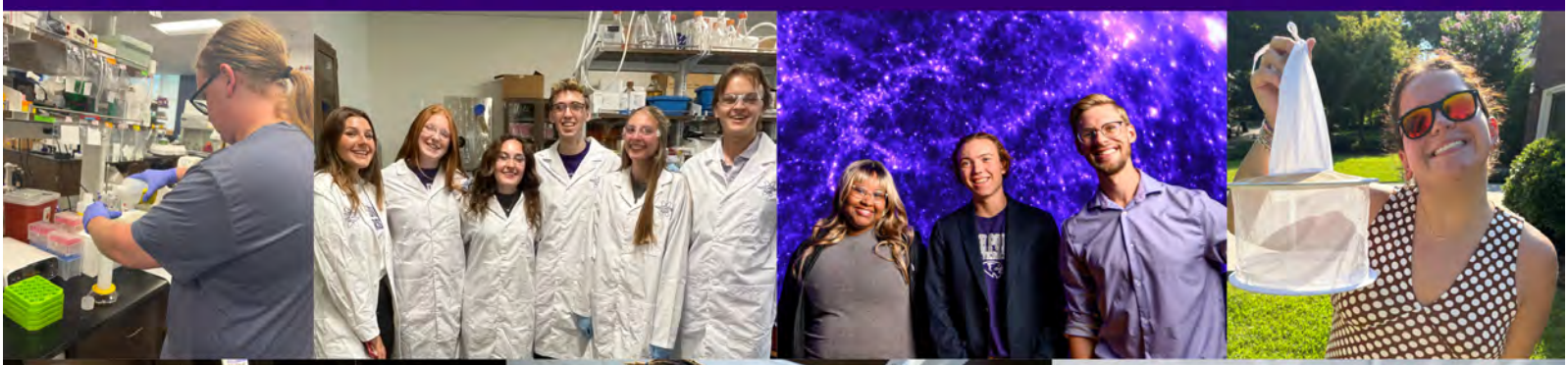


HIGH POINT UNIVERSITY

THE PREMIER LIFE SKILLS UNIVERSITY

Wanek School of Natural Sciences

Summer Research Program in the Sciences
Final Research Symposium
July 23 - 24, 2026



Scenes from SuRPS

2026 SuRPS Keynote Speaker

From Beaker to Badge: Perspectives from Blending Science and Law Enforcement

Nicholas Cutrona
Department of Chemistry, Class of 2019
Special Agent, Federal Bureau of Investigation

ABSTRACT
Scientific research and complex criminal investigations are not often considered similar. Though both have different requirements, experiences, and applications in everyday life and society, there is a common thread of shared perspectives between research and law enforcement that draws the two together in often unconsidered ways. These shared perspectives enable me to apply experiences I have collected through my scientific career to the complex investigations I now conduct in federal law enforcement. I will share my journey from aspiring undergraduate just starting their research career to experienced criminal investigator, offering a distinct look into how perspectives I have gained from my time in the biological sciences have been implemented into my investigations into organized criminal activity.

BIOGRAPHY
Nicholas Cutrona received a B.S. degree in biochemistry from High Point University in 2019. While at HPU, Nicholas participated in the SuRPs program twice in Dr. Meghan Blackledge's lab researching adjuvant therapy approaches to treating Methicillin-resistant *Staphylococcus Aureus*. He subsequently pursued his M.S. in biochemistry and molecular biology from Georgetown University. While at Georgetown, Nicholas participated in pediatric cancer research, studying the growth of Ewing's sarcoma tumors in a hypoxic environment. Following the completion of his M.S., Nicholas joined the Laboratory of Immune System Biology at the National Institute of Allergies and Infectious Diseases to conduct fetal immune system development research as it relates to Amyotrophic Lateral Sclerosis. While exploring opportunities to use his scientific background in a different way, Nicholas became a Special Agent with the Federal Bureau of Investigation in 2023. He conducts criminal investigations into drug trafficking, kidnappings, money laundering, violent crime and gangs, public corruption, and terrorism. In addition, Nicholas is a Weapons of Mass Destruction Coordinator for the FBI, where he addresses chemical, biological, radiological, nuclear, and explosive threats across the country. The mentorship, experience, and, most importantly, perspectives he has gained throughout his career have enabled him to approach complex criminal investigations through a uniquely scientific point of view.

SuRPS Final Symposium

Thursday, July 23, 2026, Culp Planetarium, Wanek School of Natural Sciences

Posters will be set up in the hall and lobby of the Wanek School of Natural Sciences.
All posters should be set up by 9 am on Thursday for both poster sessions and will be taken down after the symposium completes on Friday.

Session I: Oral Presentations: Dr. Eric Rokni, Department of Physics, Presiding

	8:30 – 9:00		*COFFEE, TEA RECEPTION (WSNS Lobby)*
	9:00 – 9:20	Dr. Kelsey Kean	Opening Remarks and Announcements Afternoon Poster Session Elevator Pitch Videos
Th.1	9:20 – 9:40	Angelina Roy	Mechanisms and Prevention of Age-Related Cataractogenesis: Glutathione Depletion, Carbamylation, and the Protective Role of Alpha-Tocopherol
Th.2	9:40 – 10:00	Scarlett Peabody	Assessing Ecosystem Services in Native vs. Ornamental Botanical Gardens at High Point University
Th.3	10:00 – 10:20	Eleanor Lee & Justin Allan	A New Hsisosuchid Crocodyliform from the Early Jurassic Lufeng Formation (Yunnan, China) and the Evolution of the Crocodyliform Pterygoid
Th.4	10:20 – 10:40	Sophia Bellino & Sophia Castillo	Evaluating the Effects of Fused Tricyclic Compounds as Mitochondrial-Targeting Drugs in *Toxoplasma gondii*
Th.5	10:40 – 11:00	Josephine Bertuna	A Four-enzyme Cocktail Allows Knockout of Candidate Dimorphic Genes in *Knufia petricola*
Th.6	11:00 – 11:20	Nicole Phillips	The Wood's Hidden Voice: Investigating Phantom Partials in String Instruments
	11:20 – 11:30		*BREAK*

Keynote Address: Introduction by Dr. Meghan Blackledge, Department of Chemistry

11:30 am – 12:30 pm	**Nicholas Cutrona,** HPU Class of 2019 Special Agent, Federal Bureau of Investigation
	From Beaker to Badge: Perspectives from Blending Science and Law Enforcement
12:30	*Assemble for group picture in WSNS Lobby*
12:30 – 1:45	*LUNCH BREAK*

Session II: Poster Presentations Part A: Wanek School of Natural Sciences Lobby, 2:00 – 3:00 pm

P1. Samantha Dowd: "Secondary Metabolites From Freshwater Fungi Inhibit Human Acetylcholinesterase"
P2. Nathan Dwier & Gavin Agahigian: "Insect Abundance Along an Urbanization Gradient in the Central Piedmont Region of North Carolina"
P3. Gustavia Gooding: "Building a Microfluidic platform to Study Glymphatic CSF Flow"
P4. Nelia Kelleher: "Investigating Enzymatic Activity and Disease-Linked Mutations of Non-Lysosomal β-Glucosylceramidase 2 from *Drosophila melanogaster*"
P5. Daniel Kent: "Creation of a Gas Handling System"
P6. Sophia Messerly: "Expanding the Landscape of Lactate Monooxygenases: Insights from *Beauveria bassiana*"
P7. Philip Morriseau: "Quantifying NAD+ Precursors in Common Foods"
P8. Maia Ramirez: "Following the Flow: How Ultrasound May Enhance Glymphatic Flow in a Physical Brain Model"
P9. Logan Rampetstreiter: "Identifying the protein target of an antibiotic adjuvant in MRSA through affinity-based protein purification."
P10. Haven Tucker: "Effects of nitrogen and water stress on gene expression and autumn leaf color in oaks (genus *Quercus*)"

3:00 – 3:15 *BREAK*

Session III: Oral Presentations: Dr. Megan Rudock Bowman, Department of Biology, Presiding

Th.7	3:15 – 3:35	Caitlin Michaelis	Loratadine's Inhibition of Efflux in MRSA to Decrease Antibiotic Resistance
Th.8	3:35 – 3:55	Lanie Gardner & Dariann Adams	Developmental filtering and the hierarchical organization of genetic contribution in evolution
Th.9	3:55 – 4:15	Thyliah Coleman	Nucleotide Hydrolysis Rates Regulate Septin-Septin Interactions
Th.10	4:15 – 4:35	Sencerity Baker	Dark Matter Halos
Th.11	4:35 – 4:55	Nick Gonzalez & Koby Mante	Interaction Interface between the mTOR Pathway and Circadian Clock in *Neurospora crassa*
Th. 12	4:55 – 5:15	Paul Cusumano	Reconstructing Input Signals to Predict Particle Behavior in Time Projection Chambers

SuRPS Final Symposium

Friday, July 24, 2026, Culp Planetarium, Wanek School of Natural Sciences

Session IV: Oral Presentations: Dr. Grace Hamilton, Department of Chemistry, Presiding

	8:30 – 9:00		*COFFEE, TEA RECEPTION (WSNS Lobby)*
	9:00 – 9:20	Dr. Kelsey Kean	Opening Remarks and Announcements Morning Poster Session Elevator Pitch Videos
Fr.1	9:20 – 9:40	Holley Lowe	Applications of Extracellular Vesicles in an *In-Vivo* Model
Fr.2	9:40 – 10:00	Samantha Dowd	Secondary Metabolites from Freshwater Fungi Inhibit Human Acetylcholinesterase
Fr.3	10:00 – 10:20	Trip Donaldson	Functional Analysis of a Tardigrade β-Carbonic Anhydrase
Fr.4	10:20 – 10:40	Gustavia Gooding	Building a Microfluidic platform to Study Glymphatic CSF Flow
Fr.5	10:40 – 11:00	Nathan Dwier & Gavin Agahigian	Insect Abundance Along an Urbanization Gradient in the Central Piedmont Region of North Carolina
Fr.6	11:00 – 11:20	Blake Bird	Competing Halo Predictions Behind JWST's Galaxies
	11:20 – 11:30		*BREAK*

Session V: Poster Presentations Part B: Wanek School of Natural Sciences Lobby, 11:30 am – 12:30 pm

