Winthrop University
Summer Undergraduate Research Experience (SURE)
2025 Abstract Book

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The Standard and Misère Ramsey Game for Stars

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Dom Luca (2026)
Justin Stone (2027)
Gwen Tomlin (2027)

Mentors: Dr. Arran Hamm
Dr. Jessie Hamm

Given a graph H and a number n, define the following two-player game between the players Blue and Red played on the complete graph with n vertices. The players will alternate turns coloring an uncolored edge with Blue going first. In the standard version of the game, the player who creates H in their colors is the winner. Define RG(H) to be the smallest n value for which Blue has a *winning strategy* (i.e. a set of moves which result in Blue winning no matter what moves Red makes). In the misère version of the game, the player who creates G in their color loses.

A star on m vertices is a graph containing m vertices in which one vertex has an edge to each other vertex with no other edges present in the graph. Prior work on the standard Ramsey game in which H is a star on m vertices established some values and upper bounds on RG(H); see Ramsey game numbers by W. Garsarch, C. Kruskal, D. Lu, E. Weaver, and N. Wilkinson for more details. Our work focused on extending these results and improving the upper bounds for larger values of m with some partial results obtained. Prior work on the misère Ramsey game in which H is a start on m vertices demonstrated that Red has a winning strategy so long as n is much larger than m; see The star avoidance game by A. Beker for more details. Our work focused on reducing the ratio of n to m and some partial results were obtained in this direction.

This work was supported primarily by SC INBRE.

Expression and Purification of YopJ Novel Acetyltransferases from Xanthomonas Vesicatoria

Payten Baldwin (2027) **Mentor: Jason Hurlbert, PhD**

Genes, *xopJ2A* and *xopJ2B* of the Xanthomonas family were found to increase the virulence of phytopathogens that cause bacterial spot disease. This study aims at expressing and purifying XopJ2 proteins, which matters because it can reveal information about the proteins structure, function, and interactions. This was studied first through the transformation of recombinant XopJ2 proteins in *Escherichia coli* and then through expression testing, lysis, and purification protocols. After testing I expect to find the presence of pure XopJ2 protein. These findings will contribute to future structural and functional predications and aiding the development of future strategies to inhibit these genes.

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Effects of Invasive Vegetation on Invertebrate Communities in a Piedmont Woodland

Alexis Becht (2025),
Kasey Long (2025)

Mentor: Dr. Kiyoshi Sasaki

Nonnative plants are widely assumed to degrade habitat quality for native animal communities, yet empirical studies evaluating their ecological impacts remain limited. In this study, we examine how invasive plant species influence invertebrate community structure in Winthrop Woods, Rock Hill, South Carolina. We assess changes in species richness and abundance across multiple invertebrate taxa in relation to the cover of six invasive plant species. Lophotrochozoans, including annelid worms (Phylum: Annelida) and mollusks (Phylum: Mollusca), exhibited higher species richness in areas with greater cover of *Elaeagnus umbellata* (autumn olive). In contrast, arthropods (Phylum: Arthropoda) showed no consistent relationship with any of the invasive plant species surveyed. Invertebrate richness showed little or no directional change in response to *Ligustrum sinense* (Chinese privet), *Wisteria sinensis* (Chinese wisteria), *Vinca major* (bigleaf periwinkle), *Microstegium vimineum* (Japanese stiltgrass), or *Phyllostachys aurea* (golden bamboo). Earthworms (Family: *Lumbricidae*) and snails (Class: *Gastropoda*) were more abundant in areas with higher *E. umbellata* cover, whereas millipedes (Class: *Diplopoda*) and woodlice (Order: *Isopoda*) were less abundant. Earthworms and millipedes also tended to be more abundant in areas dominated by *V. major*, while flatworms (Phylum: *Platyhelminthes*), cockroaches (Order: *Blattodea*), and woodlice were less abundant. These findings demonstrate that invertebrate responses to invasive plants vary across taxonomic groups, with both increases and declines observed. Such taxon-specific patterns suggest that nonnative vegetation alters invertebrate communities in complex and context-dependent ways.

This project was funded by SC-INBRE

Investigating the Role of miRNAs in RYBP Downregulation in Glioblastoma Cells

Israel A. Bellinger (2026) **Mentor: Daniel B. Stovall, PhD**

Glioblastoma multiforme (GBM) is an aggressive, malignant tumor of the central nervous system (CNS) with poor clinical outcomes and limited treatment options. The standard treatment of care is combined radiation and chemotherapy, which only increased patient survival by about 2.5 months compared to radiotherapy alone. However, these treatments also damage healthy cells, and tumor recurrence is functionally inevitable. Thus, research that investigates and targets the underlying cellular and molecular mechanisms that allow for GBM cell survival and proliferation is needed in hopes of discovering more targetable therapeutic pathways. One of these mechanisms is the alteration of the expression of RING1- and YY1-binding protein (RYBP), a Polycomb group (PcG) protein that is typically a tumor suppressor in various cancers and is frequently downregulated in GBM patients. However, the method of downregulation that GBM cells utilize to silence RYBP is currently unknown. One possible method of downregulation that we investigated is the overexpression of microRNAs (miRNAs): small, single-stranded, noncoding RNA fragments that bind to mRNA transcripts via complementary base pairing to inhibit protein synthesis. After observing the endogenous expression of RYBP protein levels in a panel of five different human GBM cell lines, we transfected "RYBP-low" U-251, U-87, and T-98 cells with specific miRNA inhibitors, isolated and quantitated total protein, and ran SDS-PAGE and Western blotting to observe any increase in RYBP expression. While we observed that endogenous RYBP expression differs in GBM cells, our miRNA inhibitor results were inconclusive, as we were not able to detect RYBP post-transfection. Therefore, further investigation into the miRNA-RYBP-GBM signaling axis is warranted in future studies.

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New Catalysts for Visible-Light Photoredox Chemistry

Sarah Buchanan (2027) **Mentor: Dr. Grattan**

Most chemical reactions require a catalyst to occur. Catalysts can be dangerous to work with and require numerous safety precautions. A relatively new field of chemistry called photoredox catalysis utilizes light to excite the catalytic cycle. These catalysts are cheaper to produce and safer to use when compared to traditional catalysts. A new organic catalyst with a unique central structure has been synthesized to be more efficient, safer, and cheaper to make. So far, these unique catalysts have been tested in an imine alkylation reaction, fluorination reaction, and lactonization reaction. All three reactions show better yield when compared to the commercial acridinium photoredox catalysts; in some cases, the yield is doubled compared to the commercial catalyst. Variations of the catalyst with the same unique central structure have been designed to produce better results for specific reactions. Future research plans include testing the catalyst in new reactions and testing the new variance catalysts.

This research is sponsored by a grant from the National Science Foundation under award number 2400166, Collaborative Research: Exploration and Development of High Performance Thiazolothiazole Photocatalysts for Innovating Light-Driven Organic Transformations.

