that the dysregulation of proline in FL-HCC leads to an increase of FL-E expression, which is degraded by NE creating LMW-E and in turn causes oncogenic effect in FL-HCC. Our preliminary results show presence of LMW-E in FL-HCC samples with a molecular weight of ~43 kDa. Moreover, tumor liver samples were found to have less amount of FL-E when compared to normal liver sample. We hypothesize this may be due to the conversion of FL-E into LMW-E in the tumor.

BISPHENOL-A LEADS TO OVEREXPRESSION OF ESTROGEN RECEPTORS AND DIMINISHES PROTECTIVE CHEMOKINE RESPONSES IN A ZEBRAFISH MODEL

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Bisphenol-A (BPA), widely used in thermal receipts and food containers, binds to both estrogen receptor (ER) a and b, disrupting estrogen activity and challenging the immune system of humans and wildlife. Zebrafish exposed to 100 ng/ml BPA immediately following fertilization (day 0) show a two to fourfold reduction in gene expression of CXCL8, the chemokine that recruits neutrophils to the site of infection on days 3 through 6 post fertilization (dpf). To determine if reduced chemokine expression has a functional outcome, we studied MPO::GFP zebrafish expressing GFP under a neutrophil-specific myeloperoxidase promoter, which allows tracking of neutrophil movement to a tail cut injury. Compared to controls, 4 dpf BPA-exposed zebrafish show significantly reduced neutrophil recruitment to the site of injury ($p=0.004$). Control zebrafish receiving a tail cut injury at 4 dpf show a fourfold upregulation in CXCL8 expression one-hour post-injury, whereas the BPA-exposed embryos display a blunted CXCL8 response. Estradiol reduces CXCL8 expression via the ER, and we found that BPA upregulates ER-a and -b gene expression by 3 dpf. During the first week of development, control zebrafish show a pattern of

expression in all four tested genes that differs from that of BPA-exposed embryos. Our findings suggest that BPA leads to the overexpression of ER's, thus reducing CXCL8 expression and diminishing key protective innate immune responses.

CLONING AN AMMONIUM TRANSPORTERS FROM AN EARLY LAND PLANT *Marchantia polymorpha*

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Ammonium is a vital source of nitrogen, a requirement of life, for many plants. Plants acquire ammonium through Ammonium Transporters/Ammonia Permeases (AMTPs), which are membrane spanning proteins. Land plants have different AMTPs than their ancestors the green algae. Algae have AMTs and RhS but land plants have AMTs and MEPs. The nonvascular land plant *Marchantia polymorpha* is one of the earliest model plants to have a MEP, making it important for understanding the evolutionary history of AMTPs. While the AMTs of *M. polymorpha* have been previously characterized and shown to be electrogenic—they carry a charged particle across the membrane—the MEPs have not, and therefore it has not been shown if the MEPs are electroneutral as is predicted. The gene of a *M. polymorpha*MEP was cloned into a plasmid and transformed into *E. coli*. In order to test the functionality of the transporter, the gene was recombined into a plasmid for expression in yeast, and then transformed into a yeast strain with no functional ammonium transporters. Yeast with the *M. polymorpha*MEP transporter were then grown on media in which ammonium sulfate was the only nitrogen source. Yeast that expressed the *M. polymorpha*MEP transporter were able to grow, showing that the transporter is functional. The next step is to perform electrophysiology to determine if the transporter is electroneutral.

COMMERCIALY AVAILABLE *Copaifera reticulata* ESSENTIAL OIL DECREASES MARKERS OF INFLAMMATION IN RAW 264.7 CELLS

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Essential oils have long been used in medicine as a natural alternative to lab derived pharmaceuticals. Although research has yet to identify and confirm their direct chemical benefits, preliminary *in vitro* trials indicate an anti-inflammatory advantage behind a group of oils containing β -Caryophyllene. The aim of the present study was to run trials on an oil derived from the plant species *Copaifera reticulata*, to determine its efficacy in combating prolonged inflammation by using a macrophage model, RAW 264.7 cells. With the use of a “therapeutic” treatment model, in which Copaiba essential oil (CO) was added to cells in a culture 2 hours after induction by INF-g and LPS, nitric oxide production and phagocytic responses were assayed to look for a correlation between the oil and the inflammatory response. Copaiba oil treatment of classically activated RAW 264.7 macrophages resulted in the reduction of phagocytic activity, capacity, and index ($p < 0.05$). CO treatment also resulted in decreased NO levels ($p < 0.05$). While therapeutic treatment with Copiaba oil shows promise as a future regulator of the inflammatory response, further analysis of the oil and its interactions within the cell model should be further explored to determine which molecular targets are impacted in this response.

CONTINUING WITH TINY EARTH AT RIVER FALLS

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The University of Wisconsin River Falls offered its second semester of the Tiny Earth project as a research elective course (Bio-195) for students who took the first-year research experience course (Bio-160). In this semester (195 course), students did further research on specific antibiotic producing isolates collected during the first semester. Our group chose two isolates (4 & 8) that showed the highest activity of *Acinetobacter baylyi* and *Enterobacter aerogenes*. We hypothesized that antibiotic production from these isolates will be increased by changing their culture conditions. We used agitation (incubator with shaking and without), carbon source additives (glucose, fructose and sucrose at 1%), protein additives (casein, tryptone and beef extract at 1%), and different types of growth medias to test the production of antibiotics against the same ESKAPE pathogens. Antibiotic production was tested using well-diffusion assay; all the tests were conducted in 3 biological replicates. PCR was performed using full-length 16s rRNA primers (27F/ 1428R) and the PCR products were re-sequenced. Isolate 4 produced a clearance zone of 15mm against *A. baylyi* on Mueller Hinton Agar; isolate 8 had a zone of 14mm against *E. aerogenes* on potato dextrose agar. The antibiotic activity of Isolate 8 increased under agitation at 100 rpm when compared to no agitation conditions; sucrose and lactose showed a positive effect on antibiotic production. Results for the effect of protein are yet to be observed; future tests will focus on phylogenetic analysis of all the antibiotic isolates from our 195 class and extraction analysis of the antibiotic compounds.

EFFECT OF RESVERATROL ON GENE EXPRESSION DURING MACROPHAGE ACTIVATION

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Macrophages are phenotypically diverse cells central to innate immunity. The M1, or classically activated, phenotype can be modeled in vitro using IFN- γ alone or in combination with LPS. This phenotype is characterized in part by the induction of nitric oxide secretion, which is catalyzed by the product of the iNOS gene. Resveratrol, a defense phytoalexin found in a variety of plants, has been shown to attenuate this nitric oxide production by macrophages, but it remains unclear if this is due to activity at the gene level. Therefore, RAW 264.7 macrophage-like cells were cultivated in the absence or presence of both resveratrol and IFN- γ , and expression of genes essential for nitric oxide synthesis were assessed with quantitative real-time PCR. Gene expression levels for the IRF-1 and iNOS gene were quantified; the housekeeping gene G3PDH was also analyzed as an internal control for the effect of cell stimulation on basal metabolic activities. Resveratrol pretreatment prior to stimulation of cells appeared to show a trend of reduction in expression for both iNOS and IRF-1. However, no significant p-values of interest were noted upon T-Tests of DNA concentration. Even so, the trends in these data suggest that resveratrol may attenuate nitric oxide production at the level of gene expression of iNOS and IRF-1; additional trials will be required to improve the statistical robustness of the sample. This suggests that resveratrol may potentially provide anti-inflammatory effects in reference to the inflammatory response involving nitric oxide.

THE EFFECTS OF FGF10 KNOCK DOWN ON GENE EXPRESSION IN LUNG DEVELOPMENT OF *Xenopus laevis*

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If an organism fails to have functional lungs, quality of life is greatly affected, and sometimes fatal. The lungs are an essential organ for any complex organism which functions in gas exchange through respiration. Fibroblast growth factor 10 (FGF10) is known to be a major contributor in the growth and development of lung tissue. In this research, the effects of FGF10 knock down on lung and other tissue development was studied. This was done by using translation blocking morpholinos to inhibit FGF10 translation in *Xenopus laevis* embryos. It was concluded that with decreased FGF10 expression, there was reduced growth of the endodermal tissues such as lung, stomach, and pancreas.