P11. Justin Allan & Eleanor Lee: "First occurrence of Shuvosauridae from the Norian (Upper Triassic) Snyder Quarry Locality based on Hindlimb Elements"
P12. Sophia Bellino & Sophia Castillo: "Evaluating the Effects of Fused Tricyclic Compounds as Mitochondrial-Targeting Drugs in *Toxoplasma gondii*"
P13. Josephine Bertuna: "A Four-enzyme Cocktail Allows Knockout of Candidate Dimorphic Genes in *Knufia petricola*"
P14. Madison Burnett: "How to NOT Study Mosquitoes: Lessons Learned in Field Research"
P15. Thyliah Coleman: "Nucleotide Hydrolysis Rates Regulate Septin-Septin Interactions"
P16. Lanie Gardner & Dariann Adams: "Developmental filtering and the hierarchical organization of genetic contribution in evolution"
P17. Nick Gonzalez & Koby Mante: "Interaction Interface between the mTOR Pathway and Circadian Clock in *Neurospora crassa*"
P18. CJ Gulla: "Advanced Characterization of Milk-Derived Extracellular Vesicles"
P19. Scarlett Peabody: "Assessing Ecosystem Services in Native vs. Ornamental Botanical Gardens at High Point University"
P20. Nicole Phillips: "The Wood's Hidden Voice: Investigating Phantom Partials in String Instruments"

Lunch at Café / Lab Clean Up

STUDENT ABSTRACTS ORAL PRESENTATIONS:

Note: presenting author(s) is underlined, * denotes faculty advisor(s)

(Th.10) Dark Matter Halos

Sencerity Baker and Alex Sobotka*
Department of Physics, High Point University

Dark matter halos are regions of dark matter that are located on the outer regions of galaxies. Halos form over time due to gravity acting on their mass, and this formation process depends on the history of the universe. Different assumptions on how dark matter halos form can be encapsulated into something called a fitting function. For a given cosmology these fitting functions make significantly different predictions on how many halos are produced. Our goal is to see whether the differences between these fitting functions change when cosmological parameters—like the expansion rate of the universe—are varied. To test this, we use different fitting functions to model the predicted halo population across different cosmologies. We find that smaller halos are sensitive to cosmological parameters. We find that that the difference between what two fitting functions predict in regards to small-mass halos is sensitive to cosmological parameters.

(Th.4) Evaluating the Effects of Fused Tricyclic Compounds as Mitochondrial-Targeting Drugs in *Toxoplasma gondii*

Sophia Bellino, Sophia Castillo, Meghan Blackledge, and Robert Charvat*
Department of Biology, High Point University

Toxoplasma gondii is an intracellular protozoan parasite that infects approximately one-third of the world's population. *T. gondii* can cause severe disease in immunocompromised individuals as well as cause devastating effects during pregnancy, especially for the developing fetus. Current treatment options have limitations, creating a need for new therapeutic strategies. This study investigates the effects of loratadine derivatives on *Toxoplasma gondii*, with a particular focus on the sole parasite mitochondrion. Prior studies employing RNA sequencing analysis revealed that genes involved in mitochondrial metabolism and function were differentially expressed between vehicle- and drug-treated parasites. Therefore, we hypothesize that loratadine-based treatment disrupts mitochondrial function, reducing parasite viability and replication. By examining changes in mitochondrial morphology and function following treatment, this research aims to determine whether loratadine has potential as an adjunct therapeutic approach against *T. gondii*. The findings may contribute to the development of more effective treatments by identifying mitochondrial pathways as promising drug targets.

(Th.5) A Four-enzyme Cocktail Allows Knockout of Candidate Dimorphic Genes in *Knufia petricola*

Josephine Bertuna, Daniel Sapozhnikov, Sophia Cima, Caden Reedy, and Grace Hamilton*
Department of Chemistry, High Point University

Knufia petricola is a black fungus capable of surviving extreme environmental pressures. When grown on carbon-starved media, it adapts by changing cell shape. There is an untested hypothesis that cell shape change is an adaption for extremotolerance, but the genetic basis of extremotolerance is unknown. We aim to identify the genes responsible for extremotolerance in *K. petricola* and someday transfer these extremotolerant traits to non-extremotolerant organisms, such as budding yeast. Thus, we may be able to advance astronautical missions by allowing organisms previously incapable of surviving the harsh conditions to be used for pharmaceutical or agricultural purposes in space. However, one major challenge is genetically manipulating the *K. petricola*. This is due to their heavily melanized cells walls, which must be removed to allow foreign DNA in. At present, we have found a mix of four enzymes that facilitate cell wall removal and begun knockout trials with twenty genes of interest that are upregulated when *K. petricola* is deprived of carbon. To date, we have attempted to knock out six of them. If our knockouts result in the removal of *K. petricola*'s ability to adapt to high stress environments—specifically its ability to change its cell shape—then we can conclude that we have discovered a gene that is necessary for extremotolerance.

(Fr.6) Competing Halo Predictions Behind JWST's Galaxies

Blake Bird and Alex Sobotka*
Department of Physics, High Point University

The James Webb Space Telescope has found unexpectedly bright, potentially massive galaxies during the first billion years. Because galaxies form in dark-matter halos—invisible gravitational structures—were enough massive halos present? Early dark energy (EDE) altered expansion before neutral atoms formed, then faded. We compare benchmark best-fit EDE and ΛCDM—the standard cosmology—testing enhancement across mass, redshift (a cosmic-time marker), and fitting-function choice. AxiCLASS computes each model's linear matter power spectrum, showing density-fluctuation strength across scales. A top-hat filter averages fluctuations within a sphere enclosing mass M, yielding $\sigma(M)$, their typical strength on that scale. Press–Schechter and Sheth–Tormen are statistical fitting functions, not simulations; they estimate halo abundance from σ(M). At redshift $z = 8$, the EDE fit predicts 2.62 times as many halos above 10^{10} $M_\odot$ as ΛCDM with Press–Schechter and 2.09 times with Sheth–Tormen. Under both prescriptions, the excess grows toward earlier times and rarer, more massive halos, then fades toward the present. For rare halos, small fluctuation differences produce large abundance shifts. Because the fits differ in matter density, expansion rate, and primordial fluctuations, the enhancement is not due to EDE alone. Within these benchmarks, the EDE fit predicts more potential hosts; fitting-function choice changes the signal's magnitude, not its direction.

(Th.9) Nucleotide Hydrolysis Rates Regulate Septin-Septin Interactions

Thyliah Coleman, Shauna Skow, and Grace Hamilton*
Department of Chemistry, High Point University

Septins are cytoskeleton proteins that are conserved across many eukaryotic species, such as yeast and humans. Septins are GTP-binding proteins, some of which also hydrolyze GTP. Single septin subunits form rods and then polymerize to form filaments that can assemble into high-order structures. Septins regulate many cellular processes such as morphogenesis, plasma membrane organization, and cellular division. Because septins rely on nucleotide hydrolysis to perform their cellular functions, changes to this septin function should affect cells' ability to form certain structures and completely separate during cytokinesis. AspE is a member of an under-studied family of septins unique to fungi. AspE can bind to one other septin, Cdc11. This AspE-Cdc11 binding interaction may be incorporated into high-order structures. We expressed and purified AspE proteins with mutations to its GTP-binding domain. We found that two of the mutations, T200A and K163A, conduct less GTP hydrolysis than the wild-type AspE. One of the mutations, D219A, outperforms wild-type AspE, and the last mutation, R447A, performs similarly to wild-type AspE. Wild-type AspE commonly behaves as a dimer, however the mutations T200A and K163A behaved as monomers. Subsequent steps will include using yeast two-hybrid assays to see if the slowed GTP hydrolysis mutations affect AspE interactions with Cdc11. Determining the rules for septin-septin interactions lays the groundwork for further research developing novel anti-fungal drugs.

(Th.12) Reconstructing Input Signals to Predict Particle Behavior in Time Projection Chambers

Paul Cusumano, and Adam Anthony*
Department of Physics, High Point University

A Time Projection Chamber (TPC) functions as a 4d camera, recording the 3d position and energy loss of charged particles travelling near lightspeed. When a particle travels through the chamber, it interacts with the gas, losing energy and producing electrons. These electrons drift to the pad plane where a signal is produced that represents the particle's location and how much charge was collected. Traditionally, a linear preamplifier is used to amplify the signal of the electrons collected at the pad plane, but this limits the types of events that can be measured by the TPC. Replacing the linear preamp with a logarithmic one allows a much wider range of charge signals to be recorded. The primary research challenge involves "undoing" the effects of these amplifiers to isolate the original signal of the electrons. This is achieved by employing a deconvolution framework to calculate the initial electrical current from the recorded amplified output. By leveraging this signal processing approach, we can more accurately model particle behavior within a TPC. Developing these reconstruction techniques enables a wider range of experiments by providing a foundation for studying low-energy particle events that are outside the operational range of linear TPCs.

(Fr.3) Functional Analysis of a Tardigrade β-Carbonic Anhydrase

Trip Donaldson, Parker Nyboer, Nadia Khan, and Kelsey Kean*
Department of Chemistry, High Point University

Tardigrades, also known as Water Bears, are microscopic extremophiles that are capable of surviving conditions that would be lethal to almost all organisms. This makes them valuable models for studying proteins that contribute to the survival of extreme environments. Carbonic Anhydrases (CAs) are metal-dependent enzymes that catalyze the reversible reaction of carbon dioxide and water into bicarbonate and protons. They regulate the body's pH balance, aid in the transport of CO_2 from tissues to the lungs for exhalation, and assist in digestion and fluid balance. While CAs have been extensively characterized in humans and many other organisms, relatively little is known about the β-carbonic anhydrase (HeCAβ) found in tardigrades. The goal of this study is to experimentally characterize HeCAβ and to investigate its metal cofactor. Previous experiments suggest it may bind a metal other than the typical zinc in its active site. HeCAβ was recombinantly expressed in Escherichia Coli and purified for the assessment of enzymatic properties. Protein activity was assessed using a colorimetric CO_2 hydration assay with different enzyme solutions consisting of varying metal ions to quantify their catalytic activity. Ongoing experiments intend to identify what metal ion HeCAβ utilizes and to further define the enzyme's biochemical properties. Understanding how HeCAβ operates in tardigrades may reveal more about the adaptations that have allowed these organisms to survive all five major extinctions.

(Fr.2) Secondary Metabolites From Freshwater Fungi Inhibit Human Acetylcholinesterase

Samantha Dowd, Jordan Havert, Tyler Janick, Blake Horne, Rutwa Patil, and Grace Hamilton*
Department of Chemistry, High Point University

Alzheimer's Disease (AD) is a progressive neurodegenerative disease that affects over 7.5 million Americans. With few treatment options available and significant adverse side effects from existing medications, novel treatments for the disease are needed. Acetylcholinesterase is an enzyme found in the nervous system that breaks down the neurotransmitter acetylcholine; reduced amounts of this neurotransmitter is a hallmark of AD. Therefore, targeting this enzyme is the main mechanism of action for many AD medications. Fungi have been shown to produce inhibitors for this enzyme, making them promising potential sources of new treatments. We made organic extracts from aquatic fungi and tested their ability to inhibit acetylcholinesterase. After identifying the fungi whose metabolites were successful inhibitors of acetylcholinesterase, we identified the compounds responsible for this activity using gas chromatography mass spectrometry. We identified six fungal extracts that inhibited human acetylcholinesterase *in vitro*, through competitive and non-competitive inhibition. These natural compounds offer promising scaffolds for the development of new AD treatments.