Patterns of amphibian and reptile diversity across habitat types in a restored Piedmont agricultural landscape

Wyatt Burton (2025) **Mentor: Dr. Kiyoshi Sasaki**
Zainah Villa Mora (2028)

Understanding how different habitat types influence species richness is essential for effective biodiversity conservation. This study examined amphibian and reptile richness across a range of habitats within a Piedmont landscape in South Carolina, a former agricultural area now undergoing private restoration to promote wildlife habitat. Amphibian richness was highest in bottomland hardwood, upland mixed, and water-associated habitats. Notably, Chamberlain's dwarf salamander (*Eurycea chamberlaini*), a species with data-deficient conservation status, was found in bottomland hardwood forests, while spotted salamander (*Ambystoma maculatum*), which is experiencing population declines in parts of its range, was observed in upland mixed forests. Amphibians were largely absent from pine plantations, upland hardwood, and restored prairie habitats. Reptile richness showed similar patterns, with elevated richness also observed in infrastructure-associated habitats, which may provide thermal and structural benefits. These results highlight the importance of preserving and restoring a mosaic of structurally complex and moisture-rich habitats to support amphibian and reptile diversity in Piedmont landscapes.

This project was funded by Carolina Wildlands Foundation and SC-INBRE

Bacteriophage Isolation on Novel Hosts

Simon Cherry (2028) **Mentor: Dr. Victoria J. Frost**
Sasha Vorontsov (2028)

Bacteriophages (phages) are viruses found wherever their bacterial hosts exist. Phages require these hosts because they use the cell's replication machinery to produce more copies of themselves. Last summer, research students in our lab investigated the host range of Winthrop's collection of sequenced phages, initially isolated on the bacterial host *Mycobacterium smegmatis*. Some of these phages could cross-infect alternative hosts within the same genus, such as *Mycobacterium nonchromogenicum* or *Mycobacterium aurum*. The goal of this research was to isolate novel phages using *M. nonchromogenicum* and *M. aurum* as the original hosts and to add to the diversity of phages in Winthrop's collection for future studies. Twenty-three soil samples were collected from various sites around campus, shaken for 2-16 hours, and then filtered. The filtrates were incubated with bacterial hosts and plated. We observed areas of lysis caused by four different phage samples. Two phages were isolated on *M. nonchromogenicum*: PinkLady and LadyMaria, and another two on *M. aurum*: GreatGreta and Midna. PinkLady and LadyMaria formed clear plaques (PinkLady's were tiny, 2.5-5 mm in diameter) on *M. nonchromogenicum*. Midna also produced clear plaques on *M. aurum*, while GreatGreta formed larger, turbid plaques. After purifying and amplifying each phage, high-titer lysates (HTLs) were obtained for DNA extraction. Restriction digest patterns of the DNA allowed initial molecular characterization, which will be followed by selecting phage(s) for genomic sequencing and annotation. Increasing the variety of phages isolated on different hosts will broaden the diversity of phages for future comparative studies and enhance our understanding of their biology.

Support was provided by an SC-INBRE grant from the National Institute for General Medical Sciences (P20GM103499), Winthrop Biology Department, and HHMI.

Investigating L1 cell adhesion molecule and LPA signaling modulation on axonal outgrowth of chicken embryonic retinal ganglion cells

Marisela Chicas (2027) **Mentor: Dr. Eric Birgbauer**

Retinal ganglion cells (RGCs) transmit visual stimuli from the retina to the brain via the optic nerve. During the process of visual development, axons navigate through the extracellular environment through growth cones. Growth cones are sensory motile structures on the ends of developing axons. These specialized structures ensure proper axon navigation; growth cones are guided by molecules that attract or repel the axon through receptors, cell adhesion molecules and their signaling pathways. Previous experimentation has shown that in vitro, Lysophosphatidic acid (LPA) causes dose-dependent growth cone collapse or retraction. In contrast, L1 is a cell adhesion molecule that plays a significant role in fasciculation and neuronal migration. These signaling molecules have the ability to influence growth cone behavior and guidance. We investigated neurite outgrowth on the L1 substrate. Initial effort for a standard LPA treatment on neurons was conducted. To examine the relationship between L1 cell adhesion molecule and LPA, further investigation will be performed.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number P20GM103499 (SC-INBRE)

SDF-1/CXCR4 Modulates LPA Responses in Chicken Embryo Retinal Ganglion Cells (RGCs)

Marsenia Chicas (2027) **Mentor: Dr. Eric Birgbauer**

Retinal ganglion cells (RGCs) are neurons located in the eye that are responsible for transmitting visual information to the brain. RGCs have long projections called axons that bundle together to form the optic nerve that acts as the pathway for visual information relay to the brain. Axonal guidance is necessary for the axons from retinal ganglion cells to ensure proper development of the visual system. During development, on the ends of axons are growth cones, which are responsible for axonal growth and guidance as they explore the extracellular environments. These structures navigate through the extracellular environment via adhesion receptors and actin-based protrusions. Growth cones have been shown to react to molecular cues, which include inhibitory molecules. Previously it has been shown that lysophosphatidic acid (LPA) causes a dose-dependent growth cone collapse in embryonic chicken retinal neurites in vitro, indicating that LPA is an inhibitory molecule. Previous experiments have also shown that the chemokine SDF-1 modulates this response to LPA, effectively preventing growth cone collapse. The chemokine SDF-1 binds to and activates the G protein-coupled receptor CXCR4, which leads to a signaling cascade within the growth cone. To investigate the role of the receptor CXCR4, we used the antagonist AMD3100, which prevents the binding of SDF-1. We found that AMD3100 decreases SDF-1's effectiveness in preventing LPA induced growth cone collapse. In the future, investigation of SDF-1's second receptor CXCR7 is necessary to ensure deeper understanding of SDF-1's role in visual development.

This research was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number P20GM103499 (SC-INBRE).

Discovery Research on Zinc Oxide and Soil Composition

Brenleigh Dailey (2027),
Kenneth Raudales (2027),
Ceseley Trower (2027)

Mentor: Dr. Maria C. Gelabert

The *STEM Preprofessional Experience* (*STEMPE*) engaged Year 1 and Year 2 STEM majors in authentic research, educational field trips, and career explorations (including experience in area middle and high school STEM classrooms). All activities focused on water—specifically, the Catawba River.

Our project focus was twofold: to investigate local soil samples and a separate discovery project on doped Zinc Oxide (ZnO). For the soil composition research, dirt and mud samples were collected and compared to USGS and local mineralogy. Soil samples were first dried, then ground into a fine powder for X-ray diffraction analysis with a Rigaku MiniFlex-600 instrument. The Match! Software was used to compare the diffraction results with other patterns in a database to identify possible compounds. The soil samples closely aligned with the elements that were expected to be found from USGS statewide analysis, such as quartz, alumina, and potassium nitrate.