ISOLATION AND ANALYSIS OF *Arthrobacter globiformis* PHAGE QUI

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The SEA-PHAGES classes at UW-River Falls isolated several phages from soil that can infect *Arthrobacter globiformis*. The phages were plaque purified, and DNA was extracted for restriction enzyme analysis. Electron microscopy showed that one of these phages, Qui, has a prolate head with the length approximately three times its width. The rest of the *A. globiformis* phages had isometric heads. The genome of Qui was completely sequenced and annotated. The Qui genome is longer than average at 113,655 bp, including 243 protein-coding genes. Qui has not been assigned to a particular genetic cluster, but it shares about 20% of its genes with *Arthrobacter* phages in cluster AM and AU, and 10-15% of its genes with phages infecting other Actinobacteria hosts (clusters BI, CC, DJ, EL). The shared genes include those encoding terminase, tape measure protein, and DNA polymerase/primase. Another unique feature of the Qui genomes is the presence of many genes encoding proteins with transmembrane domains, and the presence of several sets of duplicated genes. More than half of Qui's genes have no homologue among the almost 3,000 sequenced Actinobacteria phages, and most if its gene products have no predicted function.

ISOLATION AND ANALYSIS OF TWO PHAGES INFECTING *Microbacterium paraoxydans*

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The SEA-PHAGES classes at UW-River Falls isolated several phages from soil that can infect *Microbacterium paraoxydans*. The phages were plaque purified, and DNA was extracted for restriction enzyme analysis. The genomes of two of these phages, WaterT and LeeroyJenkins, were completely sequenced and annotated. Both of these phage genomes were unique, with no significant nucleotide matches to any of the 3,000 previously sequenced Actinobacterium phages. However, they are similar enough to each other to place them in the same genetic cluster, creating new cluster GB. Their genomes are 61,090-62,439 bp long, with 1545-1807 direct terminal repeats and containing 130-138 protein-coding genes. Most of the gene products have no predicted function, but we were able to identify the predicted terminase, portal protein, capsid maturation protease, major capsid protein, and tail proteins.

ISOLATION AND ANALYSIS OF VIBAKI, A PHAGE INFECTION *Arthrobacter globiformis*

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The SEA-PHAGES classes at UW-River Falls isolated several phages from soil that can infect *Arthrobacter globiformis*. The phages were plaque purified, and DNA was extracted for restriction enzyme analysis. Electron microscopy showed that one of these phages, Vibaki, has a contractile tail, placing it in the family Myoviridae. The rest of the *A. globiformis* phages had long, flexible tails. The genome of Vibaki was completely sequenced and annotated. The Vibaki genome is 48,201 bp long and contains 77 genes. Vibaki has not been assigned to a particular genetic cluster, but it shares about 25% of its genes with *Arthrobacter* phages in cluster AO. Most of the shared genes include those encoding structural proteins such as terminase, portal protein, capsid protein, and tail proteins. More than half of Vibaki's genes have no homologue among the almost 3,000 sequenced Actinobacteria phages, and most of its gene products have no predicted function.

NOVEL ANTIBIOTIC PRODUCTION IN ANTIBIOTIC-RESISTANT BACTERIA

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Feed-additive antibiotics promote animal health, especially in high-volume commercial farms. Previous work has demonstrated that there is a link between feed-additive antibiotics and antibiotic resistant bacteria. Forty-seven bacterial colonies have been isolated and purified using the streak-plate technique. These strains were classified morphologically and examined with gram staining. These strains were then tested as resistant to ampicillin, penicillin, and sensitive to tetracycline. This work desires to expand on this work in the hope to find novel antibiotics. Antibiotics may be classified based on their cellular/molecular targets, bacterial processes they impede, or based on their structures chemically. Because of this, antibiotics do not behave like proteins, in that they are not encoded for by DNA and RNA, but rather, they undergo a biosynthesis pathway with many steps involving catalyzation and enzymatic processes. These pathways allow for antibiotics to be classified in a variety of ways. In order to test the 47 bacterial colonies for novel antibiotics, four strains were first isolated and purified as the most likely to produce antibiotics. These strains have been regrown, re-isolated and re-purified five times, to ensure for repetition. These four strains were then gram stained. It is important to consider, that these four strains, not only survived an environment of feed-additive antibiotics, but also proved resistant to penicillin and ampicillin. The properties of these strains demonstrate a capability to resist antibiotic targets and it is the goal of this project to determine if they may be able to grow their own novel antibiotics.

OVER-EXPRESSION OF MEIS-1 IN *Xenopus laevis*

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Meis-1 is a transcription factor and a homeobox imitator used during development for proper formation of endoderm organs. It's a universal transcription factor, meaning it's preserved and used in similar forms in multiple organisms. Over-expression and misexpression of Meis-1 causes myeloid leukemia in humans and this process/development is well understood in multiple organisms. However, its expression and influence are not well understood during embryonic development, especially in *Xenopus laevis*. In order to understand the importance of Meis-1 in this organism, it is overexpressed in embryos by injecting them during very early stages of development either on the dorsal or vegetal poles. The goal is to see what organs are affected during development if Meis-1 is prematurely expressed, since this could have potential human implications given that the

same gene is also involved in human development. The embryos are then grown until stage 39 and sacrificed for *in-situ* hybridization.

PREVENTATIVE ADMINISTRATION OF TOPICAL Δ^9 -TETRAHYDROCANNABINOL (THC) REDUCES MAST CELL ACCUMULATION AND MECHANICAL SENSITIVITY IN A MURINE MODEL OF HAPTEN-INDUCED VULVAR PAIN

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Vulvodynia is a chronic vulvar pain condition with a complex etiology, affecting 10-28% of women of reproductive age. Vulvar tissues from vulvodynia patients are characterized by increased mast cell infiltration, key effector cells of the allergic immune response, indicating that chronic vulvar pain may be initiated by a local inflammatory immune response. Our lab has established a murine model of methylisothiazolinone (MI)-induced vulvar pain, in which 10 MI challenges in the vaginal canal lead to prolonged local mast cell accumulation and mechanical hypersensitivity. Δ^9 -Tetrahydrocannabinol(THC), the main psychoactive phytocannabinoid of cannabis, has also been identified as a compound of therapeutic potential with antinociceptive and anti-inflammatory properties. We found that topical THC administered before the onset of pain leads to reduced mast cell accumulation and mechanical sensitivity. These results indicate that THC reduces mechanical sensitivity via a mast cell-mediated pathway. Since little is known about effective vulvodynia treatments, more research should be conducted on the antihyperalgesic mechanisms of THC.

PROTEOME QUANTIFICATION DURING CELL CYCLE TRANSITIONS IN CANCER CELLS

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The cell cycle is a ubiquitous process that involves the growth and replication of cells. Abnormal cell cycle signaling is a hallmark of cancer. Manipulating the cell cycle pathway with inhibitors has emerged as a promising area of drug research. We propose to identify the composition of cytoplasmic protein complexes during cell cycle transitions, utilizing Stable Isotope Labeling in Cell Culture (SILAC) with mass spectrometry to quantitatively assess adjustments of protein expression. The leukemic cell line was arrested in the G1/S stage and the G2/M stage under different stable isotope-labeled conditions. We then performed immunoprecipitation with anti-ELAVL1 antibody to identify ELAVL1 binding partners; the eluates were analyzed by LC-MS/MS. We identified 465 proteins with significant changes in expression levels throughout cell cycle checkpoints, the dominant functional networks of which were cell cycle and apoptosis. Among them were numerous RNA-binding proteins, such as protein ELAVL1, which can bind to and increase the stability and translation of thousands of mRNAs that contain AU-rich 3'UTRs. Interestingly, ELAVL1 and several ELAVL1 mRNA target products were significantly downregulated at both G1/S and G2/M checkpoints. Thus, changes in ELAVL1 protein levels during transitions may have downstream consequences for the expression of other target genes. We detected significant differences in ELAVL1-immunoprecipitated interactions that are formed during cell cycle transitions and are analyzing interacting partners. Once we identify changes in protein complex composition between dividing and non-dividing cells, we will begin testing novel cell cycle inhibitors that stop malignant cell growth and proliferation.