(Fr.5) Insect Abundance Along an Urbanization Gradient in the Central Piedmont Region of North Carolina

Nathan O. Dwier, Gavin H. Agahigian, Scarlett E. Peabody, Madison M. Burnett, Haven A. Tucker, Megan E. Rudock Bowman, and A. Daniel Greene*
Department of Biology, High Point University

The process of urbanization is associated with environmental disturbance and fragmented, modified landscapes. Although urbanization is a significant cause of extinction of native species and has been shown to lead to a decline in species diversity, the effects of urbanization are not consistent across taxa. In our study, we chose to assess the effect of urbanization on the abundance of insects belonging to the orders Diptera, Lepidoptera, Coleoptera, Hemiptera, and Trichoptera. Insects were collected from 28 sampling sites belonging to 2 transects (West-East Transect: sites 1-14 [Davidson & Guilford County, North Carolina) and North-South transect: sites 15-28 [Guilford County, NC]) during calendar weeks (CW) 24-27 (June-July) of 2026. Each sampling site featured a covered (1.3 m diameter black umbrella) sampling station that included a Dynatrap® ½ Acre LED Mosquito & Insect Trap (DT1130-GRSR) and a BirdWeather Portable Universal Codec (PUC; collected bioacoustic and environmental data) attached to a shepherd's hook (at 1.5 m in height). During each sampling event (4), insect, bioacoustic, and environmental data were collected from ≈ 1500 – 1100 hours for 18.4 ± 0.65 hours (average ± SE). In a 125 m radius surrounding each sampling site, the amount of developed, agricultural, and natural land cover was calculated using QGIS. A separate generalized linear mixed model was constructed for each insect order (Diptera, Lepidoptera, Coleoptera, Hemiptera, and Trichoptera) to assess the effect of environmental and land cover variables on insect abundance.

(Th.8) Developmental filtering and the hierarchical organization of genetic contribution in evolution

Lanie Gardner, Dariann Adams, and Kenneth McKenna
Department of Biology, High Point University

Have you ever considered the importance of the hierarchical structure of gene pathways? Developmental systems determine not only how organisms are built but also how genetic variation contributes to phenotypic evolution. Although genome-wide association studies (GWAS) have identified numerous loci associated with complex traits, the developmental principles governing why some genes repeatedly contribute to variation while others remain highly constrained are poorly understood. Our main objective is to understand whether network positions determine phenotypic importance. Using the *Drosophila melanogaster* wing as a model system, we will integrate population genetics, developmental biology, and network analysis to determine how developmental organization shapes phenotypic variation and evolvability. To test this mechanistic prediction, targeted RNAi knockdowns were performed using wing specific GAL4 drivers across a curated set of genes spanning the inferred developmental hierarchy. Phenotypic consequences were quantified under baseline, nutritional stress, and heat stress conditions to determine whether developmental necessity interacts with environmental state. In conclusion, by linking developmental hierarchy, plasticity, genetic variation, and evolutionary constraint within a unified framework, this work will establish a mechanistic basis for developmental filtering and provide new insight into how developmental architecture governs the evolutionary potential of complex traits.

(Th.11) Interaction Interface between the mTOR Pathway and Circadian Clock in *Neurospora crassa*

Nick Gonzalez, Koby Mante, and Alexander Mosier*
Department of Biology, High Point University

The circadian clock is a molecular system found across all branches of life. This clock does not simply tell an organism what time it is, but rather it allows an organism to be more proactive towards environmental changes. The conserved molecular nature of the clock allows the use of model organisms such as the filamentous fungus, *Neurospora crassa*. Within the core circadian clock of *N. crassa*, a core clock protein, FREQUENCY, has recently been studied to define its overall interactome and give a starting point for clock regulation at the proteomic level. The goal of this project is to examine how recently discovered interactors to the core circadian clock explain how the clock temporally regulates downstream processes. Reviewing the list of interactors, we found the quantity of those connected to the mTOR pathway to be particularly interesting. We studied how the proteins mTOR, PP1, WD-Repeat, and α-Tubulin facilitate interaction between the mTOR pathway and the overall negative feedback loop that underlies the circadian clock. To do so, we studied the selected proteins by Western Blot analysis. Using samples of proteins collected at various periods of total darkness, no darkness, 4 hours, and 8 hours, along with antibodies specific for the proteins and their phosphorylation state we measured relative abundance and phosphorylation across circadian time. Our findings create a baseline for how mTOR pathway proteins oscillate over circadian time, in both abundance and phosphorylation state, as well as how they act back on the core circadian clock to maintain proper timing.

(Fr.4) Building a Microfluidic platform to Study Glymphatic CSF Flow

Gustavia Gooding, Maia Ramirez, Eric Rokni, and Jacob Brooks*
Department of Physics, High Point University

The glymphatic system is the brain's waste-clearance system, in which cerebrospinal fluid (CSF) flows through perivascular spaces surrounding blood vessels and carries away metabolic waste, including the amyloid-beta and tau proteins associated with Alzheimer's disease. Because this clearance can be disrupted in neurodegenerative diseases, there is growing interest in whether ultrasound can enhance CSF flow as a therapeutic strategy. Testing this requires a controlled physical model in which flow can be measured and manipulated. This project developed a 3D-printed microfluidic platform to mimic perivascular flow and enable imaging during ultrasound exposure. The device was designed parametrically in Python and OpenSCAD, allowing rapid iteration, and printed using flexible resin to approximate the mechanical properties of soft brain tissue. Surrounding agar gel was characterized by rheometry, confirming solid-like, tissue-mimicking behavior. To analyze fluid motion within the model, a custom Python-based particle-tracking pipeline was developed to quantify particle transport and diffusion. Together, these components establish a validated, tunable testbed for studying CSF dynamics. The long-term aim is to tune this platform to represent both healthy and impaired flow states, creating a controlled system to test how ultrasound influences glymphatic flow, a foundation for evaluating ultrasound as a therapeutic approach to neurodegenerative disease. Ongoing work focuses on refining channel geometry and preparing for trials with rat CSF.

(Th.3) A New Hsisosuchid Crocodyliform from the Early Jurassic Lufeng Formation (Yunnan, China) and the Evolution of the Crocodyliform Pterygoid

Eleanor Lee, Justin Allan, and Josef Stiegler*
Department of Biology, High Point University

In 2018 an expedition to the Lufeng Formation of Yunnan, China collected a partial skeleton of a crocodyliform which comprises of a complete skull, hemimandibles, and the anterior half of the postcranial skeleton. This represents the largest and most complete crocodyliform collected from the Lufeng Formation. We used CT scan data of the specimen to generate a 3d model of the skull. Using the software Dragonfly, we segmented bones into individual models. This anatomical model formed the basis for our coding of the specimen into a morphological data matrix for phylogenetic analysis. Our phylogenetic analysis places the specimen with the Hsisosuchidae, a clade of terrestrial crocdyliformes endemic to Southern China, and represents the chronologically earliest member of this clade. The Hsisosuchidae are near the origin of several of the first terrestrial to semi-aquatic transitions within Crocodyliformes. The analysis recovers a specimen previously collected from the Lufeng Formation as the sister taxon of our primary specimen, suggesting it is a juvenile belonging to the same species. Optimization of morphological characters on our phylogenetic tree illustrates that the Hsisochidae are more like extant crocodylians in terms of their enlarged pterygoid bones and less like protosuchians which had a weaker bite force due to less pterygoid surface area for muscle attachment.

(Fr.1) Applications of Extracellular Vesicles in an *In-Vivo* Model

Holley Lowe. CJ Gulla, Steve Ray, Steve Grekin, David Coltan, Elyse Zeffiro,* and Elijah Sage*
Grekin Labs

Applications of extracellular vesicles (EVs) in healing and cell restoration/regrowth have become a popular focus in modern anti-aging research. EVs are lipid-bilayer bound nano-sized particles that contain DNA, RNA, and proteins from the cells they bud from. After a series of *in vitro* experiments to determine an optimal concentration of EVs to cells for promoting cell growth, we sought to apply those findings to an *in vivo* doxorubicin aging model. Four experimental groups of Long-Evans rats (n=8 per group) were used to evaluate the effects of EVs over the course of a six-week protocol. The first three weeks consisted of an induced accelerated aging phase, in which the rats received either a doxorubicin injection or no injection. During the last three weeks, each specimen received an EV treatment, saline, or no injection, determined by experimental group. All rats were euthanized following the six-week protocol, and tissues were collected for histological analysis. Findings from tissue analysis will inform future *in vivo* studies to explore EV treatment through oral administration.

(Th.7) Loratadine's Inhibition of Efflux in MRSA to Decrease Antibiotic Resistance

Caitlin Michaelis, Bryce Grier, and Heather Miller*
Department of Chemistry, High Point University

Antibiotic resistant bacteria is a growing issue affecting populations worldwide. Methicillin-resistant *Staphylococcus aureus* (MRSA), a very common kind of antibiotic-resistant bacteria is present in both healthcare and community settings. Due to its many antibiotic resistance mechanisms, it is difficult to treat. One mechanism that leads to antibiotic resistance is the bacterial efflux pumps ejecting antibiotic from the cell before they can work. It has been discovered that loratadine, the FDA-approved active ingredient in Claritin, is an effective antibiotic adjuvant in vitro against MRSA, being able to consistently inhibit growth when paired with antibiotics. Results from our lab reveal that loratadine triggers pleiotropic changes to gene expression in key antibiotic resistance genes and some efflux pumps. We aimed to discover if loratadine treated MRSA cultures lowered the efflux of antibiotics from the cell. Quantitative fluorescence studies using ethidium bromide helped discover that there was efflux inhibition at certain concentrations of loratadine. We report that loratadine has an IC50 value of approximately 15 μM in this USA 300 strain. In comparison to a known efflux pump inhibitor, nilotinib, a drug marketed for leukemia, there was a similar level of inhibition. These results add to our knowledge of loratadine and yet another antibiotic resistance mechanism that it derails.