For the ZnO research, our goal was to incorporate nitrogen into the zinc oxide compound (*p*-type ZnO) which could be used for material for biosensors, or antiviral/antibacterial applications. Zinc solutions were prepared from zinc nitrate, elemental zinc, KOH, and an EDTA chelating agent with variable polymer and pH. Aqueous samples were placed into Teflon-lined autoclaves for oven synthesis between 95 and 180 °C. After synthesis, centrifuging revealed very little solid product, and fluorescent lighting indicated luminescence. Excitation and emission characteristics were investigated with a PTI Spectrophotometer. While the N-doped ZnO syntheses produced virtually no powder, fluorimetry emissions and excitations were observed that are consistent with ZnO nanoparticles. Sample comparison revealed that polymer-containing samples showed more shifts in emission with increasing KOH.

Support was provided by the National Science Foundation's Robert Noyce Teacher Scholarship Program (NSF2345156) and the Winthrop Biology Department.

Effects of Rain Events on Fish Gill Physiology and *Escherichia coli* Presence in Freshwater Streams

Lily Doyle (2025) **Mentors: Dr. Frost and Dr. Blair**

Rain events affect water chemistry and can lead to contamination of river systems including increased bacterial loads. The presence of *Escherichia coli (E. coli)* is a common indicator of fecal contamination in river systems. Changes in water quality can affect fish health and trigger physiological responses such as gill remodeling, whereby the structure of their gills is altered in response to changes in a variety of environmental abiotic factors. This change in the surface area of the gill occurs via shrinkage and growth of the interlamellar cell mass (ILCM). This project aimed to understand how rainfall impacts microbial populations in river systems, as well as its effects on fish gills, skin, and gill physiology. The hypothesis is that precipitation events will cause increased turbidity and bacterial concentrations, specifically an increase of *E. coli* in river systems, as well as changes in fish gill physiology. Fish (Bluegill and Redbreast sunfish) and water samples were collected in Fishing Creek before and after a rain event. *E. coli* colony counts (Colony Forming Units; CFU) and bacterial density (OD_{600}) were measured from water samples and swabs of the fish skin and gills. ILCM to lamellae ratio measurements were taken, and water chemistry data were analyzed. After the rain event occurred, there was a significant increase in bacterial density in the water samples, skin swabs, and gill swabs. There was also a significant increase in *E. coli* colonies in the water samples. Interestingly, a significant decrease in the ILCM-to-lamellae ratio occurred in the fish gills, indicating an increase in lamellae surface area. These results suggest that rainfall events can elevate bacterial exposure as well as influence gill physiology of fish in small freshwater river systems.

Support was provided by an SC-INBRE grant from the National Institute for General Medical Sciences (P20GM103499), and Winthrop Biology Department.

Synthesis of Zone 2 Modification of Sphingosine Kinase Inhibitor 1 for Cancer Treatment

Morgan Dukes (2026) **Mentor: Dr. T. Christian Grattan**

Sphingosine kinase-1 (SK1), an enzyme in the sphingomyelin metabolic pathway, regulates whether the cell undergoes apoptosis or cell proliferation. Cancer prevents apoptosis from occurring by hyperactivating SK1 converting sphingosine to sphingosine-1-phosphate (S1P) signaling for proliferation. Inhibitors for SK1 are needed to stop S1P production. Using a known sphingosine kinase inhibitor (SKI-1), three new derivatives were created to improve the oral bioavailability while improving or maintaining interactions with SK1. Modifications were made to the central pyrazole ring and terminal naphthalene ring of SKI-1. Through multiple syntheses, the final products of 24A, 24C, and 24D were successfully produced and verified by 1H-NMR.

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Studying Homology Directed DNA Repair in *Drosophila*

Hannah Duncan (2026) **Mentor: Dr. Evan Dewey**

For multicellular life to survive, genome stability must be maintained. DNA is exposed to tens of thousands of sources of damage each day, and it must combat this damage to prevent genome instability and cancer. One repair pathway for double strand breaks is Homology Directed DNA Repair (HDR), which uses an undamaged chromosome as a template. HDR must be appropriately regulated to ensure use of the identical sister chromatid, and not the non-identical homologous chromosome. This is to prevent crossovers between non-identical homologs, which can potentially lead to cancer and disease. It is still unknown exactly how and why these crossovers occur, however. Our lab studies *fancm,* which encodes a protein in the FA anchor complex for resolving interstrand crosslinks, a process that includes HDR repair of a double strand break. Additionally, CRISPR/Cas9 genome editing tools require accurate and predictable HDR, but it is not yet thoroughly understood. To better understand both *fancm* and CRISPR/Cas9, *fancm* mutant male flies with DNA double strand breaks induced by CRISPR/Cas9 in the *ry* gene were crossed with females containing a deletion in the same gene. The paternal chromosome was amplified from the progeny to determine whether a crossover event occurred during repair. Further investigation is required to fully understand the mechanisms that lead to CO and NCO products.

This work was supported by SC INBRE, a grant from the National Institutes of Health National Institute of General Medical Sciences (P20GM103499).

Stabilization of G-Quadraplex Structures Increases RYBP Transcription in Glioblastoma Cells

Ariyana Felder-Grooms, **Mentor: Dr. Daniel Stovall**
Evonna Kinloch,
Hannah Nation (2026), (2027)

Glioblastoma Multiforme (GBM) is the most common and lethal CNS tumor with a median survival rate of less than 15 months (Kanderi et. Al 2022). Standard treatment for GBM currently is surgery and chemotherapy using temozolomide. GBM alters the expression of the Polycomb (PcG) group of proteins. The PcG protein Ring1- and YY1-Binding protein (RYBP) is a component of the non-canonical Polycomb Repressive Complex 1 (PRC1) and modifies and compacts chromatin to regulate cell identity (Araujo-Abad et. Al 2023). RYBP is downregulated in about 50% of GBM patients (Li et al., 2013), but no mechanism has yet been proposed. G-Quadruplexes (G4) are secondary structures formed by guanine-rich DNA or RNA sequences that can increase or decrease transcription (Spiegel et. Al 2020). They can be resolved by helicases called resolvases, such as RecQL4 and DHX36 (Hansel-Hertsch et. Al 2016). Meanwhile, pharmacological ligands have been deveoped to stabilize G4s, including Phendc3, Pyridostatin, and Tmpyp4. Our results show that the G4 ligands Phendc3 and Pyridostatin significantly increased RYBP expression after 24 hours in multiple GBM cell lines. We also tested Tmpyp4, which modestly but statistically increased RYBP expression in U-251 and T-98 cells, but not U-87 cells. Interestingly, knockdown of DXH36 did not affect RYBP expression in U-87, T-98, or U-251 cells, whereas RecQL4 did not affect RYBP expression in U-251 cells but caused significantly decreased RYBP in T98 cells. Overall, our results suggest that G4 stabilization by pharmacological ligands increases RYBP expression in GBM, and that DHX36 nor RecQL4 are likely involved in RYBP silencing.