RESISTING ANTIBIOTIC RESISTANCE: DISCOVERY AND EXTRACTION OF AN ANTIBIOTIC FROM *Bacillus cereus*

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By the year 2050 it is estimated that uncontrollable common infections due to antibiotic resistance will kill more people than diabetes and cancer. The current supply of antibiotics is quickly losing effectiveness against the most serious bacteria, identified by the NCBI as the ESKAPE pathogens. Their resistance makes them very difficult to treat and nearly impossible to control in a hospital environment. The goal of our research is to discover bacterial species that produce antibiotics effective against ESKAPE pathogens. We began this process by collecting soil from Sheridan Elementary in Northeast Minneapolis. We hypothesized we would discover antibiotic producing bacteria in soil due to the lengthy history of significant antibiotic discoveries from soil. After collecting our sample, diluting the soil, and selecting isolates, we began to further analyze whether our isolates produced a zone of inhibition against ESKAPE pathogen safe relatives. With this information, we selected a single isolate for further study which included PCR amplification, gel electrophoresis, gene sequencing, and biochemical testing. With all this information we were able to identify our soil isolate as *Bacillus cereus*. After discovering the identity of this antibiotic producing bacterium, further work was completed to chemically extract the antibiotic from the bacterium. Continued research will further analyze whether this antibiotic is a novel antimicrobial compound. The antimicrobial compound's effects will also be applied to yeasts and other simple eukaryotes to assess its therapeutic index.

ROLE OF *etv1* AS A POTENTIAL DOWNSTREAM TRANSCRIPTION FACTOR OF FGF SIGNALING IN *Xenopus laevis* LUNG DEVELOPMENT

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Proper lung formation is crucial to ensure the vitality of air breathing animals. The fibroblast growth factor (FGF) signaling pathway is a key component of lung development. *In vivo*, prolonged FGF signaling originating from the mesoderm allows the specification and differentiation of lung tissue from the endoderm. The upregulation of FGF signaling increases lung formation, whereas the downregulation of FGF signaling causes a reduction in lung size. Many of the transcription factors initiated by FGF signaling and involved in early lung development are not well identified. ETS variant 1 (*etv1*) is a known transcription factor that has been shown to respond to FGF signaling in *Xenopus* retinal development and in vegetal cap assays. Additionally, *etv1* expression is localized to the lung, presenting as a good candidate for a potential transcription factor involved in lung development. In this study we used *Xenopus* embryos to examine *etv1* as a potential downstream transcription factor of FGF signaling in early lung development. We used whole mount *in-situ* hybridization to show that when FGF signaling is overexpressed there is an increase in *etv1* expression and an increase in lung size. When we inhibited FGF signaling we saw a reduction of *etv1* expression and lung size. However, when we overexpressed *etv1* we observed normal lung formation. These results infer that *etv1* expression is localized in the lung and no other endodermally derived organ and appears to respond proportionally to FGF signaling. Additionally, these results suggest that *etv1* expression is not conducive to increasing lung size.

SEQUENCING AND ANALYSIS OF ANTIBIOTIC PRODUCING BACTERIA FROM RABBIT FECES

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It has been estimated that over 2 million people in the United States acquire serious infections per year as a result of antibiotic resistant strains of bacteria, and over 23,000 of these people die. The antibiotic resistance that causes these deadly diseases results from the overuse of antibiotics. Researchers attempting to solve this problem are making few antibiotic discoveries and cannot keep up with the rate of new antibiotic resistant strains of bacteria. The six bacteria that are major threats are known as the ESKAPE pathogens, and they include *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and many species of *Enterobacter*. They are the most common bacteria to cause diseases in health care settings, and they are continuing to develop more antibiotic resistant strains. The goal of the research was to discover antibiotic producing bacteria in rabbit feces. Bacteria were isolated from rabbit feces and were then tested on Tryptic Soy agar, Mannitol Salt agar, Nutrient agar, and Brain Heart Infusion, to see if they could inhibit the growth of safe relatives of the ESKAPE pathogens, including *B. subtilis*, *S. aureus*, *P. aeruginosa*, and *E. coli*. One isolate from rabbit feces produced zones of inhibition against *B. subtilis*, *S. aureus*, and *P. aeruginosa*. The 16s rRNA gene was PCR amplified and sequenced at the University of Minnesota. The results showed that the isolate was in the genus *Paenibacillus*. The isolate was also analyzed using various biochemical methods to confirm identity.

SEQUENCING THE GM2A GENE: IMPLICATIONS FOR LATE-ONSET TAY-SACHS

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Late-onset Tay-Sachs (LOTS) is a neurodegenerative disease found more frequently in French Canadians, Cajuns, and Ashkenazi Jews. LOTS symptoms include neuromuscular problems such as gait issues and ataxia. LOTS symptoms are caused by slow accumulation of GM2 gangliosides in the lysosomes of neurons in the central nervous system. Hexosaminidase A (HEXA) is the enzyme that cleaves GM2 gangliosides to GM3 gangliosides, preventing lipid accumulation. GM2 gangliosides must first be extracted from the lysosomal membrane by GM2 activator complex (GM2A) before HEXA can cleave them. Mutated GM2A could result in build-up of GM2 gangliosides in nerve cells. In a previous study, the *HEXA* genes of the offspring of a deceased Ashkenazi Jewish male (SG) suspected of having LOTS were sequenced and found to be normal. In this study, the exons of the *GM2A* gene were sequenced in four individuals to see if it could have accounted for the LOTS symptoms in SG. DNA from SG's daughters (JG and ME), a woman of Ashkenazi Jewish descent and the mother of SG's offspring (AD), and a control (KM) of non-Jewish descent were sequenced for the *GM2A* exons. Exons 1-4 were successfully sequenced for all subjects. JG and KM shared similar mutations in exon 2 with two methionine to valine changes. Only JG had a SNP in exon 4, changing a valine to an alanine. In summary, this mutation in SG's offspring is a conservative amino acid substitution that very likely would not affect GM2A protein function.

SEQUENCING THE HEXB GENE: IMPLICATIONS FOR LATE ONSET TAY-SACHS

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This research examines the possible correlations between mutations in the Hexosaminidase B gene (HEXB) and Late Onset Tay-Sachs (LOTS). LOTS is a lysosomal disorder that impairs neurological functions. Symptoms exhibited during early adulthood includes seizures, muscle weakness, mood alterations, and speech impairment. HEXB protein subunit combines with the Hexosaminidase A (HEXA) subunit to form a functional HEXA protein

that breaks down glycolipids in the brain. Loss of HEXA subunit function has been associated with LOTS as glycolipids accumulate, causing the lysosome to swell and damage nerves cells. DNA extracts were used to sequence the HEXB exons from family members of an Ashkenazi Jew suspected of having LOTS. There is a higher prevalence of the disease in Ashkenazi Jew with 1 in 25 of the population being carriers. Previous sequencing of the HEXA subunit exons in these individuals revealed normal DNA sequences. Most exons in HEXB were successfully amplified using polymerase chain reaction (PCR) and purified to obtain DNA sequencing data. The sequencing results were analyzed and compared to the HEXB template DNA to scan for single nucleotide polymorphism (SNPs). The results suggest that mutations in the second half of the exons of the HEXB is not associated with LOTS. All of the exons (9-14) that were successfully amplified did not have any SNPs when using the DNA of the two daughters of the subject. Another study was able to detect SNPs in the first half set of exons in HEXB that could be significant to alter the function of HEXB.