(Th.2) Assessing Ecosystem Services in Native vs. Ornamental Botanical Gardens at High Point University

Scarlett Peabody, Madison M. Burnett, Haven A. Tucker, Brian R. Ragoobir, Ellie Marcella V. Ratta, Kara E. Vaartjes, Nicole Korzcyk, Connor S. Spitler, A. Daniel Greene, and Megan E. Rudock Bowman*
Department of Biology, High Point University

The Mariana H. Qubein Arboretum and Botanical Gardens at High Point University is an extensive network of over 30 campus gardens, which include a diverse range of native and ornamental flowering plants. In this study, ecosystem services of pollination, predation, decomposition, and nutrient cycling were assessed in two gardens of similar size (i.e., area) and plant diversity but varying significantly in terms of plant species identity – Native vs. Ornamental. The Scarborough Butterfly Garden contains a wide array of native plants selected to support pollination services, while the Conservatory Garden is primarily planted with annuals selected for their aesthetic appeal. To compare ecosystem services between the two, pitfall traps were used to collect epigeal arthropods while aerial nets were used to assess insect pollinators. Pitfall traps were placed in each garden randomly within 4 quadrants at equal area density. Traps were collected weekly from March - April 2025 and June - July 2026, after which arthropods were grouped and counted. Using aerial nets, garden areas were actively sampled 14 times for 30 minutes each (August – September 2025 and March - July 2026). Collected insects were chilled on ice for 20 minutes, photographed on a 1cm x 1cm grid for identification using iNaturalist, and released. The diversity of epigeal arthropods and pollinators was higher in native gardens when compared with ornamental gardens. The application of granular systemic insecticide Imidacloprid to the mulch in the Butterfly Garden in May 2026 dramatically decreased the abundance of species and specimens collected compared to previous surveys.

(Th.6) The Wood's Hidden Voice: Investigating Phantom Partials in String Instruments

Nicole Phillips and Eric Rokni*
Department of Physics, High Point University

Stringed instruments, such as violins, cellos, and pianos, produce harmonics when the string is set into motion. Phantom partials are frequencies outside of the harmonic series that also appear in an instrument's output. While originally attributed to forced longitudinal motion in the string, recent studies have determined that phantom partials are likely produced from the wood of the instruments, possibly through nonlinearities from wood-on-wood contact. The goal of this research was to determine whether wood-on-wood contact and a violin's soundpost impact the strength of phantom partials. A wooden box with a removable bottom was designed to replicate the inside of a string instrument. A piezoelectric transducer (PZT) drove the box at two simultaneous frequencies; 330 Hz at a constant amplitude and 440 Hz with a linearly increasing amplitude. An accelerometer was placed next to the PZT to measure the resulting frequencies. Five configurations were tested: a single spruce plate, two spruce plates resting on top of each other, a spruce plate resting on the box, a spruce plate glued to the box, and the box fitted with a soundpost. Whilst we found that wood-on-wood contact increases the strength of the phantom partials, the addition of a soundpost had no major impact on their strength. These results help narrow down the physical origins of phantom partials, helping explain what gives each instrument its unique sound.

(Th.1) Mechanisms and Prevention of Age-Related Cataractogenesis: Glutathione Depletion, Carbamylation, and the Protective Role of Alpha-Tocopherol

Angelina Roy and Jeremy Whitson*
Department of Biology, High Point University

Age-related cataracts result from the progressive aggregation of lens crystallins, presumably driven by post-translational modifications such as oxidation and carbamylation. Our study investigated the molecular mechanisms of cataractogenesis and evaluated potential protective interventions using mammalian lens models. Over eight weeks, we employed multiple complementary approaches. Western blot analysis of mouse lens proteins revealed increased SNAIL expression in glutathione-deficient lenses. This suggests the activation of epithelial-mesenchymal transition. Carbamylation-specific Western blots following potassium cyanate (KOCN) incubation demonstrated enhanced protein modification in glutathione-deficient lenses, indicating that glutathione directly protects lens proteins from damage. *Ex vivo* porcine lens culture experiments tested anti-cataract agents against photooxidative stress. Treatment with alpha-tocopherol (a vitamin E derivative) showed the highest percentage of opacity inhibition compared to controls. Daidzein had no significant effect, while, in contrast to previous *in vitro* studies, apigenin showed the lowest percentage of opacity inhibition.Additionally, in vitro aggregation assays in KOCN solutions unexpectedly revealed that KOCN surprisingly did not promote aggregation but rather inhibited it. These results are interpreted within the broader framework of lens aging, where oxidative stress depletes glutathione, increases cyanate availability, and enhances carbamylation. This further links protein damage to cataract formation. Our findings highlight alpha-tocopherol as a promising protective agent, along with carbamylation dynamics, which may represent a middle ground between helpful and harmful effects on lens health. These findings contribute valuable insights toward strategies for delaying cataract progression and, more broadly, understanding protein homeostasis in age-related diseases.

STUDENT ABSTRACTS POSTER PRESENTATIONS:

Note: presenting author is underlined, * denotes faculty advisor(s)

THURSDAY, JULY 24 POSTER PRESENTATIONS PART A (2:00 – 3:00 pm):

(P.1) Secondary Metabolites From Freshwater Fungi Inhibit Human Acetylcholinesterase

Samantha Dowd, Jordan Havert, Tyler Janick, Blake Horne, Rutwa Patil, and Grace Hamilton*
Department of Chemistry, High Point University

Alzheimer's Disease (AD) is a progressive neurodegenerative disease that affects over 7.5 million Americans. With few treatment options available and significant adverse side effects from existing medications, novel treatments for the disease are needed. Acetylcholinesterase is an enzyme found in the nervous system that breaks down the neurotransmitter acetylcholine; reduced amounts of this neurotransmitter is a hallmark of AD. Therefore, targeting this enzyme is the main mechanism of action for many AD medications. Fungi have been shown to produce inhibitors for this enzyme, making them promising potential sources of new treatments. We made organic extracts from aquatic fungi and tested their ability to inhibit acetylcholinesterase. After identifying the fungi whose metabolites were successful inhibitors of acetylcholinesterase, we identified the compounds responsible for this activity using gas chromatography mass spectrometry. We identified six fungal extracts that inhibited human acetylcholinesterase *in vitro*, through competitive and non-competitive inhibition. These natural compounds offer promising scaffolds for the development of new AD treatments.

(P.2) Insect Abundance Along an Urbanization Gradient in the Central Piedmont Region of North Carolina

Nathan O. Dwier, Gavin H. Agahigian, Scarlett E. Peabody, Madison M. Burnett, Haven A. Tucker, Megan E. Rudock Bowman, and A. Daniel Greene*
Department of Biology, High Point University

The process of urbanization is associated with environmental disturbance and fragmented, modified landscapes. Although urbanization is a significant cause of extinction of native species and has been shown to lead to a decline in species diversity, the effects of urbanization are not consistent across taxa. In our study, we chose to assess the effect of urbanization on the abundance of insects belonging to the orders Diptera, Lepidoptera, Coleoptera, Hemiptera, and Trichoptera. Insects were collected from 28 sampling sites belonging to 2 transects (West-East Transect: sites 1-14 [Davidson & Guilford County, North Carolina) and North-South transect: sites 15-28 [Guilford County, NC]) during calendar weeks (CW) 24-27 (June-July) of 2026. Each sampling site featured a covered (1.3 m diameter black umbrella) sampling station that included a Dynatrap® ½ Acre LED Mosquito & Insect Trap (DT1130-GRSR) and a BirdWeather Portable Universal Codec (PUC; collected bioacoustic and environmental data) attached to a shepherd's hook (at 1.5 m in height). During each sampling event (4), insect, bioacoustic, and environmental data were collected from ≈ 1500 – 1100 hours for 18.4 ± 0.65 hours (average ± SE). In a 125 m radius surrounding each sampling site, the amount of developed, agricultural, and natural land cover was calculated using QGIS. A separate generalized linear mixed model was constructed for each insect order (Diptera, Lepidoptera, Coleoptera, Hemiptera, and Trichoptera) to assess the effect of environmental and land cover variables on insect abundance.

(P.3) Building a Microfluidic platform to Study Glymphatic CSF Flow

Gustavia Gooding, Maia Ramirez, Eric Rokni, and Jacob Brooks*
Department of Physics, High Point University

The glymphatic system is the brain's waste-clearance system, in which cerebrospinal fluid (CSF) flows through perivascular spaces surrounding blood vessels and carries away metabolic waste, including the amyloid-beta and tau proteins associated with Alzheimer's disease. Because this clearance can be disrupted in neurodegenerative diseases, there is growing interest in whether ultrasound can enhance CSF flow as a therapeutic strategy. Testing this requires a controlled physical model in which flow can be measured and manipulated. This project developed a 3D-printed microfluidic platform to mimic perivascular flow and enable imaging during ultrasound exposure. The device was designed parametrically in Python and OpenSCAD, allowing rapid iteration, and printed using flexible resin to approximate the mechanical properties of soft brain tissue. Surrounding agar gel was characterized by rheometry, confirming solid-like, tissue-mimicking behavior. To analyze fluid motion within the model, a custom Python-based particle-tracking pipeline was developed to quantify particle transport and diffusion. Together, these components establish a validated, tunable testbed for studying CSF dynamics. The long-term aim is to tune this platform to represent both healthy and impaired flow states, creating a controlled system to test how ultrasound influences glymphatic flow, a foundation for evaluating ultrasound as a therapeutic approach to neurodegenerative disease. Ongoing work focuses on refining channel geometry and preparing for trials with rat CSF.

(P.4) Investigating Enzymatic Activity and Disease-Linked Mutations of Non-Lysosomal β-Glucosylceramidase 2 from *Drosophila melanogaster*

Nelia Kelleher, Macie Fox, Chris Abdullah,[1] and Kelsey Kean[2]*
[1]Department of Biology/Chemistry, Springfield College
[2]Department of Chemistry, High Point University

Lipids are essential components of neuronal membranes, and their metabolism plays a crucial role in maintaining cellular homeostasis. Disruptions in enzymes involved in lipid metabolism, for example non-lysosomal β-glucosylceramidase 2 (GBA2), have been implicated in motor neuron disorders including recessive spastic ataxias and Gaucher's disease, a genetic disease that is characterized by a toxic accumulation of glucosylceramides due to disrupted lipid metabolism enzymes. GBA2 catalyzes the breakdown of glucosylceramides, but despite this clinical relevance, the molecular mechanisms by which GBA2 contributes to these pathologies remain unclear. In this collaborative project with Springfield College, we have identified putative GBA2 orthologs in *Drosophila melanogaster* and are utilizing this model organism to study GBA2 function. Previously in our lab, recombinant expression in *E. coli* and fluorescence-based assays with 4-methylumbelliferyl-β-D-glucopyranoside (4-MUG) were used to confirm the enzymatic activity of putative GBA2 orthologs as genuine glucosylceramidases. Here, we continue to characterize GBA2 from *Drosophila melanogaster,* including characterizing the effects of disease-related mutations on enzymatic activity and pH dependence. This project advances our understanding of GBA2 and the biochemical mechanisms of its disease-causing mutations at both the molecular and organismal levels.