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Nucleic Acid Aptamer Gold/Silver Nanoparticle Conjugates as Trojan-Horse Drug Delivery Vehicles in the Fight Against Bacterial Infections

Ashely Francisco (2026),
Cierra Ari Randolph (2026)
Mentor: Dr. Timea G. Fernandez

The alarming rise in antibiotic resistance is extensively documented, with studies indicating that the misuse and over-prescription of antibiotics contribute significantly to this crisis. Our research proposes the fabrication of modular nanodevices for the targeted delivery of antibiotics to bacterial strains using aptamers. We investigated the therapeutic potency of nucleic acid-gold/silver nanoparticle conjugates as carriers of tetracycline and ampicillin to treat infections caused by *E. coli*. Currently, we are investigating how the morphology, dimensions, and surface coatings of silver/gold nanoparticles can augment their antimicrobial activity in the context of targeted antibiotic treatments.

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The Devonian Mass Extinction: approaching big problems from a microscopic perspective

Kylie Full (2026) **Mentor: Dr. Diana Boyer**

The Devonian Period was characterized by high marine biodiversity, but environmental instability led to several extinction events, including the Hangenberg and Kellwasser Events. The Late Devonian Extinction is considered one of the top 5 biggest mass extinctions and is still a mystery to this day. It went from a reef ecosystem dominated by stromatoporoids and brachiopods to being dominated by other organisms. This study aims to quantify changes in marine communities by analyzing fossil composition in petrographic thin sections from the Guilmette Formation, pre-extinction, and the Joana Limestone, post-extinction, in the Great Basin, U.S.A. Using the point count method, we assessed structural shifts in marine life before and after the extinction. While this method has limitations, it provides a valuable opportunity to describe ecological transitions and the long-term impacts of extinction events on marine biodiversity. While many invertebrate taxa remained present before and after the extinction, there was a large increase in echinoderms, with the average counts per slide for echinoderms before the extinction being 1.8 and after being 62.4. There was a small shift in brachiopods, with 15.2 average counts per slide pre extinction and 11.74 post extinction. The evenness in taxa remained relatively similar comparing pre/post extinction slides, before being 0.6 and after being 5.2. Taxonomic richness is also very similar at 6.1 before and 5.2 after. One of the main takeaways from this research is that the communities from before and after show a shift in dominance from brachiopods and stromatoporoids to echinoderms.

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Total Synthesis of Sphingosine Kinase Inhibitor 1 Derivatives for Cancer Treatments

Kalli Green (2027) **Mentor: Dr. Christian Grattan**

Targeted chemotherapy is a new and developing technique that has the ability to identify a specific molecule and pathway, increasing the efficiency by only affecting abnormal cancerous cells. The sphingomyelin pathway is important in cell regulation, signaling, and determining cellular fate. Inhibition of sphingosine kinase isoform 1 (SK1), within this pathway, leads to a buildup of sphingosine and ceramide, two molecules directly linked to cell apoptosis. It also decreases the intracellular concentration of sphingosine-1-phosphate (S1P), a molecule linked to cellular proliferation. Recently, an inhibitor, sphingosine kinase inhibitor 1, SKI-1) was identified which showed promising inhibitory ability of SK1. Due to the inhibitor's hydrophobic properties, it is incapable of metabolizing in the body. A set of compounds will be designed to assess the binding influence of the naphthalene by substituting pyridine rings into the template compound with the target enzyme in an attempt to obtain a compound with increased efficacy *in vivo*. These inhibitors were synthesized and evaluated using NMR. Microwave heating was used to synthesize modifications of the template inhibitor in an attempt to produce a more efficient candidate capable of at least maintaining the inhibition of SK1 *in vitro*, while also improving the bioavailability of the compound for *in vivo studies*. These novel derivatives will be submitted for assay testing to identify the best modifications throughout the structure separately and then combined to produce a promising drug candidate for the targeted therapy of cancerous cells.

Culturally Responsive Teaching and Student Outcomes in K-12 Classrooms: A Synthesis of Research-Based Practices

Ja'Niyah Heyward (2027) **Mentor: Dr. Minnie Mize**

This synthesis examined the impact of culturally responsive teaching (CRT) on student outcomes in K–12 classrooms. As school populations become increasingly diverse, CRT offers a structured approach to addressing students' academic, cultural, and social needs. We conducted a mixed methods review of peer-reviewed studies published between 2010 and 2025, encompassing both qualitative and quantitative research. Findings consistently associated CRT practices with improved student engagement, academic achievement, and behavioral outcomes. While the heterogeneity of study designs limited formal statistical aggregation, the consistency of results across contexts supports the reliability of CRT's positive effects. These findings underscore CRT's potential as a promising framework for advancing equity and enhancing student success in diverse educational settings.

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The STEMPE Experience: Analysis of Water Samples Collected from the Catawba River Basin, and an Introduction to Local Middle and High School Teaching Practices

Kierra Hicks (2028),
Dylan Incorvaia (2026),
Jay Smith (2029)

Mentors: Dr. J. Chism and Dr. V. Frost

The STEM Preprofessional Experience (STEMPE) engaged Year 1 and Year 2 STEM majors in authentic research, educational field trips, and career explorations, including experience in area middle and high school STEM classrooms. All activities focused on water—specifically the Catawba River. The STEMPE biology students studied the water quality in the Rock Hill area of the Catawba River Basin, assessing its safety for human recreational activities. Water samples were collected at five different locations, either from tributaries or directly from the Catawba River. Each sample was collected in triplicate and tested for the presence of *Escherichia coli* (*E. coli*) using Petrifilm media plates. One milliliter of each sample was inoculated onto individual plates and incubated at 37° C for 24 hours. Colony-forming units (CFU/mL) were enumerated following incubation. The water samples collected at this time did not contain *E. coli* levels above the U.S. Environmental Protection Agency's recommended safety thresholds for recreational use. Students' exploration of water also examined how rising sea levels lead to saltwater intrusion into freshwater habitats. To assess the effects of this process on living organisms, students investigated the effects of increasing salt concentration on *E. coli*. In addition to these research activities, biology students also visited local middle and high schools in Rock Hill to shadow biology teachers. This provided students with the opportunity to interact with both students and teachers during ongoing lessons and observe the implementation of teaching practices in a real-world setting.

Support was provided by the National Science Foundation's Robert Noyce Teacher Scholarship Program (NSF2345156) and the Winthrop Biology Department.