CHEMISTRY

A COMPUTATIONAL ANALYSIS OF CANDIDATE NON-COVALENT ORGANOCATALYSTS FOR AN ASYMMETRIC [2,3]-WITTIG REARRANGEMENT

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The [2,3]-Wittig rearrangement is a useful pericyclic reaction for the synthesis of natural products. As it forms a new carbon-carbon bond, it can also be useful for growing simple molecules into larger, more complex ones. When uncatalyzed or symmetrically catalyzed, it yields a racemic mixture. In recent years, experimental chemists have sought to asymmetrically catalyze the reaction, but they have fallen short of a fully enantiopure outcome. The goal of this study is to identify effective methods for the computational study of the [2,3]-Wittig rearrangement and ultimately, to identify the ideal catalyst for an enantioselective [2,3]-Wittig rearrangement of 3-(allyloxy)-1-benzyl-2-oxindole. Density Functional Theory has been used to model the reaction and effects of two different catalysts studied experimentally. Issues identifying the lowest energy conformations of the catalysts and substrates, as well as the lowest energy alignment of the catalyst upon the substrate, have presented challenges for a proper description of the reaction energy. To solve this problem, molecular docking studies are being implemented to determine the proper bimolecular alignment prior to density functional theory optimization of the structures.

COMPUTATIONAL PREDICTIONS OF AIR SENSITIVITY FOR PRIMARY PHOSPHINES

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A variety of phosphines have been modeled using semi-empirical and *ab initio* methods to determine air-stability. First primary, secondary, and tertiary phosphines with known air-stabilities were modeled and calculations were run to determine the SOMO energies of the related radical cation. A previously published benchmark of SOMO energies were reproduced with similar trends using less "costly" semi-empirical PM6 and RM1 and simple Hartree-Fock methods using MIDI and 3-21G basis sets. A variety of substituted aryl primary phosphines were modeled using the previous methods. Substituents exhibiting electron donating and withdrawing effects, via both induction and resonance were examined in the *ortho*, *meta*, and *para* positions in pursuit of disubstituted phenylphosphines stabilized by electronic effects alone.

DEGRADATION PROFILE OF AN IRON-POLY(LACTIC ACID) COMPOSITE

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Poly(lactic acid) (PLA) and PLA composites are increasingly useful materials for 3D printing. Their growing popularity warrants a better understanding of their chemical properties. This work describes degradation of an iron-PLA polymer composite intended to increase structural stability of PLA filaments. By understanding the effects of the iron particulate on the degradation of the polymer composite, we will be able to better predict its properties and performance during environmental and physiological degradation processes.

DESIGN AND TESTING OF A MERCURY-FREE SCHLENK LINE BUBBLER

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The Schlenk line (air-free vacuum manifold) is a staple of modern synthetic organic and inorganic labs, enabling the relatively easy handling of air- and moisture-sensitive materials. A necessity of these systems is the ability to provide an environment of inert gas, such as N₂ or Ar, that is above atmospheric pressure. This "overpressure" is enabled by use of a mercury bubbler. Given mercury's high cost and deleterious health and environmental effects, we have sought to design a new bubbler system as a replacement. We have developed a mercury-free bubbler system from simple and common laboratory glassware that provides as much or more overpressure than a commercial mercury bubbler and uses inexpensive and environmentally benign mineral oil. Our apparatus has been successfully implemented for use in both research and teaching lab settings.

DEVELOPMENT OF A NEW MOLECULAR GEOMETRY OPTIMIZER FOR THE QUANTUM CHEMISTRY COMMON DRIVER AND DATABASES ENVIRONMENT

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Previously, for any quantum chemistry package, a built-in molecular geometry optimizer has been included, unique to each chemistry package and unable to function outside the larger program. A full rewrite of the molecular geometry optimizer Optking into Python was undertaken, as part of the Quantum Chemistry Common Driver and Databases (QCDB) project to develop programs and drivers capable of interfacing with various quantum chemistry packages. This allows for researches to take advantage of the strengths of each program and enables workflows to easily incorporate multiple quantum chemistry packages. Optking is the first molecular geometry optimizer, capable of high-accuracy convergence, intentionally written to interface with a number of quantum chemistry packages.

DONOR ATOM AND RING SIZE EFFECTS OF PLATINUM (II) COMPLEXES WITH SULFUR CONTAINING LIGANDS

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Coordinatively unsaturated transition metal complexes of d^8 metals (including Pt(II) and Pd(II)) are widely used in catalytic transformations. Macrocyclic ligands that bond in a facial geometry at metal atoms that prefer a square planar geometry result in metal complexes with either five-coordinate square pyramidal or six-coordinate octahedral geometries. The mismatch of ligand and metal geometry preferences allows for possible weak axial interactions involving donor atoms (such as sulfur or oxygen) that can alter properties at the metal such as electrochemical oxidations, electronic transitions, and fluxional NMR. These axial interactions could be exploited in catalyst design. In an effort to explore macrocycle ring size and donor atom effects in Pt(II) complexes, we synthesized $[\text{Pt}(\text{9[ane]S}_3)_2](\text{PF}_6)_2$, $[\text{Pt}(\text{9[ane]S}_3)(\text{9[ane]S}_2\text{O})](\text{PF}_6)_2$, and *cis*-Pt(6[ane]S₃)(DMSO)Cl₂(9[ane]S₃ = 1,4,7-trithiacyclononane, 9[ane]S₂O = 1-oxa-4,7-dithiacyclononane, 6[ane]S₃ = 1,3,5-trithiane). X-ray crystal structures obtained show short axial Pt-S distances in the homoleptic and heteroleptic complexes of 9[ane]S₃. Only monodentate bonding is observed in *cis*-Pt(6[ane]S₃)(DMSO)Cl₂. Solution NMR is consistent with fluxional 9[ane]S₃ ligands. Electrospray mass spectroscopy was also used to verify metal/ligand stoichiometries. Electrochemical studies are underway to probe the observed axial donor atom and ring size effects.

GREEN, FACILE METHOD FOR THE SYNTHESIS OF PHOSPHINE SULFIDES AND SELENIDES

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Phosphines were oxidized by elemental sulfur and selenium. In contrast to the standard 8-36 h toluene reflux, 30 min microwave irradiations with environmentally friendlier solvents (i.e. ethyl acetate, acetonitrile, ethanol, and heptane) were analyzed with triphenylphosphine. Ethyl acetate revealed to be the best solvent for this greener method and adapted to various aryl, tertiary phosphines. 30-120 min microwave reaction times at 170°C were observed to produce the tertiary phosphine chalcogenides with conversion rates of greater than 74% and purities of greater than 97%, with multiple targets crystallizing directly from the reaction solution. Products were confirmed by melting point, IR, and heteronuclear (³¹P, ⁷⁷Se) NMR. This faster, and greener procedure was an easy alternative protocol for the oxidation of phosphines with heavier chalcogens.

THE MITIGATION OF PHOTOINDUCED DNA-OXIDATION BY USING ANTIOXIDANTS FOUND IN FOODS UNDER DIFFERENT TEMPERATURE SETTINGS

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Antioxidants are beneficial to human health. They prevent oxidation reactions that produce free-radicals which can cause harm to the body. Rudimentarily, the existing undergraduate experiments at the Rochester Community and Technical College have provided students with an experimental model to observe the effectiveness of antioxidants found in different food sources in the prevention of DNA oxidation. The purpose of this research is to not only explore additional antioxidant-containing food sources and their effectiveness but also to take into consideration of temperature, a factor that potentially affects the activity of antioxidants. Given that cooking temperatures often reach or surpass the boiling point and the ingested foods eventually reach the digestive system, antioxidant samples were subjected to room temperature (21° C), human body temperature (37° C), and water boiling point (100° C). Three types of foods were used to provide antioxidants: tomato, dark chocolate, and green

tea. Before mixing each food with the DNA and proflavin, the food samples were subjected to a heat treatment until the designated temperature has been reached. After the sample mixtures were prepared, they were subjected to photo-oxidation. This experiment allowed undergraduate students to explore the relationship between temperature and antioxidant activity as well as comparing the extent of oxidation mitigated by the respective food sources.