(P.5) Creation of a Gas Handling System

Daniel Kent and Adam Anthony*
Department of Physics, High Point University

Fission, or the splitting of a nucleus in two, has applications which span from power generation to nucleosynthesis, the creation of elements in the universe. In the case of nucleosynthesis, very unstable nuclei are involved with half-lives much shorter than a second. Studying nuclei like this necessitates the use of a rare-isotope beam (RIB). In RIB experiments, an unstable nucleus is created and its physical properties measured within milliseconds. When studying fission with a RIB, there is a tension: the creation of the nuclei must be done at high energy, while the fission measurement must be done at low energy. This project focuses on the slowing down, or degrading, of the RIB. In a previous experiment, a thin piece of iron was used. The non-uniformity of the iron meant the energy of the fission nuclei was poorly constrained. Previous work demonstrated the feasibility of using a gas degrader. This project began developing a gas handling system (GHS) to maintain a uniform pressure in the degrader. Over this project, I designed and built a temporary version of the GHS; additionally, I wrote firmware for a user interface to view and control conditions within the GHS. Future work in this project includes the construction of a permanent version of the GHS proper for testing.

(P.6) Expanding the Landscape of Lactate Monooxygenases: Insights from *Beauveria bassiana*

Sophia Messerly, Imogen Irons, and Kelsey Kean*
Department of Chemistry, High Point University

Lactate monooxygenase (LMO) is a flavoenzyme that uses flavin mononucleotide (FMN) as a cofactor to catalyze redox reactions. LMOs are unique because they use a coupled pathway to convert lactate into acetate, H_2O, and CO_2, unlike other flavoenzymes in the family that catalyze uncoupled pathways. LMOs are commonly found in bacteria, but recent genomic analyses and biochemical studies have also identified them in archaea and fungi. However, fungal LMOs remain poorly characterized, and it is unclear whether they retain the catalytic behavior observed in bacterial enzymes. In this study, we focus on an LMO from the fungus *Beauveria bassiana* and report its expression, purification, and enzymatic activity. The recombinant protein was expressed in *Escherichia coli,* purified by affinity chromatography, and analyzed by Gel electrophoresis and UV-visible spectroscopy. Enzymatic activity was evaluated using an acetate-dependent assay that monitored the formation of acetate and its conversion to an intermediate, with absorbance at 450nm measured. These findings expand current knowledge of LMOs and suggest functional conservation across different domains of life.

(P.7) Quantifying NAD+ Precursors in Common Foods

Philip Morriseau and Jeremy Whitson*
Department of Biology, High Point University

Nicotinamide adenine dinucleotide (NAD+) is an essential electron carrier for cellular energy metabolism and a coenzyme for DNA repair. NAD+ levels drop as we age, so dietary precursors like NAM, NMN, NR, and NA are getting more attention as something we can increase through diet to support healthy aging. This project tested a diverse selection of common foods to quantify the levels of these NAD+ precursors to construct evidence-based diet recommendations that promote healthy aging. Fifty food items were selected to represent major dietary categories, including meats, vegetables, fruits, fungi, grains, and herbs. Each food sample was analyzed in triplicate to ensure reproducibility. Samples were homogenized in a 0.1% formic acid and buffered methanol solution spiked with isotopically-labeled NAM internal standard and analyzed using liquid chromatography-mass spectrometry (LC-MS). External calibration curves were made from standards that contained all the metabolites at a 50uM concentration, and a series of 1:10 serial dilutions down to 500pM. Meats showed the most concentrated levels of total vitamin B3, making them the most efficient way to meet daily vitamin B3 requirements. Broccoli, raw cabbage, white flour, mushrooms, thyme, cooked spinach, and green tea were the most concentrated in NR and NMN. A diet emphasizing these foods can deliver up to 250mg of NR and NMN combined daily, reaching a similar level to supplements. Overall, meats are recommended for total vitamin B3 delivery for daily health, while broccoli, cabbage, and fungi are recommended for targeted NMN and NR intake to promote healthy aging.

(P.8) Following the Flow: How Ultrasound May Enhance Glymphatic Flow in a Physical Brain Model

Maia Ramirez, Gustavia Gooding, Jacob Brooks, and Eric Rokni*
Department of Physics, High Point University

The brain produces metabolic byproducts that must be cleared every day to maintain healthy function. This waste is cleared out by the glymphatic system, a waste-removal pathway discovered in 2012. This system uses cerebrospinal fluid (CSF) that flows through brain tissue to remove proteins such as amyloid-beta. When this system is not functioning well, such as after traumatic brain injuries or sleep deprivation, these proteins can build up in the brain and are associated with neurodegenerative disorders such as Alzheimer's disease. Because of this, researchers have been interested in finding methods to improve this glymphatic flow. Focused ultrasound (FUS) is a noninvasive therapy that has potential to mechanically stimulate CSF flow. To investigate this, we created a physical model of this system using 3D-printed elastic resin surrounded by an agarose gel fabrication to mimic the perivascular spaces CSF flows through and the surrounding brain tissue. A synthetic CSF mimic was also developed to flow through the system. Rheological characterization of both the agarose gel and synthetic CSF was performed to best match the mechanical properties of biological brain tissue and CSF, respectively. Fluorescence particle tracking was then used to quantify the fluid movement of both a normal flow and FUS exposure. By understanding how different ultrasound parameters affect the movement of CSF, we can develop a deeper understanding of the system's mechanics which can help inform future therapies.

(P.9) Identifying the protein target of an antibiotic adjuvant in MRSA through affinity-based protein purification.

Logan Rampetstreiter, Gabriel Valenzano, Meghan Blackledge, and Heather Miller*
Department of Chemistry, High Point University

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a gram-positive bacterium that has developed resistance to many antibiotics. MRSA's antibiotic resistance poses a serious health risk to communities and hospitals across the globe. Previous results from our lab have shown that small molecules such as loratadine, the active ingredient in the common allergy medication Claritin, inhibit resistant bacteria's growth when co-treated with antibiotics. Compounds that resemble the three-ring structure of loratadine have also shown inhibition of bacterial growth, suggesting that the structural scaffold plays a large role in the antibiotic adjuvant activity of these compounds. Our research focuses on a brominated carbazole (compound 8), which acts as an adjuvant when co-treated with oxacillin in vitro. Previous experiments have theorized serine/threonine kinase 1 (STK1) as the target protein for adjuvant activity, although this has not been directly demonstrated. We aim to isolate and characterize the protein(s) that compound 8 interacts with in or on MRSA cells through protein purification techniques. Identifying the protein target(s) of compound 8 will provide a better understanding of its mode of action and how it enhances antibiotic activity.

(P.10) Effects of nitrogen and water stress on gene expression and autumn leaf color in oaks (genus *Quercus*)
Haven Tucker, Nicole Hughes, and Megan E. Rudock Bowman*
Department of Biology, High Point University

The adaptive function of autumn leaf coloration is an issue currently debated by plant physiologists and evolutionary biologists. Plant physiologists argue that red anthocyanin pigments evolved in trees adapted to cold and bright conditions in autumn and help reduce damage from sunlight and free radicals during leaf senescence. Evolutionary biologists argue that red coloration may have coevolved to signal poor nutritional quality to insects choosing host trees during autumn (e.g., aphids), since these insects tend to be attracted to lighter-colored leaves. These functions are not mutually exclusive, as photosynthetically vulnerable tissues (e.g., drought-stressed or low-nitrogen plants) would both benefit from photoprotection and also make poor hosts. Additionally, UV-absorbing phenolic compounds increase under nitrogen and water stress and should be visible to insects that can see UV, even in yellow leaves. We hypothesized that anthocyanins and UV-absorbing phenolics would increase under water and nitrogen stress, with the highest levels occurring under combined stress. To test this hypothesis, we grew saplings of two oak species with red autumn leaf color (*Quercus rubra* and *Q. bicolor*) and two with yellow autumn leaf color (*Q. acutissima* and *Q. robur*) under combinations of high versus low nitrogen and high versus low water during the growing season. In the fall, we will quantify anthocyanin and phenolic levels in leaves from each treatment using a spectrophotometer and examine gene expression.

FRIDAY, JULY 25 POSTER PRESENTATIONS PART B (11:30 am – 12:30 pm):

(P.11) First occurrence of Shuvosauridae from the Norian (Upper Triassic) Snyder Quarry Locality based on Hindlimb Elements
Justin Allan, Eleanor Lee, and Josef Stiegler*
Department of Biology, High Point University

From 2023-2026, expeditions to the Upper Triassic Chinle Formation of northern New Mexico's Carson National Forest focused excavation on the Snyder Quarry locality. The locality is within the Chinle Formation, an Upper Triassic unit spanning much of the American Southwest which is exposed in the Chama Basin. Our excavations yielded thousands of vertebrate fossils, including several hindlimb elements representing shuvosaurid poposauroid hindlimb material. Shuvosauridae is a clade of pseudosuchian archosaurs in the clade Poposauroidea characterized by bipedality and complete edentulism. Shuvosaurids have been previously recovered from several Chinle Fm localities, and two new species have been recently named, including Sonselasuchus from Petrified Forest National Park, and Labrujasuchus from very near the Snyder Quarry locality. The hindlimb material includes an associated femur and tibia, as well as several isolated femora and isolated metatarsals. In our phylogenetic analysis, we treated the material as belonging to a single species of shuvosaurid due to femora comprising most of our material, and the association of the femur and tibia in one individual. The results of our analysis unite several taxa in a shuvosaurid clade, including Effigia and Labrujasuchus (also from the Chama Basin) and Shuvosaurus from chronologically equivalent deposits in Texas. Our specimens lack diagnostic features of Labrujasuchus, however, it is unclear whether this is due to individual variation or taxonomic difference.

(P.12) Evaluating the Effects of Fused Tricyclic Compounds as Mitochondrial-Targeting Drugs in *Toxoplasma gondii*
Sophia Bellino, Sophia Castillo, Meghan Blackledge, and Robert Charvat*
Department of Biology, High Point University

Toxoplasma gondii is an intracellular protozoan parasite that infects approximately one-third of the world's population. *T. gondii* can cause severe disease in immunocompromised individuals as well as cause devastating effects during pregnancy, especially for the developing fetus. Current treatment options have limitations, creating a need for new therapeutic strategies. This study investigates the effects of loratadine derivatives on *Toxoplasma gondii*, with a particular focus on the sole parasite mitochondrion. Prior studies employing RNA sequencing analysis revealed that genes involved in mitochondrial metabolism and function were differentially expressed between vehicle- and drug-treated parasites. Therefore, we hypothesize that loratadine-based treatment disrupts mitochondrial function, reducing parasite viability and replication. By examining changes in mitochondrial morphology and function following treatment, this research aims to determine whether loratadine has potential as an adjunct therapeutic approach against *T. gondii*. The findings may contribute to the development of more effective treatments by identifying mitochondrial pathways as promising drug targets.