Investigating the Role of Pax6 in Embryonic Chicken Corneas in Relation to Immunity

Mitchell Hill (2026),
Nadia Smith (2026),
Abby Weber (2025)

Mentor: Dr. Jena Chojnowski

Aniridia is a congenital disease characterized by a partial or complete absence of the iris. This condition is known to be caused by a mutation in the PAX6 gene, a highly conserved transcription factor essential for development, cellular maintenance and repair, and immune function. The objective of this research is to investigate the immunological role of PAX6 while establishing techniques for future studies. PAX6 expression has been shown to influence cellular repair in the cornea, but its specific role in regulating immune responses remains unclear. This work investigates the role of PAX6 in immune function and wound healing within the corneas of embryonic chicken eyes. The chicken cornea was utilized as the model tissue for this work, due to the well-conserved nature of PAX6 and the frequent use of chicken eyes as human analogs. Whole corneal dissections and dissociated corneal cells were employed to perform histological and immunohistochemical analyses. We focused on the differences in structure and expression in the limbal (peripheral) and central regions of the cornea and their respective responses to induced damage. The preliminary findings from this work demonstrate PAX6 expression in stromal and epithelial cells of the limbal region, as well as in the central corneal epithelium. This work establishes a foundation for future studies investigating PAX6-mediated immune and repair pathways in a human model and has potential applications in developing therapies that target immune and repair dysfunctions in aniridic patients.

Grant support: SC INBRE and the Research Council Grant

CAIN55 mycobacteriophage gene allosteric modulation of transcription termination factor NusA

Be Kuehn (2026) **Mentor: Dr. Jason Hurlbert**

An environmentally isolated phage gene has recently been identified as cytotoxic to members of the *Mycobacterium* genus. The gene, CAIN55, encodes a 308 amino acid protein that was found to bind to the transcription termination factor, NusA, by a two-hybrid assay. COBALT Multiple Alignment indicated high conservation between CAIN55 and the NusA/λN antitermination complex. λN protein is a bacteriophage protein with a solved structure that promotes termination pause in complex with NusA. From the CAIN55 and λN protein alignment, a conserved 18 amino acid fragment was identified. The conserved region on λN protein contains residues within 3.5 Å of NusA, indicating this region as a potential region of importance for the protein's antitermination activity. We have expressed and purified E. coli NusA for ITC analysis with the CAIN55 fragment to confirm binding and determine kinetic and stoichiometric parameters.

Winthrop University Ronald E. McNAir Postbaccalaureate Achievement Program, Grant #P217A230073.

A Dynamics Informed Neural Network Model for Measles Transmission

Jake Matthews (2028),
Eddie Wenker (2028),
Camryn Whipple (2027)

Mentors: Dr. Kristen Abernathy,
Dr. Zach Abernthy

Dynamics Informed Neural Networks (DINNs) combine traditional compartmental models within the architecture of a neural network. With the outbreak of COVID-19, the use of DINNs have been applied to published COVID data to more accurately predict transmission rates with limited data. In this project, we apply this technique to the study of measles transmission in the United States. We use an SEIRV compartmental model to track the spread of measles through the population. We then construct a DINN that uses the SEIRV compartmental model with current US measles data to predict transmission rates and numbers of infections. We compare the results from the DINN to predictions from a corresponding neural network that excludes the dynamics structure. We find that excluding dynamics in the neural network architecture produces a transmission rate profile and basic reproductive ratio that are not supported by data. Predicted SEIRV compartments without dynamic architecture fail to make sense in a real world setting. With the dynamics architecture, the neural network produces a transmission profile with peaks preceding rises in infection. Additionally, the corresponding basic reproductive ratio is within statistically validated basic reproductive ratio ranges for a measles outbreak.

This work was supported primarily by the National Science Foundation EPSCoR Program under NSF Award #OIA-2242812.

Effects of Ectopic RYBP Expression on Glioblastoma Cell Proliferation

Rachell McCollum (2025) **Mentors: Dr. Dan Stovall**

Glioblastoma multiforme (GBM) is the most common and lethal cancer of the central nervous system with a median survival rate of around 15 months. The RING1 and YY1 binding protein (RYBP), a transcription factor, displays decreased expression in GBM and is a member of the Polycomb group (PcG) of proteins. We hypothesized that RYBP exerts tumor suppressive effects in glioblastoma cells by inhibiting cell proliferation. Based on extensive research in other cancers, RYBP widely behaves as a tumor suppressive gene across tissue types and can lead to inhibiting cell proliferation. However, there is no current research on the phenotypic effects of losing RYBP in GBM. We first cultured five GBM cell lines and determined the endogenous RYBP levels in each. U-87 and U-251 GBM cell lines, which had the lowest endogenous level of RYBP, were then transduced with lentivirus to force ectopic expression of RYBP. Infection with a control virus that did not express RYBP was also included. After optimizing transduction and confirming successful RYBP expression, we determined that there was no statistically significant difference between cell proliferation in RYBP-expressing and control cells for either U-87 or U-251 cell lines, based on two independent experiments in each cell line. These experiments need to be repeated with greater technical precision. Future directions will also focus on studying the effects of RYBP on other GBM cell phenotypes, such as invasiveness, and determining RYBP's direct gene targets.

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Plant species interactions in Florida rosemary scrub

Amber Mercer (2027) **Mentor: Dr. Jennifer Schafer**
Kerrington Norman (2025)

The Florida scrub ecosystem contains a multitude of endangered plant species, which are threatened due to habitat loss. Florida rosemary scrub, a vegetation type within the Florida scrub ecosystem, has open gaps among the shrubs. Florida rosemary produces allelopathic chemicals, which contribute to maintenance of gaps and affect germination and survival of endangered and endemic herbaceous species. The ground cover species *Licania michauxii* (gopher apple) and *Selaginella arenicola* (sand spikemoss) co-occur with endangered species in the gaps. We investigated whether ground cover species interact with herbaceous plant species in Florida rosemary scrub gaps. We established paired 20 x 20 cm plots in gaps; one plot had a high amount of bare soil, and one plot had high cover of one of the ground cover species. We identified and counted plant species present in the plots. There was a significant association between plot type and presence of other plant species for *Selaginella*, but not for *Licania*. Bare plots tended to have other plants in them more often than *Selaginella* plots. There was an effect of *Licania*, however, on the number of plant species present; there were more plant species present in *Licania* plots than in bare soil plots. In contrast, we found that bare soil plots had a significantly higher number of other plants than *Selaginella* plots. Our results suggest that *Licania* facilitates occurrence of other plants, while *Selaginella* inhibits herbaceous plants in Florida rosemary scrub gaps. This research has implications for scrub restoration.

Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number P20GM103499. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Using Graph Theory to Model the Flow of Water

Winnie Moore (2027) **Mentor: Dr. Jessie Hamm**

The *STEM Preprofessional Experience* (*STEMPE*) engaged Year 1 and Year 2 STEM majors in authentic research, educational field trips, and career explorations (including experience in area middle and high school STEM classrooms). All activities focused on water—specifically, the Catawba River.

My research experience was in the area of math called graph theory. The objective of our research was to use graph theory to model and analyze the capacity of the water systems in Rochester, NY.