MODIFYING GLASSY CARBON ELECTRODES WITH GRAPHENE OXIDE DERIVATIVES TO CONTROL CONDUCTIVITY

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Graphene oxide and its derivatives have been used in ground breaking technological developments because of their unique conductive properties and notable strength. With these new applications, it will be important to understand the properties of these materials to further their utilization. A series of studies described here demonstrate a way to control the conductivity of reduced graphene oxide using a benign reagent, ascorbic acid. To monitor the reduction, a λ_{\max} peak shift of 230nm to 270nm was observed confirming reduction of graphene oxide. Data presented in this study shows that by varying the concentration of ascorbic acid, the extent of reduction can be controlled. After this confirmation of control, studies were performed to characterize the conductive properties of the derivatives of reduced graphene oxide. Glassy carbon electrodes were modified to host depositions of reduced graphene oxide derivatives. A three electrode potentiostat with modified glassy carbon electrodes were used to measure the current produced in a linear sweep voltammogram from a hexacyanoferrate(III) test system. Data show the current produced is influenced by the concentration of ascorbic acid used in the reduction of graphene oxide. When graphene oxide was deposited on a glassy carbon electrode, the current was inhibited compared to the current produced on a bare electrode. In contrast, the ascorbic acid + graphene oxide modified electrodes showed an increased current with increased ascorbic acid concentration indicating increased conductivity. These results demonstrate reduction by ascorbic acid is a viable, inexpensive, and green method for influencing the conductive properties of graphene oxide.

MONOPHOSPHONIUM SALTS OF BISPHOSPHINES AS FACILE PRECURSORS TO BISPHOSPHINE MONOXIDES

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Bisphosphine mono-oxides (BPMOs) are hemi-labile ligands useful for stabilizing metals for a variety of applications including inorganic synthesis, metal complex catalysis, pharmaceutical development, and analytical chemistry. Current synthetic routes are limited since normal oxidizers such as hydrogen peroxide produce a mixture of unoxidized, mono-oxidized, and bis-oxidized phosphines. Current methods used include selective oxidation via a Pd-catalyzed reaction¹, which is expensive and air-sensitive, and mono-reduction of bisphosphine dioxides using an anhydride, a thiol, and N,N-diisopropylethylamine. We are developing a simpler method to produce mono-oxidized bisphosphines in high purity by preparing a monophosphonium salt using the well-established Wittig reaction to selectively oxidize one phosphorus center. $^{31}\text{P}\{^1\text{H}\}$ NMR is used as the primary means to characterize the products and their ratios in our attempts to optimize the protocol.

A MORE EFFICIENT SYNTHETIC PATHWAY TO A MULTITUDE OF NOVEL OXAZOLIDINONE ANTIBACTERIAL AGENTS

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A new pathway to synthesize a multitude of novel Oxazolidinone antibacterial agents was designed. The route incorporates a starting material with a bromine substituent that ends up on a benzene ring furthest from the Oxazolidinone ring. The synthesis of the final bromine substituted Oxazolidinone compound has been successfully completed in eight steps. It will now be tested for antibacterial activity and bioavailability at Johns Hopkins University. The successful route to the bromine containing Oxazolidinone can now be used to create a variety of new Oxazolidinone derivatives by substituting the bromine with various functional groups using Suzuki or Sonogashira reactions.

NOVEL SYNTHESIS OF AN OXAZOLIDINONE ANTIMICROBIAL AGENT

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With a rising increase in antibiotic resistant strains of bacteria, there is a constant need to innovate new antibiotic designs, particularly those that work by novel bacterial inhibition mechanisms. The current FDA approved drug Linezolid contains an oxazolidinone ring and has shown to be effective against resistant strains of bacteria, including those of the disease tuberculosis. The purpose of this research is to synthesize an oxazolidinone derivative, which can be tested for efficacy against resistant bacteria and bioavailability. This novel derivative will be synthesized in a seven-step synthesis, three of the steps have been completed successfully. The products of those steps have been characterized by NMR spectroscopy. The first step includes protecting dopamine with a Boc protecting group to inhibit the nucleophilic properties of the primary amine for the rest of the synthesis. At the end of the synthesis, the Boc protecting groups will be removed to reveal the primary amine which will aid in increasing hydrogen bonding within the active site and water solubility, thus increasing bioavailability. The compound will be sent to Johns Hopkins University to test its antimicrobial properties; it will also be used to synthesize further oxazolidinone derivatives.

OPTIMIZING THE SYNTHESIS OF A NOVEL TETRADENTATE MIXED DONOR LIGAND

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Late row transition metal complexes are often used in industrial processes as catalysts. The metals used are typically rare and expensive metals such as platinum and palladium. An exciting area of research investigates the use of more abundant and less expensive first row transition metal complexes for use in these reactions. To this end, a new family of ligands with mixed donor atoms has been developed to stabilize first row transition metals in their reactive low oxidation states.

POLYMERIZATION OF THERMAL ASPARTATE BY GREEN CHEMISTRY

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Green chemistry refers to the reactions that are more environmentally friendly. It aims to minimize the use of hazardous substances during lab procedure by using less hazardous reagents, safer solvents, maximizing atom economy as well as providing renewable feedstocks. Polymers have proven to be of great use in the water treatment industry as a scale inhibitor to prevent buildup of insoluble materials. One of the most widely used scale inhibitors is a polymer called poly(acrylate) (PAC), which is relatively non-toxic and environmentally benign, but it is non-biodegradable. To address this limitation, we have conducted a polymerization reaction to create thermal poly(aspartate) (TPA) which is a biodegradable polymer alternative to PAC. No organic solvents are used and little to no waste is produced during the synthesis. Current research has the potential to incorporate green chemistry into the organic curriculum for second semester students in order to prepare them for the current workforce and help them be conscious of the environment.

PRIMARY PHOSPHINES: NEW SYNTHETIC METHODS AND NEW TARGETS

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Primary phosphines, compounds of the type RPH_2 , are notorious for their reactivity with oxygen; many exhibit pyrophoric behavior. This reactivity has hindered the development of its chemistry despite its potential utility as a synthon and its analogy to well-explored primary amines. Herein, two new approaches for aryl and alkyl primary phosphines are reported. We also report the first aryl, air-stable primary phosphine that is not kinetically stabilized by bulky *ortho* substituents. Phosphines are identified primarily by ^{31}P spectroscopy. Experimental air-stability observations are compared to molecular modeling predictions.

RATIONAL DESIGN OF TRIBOLUMINESCENT MANGANESE (II) COMPLEXES

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Triboluminescence is the property of a class of compounds that spontaneously emit light upon mechanical fracture. Compounds that exhibit triboluminescence can be used in applications including pressure sensors. The optical and structural features required for triboluminescence to occur are poorly understood. Evidence suggests that noncentrosymmetric packing is a requirement for compounds to exhibit triboluminescence. Salts involving chiral cations paired with photoluminescent metal complexes were chosen as potential triboluminescent synthetic targets. As single enantiomer compounds are either expensive or difficult to obtain, we looked to employ cinchonine, a readily available and inexpensive single enantiomer natural product obtained from cinchona trees. An N-benzyl derivative of cinchonine (N-Bzcinch)Br (N-Bzcinch = N-benzylcinchonidinium), was synthesized and characterized by 1H NMR, solid-state photoluminescence, and X-ray structures. Two X-ray structures were obtained of N-benzylcinchonidinium bromide, an anhydrous form and a 1.5 hydrate. Both single enantiomer structures crystallize in chiral space groups but exhibit different packing in large part due to hydrogen-bonding. Both salts also exhibit green solid-state photoluminescence. As several salts of $[MnBr_4]^{2-}$ exhibit triboluminescence, our next goal is to synthesize salts of the form $(N-Bzcinch)_2[MnBr_4]$.