(P.13) A Four-enzyme Cocktail Allows Knockout of Candidate Dimorphic Genes in *Knufia petricola*

Josephine Bertuna, Daniel Sapozhnikov, Sophia Cima, Caden Reedy, and Grace Hamilton*
Department of Chemistry, High Point University

Knufia petricola is a black fungus capable of surviving extreme environmental pressures. When grown on carbon-starved media, it adapts by changing cell shape. There is an untested hypothesis that cell shape change is an adaption for extremotolerance, but the genetic basis of extremotolerance is unknown. We aim to identify the genes responsible for extremotolerance in *K. petricola* and someday transfer these extremotolerant traits to non-extremotolerant organisms, such as budding yeast. Thus, we may be able to advance astronautical missions by allowing organisms previously incapable of surviving the harsh conditions to be used for pharmaceutical or agricultural purposes in space. However, one major challenge is genetically manipulating the *K. petricola*. This is due to their heavily melanized cells walls, which must be removed to allow foreign DNA in. At present, we have found a mix of four enzymes that facilitate cell wall removal and begun knockout trials with twenty genes of interest that are upregulated when *K. petricola* is deprived of carbon. To date, we have attempted to knock out six of them. If our knockouts result in the removal of *K. petricola*'s ability to adapt to high stress environments—specifically its ability to change its cell shape—then we can conclude that we have discovered a gene that is necessary for extremotolerance.

(P.14) How to NOT Study Mosquitoes: Lessons Learned in Field Research

Madison Burnett, Scarlett E. Peabody, Nathan O. Dwier, Gavin H. Agahigian, Haven A. Tucker, A. Daniel Greene, and Megan E. Rudock Bowman*
Department of Biology, High Point University

Studying mosquitoes is important regarding public health, disease management, and ecological research due to several species serving as vectors for human disease pathogens. CDC light traps are widely regarded as the gold standard for adult mosquito surveillance. However, modified DynaTraps® have demonstrated improved mosquito capture rates while offering a more cost-effective alternative. DynaTrap®, commercially available mosquito UV light traps, were placed at 28 field sites, along 2 urbanization gradients (North-South or East-West) in Greensboro and High Point, North Carolina, overnight weekly for 4 weeks in the summer of 2026. Samples collected were placed in a -80ºC freezer and sorted to taxonomic order. Mosquitoes represented a small minority of the insects trapped each week, less than 0.5% of the total specimens collected during week 2. There was a significant amount of by-catch, most commonly other Dipterans. The low mosquito capture rate could potentially be due to the trap placement, environmental conditions such as temperature, rainfall, humidity, and wind, or the attractant effectiveness, all of which can greatly influence the trap performance. Despite this setback, the samples collected provide information on the biodiversity of these areas across a gradient of urbanization. Future work can pivot towards analyzing the composition and diversity of the by-catch, comparing the trap efficiency across the 28 locations, or using different mosquito traps for further studies.

(P.15) Nucleotide Hydrolysis Rates Regulate Septin-Septin Interactions

Thyliah Coleman, Shauna Skow, and Grace Hamilton*
Department of Chemistry, High Point University

Septins are cytoskeleton proteins that are conserved across many eukaryotic species, such as yeast and humans. Septins are GTP-binding proteins, some of which also hydrolyze GTP. Single septin subunits form rods and then polymerize to form filaments that can assemble into high-order structures. Septins regulate many cellular processes such as morphogenesis, plasma membrane organization, and cellular division. Because septins rely on nucleotide hydrolysis to perform their cellular functions, changes to this septin function should affect cells' ability to form certain structures and completely separate during cytokinesis. AspE is a member of an under-studied family of septins unique to fungi. AspE can bind to one other septin, Cdc11. This AspE-Cdc11 binding interaction may be incorporated into high-order structures. We expressed and purified AspE proteins with mutations to its GTP-binding domain. We found that two of the mutations, T200A and K163A, conduct less GTP hydrolysis than the wild-type AspE. One of the mutations, D219A, outperforms wild-type AspE, and the last mutation, R447A, performs similarly to wild-type AspE. Wild-type AspE commonly behaves as a dimer, however the mutations T200A and K163A behaved as monomers. Subsequent steps will include using yeast two-hybrid assays to see if the slowed GTP hydrolysis mutations affect AspE interactions with Cdc11. Determining the rules for septin-septin interactions lays the groundwork for further research developing novel anti-fungal drugs.

(P.16) Developmental filtering and the hierarchical organization of genetic contribution in evolution

Lanie Gardner, Dariann Adams, and Kenneth McKenna
Department of Biology, High Point University

Have you ever considered the importance of the hierarchical structure of gene pathways? Developmental systems determine not only how organisms are built but also how genetic variation contributes to phenotypic evolution. Although genome-wide association studies (GWAS) have identified numerous loci associated with complex traits, the developmental principles governing why some genes repeatedly contribute to variation while others remain highly constrained are poorly understood. Our main objective is to understand whether network positions determine phenotypic importance. Using the *Drosophila melanogaster* wing as a model system, we will integrate population genetics, developmental biology, and network analysis to determine how developmental organization shapes phenotypic variation and evolvability. To test this mechanistic prediction, targeted RNAi knockdowns were performed using wing specific GAL4 drivers across a curated set of genes spanning the inferred developmental hierarchy. Phenotypic consequences were quantified under baseline, nutritional stress, and heat stress conditions to determine whether developmental necessity interacts with environmental state. In conclusion, by linking developmental hierarchy, plasticity, genetic variation, and evolutionary constraint within a unified framework, this work will establish a mechanistic basis for developmental filtering and provide new insight into how developmental architecture governs the evolutionary potential of complex traits.

(P.17) Interaction Interface between the mTOR Pathway and Circadian Clock in *Neurospora crassa*

Nick Gonzalez, Koby Mante, and Alexander Mosier*
Department of Biology, High Point University

The circadian clock is a molecular system found across all branches of life. This clock does not simply tell an organism what time it is, but rather it allows an organism to be more proactive towards environmental changes. The conserved molecular nature of the clock allows the use of model organisms such as the filamentous fungus, *Neurospora crassa*. Within the core circadian clock of *N. crassa*, a core clock protein, FREQUENCY, has recently been studied to define its overall interactome and give a starting point for clock regulation at the proteomic level. The goal of this project is to examine how recently discovered interactors to the core circadian clock explain how the clock temporally regulates downstream processes. Reviewing the list of interactors, we found the quantity of those connected to the mTOR pathway to be particularly interesting. We studied how the proteins mTOR, PP1, WD-Repeat, and α-Tubulin facilitate interaction between the mTOR pathway and the overall negative feedback loop that underlies the circadian clock. To do so, we studied the selected proteins by Western Blot analysis. Using samples of proteins collected at various periods of total darkness, no darkness, 4 hours, and 8 hours, along with antibodies specific for the proteins and their phosphorylation state we measured relative abundance and phosphorylation across circadian time. Our findings create a baseline for how mTOR pathway proteins oscillate over circadian time, in both abundance and phosphorylation state, as well as how they act back on the core circadian clock to maintain proper timing.

(P.18*)* Advanced Characterization of Milk-Derived Extracellular Vesicles

CJ Gulla, Holley Lowe, David Coltan, Stephen Ray, Steve Grekin, Elyse Zeffiro*, and Elijah Sage*
Grekin Labs

Extracellular vesicles (EVs) are nano-sized particles that are naturally released by all living cells. EVs play a key role in cellular communication, which makes them useful in targeted drug delivery and cell-free therapeutics. This summer, we isolated EVs from various milk sources in order to characterize their differences to determine whether or not EVs isolated using our methodology meet the standards for human consumption. To evaluate the size distribution and concentration of our EVs, we used nanoparticle tracking analysis (NTA). Next, we observed individual EV morphology using both the scanning electron microscopy (SEM) and atomic force microscopy (AFM). Finally, we assayed for different proteins found in the membrane and the cytosol of milk EVs using SDS-PAGE to confirm sample quality. Analysis of our data suggests that we met the MISEV standards for each milk sample. In the future, we intend to adapt our results to develop a release assay, which will ensure the quality of EVs produced when manufacturing begins.

(P.19*)* Assessing Ecosystem Services in Native vs. Ornamental Botanical Gardens at High Point University

Scarlett Peabody, Madison M. Burnett, Haven A. Tucker, Brian R. Ragoobir, Ellie Marcella V. Ratta, Kara E. Vaartjes, Nicole Korzcyk, Connor S. Spitler, A. Daniel Greene, and Megan E. Rudock Bowman*
Department of Biology, High Point University

The Mariana H. Qubein Arboretum and Botanical Gardens at High Point University is an extensive network of over 30 campus gardens, which include a diverse range of native and ornamental flowering plants. In this study, ecosystem services of pollination, predation, decomposition, and nutrient cycling were assessed in two gardens of similar size (i.e., area) and plant diversity but varying significantly in terms of plant species identity – Native vs. Ornamental. The Scarborough Butterfly Garden contains a wide array of native plants selected to support pollination services, while the Conservatory Garden is primarily planted with annuals selected for their aesthetic appeal. To compare ecosystem services between the two, pitfall traps were used to collect epigeal arthropods while aerial nets were used to assess insect pollinators. Pitfall traps were placed in each garden randomly within 4 quadrants at equal area density. Traps were collected weekly from March - April 2025 and June - July 2026, after which arthropods were grouped and counted. Using aerial nets, garden areas were actively sampled 14 times for 30 minutes each (August – September 2025 and March - July 2026). Collected insects were chilled on ice for 20 minutes, photographed on a 1cm x 1cm grid for identification using iNaturalist, and released. The diversity of epigeal arthropods and pollinators was higher in native gardens when compared with ornamental gardens. The application of granular systemic insecticide Imidacloprid to the mulch in the Butterfly Garden in May 2026 dramatically decreased the abundance of species and specimens collected compared to previous surveys.