We created a graph to model the water system within Rochester, NY. This weighted graph consisted of locations within the region as well as capacities to represent the piping infrastructure in place. We then analyzed this graph and used free online software to find the maximum flow and minimum cut values for the network. We found that the maximum amount of water that can flow through the entire water system at once is 24 million gallons per day.

Support was provided by the National Science Foundation's Robert Noyce Teacher Scholarship Program (NSF2345156) and the Winthrop Biology Department.

Women's Resistance, the Colonized Mind, and Bridging Multigenerational Experiences of Women in the Latin Caribbean

Ariel Moscat (2026) **Mentor: Dr. Heather Listhartke**

Women's resistance literature offers a first-hand recount of the injustice experienced by Latin Caribbean women during historical times of corruption. While utilizing Gloria Anzaldúa's Colonial Mindset's framework, I analyzed the narratives of these women specifically in Puerto Rico, the Dominican Republic, and of Latin Caribbean descent in the United States to draw connections to the shared identity struggle that Latina women have inherited through colonial influences to understand how Latin culture has shifted through generations of resistance. This presentation offers implications to understanding the multifaceted identity of Latina women and how they navigate political and social constructs.

Winthrop University Ronald E. McNair Postbaccalaureate Achievement Program, Grant # P217A230073

Isolation of ExplosioNervosa lysogens and subsequent investigations of their superinfection immunity

Ciaran L. Murphy (2026), **Mentor: Dr. Victoria J. Frost**
Karissa Wilczak (2026)

ExplosioNervosa is a cluster A9 bacteriophage (phage) that infects the bacterial host *Mycobacterium smegmatis* (*M. smegmatis*). ExplosioNervosa is a temperate phage capable of incorporating its genome into a bacterial cell, forming a lysogen. Studies of lysogeny-related phage genes indicate that some lysogens can protect against repeated phage infections (superinfection) using an immunity repressor encoded by the prophage. The immunity repressor is also believed to play a role in lysogeny. ExplosioNervosa has a mutant population with a genome deletion of approximately 4,000 bp, which includes the predicted immunity repressor gene. We hypothesize that this mutant is selected for in the laboratory, where lysogeny may not be necessary. This was tested by attempting to create lysogens of both wild-type and mutant ExplosioNervosa using *M. smegmatis*. Plates were first seeded with a high concentration of phage, then each plate was spread with a dilution curve of *M. smegmatis* to promote lysogeny by gradually decreasing host density. Selected colonies were quadrant-streaked to purify lysogen candidates. Because lysogens continually release phage due to spontaneous reversion to the lytic cycle, they were verified by testing for both bacterial growth and phage release. Only one stable wild-type ExplosioNervosa lysogen was identified. Superinfection immunity assays on this lysogen demonstrated that it is resistant to reinfection by the same phage (homotypic defense) and may have some ability to defend against other phages from different clusters (heterotypic defense). This supports the idea that the immunity repressor is essential for both a stable lysogen and superinfection defense, but more candidate lysogens are being tested to confirm these findings.

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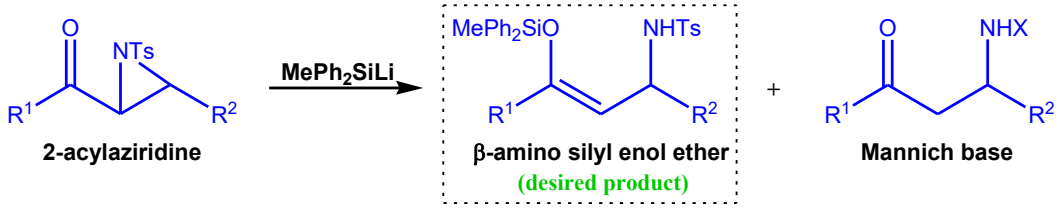
Synthesis of silyl enol ethers from 2-acylaziridines using silyllithium reagents

Abbie Nation (2026) **Mentor: Dr. Aaron M. Hartel**

Silyl enol ethers are useful intermediates in organic synthesis, capable of serving as enolate equivalents in many valuable nucleophilic addition reactions. This research is focused on developing a regio- and stereoselective method for preparing silyl enol ethers from 2-acylaziridines using silyllithium reagents.



The reaction mechanism begins with nucleophilic attack of silylllithium at the carbonyl carbon of the 2-acylaziridine. This is followed by a Brook rearrangement – migration of silyl group from carbon to oxygen – which promotes opening of the aziridine ring and leads to the formation of the silyl enol ether. So far, we have optimized reaction conditions including temperature, solvent, and the amount of silyllithium reagent added for selective formation of silyl enol ether over Mannich base. Current efforts are focused on the isolation and purification of silyl enol ether products via column chromatography.

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Family of Generalized Continuous Bernoulli Distributions: Properties and Applications

Garrett Nix (2027) **Mentor: Dr. Dodamgodage Gihanee Senadheera**

This research aims to introduce new families of generalized continuous Bernoulli distributions using the T−R{Y} framework. These distributions are called T-continuous Bernoulli{Y} families, and arise from the quantile functions of the exponential, Weibull, logistic, Cauchy, and extreme value distributions. Some of the general properties of the T-continuous Bernoulli{Y} families are investigated and discussed. Two new generalized continuous Bernoulli distributions are discussed and applied to three different datasets to observe the performance of these generalizations.

This project is supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences (P20GM103499-20) from the National Institutes of Health. We would like to thank the South Carolina INBRE Program, Winthrop University Summer Undergraduate Research Experience Program, and the Winthrop Department of Mathematics for both the support and funding of this project.

Mammalian Cell Viability Evaluation of Nucleic Acid Aptamer Gold and Silver Nanoparticle Conjugates

Julianne Phu (2026) **Mentors: Dr. Timea Fernandez, Dr. Kirill Afonin**

Illnesses caused by bacteria are a major public health concern since microorganisms have become increasingly resistant to available antibiotics. At the same time, big pharma has gradually shifted its focus from developing drugs that cure diseases to those that treat chronic conditions. Thus, rediscovering old drugs and using them for new purposes is becoming more important. The long-term goal of this project is to use nucleic acid aptamer-nanoparticle conjugates as vehicles for targeted delivery of antibiotics to bacteria that are resistant to them.

In previous work, the therapeutic potency of nucleic acid-gold and silver nanoparticle conjugates as carriers of tetracycline and ampicillin to treat infections caused by Gram-Negative model organisms was investigated. It was hypothesized that by attaching nucleic acids that binds to these antibiotics to gold and silver nanoparticles, the resulting conjugates will work as a "Trojan-horse" antibiotic-delivery vehicle that smuggles the antibiotic into the cell without being detected by cellular defense systems.