SOLID-STATE STUDIES OF DERIVATIVES FORMED BY REACTION OF NITROGENOUS BASES WITH ALDOSES: THE CRYSTAL STRUCTURE OF THE 2-FLUOROPHENYLHYDRAZONE OF D-MANNOSE

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We are chemically combining aldoses with nitrogenous bases to determine by single-crystal X-ray diffraction whether the derivatives formed are either open-chain Schiff bases or cyclic glycosylamines. Previous work in our laboratory has shown that D-mannose tends to yield glycosylamines upon reaction with substituted anilines but Schiff bases upon reaction with substituted phenylhydrazines, which differ from the anilines by only a single N-H moiety; we are now extending this investigation to other aldoses. Concurrently we are using these carbohydrate derivatives as a context in which to investigate the possible role of close intermolecular fluorine-hydrogen interactions in defining their crystal structures. Our previous work has shown that the 3-fluorophenylmannopyranosylamine and the 4-fluorophenylmannopyranosylamine are isomorphous (exhibiting the same solid-state molecular packing arrangement) while the 2-fluorophenylmannopyranosylamine assumes a different molecular packing arrangement, one isomorphous with the non-halogenated *N*-phenylmannopyranosylamine. A characteristic fluorine-hydrogen interaction is conserved in the isomorphous 3-fluoro and 4-fluoro compounds. To examine such interactions further, we have now synthesized and determined the crystal structure of the 2-fluorophenylhydrazone of D-mannose. In this Schiff base structure the fluorine atom interacts with neighboring C-H groups but not with neighboring O-H groups. Future work will include determination of the crystal structures of the 3-fluoro and 4-fluoro analogues.

A SUSTAINABLY SOURCED DEGRADABLE POLYMER FROM LIGNIN

Cecelia Kinane¹, Brittany Nelson-Cheeseman² (Advisor), Dr. Eric Fort¹ (Advisor)

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Sustainable sources of organic compounds are needed to decrease use of fossil fuels in making plastics. Lignin derived molecules can be readily obtained from wood biomass waste. We are preparing triblock copolymer featuring vanillic acid as a lignin model molecule in order to create a bio-based thermoplastic elastomer.

SYNTHESIS AND CHARACTERIZATION OF HYDROGEL-GRAPHENE/MAGNETITE COMPOSITE MATERIALS

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Department of Chemistry and Biochemistry

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The goal of this research is to synthesize and characterize hydrogel composites made with nanoparticles of graphene and magnetite, specifically to determine variation of magnetic and thermal properties of hydrogel-graphene/magnetite composites. The hydrogel polymers will be made from acrylamide. The ultimate goal is to synthesize a superior material for the use in electronic devices. The superior hydrogel would have the capacity to remove more heat from the electronic components, thereby reducing the degradation due to heat. The objective of the research project is to understand the impact of immobilizing nanoparticles within the hydrogel structure. The comparison should reveal how properties of the nanoparticles are modified by hydrogels.

SYNTHESIS OF A NOVEL OXAZOLIDINONE ANTIBACTERIAL AGENT

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Due to evolutionary stresses, bacteria are becoming resistant to current antibiotics. New antibacterial agents are required to fight these resistant strains of bacteria. After the release of a new class of antibiotics, oxazolidinones, Dr. J. Thomas Ippoliti created his own derivative which was shown to be more effective than linezolid against tuberculosis but less water soluble. Building off this success, a new derivative incorporating a morpholine ring was targeted for synthesis with the goal of increasing the water solubility of the molecule. This would hopefully allow for smaller doses to be taken while reducing negative side-effects of treatment. A nine-step synthetic route was developed. The first step is a double nucleophilic aromatic substitution. In the next reaction the morpholine ring is added via a reductive amination to an aldehyde group using triacetoxyborohydride. This step was surprisingly low yielding, but we were able to increase the yield by increasing the equivalencies of morpholine. An interesting side reaction occurred in the fourth step where the morpholine ring was substituted by a chlorine via benzyl chloroformate. The morpholine was then substituted back on in an S_N2 fashion in a later reaction. Currently steps one through four have been completed. Once the final product is synthesized it will be sent to Johns Hopkins University to be tested against resistant strains of tuberculosis and other bacteria.

TOWARDS ISOMORPHOUS “BRIDGE-FLIPPED ISOMERS”: INVESTIGATIONS OF 4-PYRIDYL AND GLOXAL-BASED SYSTEMS

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We are investigating the crystal structures of pairs of molecules we define as “bridge-flipped isomers.” These molecules differ structurally only in the orientation of an atom bridge connecting two major components of the molecules, such as aryl groups. Examples can be found among the benzylideneanilines, where the isomerism is $Ar_1-CH=N-Ar_2$ vs. $Ar_1-N=CH-Ar_2$, and among the phenylhydrazones, where the isomerism is $Ar_1-NH=N-CH-Ar_2$ vs. $Ar_1-CH=N-NH-Ar_2$ ($Ar = aryl$). Using single-crystal X-ray diffraction, we are determining how frequently such pairs are isomorphous, crystallizing into the same molecular packing arrangement in the solid state. Isomorphous pairs may form interesting solid solutions. Based on the premise that the occurrence of similar molecular packing motifs in at least one dimension in both members of a bridge-flipped isomeric pair might encourage their isomorphism, we have begun the synthesis and crystallization of a 4-pyridine-derived system of isomers with iodine substituents; the anticipated shared motif would be close intermolecular $N \cdots I$ Lewis acid-base contacts. We now have successfully grown crystals of the benzylideneaniline formed by reaction of 4-iodoaniline with 4-pyridinecarboxaldehyde and have determined the crystal structure. As predicted, molecules are linked into chains in the solid state by close $N \cdots I$ contacts. We are pursuing the synthesis and crystallization of the bridge-flipped isomer of this compound while concurrently beginning the synthesis and crystallization of analogous diimines based on glyoxal. Crystal structures of these derivatives will be compared to their bridge-flipped analogues, the corresponding diimines based on hydrazine. Samples are now in preparation for submission for X-ray crystal structure analysis.

ECOLOGY AND ENVIRONMENTAL SCIENCE

BACTERIAL GROWTH FROM VARIOUS SOIL SOURCES

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Crown College, St. Bonifacius, MN

Antibiotic resistance is a growing issue in our world today. Soil is a good source of microorganisms, including possibly new antibiotic producers. By testing diverse sources of soil, we can hopefully isolate a number of antibiotic producers that could potentially lead to the discovery of an unknown antibiotic. The goal of this study was to look at the bacterial content of four very diverse ecological environments, and then eventually find different antibiotic producers from these samples. The environments used were selected based on the plant life found in the surrounding area and are named accordingly. A second goal of this study was to determine the effect of conducting burns on the bacterial content of soil. The different environments consisted of an evergreen area, cattail area, a woodland area, and a pre-burn prairie soil sample. Two additional samples were collected from the prairie soil, two weeks and five months after a burn was conducted in the area. Data were collected on the number of bacteria colonies formed and the colony forming units per gram were calculated. The prairie soil had the lowest bacterial content of all the soil samples. The microbial content increased with burning, which suggests that the burn plausibly helped to revive the soil bacteria ecosystem. Future plans are to test for antibiotic production by the bacteria isolated from the soils, against relatives of pathogens.

THE EFFECT OF MARINE TRAFFIC ON BOTTLENOSE DOLPHIN (*Tursiops truncatus*) BEHAVIOR IN THE RÍA DE AROUSA IN GALICIA, SPAIN

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Understanding the dynamics between bottlenose dolphin (*Tursiops truncatus*) behavior and anthropogenic behavior is essential for the creation and implementation of effective conservation strategies for the species. Due to a general trend towards coastal urbanization, bottlenose dolphins encounter frequent disturbances due to human activities, facing increased threats to fitness and survival. This study examined the effects of marine vessel traffic on a resident population of bottlenose dolphins in the Ría de Arousa of Galicia, Spain. Marine vessel traffic, specifically commercial mussel farm boats, fishing boats, and tourist catamarans, is the most common anthropogenic threat faced by Ría's dolphins. Using land-based observations, data were collected on group behavior and marine vessels interacting with a group. These data were used to compare differences in behavioral transitions, behavioral budgets, and bout durations in the presence and absence of marine vessel interactions. The Ría's resident bottlenose dolphin population was more likely to continue traveling and less likely to remain resting in the presence of marine vessel traffic. The behavioral budget analyses indicated they also spent a higher proportion of time traveling and a lower proportion resting. The average length of behavioral bouts was significantly different in impact situations, during which dolphins experienced longer traveling and socializing bouts and shorter resting bouts. These short-term consequences may result in long-term decreases in reproductive success and survival at the individual and population levels. Thus, steps should be taken to improve local legislation and increase public awareness with the goal of conserving this resident population of bottlenose dolphins.