(P.20) The Wood's Hidden Voice: Investigating Phantom Partials in String Instruments

Nicole Phillips and Eric Rokni*
Department of Physics, High Point University

Stringed instruments, such as violins, cellos, and pianos, produce harmonics when the string is set into motion. Phantom partials are frequencies outside of the harmonic series that also appear in an instrument's output. While originally attributed to forced longitudinal motion in the string, recent studies have determined that phantom partials are likely produced from the wood of the instruments, possibly through nonlinearities from wood-on-wood contact. The goal of this research was to determine whether wood-on-wood contact and a violin's soundpost impact the strength of phantom partials. A wooden box with a removable bottom was designed to replicate the inside of a string instrument. A piezoelectric transducer (PZT) drove the box at two simultaneous frequencies; 330 Hz at a constant amplitude and 440 Hz with a linearly increasing amplitude. An accelerometer was placed next to the PZT to measure the resulting frequencies. Five configurations were tested: a single spruce plate, two spruce plates resting on top of each other, a spruce plate resting on the box, a spruce plate glued to the box, and the box fitted with a soundpost. Whilst we found that wood-on-wood contact increases the strength of the phantom partials, the addition of a soundpost had no major impact on their strength. These results help narrow down the physical origins of phantom partials, helping explain what gives each instrument its unique sound.

2026 SuRPS Faculty Participation and Projects

Department of Biology

Dr. Megan Rudock Bowman (Molecular Ecology and Medical Entomology)

The Effect of Urbanization on Mosquito Species and Vector Distribution

My lab works on a variety of projects in the Molecular and Genetic Ecology space, often collaborating with botanists, ecologists and entomologists. This summer we will be continuing work on a Medical Entomology project in collaboration with Dr. A. Daniel Greene. The Greene and Bowman labs will collaborate to collect and identify mosquitos to the species level across both a North-South and East-West Urbanization gradient, using DynaTraps and CDC Light Traps. Mosquitos will be frozen on site and transported to the laboratory. Species identification will occur on a Cold Table in the lab, where mosquitos will be pooled by species, trap and date for analysis. Using molecular assays, such as RAMP assays and RT-PCR mosquito pools will be tested for Vector-borne diseases, such as Zika, Dengue Fever, La Crosse encephalitis, and Malaria. Test results will be added to state-wide databases and further evaluated with GIS data for correlations with Urbanization, Socio-economic status, or land utilization. Students will have the opportunity to participate in monthly field research, DNA and RNA isolation, PCR, qPCR, bioinformatics, and workshops for mosquito identification. There may also be the opportunity to present this research at the national Ecological Society of America meeting immediately following SURPs.

Dr. Robert Charvat (Molecular Parasitology)

Investigating the mechanism of action of novel antiparasitic compounds

The Charvat lab studies *Toxoplasma gondii*, a parasite found around the world infecting approximately one-third of the human population. Toxoplasmosis, the disease caused by infection with *T. gondii*, is the second leading cause of death from food-borne illness in the United States, and for which there are currently no efficacious treatments. As a result, our group is broadly interested in novel drug discovery and understanding the mechanism of action of those compounds as well as others with intriguing effects on normal parasite biology.

Dr. A. Daniel Greene (Community Ecology, Entomology, and Landscape Ecology)

Characterization of arthropod diversity and abundance across various habitats and disturbance gradients in the southeastern U.S.

In the Greene lab, we are interested in measuring how arthropod community patterns change across managed and natural landscapes in response to/alongside environmental gradients (e.g., climatic and landscape data). Specifically, we are researching how the abundance of various arthropod taxa/functional groups (e.g., decomposers, predators, etc.) differs across ecotones and disturbance (e.g., urbanization and/or fragmentation) gradients. Additionally, we are interested in assessing if biodiversity and/or abundance trends are consistent across arthropod and taxa/functional groups and sampling methods. We assess arthropod communities occupying macro- and micro-habitats (e.g., the arthropod community living within bryophytes) with commonly used sampling techniques (e.g., pitfall traps and leaf litter collection) and innovative capture methods to answer our questions. We also collect local environmental data via deployable sensors and utilize geospatial land cover data layers (e.g., USDA Copland Data Layer) to understand how arthropod communities are spatiotemporally structured. We spend our time identifying a wide variety of arthropods, learning different ecological modeling and mapping techniques, understanding our findings within the context of climate change, and enjoying our fieldwork! We love to collaborate and learn from others' experiences, so please reach out if you are interested!

Dr. Kenneth McKenna (Developmental Biology)

Developing a hierarchy of genetic contribution

My research program is motivated by a central question in evolutionary and developmental biology: how do gene regulatory networks (GRNs) and emergent properties across biological levels shape phenotypic variation and evolution? Traditional models have often reduced development to linear gene-to-trait mappings, but my work seeks to transcend this reductionism by embracing the complexity and nonlinearity inherent in biological systems. I argue that causation in development is distributed across networks of genes, cells, and physiological processes, and that understanding these networks is essential for explaining how unique traits arise from shared genetic origins.

Our lab is taking a two-pronged approach to this problem. First, using the Drosophila wing as our model, we will build a hierarchical model of genetic contribution to the phenotype. Although the field has generated a working network/GRN model of genes involved in wing development, missing from this is information that informs evolutionary biology. A list of factors needs to be massaged, manicured, and matured into a functional system so as to unveil paths of evolution. The first step in doing this is making a hierarchical model of genetic contribution rooted in the network architecture. To do so, we are using the Drosophila Transgenic RNAi Project (TRiP) to knockdown every gene in the wing GRN under a common GAL4 promoter. We will start with the core organizers (Dpp/BMP2, Wnt, Hh) and their target genes (Spalt, Distalless, Cubitus interruptus), and will continue to build out from there.

Dr. Alexander Mosier (Circadian Biology and Proteomics)

Unveiling the Regulation of and by the Molecular Clock

The Mosier lab studies the circadian clock, a molecular mechanism that keeps time so that the organism can be proactive rather than reactive to changes due to the Earth's day/ night cycle. This core clock is conserved across all branches of the tree of life. The first area of focus of the research is investigating how the core clock relays this temporal information through protein-protein interactions. Through the use of Western Blot analysis and Mass Spectrometry we look at protein function and regulation as influenced by the core clock mechanism. The second part of the lab is looking into the novel field of quantum biology and studying how quantum mechanics impact and regulate the clock's functionality. By developing computational models to simulate changes in basic quantum process we can begin developing an understanding of the impact these have on the core clock.

Dr. Josef Stiegler (Vertebrate Paleontology and Anatomy)

Anatomy and systematics of dinosaurs and other reptiles from the Late Triassic of New Mexico

The Southwestern U.S. preserves a vast sedimentary rock unit called the Chinle Formation that includes river, lake, and pond deposits from the Late Triassic Period of paleo-tropical Pangea. In Northern New Mexico, broad exposures of the Chinle Formation have yielded a wealth of fossils including dinosaurs and other lineages of terrestrial reptiles that typically come from dense multi-taxon bonebeds representing mass-death assemblages. The Stiegler lab conducts paleontological field research to collect fossils from two of these bonebeds, and is engaged in analyzing the anatomy and phylogenetic relationships of the fossils, with a focus on the dinosaurs and their close relatives.

This summer, students are encouraged (but not required) to join Dr. Stiegler in New Mexico for fieldwork beginning in May that will overlap with the first few days of SuRPS in June. There, they will collect vertebrate fossils and experience the beautiful high altitude desert biome (~6100 ft). Back at High Point in June and July, students will be engaged in various projects identifying, cataloguing, preparing, imaging, and describing the anatomy of fossils that were collected during fieldwork. These projects will involve carefully removing fossils from the rocks that encase them either mechanically with hand tools, or digitally by creating 3D models from CT scans. Students will take at least one trip to the Duke Shared Materials Instrumentation Facility to participate in the collection of CT scans of fossils with Dr. Stiegler, and all SuRPS students will learn how to generate 3D models of vertebrate anatomy from CT scan data.

Dr. Jeremy Whitson (Geroscience and Eye Lens Physiology)

Pro-longevity and anti-cataract effects of natural compounds

Biological aging is a complex and multifactorial process that involves accumulation of cellular and molecular damage, cell and tissue dysfunction, chronic inflammation, and many other physiological changes.

These changes result in a high incidence of age-related diseases, including age-related cataract, which is the leading cause of blindness globally. In the Whitson lab, we focus on characterizing the molecular changes that underlie aging and the development of age-related cataracts, as well as testing natural compounds for the ability to slow, prevent, or even reverse these molecular changes.

Ongoing projects include assessment of nicotinamide adenine dinucleotide (NAD+) precursors in foods via mass spectrometry to develop an NAD+-boosting anti-aging diet, determination of age-related protein posttranslational modifications across the spatiotemporal gradient of the eye lens, exploration of the physiological role of urea in the lens, and testing of flavonoid compounds as anti-cataract agents in lens homogenates and in whole cultured lenses.

Department of Chemistry

Dr. Grace Hamilton (Biochemistry)

Fungal cytoskeletal proteins and secondary metabolites

There are two SuRPS projects in the Hamilton Lab this summer: The first project explores how fungi control the shapes of their cells. Cell shape plasticity is a hallmark of fungal growth and hypothesized to be an adaptation for extremotolerance. Cell shape is largely controlled by the protein of the cytoskeleton. Some of the most understudied cytoskeletal proteins are septins. Septins are nucleotide-binding proteins, but we don't yet understand how their ability to bind and hydrolyze nucleotides relates to their ability to interact with one another to form polymers. SuRPS students will use biochemistry and molecular biology techniques including yeast two-hybrid assays, recombinant protein purification, and HPLC to determine how nucleotide binding and hydrolysis affect septin-septin interactions. By elucidate how fungi control their cell shape, we identify potential targets for new antifungal drugs.

The second project explores the use of small molecules produced by fungi (fungal secondary metabolites) to treat human disease. Drugs that inhibit the human enzyme acetylcholinesterase (AChE) are used to treat several neurodegenerative diseases, including Alzheimer's Disease. But current treatments are imperfect, and there is demand for novel AChE inhibitors. We have previously screened a library of freshwater and marine fungi for the production of AChE inhibitors and identified several promising hits! But we don't yet know what specific molecules are producing the inhibitory effects. SuRPS students will use analytical chemistry techniques, including mass spectrometry and NMR, to identify the specific molecules being produced by each fungus, hopefully paving the way towards novel treatments for neurodegenerative diseases

Dr. Kelsey Kean (Biochemistry)

Studying extreme proteins from extreme organisms

Proteins are among the most abundant and functionally diverse biomolecules with the ability to carry out unique and specific functions and chemistries. In the Kean Lab, we are interested in understanding how proteins evolve and are able to carry out their unique and specific chemistries. A key piece to understanding how proteins work – when working correctly, when behaving aberrantly, or when being engineered for a new function – comes from exploring and understanding protein structure and function on a molecular level. One area of interest in our group is understanding proteins from extremophiles, organisms that can survive extreme conditions such as pH, temperature, and even the vacuum of space. In order to survive, these organisms must have very stable proteins. We are curious to know how these proteins work and what makes them so stable. Student researchers in the Kean Lab will have the opportunity to learn techniques in molecular biology, biochemistry, and structural biology.