To ensure these conjugates are nontoxic for potential use as human therapeutics, MTS assays were conducted to verify that the aptamer-nanoparticle conjugates do not harm mammalian cells. Nanoparticles tend to accumulate in the liver to be processed before being excreted from the body. Therefore, streptavidin coated gold, as well as citrate coated gold and silver, were conjugated with ampicillin and tetracycline aptamer and tested on human liver carcinoma cells (HEPG2). They were also tested on human embryonic kidney cells (HEK293FT), and human ovarian cancer cells (HeLa) to determine the viability of a wider range of human cells. The conditions to attach DNA aptamers to gold and silver nanoparticles were optimized and all conjugates were tested at 10x their MIC with three biological repeats. The conjugated nanoparticles demonstrated no mammalian cell toxicity while 5nm silver nanoparticles alone showed some toxicity to HepG2 cells.

This work was supported by funding from SC INBRE #5P20GM103499 and MADE in SC EPSCoR, NSF #1655740 and by Winthrop University College of Arts and Sciences.

Expression and Purification of a Non-Secreted α-Amylase from *Xanthomonas*

Samuel Reese (2026) **Mentor: Dr. Jason Hurlbert**

α-amylases are secreted enzymes that catalyze hydrolysis of α-1,4-linked oligosaccharides during starch degradation by members of the phytobacterial pathogen *Xanthomonas.* We have identified a novel gene encoding a putative α-amylase, named XamyL (XamyLarge), which possesses an extended N-terminal region that appears to block secretion of the α-amylase, but appears to be required for virulence. The research described herein represents the first steps in the process to crystallize and characterize XamyL to better understand the role of the protein to the bacterium. To better understand the properties of this novel, non-secreted α-amylase, the gene for *XamyLarge* was cloned into a pET28-based vector and expressed in *Escherichia coli.* Optimal conditions for bacterial growth and protein expression were evaluated. Following cell growth under each condition tested, cultures were harvested, lysed and the recombinant XamyL was purified from the lysate via metal chelating affinity chromatography. Protein expression and purification was assessed by SDS-PAGE and western blotting. Optimal expression occurred at 30°C using 1 mM IPTG. This establishes the best foundation to produce XamyL for future research efforts inclyding protein structure determination via x-ray crystallography and enzymological studies to determine the mode of action of the protein.

Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under Award Number P20GM103499. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Visualizing Trafficking of Stereocilia Myosin Motors at the Single Molecule Level

Ryerson, Elizabeth (2026) **Mentor: Dr. Jonathan Bird (University of Florida)**

Stereocilia are located within the cochlea and are essential for the detection of sound and the sense of hearing. Stereocilia are actin-based structures that mediate mechanoelectrical transduction to convert fluid motion in the cochlea into electrical impulses that are transmitted to the brain. Development of stereocilia during embryogenesis is facilitated by myosin 15 (MYO15A), an ATP-dependent motor protein. Significantly, mutation of MYO15A suppresses stereocilia development and yields profound hearing loss. Previous studies have identified the role of MYO15A in the transport of essential cargo proteins to the tips of stereocilia to carry out stereocilia elongation. However, no studies up to this point have visualized the anterograde motion of single MYO15A molecules. To address this knowledge gap, this research applies Total Internal Reflection Fluorescence Microscopy to visualize Halo-tagged MYO15A motility in actin-based filopodia as a model for MYO15A movement in stereocilia. Completion of this project resulted in the development of an experimental workflow for tracking MYO15A motility as well as the preliminary quantification of an average velocity of 195 ± 132 nm/s at 37° C. Our approach reveals how proteins are trafficked within stereocilia and enables future studies to understand how pathogenic mutations in human MYO15A contribute to hearing loss.

This research was supported by the ASPET SURF Program and by NIH R01 DC 018827.

Electroreduction of CO_2 on Amino Acid Functionalized Cu Catalyst

Ethan Seidl (2026) **Mentor: Dr. Dominique Itanze**
William Wheaton (2028)

Hydrocarbon fuels serve as the main energy source in our current energy infrastructure and release dangerous byproducts into the atmosphere such as CO_2. Hydrocarbon fuels are currently sourced from fossil fuels and other biofuels. With the idea to help aid in our global climate change crisis, previous research studies have determined that Cu is a suitable catalyst to reduce CO_2 into various hydrocarbon fuels. There are a multitude of mechanistic pathways to form hydrocarbon fuels as determined by multiple studies. A pure, unaltered Cu catalyst requires substantial amounts of applied electrochemical potential (~1V) to sufficiently reduce CO_2 into reliable fuels. However, more recent studies have shown that a histidine-functionalized Cu catalyst yielded greater selectivity in the formation of hydrocarbon fuels with higher Faradaic efficiency across a wide range of applied voltage than that of pure Cu. This research aims to determine if CO_2 reduction on amino acid functionalized Cu catalysts will yield more thermodynamically favorable results through computational analysis.

Achieving excellent electrochemical performance for supercapacitors through asymmetric combination of conductive 2D MOFs

Danica G. Settles (2027) **Mentor: Dr. F. Z. Amir**

Asymmetric supercapacitors (ASCs) are utilized in various applications, including electric vehicles (EVs), portable electronics, and backup power systems. The ASCs electrodes are made from two distinct materials. One electrode utilizes redox (Faradic) reactions, with or without non-Faradic reactions (pseudocapacitor electrode), while the other primarily relies on electric double-layer electrostatic absorption/desorption (EDLC electrode).

Herein, we report the fabrication through electrophoretic deposition of an asymmetric supercapacitor using nickel hexaaminobenzene ($Ni_3(HAB)_2$) as the pseudocapacitive electrode and nickel hexaaminotriphenylene ($Ni_3(HITP)_2$) as the EDLC electrode. The morphology of the electrodes was characterized using field-emission scanning electron microscopy and transmission electron microscopy. Cyclic voltammetry, electrochemical impedance spectroscopy, and galvanostatic charge-discharge tests were used to analyze the electrochemical performance of the supercapacitors obtained. The supercapacitor displayed an outstanding electrochemical capacitive performance in Na_2SO_4 electrolyte with an areal specific capacitance of 26.83 mF cm^{-2} at a current density of 0.05mA cm^{-2}. Cyclic voltammetry curves performed at very high scan rates of up to 7000 mV s^{-1} show high-rate performance and suggests the high electrical conductivity of the electrodes and therefore a high electron transfer efficiency. Furthermore, the supercapacitor exhibited an exceptional capacitance retention. The outstanding electrochemical performance is attributed to the EPD process, the high conductivity of 2D MOFs which facilitate the electron transfer and the large surface area of the two MOFs used. These results provide great prospect for developing MOFs as a new class of materials for asymmetric supercapacitors.