FOSSIL CORAL AND OCEAN CARBON CYCLING

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An understanding of past climate change is critical for understanding how future climate will evolve. All of Earth's surface environments (ocean, atmosphere, and land) play a role in the climate system. Therefore, it is possible to use reconstructions of past oceanic environments to infer past changes in the global climate system. A primary approach toward reconstructing past environmental change is to use paleoenvironmental "proxies" as indirect archives. Recent experimental studies have suggested that the uranium concentration of fossil coral skeletons, if well-preserved, may be used as a proxy in order to glean environmental information dating back thousands of years. In this study, we aim to further test the robustness of the relationship between uranium concentration in fossil corals and indicators of the oceanic environment, including temperature, pH, and salinity in order to determine whether we can use uranium concentrations in coral as a proxy for the global climate in the past. We are examining a compilation of previous measurements of uranium concentrations in 1907 fossil and modern coral skeleton samples from three ocean basins (Atlantic, Pacific, Indian). Our dataset also contains information on the samples' growth location, species, and age. We will compare coral uranium data to secondary datasets that contain spatial information regarding ocean temperatures, pH, and salinity. Our work will enable an understanding of whether uranium concentrations of fossil corals are viable proxies for past changes in the climate system.

INTERACTION EFFECTS OF BURN TREATMENT AND FLORAL DISPLAY ON REPRODUCTIVE SUCCESS WITHIN *Liatris aspera* AND *Solidago speciosa*

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Conservation efforts to maintain tallgrass prairie rely on prescribed burns, as human activity has suppressed the natural occurrence of grassland fires. While fire has been shown to reduce seed predation, improve conditions for germination, and promote plant growth, prescribed burns applied to prairie communities may differentially affect the fitness of plant species with distinct reproductive strategies. The following study examines *Liatris aspera* and *Solidago speciosa*, two *Asteraceae* species that produce different numbers of composite flowering heads. Stalks from *S. speciosa* and *L. aspera* plants on either side of a burn break at Staffanson Prairie (Douglas County, MN) were dissected to determine the number of flowering heads on each specimen. Seed set was determined by x-raying a sample of achenes from each specimen. For *L. aspera*, flowering head count and burn treatment in the previous year statistically interacted to influence seed set. Within *L. aspera* that had not recently burned, greater head counts correlated with increased seed set; burned plants, alternately, displayed greater average head counts but no association between head count and seed set. For *S. speciosa*, an interaction model between burn treatment and head count was not statistically significant. These asters' reactions to burn treatment may be impacted by plant-pollinator relationships dependent on floral display size, though further research is needed to understand how pollinators respond to differences in flowering head count. This study demonstrates that fire may interact with variations in plant characteristics to influence reproductive success, warranting a careful approach to prescribed burns that considers species composition.

INVASIVE AND NATIVE SPECIES COFUNCTION TO CREATE SUITABLE HABITAT FOR ENDANGERED CHINOOK SALMON (*Oncorhynchus tshawytscha*)

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A fundamental goal in conservation is to determine the most efficient methods to protect an endangered species, but when it comes to the Chinook salmon (*Oncorhynchus tshawytscha*), conservationist managers struggle with the issue of smolt survival in the ocean after they are released from hatcheries. Ocean released salmon often encounter challenging and varying habitats, some of which are novel to them. Chinook salmon inhabit seagrass beds (*Zostera marina*) in estuaries of the Pacific northeast until they are large enough to transition to deeper marine environments. Recently, a potential habitat forming brown algal species *Sargassum muticum* has invaded shallow waters in the Pacific northeast, where they create mixed habits with seagrass and other species of algae. Here, we carry out an experiment at Friday Harbor Labs in San Juan island to test the nursery function of three different habitats, seagrass, invasive brown algae, and a mixture of the two as well as a control habitat with bare sand. We measure salmon growth, survival and prey availability and hypothesized that, based on the nursery habitat mosaic theory that a mixed habitat (seagrass and Sargassum) would provide the best nursery habitat compared to the other three habitats. We found that salmon growth rates were lowest in seagrass, yet survival rates were greatest and overall nursery quality was greatest in mixed habitats. Taken together these results indicate that diverse assemblage of habitats (or foundation species) is more important than a single/mono specific habitat/foundation. Even if one habitat is invasive (sargassum).

NEST CHARACTERISTICS OF *Glaucomys volans* WITHIN ITASCA STATE PARK

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Recently, the Southern Flying Squirrel (*Glaucomys volans*), a deciduous species, has expanded its range north into Itasca State Park, Clearwater, Co., MN, as the forest has transformed from coniferous to deciduous forest. This expanding range overlaps with the Northern Flying Squirrel (*Glaucomys sabrinus*), which typically inhabits coniferous forest. The change is likely due to a combination of climate change and ecological succession resulting from fire suppression. This study focused on the nesting sites chosen by *G. volans*. To conduct this study, we used three trapping methods to capture *G. volans*. We then radio collared captured individuals and tracked them using radio telemetry. Once a nest site was located, we collected habitat data to characterize the nest tree and its surrounding habitat. *G. volans* did not have a strong preference for any particular type of nest site; however, some individuals used specific tree species repeatedly throughout the study, but this was not a statistically significant trend. This outcome may be due to *G. volans* following nest choices made by previous individuals, and not selecting the nesting locations independently. One observation that was made was that *G. volans* tended not to select healthy, living trees for nesting sites (one out of 38 observations). This observation may give insight into land management practices and emphasize the need for dead snags. In the future, it would be ideal to collect habitat data from random locations within the Itasca State Park forest to compare with chosen nest site plots.

PHOTOPROTECTION IN RESPONSE TO DESICCATION IN BRYOPHYTES

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Desiccation tolerance, the ability to survive complete dehydration and recover upon hydration, is rare among vascular plants but is relatively common in bryophytes. In the desiccated state, all light is damaging to photosynthetic tissues, but is mitigated by photoprotective mechanisms. The xanthophyll cycle is a photoprotective mechanism that dissipates excess light using the pigment zeaxanthin (Z). We analyzed three moss species, with low (*Sphagnum*), medium (*Calliergon*) and high tolerance (*Dicranum*) to desiccation to characterize the fluorescence response to desiccation, the role of the xanthophyll cycle in this response, and recovery of each species. Mosses were hydrated overnight to get initial measurements and then desiccated in either darkness or natural light for 0, 1 and 3 weeks, monitoring recovery after each desiccation period. We found that recovery was more rapid for tolerant species and dark desiccated mosses and decreased in rate as time of desiccation increased. In addition, tolerant species desiccated in the light retained Z after desiccation at all timepoints. Dark desiccation did not result in accumulation of Z at any timepoint. There was no change in total photoprotective pigments in tolerant species with a decrease occurring in low tolerant sphagnum. No other significant change occurred in pigments overtime across all species. Our data show that some bryophytes have high desiccation tolerance and can rapidly downregulate photochemistry, recovering upon hydration. However, our data demonstrates photoprotection from xanthophyll cycle pigments is not essential for tolerance, but instead plays a supplementary role in natural light.

RESOURCE USE OF SMALL PRAIRIE MAMMALS

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Since small prairie mammals, such as voles and mice, strongly affect prairie plant communities, understanding their roles in restored (planted) and remnant prairies is of value. We used stable isotope ratios of carbon and nitrogen in fur samples of live trapped prairie mammals to explore their diets. Fur serves as a record of diet across months and provides a broad snapshot of the degree to which individuals are consuming C₃ and C₄ plants and the amount of animal matter in their diet. Through data wrangling techniques and linear mixed-effects model comparisons we gained an understanding of the resources different small mammals are using in restored and remnant prairies. Together our analyses suggest significant differences in the isotope ratios of carbon for voles and mice and differences in nitrogen between individuals inhabiting restored as compared to remnant prairies.