Dr. Heather Miller (Molecular Biology & Biochemistry)

Disruption of Virulence and Antibiotic Resistance by Novel Molecules

The Miller Lab is engaged in a range of collaborative research projects designed to explore critical molecular aspects of human pathogens. One of our main goals is to understand how novel antibiotic adjuvants we are studying exert their effects. We have data that supports multiple antibiotic adjuvants working against methicillin-resistant *Staphylococcus aureus* (MRSA), as well as other human pathogens. These antibiotic adjuvants likely bind and inhibit a major regulatory protein in *S. aureus* called serine-threonine kinase 1 (Stk1). In doing so, many downstream gene expression changes occur, dismantling S. aureus virulence and antibiotic resistance.

Summer projects will center on three areas: 1) preparing and examining high-throughput RNA-seq data from multiple strains of bacteria to identify consequences of antibiotic adjuvants on gene expression. These experiments aim to shed light on which genes are always disrupted by adjuvant molecules and determine if these changes correlate with the bacteria's genetic background or environment in which it is acquired by humans. These analyses will offer predictive ability to other medically relevant strains. Students will gain experience in bioinformatic tools, as well as RNA purification and reverse transcription-quantitative PCR. 2) analyzing the consequences of these adjuvants on an animal infection model. This collaborative project will involve the enumeration of bacteria and the host animal's molecular response to infection. Students will gain experience in techniques such as spot plating, microscopy, and enzyme-linked immunosorbent assays (ELISAs). 3) analyzing novel molecules as inhibitors of efflux. These experiments will quantify any disruption to bacterial cells' ability to accumulate and/or pump out antibiotics, contributing to resistance. Students will learn aseptic technique and fluorescence accumulation and efflux assays.

Department of Physics

Dr. Adam Anthony (Nuclear Physics)

Imaging Nuclear Reactions with Time Projection Chambers

My group's work focuses on studying nuclear reactions with a class of detector called a Time Projection Chamber (TPC). TPCs are gas-filled detectors that act like a camera, allowing us to take 3D "images" of individual nuclear reactions where the nuclei are typically moving at more than 20% the speed of light. By measuring where and how the nuclei interact with the gas we can deduce both the path nuclei take through the detector, as well as their speed. This lets us understand the details of nuclear reactions from fission to the transfer of a single neutron between nuclei.

This project will focus on the development of new electronics and computational tools for analyzing TPC experiments. One of the more difficult things to measure in a TPC is how the particles lose energy in the detector. Unfortunately, this is also the hardest process to model theoretically and critical to understanding the physics of most experiments. Potential projects would involve: 1) designing and testing a new version of a circuit to allow us to measure a wider range of energy losses. 2) training and testing of a machine learning model to remove artifacts in the raw data that cannot (always) be easily removed using traditional methods. 3) testing a new computational method, developed last summer, for analyzing TPC data using data sets from institutions in Europe and the United States.

Dr. Jacob Brooks (Physics and Materials Science)

Micropatterned Surfaces for Advanced Functional Materials

Our research focuses on the design and fabrication of micropatterned surfaces to control interactions at the micro- and nanoscale. These surfaces have diverse applications, including fluid manipulation, biological interfaces, and device performance enhancement. Current projects explore strategies for biofilm prevention, development of biomimetic cilia arrays for microfluidic systems, and refinement of grayscale photolithography techniques using a maskless aligner to achieve complex 2.5-D structures. Students working in the lab will gain experience in microfabrication and characterization, including maskless photolithography, scanning electron microscopy (SEM), rheometry, atomic force microscopy (AFM), and contact angle measurements. This work integrates principles of materials science, microengineering, and biology, offering opportunities to contribute to innovations with implications for healthcare, environmental systems, and advanced manufacturing.

Dr. Eric Rokni (Biomedical Ultrasound)

Physics of Cavitation in Therapeutic Ultrasound

Our lab investigates the fundamental physics of therapeutic medical ultrasound, an emerging technology for noninvasive surgeries. Therapeutic ultrasound uses focused sound waves to generate bubbles in tissue, a process called cavitation. When these bubbles oscillate and collapse, they can destroy tissue in a controlled manner allowing for precise treatments. Current projects in the lab investigate two questions: How does cavitation behavior change in viscous environments that mimic conditions such as cystic fibrosis? And how might magnetic fields influence bubble growth and collapse? We are approaching these questions experimentally, analytically, and computationally. In the lab, students will gain hands-on experience with therapeutic ultrasound systems, performing underwater acoustic measurements, and working in MATLAB/Python. This research integrates physics, engineering, and biomedical applications, providing the perfect opportunity for students looking to engage in interdisciplinary work.

Dr. Alex Sobotka (Physics)

Predicting Dark Matter Galactic Halo Populations Resulting from Non-Standard Cosmologies

Galaxies are embedded within massive, roughly spherical halos of dark matter whose sizes and abundances are shaped by the universe's expansion history—from the Big Bang through the earliest stages of structure formation. Many proposed extensions to standard cosmology, such as modified particle dark matter properties or early periods of accelerated expansion, can leave distinctive imprints on the number and distribution of these halos. Instead of relying solely on computationally intensive simulations, this project develops and utilizes analytical tools to predict how different early-universe scenarios influence the abundance and growth of dark matter halos.

A key challenge to this analytical approach is that these predictions require assumptions about how halos collapse, evolve, and merge over time. Small changes in these assumptions can lead to significant differences in predicted halo populations. Students will explore these dependencies by comparing the halo population predicted by different collapse prescriptions and quantifying how variations among non-standard cosmologies compare under different halo collapse models. This work provides experience in theoretical astrophysics, cosmological modeling, coding, and the physics of the early universe, while contributing to our understanding of how the universe's earliest moments shaped the galaxies we observe today.

SuRPS 2026 Seminar Series

Wednesdays at 11 am, Wanek School of Natural Sciences

Date	Name	Affiliation	Seminar Title
Friday, June 5	**Dr. Emily Owens Pickle** Assistant Professor	Department of Epidemiology, Biostatistics, & Environmental Health Joint School of Public Health Old Dominion University Norfolk, VA	*From parasites to pandemics: investigation of emerging and re-emerging diseases in the United States*
Wednesday, June 10	**Dr. Cedric Schacck** Assistant Professor	Department of Chemistry Wake Forest University Winston-Salem, NC	*New Organic Scaffolds for Optical and Electronic Materials Applications*
Wednesday, June 17	**Dr. Lily Hughes** Research Assistant Professor	North Carolina State University & North Carolina Museum of Natural Sciences Raleigh, NC	*Uncovering Fish Biodiversity with Genomics Across Ancient and Recent Timescales*
Wednesday, July 1	**Dr. Caroline Proulx** Associate Professor	Department of Chemistry North Carolina State University Raleigh, NC	*New strategies for peptide mimicry and late-stage functionalization*
Wednesday, July 8	**Dr. Kennita Johnson** Assistant Professor	Lampe Joint Department of Biomedical Engineering North Carolina State University & University of North Carolina at Chapel Hill Chapel Hill, NC	*Biomedical Imaging from Different Perspectives*
Wednesday, July 15	**Dr. Catherine Denning-Jannace** Assistant Professor	Department of Chemistry University of North Carolina at Greensboro Greensboro, NC	*Beyond Cu chelation: Assessing the role of Cu in the antifungal response of C. albicans*

Past SuRPS Keynote Speakers

Year	Speaker	Title
2015	**Rachael Parker, Ph.D.** HPU Chemistry 2011 *Virginia Tech*	*Statistical and combinatorial approaches to designing repeat proteins as recognition elements in microbial sensors*
2016	**Sarah Craven Seaton, Ph.D.** HPU Chemistry/Biology 2004 *UNC Asheville Biology*	*Soirées in the Soil: Bacterial Communication, Cooperation, and Competition in the Rhizosphere*
2017	**Laura Lee, Ph.D.** HPU Biochemistry/Physics 2012 *North Carolina State University*	*Boiling Bugs Break Biomass: An Investigation Into High Temperature, Cellulolytic Microorganisms*
2018	**Gavid Coombs, Ph.D.** HPU Biochemistry 2014 *Yale University*	*A Journey Through Research: Peptide-Catalyzed Atroposelective Coupling of Arenes and Quinones*
2021	**Hailey Parry, Ph.D.** HPU Exercise Science/Chemistry 2017 *National Institutes of Health*	*Key to Success – A Note to Future Graduates*
2022	**Elizabeth Reardon** HPU Biology 2017 *Emmes Company, LLC*	*Planting Seeds: A Perspective on Alternative Paths*
2023	**Calla Telzrow, Ph.D.** HPU Biology 2016 *RFI at PPD*	*Underappreciated & Underestimated: Implications of Human Fungal Pathogens and Genetic Approaches to Understanding Them*
2024	**Alan Vasquez Soto, Ph.D.** HPU Physics 2018 *UNC Chapel Hill*	*Exploring the Fast Transient Optical Sky & Developing New Technologies for the Argus Array*
2025	**Olivia Armendarez** HPU Biochemistry 2022 *Northeastern University*	*Adaptive light-sensing and color-changing materials inspired by nature*

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Scenes from SuRPS











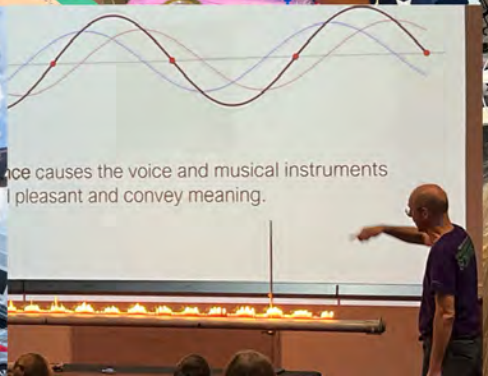

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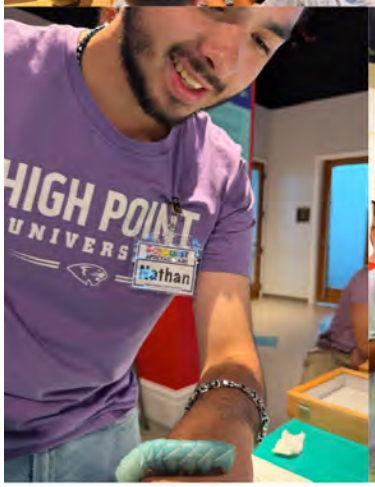

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