Winthrop University Research Council/NSF-EPSCoR

Utilizing the T-R{Y} Framework to Generalize the Kumaraswamy Distribution

Steven Stokes (2027) **Mentor: Dr. Dodamgodage Gihanee Senadheera**
Miguel Villano (2026)

This research investigates the T-R{Y} Framework, a systematic approach to constructing flexible probability distributions through compositing three generic distributions which allows for generational inheritance. In this framework, each generation passes on its parameters, bounds, skew, and other qualities to its succeeding generation, thereby resulting in a final distribution that is much more flexible than the previous. Particular emphasis is placed on the Kumaraswamy distribution, due to its bounds on the unit interval and already flexible shapes. Optimal Parameter estimation is conducted through Maximum Likelihood Estimation, which is solved through Differential Evolution and the L-BFGS-B algorithm. The proposed distributions are evaluated on New York Air Quality data, with model performance scored through AIC and BIC tests.

This project is supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences (P20GM103499-20) from the National Institutes of Health. We would like to thank the South Carolina INBRE Program, Winthrop University Summer Undergraduate Research Experience Program, and the Winthrop Department of Mathematics for both the support and funding of this project.

Mental Landscapes: How Imagined Environments Affect Emotional and Social Wellbeing

Angie Torres (2026) **Mentor: Dr. Donna Nelson**

Few studies have explored how the presence of sunlight, indoor versus outdoor settings or imagined social connection influence the effects of mental imagery. We found that compared to a control condition, participants in the mental imagery conditions reported significantly reduced negative emotions and social disconnect, and increased social trust. In addition, imagery involving a sunny environment significantly increased positive emotions compared to cloudy or indoor landscapes. Our findings suggest that positive imagery can improve emotional and social well-being. This may be a valuable tool for mental health support, especially in circumstances where real exposure to nature is not possible.

Winthrop University Ronald E. McNair Postbaccalaureate Achievement Program, Grant # P217A230073

Studying DNA Repair After CRISPR-Induced Breaks

Bryson Vaughan (2026) **Mentor: Dr. Evan Dewey**

It is estimated that our DNA is subjected to anywhere from ten thousand to one-million sources of damage each day, with ten to fifty double-strand breaks occurring per cell cycle. Damage comes from the environment around us and from our own internal metabolic processes. Our cells often use homology directed repair (HDR) to successfully repair a break using an undamaged chromosome as a template to maintain genome stability. This process must be precisely regulated to avoid detrimental outcomes that could lead to cancer. On the benchtop, it is known that CRISPR/Cas9 induces double-strand breaks (DSBs), but little is known about the role of HDR in repair stemming from a Cas9 DSB and also in how key HDR genes are regulated in this process. Our research this summer sought to make the picture clearer by focusing on one such HDR gene, *fancm,* and how it might regulate HDR for Cas9 DSBs. By using the *Drosophila melanogaster* model, we mutated *fancm* and cut a target homologous chromosome with CRISPR/Cas9 in developing male germline cells in order to watch how the cells repaired the broken target using an unbroken template. Surprisingly, we observed a lack of HDR and instead found products of backup Polymerase Theta-Mediated End Joining (TMEJ) repair pathway. In this process, DNA microhomologies anneal to each other and cause small deletions. The use of TMEJ suggests that a mutated *fancm* gene caused the cell to lose the ability to perform HDR. In the products analyzed, we also saw a lack of template integration into the target strand, suggesting that the target strand could not invade the template to perform HDR. In the future, our lab plans to sequence more flies and monitor DNA repair events to better understand the importance of *fancm* in HDR.

This work was supported by SC INBRE, a grant from the National Institutes of Health National Institute of General Medical Sciences (P20GM103499).

Physiological Effects of Dual Environmental Stressors on Redear Sunfish: Gill Protein Expression

Andrea Vega (2027) **Mentor: Dr. Salvatore Blair**

Freshwater fish are continuously and increasingly threatened by elevated temperatures and salinity changes caused by climate change and other activities. These two stressors impact the gill structure and function, by altering the balance between gas exchange and osmoregulation. This gill remodeling process happens within the interlamellar cell mass (ILCM) and forces growth or reduction, as well as the expression of certain stress proteins. The goal of this study was to examine the physiological effects that temperature (20°C vs 26°C) and salinity (0ppt vs. 17ppt) had on redear sunfish (*Lepomis microlophus)*. Gill samples were collected post-mortem and analyzed using hematoxylin and eosin (H&E) staining to clearly observe ILCM remodeling. Immunohistochemistry (IHC) was used to locate target protein expression, such as sodium-potassium ATPase (NKA), HSP70, and HSP90. As expected, increased temperature reduced the ILCM, likely associated with increased oxygen uptake ability. Salinity results were more varied, however, and while exposure resulted in elevated plasma osmolality, ILCM results were more confounding. NKA expression was mainly in mitochondrion-rich cells and increased with the salinity, which was expected due to its role in ion-regulation. HSP70 expression was inconclusive, which suggests using a different method, such as western blotting (WB) to quantify, or requires a new antibody. Overall, these results support that temperature is the stronger stressor in gill remodeling, while salinity influences ion transport mechanisms within freshwater fish. This study aimed to provide insight into how freshwater fish may respond in the future to increased simultaneous environmental stressors.

Funded by SC INBRE

Studying Non-Crossovers of Homology Directed Repair using *Drosophila* with a *fancm* gene knockout

Ella Williams (2027) **Mentor: Dr. Evan Dewey**

DNA is subject to tens of thousands of sources of damage every day. Repair of this damage is crucial to maintaining genome stability, but genes involved in the repair process genes are at risk of mutations of their own. Homology Directed Repair (HDR) is responsible for precisely repairing double strand breaks using homologous chromosomes as a template. During HDR, two products can result: a crossover, when large swaths of DNA are exchanged between homologs, and non-crossovers (NCOs), when only the minimal amount of DNA needed for repair is swapped between homologs. Misregulated HDR leading to COs can lead to genome instability and cancer. Our research examined NCOs in *Drosophila* in a *fancm* gene knockout. *Fancm* is responsible for starting the Fanconi Anemia (FA) pathway which removes Interstrand Crosslinks (ICLs), creating a double strand break (DSB) to be repaired by HDR. To study HDR products without *fancm*, we made *fancm* mutant males and induced CRISPR-Cas9 double strand breaks in their germline cells at specified locations. This is done in one allele of the *rosy (ry)* gene (target homolog), but not the other (template homolog), via a single nucleotide polymorphism (SNP). These males are then crossed with females containing a deletion in the *ry* gene to. The paternal chromosome, housing potential HDR repair products in resulting progeny, can then be selectively amplified via PCR using primers directed to the deleted *ry* region. If a NCO occurred in the parental male's germline it can be detected and reconstructed in the amplified products from the mixed presence of target and template SNPs. We see varying lengths of template DNA in NCOs in *fancm* mutant males, and more analysis is needed to fully understand the effects of *fancm* loss on HDR.

This work was supported by SC INBRE, a grant from the National Institutes of Health National Institute of General Medical Sciences (P20GM103499).