MATH AND COMPUTER SCIENCE

***Daphnia* AND MIXED ALGAE, PREDATION AND COMPETITION: A LOOK AT STOICHIOMETRIC MODELING**

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Our goal is to understand the detrimental effects of excess nutrients or nutrient imbalance related to predator prey and competition dynamics. Due to the complex behavior of natural systems, it is often difficult to observe population dynamics in nature. We are studying these dynamics by conducting laboratory experiments to observe *Daphnia* characteristics when fed *Chlamydomonas* and *Scenedesmus* grown at three different phosphorus concentrations (1.7 mM, 0.34 mM, 5 μM). We quantified the competition between our algal species by counting

Chlamydomonas and *Scenedesmus* cells throughout the study. We have growth rate, competition rate, and carrying capacity data for both algal species as a function of growth conditions. We also have phosphorus uptake and per capita phosphate content data. Similar to what was outlined in Nisbet et. al, we used dynamical systems modeling. First, we modeled the predator-prey interactions between *Daphnia* and algae. In order to analyze the competition for phosphorus between our algae, we fit a synthesis of the competitive Lotka-Volterra and Droop Cell-Quota models. To date, we have refined the lab methodology for the algae: *Daphnia* experiments and observed Pi-dependent population shifts in algal co-cultures. We found that *Scenedesmus* outcompetes *Chlamydomonas* at the lower two phosphorus concentrations while at the highest concentration, *Chlamydomonas* outcompetes *Scenedesmus*. Moreover, Pi fell below detectable levels in 5 μM algae media due to rapid consumption. Our newfound understanding will be used to improve the Mathematical Biology program at St. Olaf College and could inform decisions regarding environmental health and remediation.

FRAMING OF CULTURE WAR ISSUES IN CONGRESSIONAL CAMPAIGN WEBSITES

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Research shows that politicians strategically frame issues to gain public support for their views. Further, it is known that framing has the potential to affect individuals' opinions on issues. Previous research done on issue framing has two primary limitations: first, the labor-intensive nature of using humans to code documents, and second, the necessity of determining all possible frames of an issue. We use a unique dataset of 2008 to 2018 House of Representative candidates' campaign website pages to examine framing of culture-war issues such as LGBT+ rights and abortion. Over 2,000 pages dedicated to culture-war issues are analyzed through topic modeling and dictionary-based methods. Using the R package *stm*, we fit topic models on our data without pre-specifying possible frames. Our dictionary-based method utilizes the Moral Foundations and Linguistic Inquiry and Word Count dictionaries to score pages based on predetermined categories. The results of these methods are then built into mixed-effect models to examine how party affiliation, incumbency status, congressional district characteristics, and time affect framing. In addition to providing insight into how politicians frame issues, our results contribute to existing methods for topic modeling.

INVESTIGATING THE EFFECT OF VALUES AFFIRMATION ON THE PERSISTENCE AND PERFORMANCE OF INTRODUCTORY CHEMISTRY STUDENTS

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Previous literature has highlighted low STEM retention as a national educational issue. Specifically, certain demographic groups are underrepresented among STEM graduates due to higher STEM dropout rates within these groups. To this end, the St. Olaf College Chemistry Department has implemented values affirmation assignments within introductory chemistry courses with the goal of increasing student performance and persistence. Homologous studies have found similar assignments to be effective in improving performance and persistence specifically among underrepresented groups within other STEM disciplines, such as women in introductory physics and first-generation college students in biology courses. Herein, we will discuss the statistical modeling and methods that were used to determine if these new assignments had a significant effect on the performance and persistence of St. Olaf students in introductory chemistry.

NEUROSCIENCE

THE EFFECTS OF INTRA-BURST FREQUENCY IN COORDINATED RESET NEUROMODULATION FOR PARKINSONIAN NON-HUMAN PRIMATE

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Traditional deep brain stimulation (tDBS) utilizes a constant high frequency delivery of electrical charge to treat Parkinson's disease (PD). Despite the proven benefits of tDBS, it may lead to severe side effects like dysarthria, dysesthesia, or cerebellar ataxia (Dayal et. al, 2017). The side effects can result from the electrode's current spreading to adjacent structures of the brain associated with limbic and motor circuits. Recent studies on the pathogenesis and pathophysiology of PD show that the disease might be associated with an increased synchronization in neuronal activity patterns in the basal-ganglia-thalamocortical circuit (Alexander, 2004). Coordinated reset (CR) is a stimulation technique where multiple contacts of the DBS lead deliver bursts of brief, low-intensity pulse trains to desynchronize pathological neural oscillations. This study investigates a unique CR paradigm in the non-human primate model of PD. A female rhesus macaque with moderate parkinsonism, induced through a series of 1-Methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) injections, was trained to perform a standard reach and retrieval task. A DBS lead (NuMed) was implanted in the STN with electrical stimulation delivered using an external pulse generator (Tucker Davis). The changes in mUPDRS scores and the animal's performance (reach duration, retrieval duration, and reaction time) during the reach/retrieval task showed that CR DBS with the intra-burst frequency of 130Hz might work more efficiently than that of 150Hz and 170Hz, which have been used in current CR configurations. The lower intra-burst frequency could be a potential therapeutic alternative to traditional, high frequency DBS and high intra-burst rates in current CR paradigms.

ORGANISMAL AND PHYSIOLOGICAL SCIENCES

THE CONTRACTILE EFFECTS OF *Salvia sclarea* ON SMOOTH MUSCLE TISSUE ISOLATED FROM THE UTERINE HORNS OF *Mus musculus*

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The smooth muscles in our bodies are often overlooked though they play a crucial role in the maintenance of homeostasis in the body. In this study, an aqueous extract of *Salvia sclarea* seeds was applied to extracted uterine horns from *Mus musculus* suspended in organ baths in order to observe the effects that this herbal has on uterine contractions. Results showed that *Salvia sclarea*, commonly known as Clary, and used as a natural birth labor inducer, effectively and significantly induced uterine tissue contractions.

A NOVEL EX OVO CULTURING VESSEL DESIGNED FOR EXPERIMENTATION ON CHICKEN EMBRYO'S CHORIOALLANTOIC MEMBRANE

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Developing an ex ovo chick culturing vessel provides an opportunity to view a unique structural component relevant to standard development. This structure, the chorioallantoic membrane (CAM), is an external vasculature

system that angiogenically proliferates to provide the developing embryo with nutritional support and proper oxygenation. A model that allows a visual representation of this process with ease of manual manipulation can be advantageous for many reasons, one of which includes the testing of various scaffolding materials. In order for this to be a viable model, ex ovo development must closely mirror in ovo development and environmental conditions must remain accurate and stable. Throughout the process of literature review, we have tested many different ex ovo culturing models and determined that our trigonal hexagonal pyramid (THP) constructed of a Nylon-12 polymer and polydimethylsiloxane (PDMS) windows provides us with a high viability rate without presenting structural deformities.

SOCIAL SCIENCES

PREPARING FOR LIFE AFTER ST. OLAF

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With shifting expectations in career services, there is higher accountability for career centers such as the Piper Center to fulfill its mission to give all students equal opportunity to find jobs. In order to provide students at St. Olaf with access to meaningful career services and experiential learning, our project investigates trends and relationships related to engagement with the Piper Center, as well as participation in internships, research, and other forms of experiential learning. We are specifically interested in looking at the differences between race & ethnic groups, athletes & non-athletes, low-income/ first generation, financial needs, and majors. Using statistical analysis, we looked at the utilization rates of career services including career coaching appointments and career and networking event attendance for five class years of St. Olaf students. Additionally, our research includes analysis of self-reported engagement in experiential learning practices including internships and undergraduate research for four years of graduating classes. Finally, our research compares career center engagement and experiential learning participation with students' confidence in their ability to pursue meaningful work post-graduation.

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