Spring 2026
Biology Research Showcase
Undergraduate Poster Abstract Book
Final version

Monday, April 27, 2026
SERC Lobby

Department of Biology
Temple University

Early AM Session 1 9am–10:30am	Late AM Session 2 11am–12:30pm
Ahmer (Cordes lab)	Ahuja (Gould lab)
Ansari (Hasan lab)	Bakare (Wang lab)
Awal (Ghosh lab)	Chapin (Bonfim lab)
Bolisetti (Kulathinal lab)	Dachepalli (Rawls lab)
Brownfield (Sewall lab)	Daniel (Sutton-Hickey lab)
Duffy (Liberles lab)	Dansberger (Ghosh lab)
Elkind (Liberles lab)	Elazazy (Rawls lab)
Golugula (Kulathinal lab)	Gordon (Grattepanche lab)
Gunaydin (Wu lab)	Hartman (Liberles lab)
Ikeh (independent)	Huang (Grattepanche lab)
Khandeshi (Rajadhyaksha lab)	John (Buttaro lab)
Le (Rajadhyaksha lab)	Kazi (Tam lab)
Le (Sewall lab)	Lasalla (Rothberg lab)
Lee (Smutzer lab)	Lin (Smutzer lab)
Martin (Kutlu lab)	Linhart (Sewall lab)
McNaughton (Bonfim lab)	Merry (Sharma lab)
Miller (Bonfim lab)	Morlet (Kim lab)
Oubarri (Kang lab)	Mousseau (Kulathinal lab)
Pasyar (Buttaro lab)	Nguanpho (Darbinian lab)
Patel (Ward lab)	Ohm (Golemis lab)
Porrecca (Chen lab)	Orekhova (Chen lab)
Regan (Daws lab)	Parrucci (Sewall lab)
Reyes (Sun lab)	Reyes (Sun lab)
Seaman (Bellacosa lab)	Sun (Abdulmalik lab)
Torh (Sun lab)	Tower (Rothberg lab)
Tran (Grattepanche lab)	Tran (Smutzer lab)
Uhlfelder (Bonfim lab)	Trinh (Grattepanche lab)
Zagorski (Ward lab)	Voet (Feitelson lab)
	Weidner (Giovanniello lab)

For a detailed summary, go to the last page of this document, “Faculty PI-Student Index”.

Session 1 (9am–10:30am, SERC Lobby)

Session1/Poster-1

Temporal Partitioning Facilitates Coexistence during Invertebrate Community Assembly within Ephemeral Pools

Jack Roderick Brownfield (Ecology, Evolution & Biodiversity)

Sewall Lab | Ambler

In fall 2021, an unprecedented tornado struck the Temple Forest Observatory, forming hundreds of novel ephemeral pools in uprooted trees' root basins. We utilized this opportunity to study niche partitioning during community assembly as aquatic invertebrates colonized these pools. We hypothesized that time is an important axis of partitioning, allowing organisms to avoid interspecific competition via asynchronous recruitment. We found that temporal niche overlap decreased significantly between year 0 and year 1, while other niche axes saw no change, suggesting that time is a significant axis of partitioning for these communities during assembly. Our work uncovers how temporal factors drive coexistence, offering a rare window into the hidden dynamics of community assembly and ephemeral habitats.

Session1/Poster-2

Disturbance Driven Responses of the Soil Seed Bank in Mature Temperate Forests

Amanda Thuy Le (Ecology, Evolution & Biodiversity)

Sewall Lab | Ambler

Beneath the forest floor lies a reserve of viable seeds that hold remnants of past plant communities, can shape the future forests. Large, infrequent disturbances can cause structural changes to an ecosystem. To examine how novel disturbances interact with ecological memory to shape community assembly, this study compares two mature forest stands in Ambler, Pennsylvania, United States: one disturbed by a tornado and one undisturbed reference forest. The disturbed forest is dominated by early successional species while the undisturbed forest retains shade-tolerant woody taxa. These findings suggest that the tornado disturbance reshapes habitat heterogeneity and filter functional traits allowing colonizers to dominate open microsites and survivors to shape ecosystem legacy. Climate change is increasing the frequency and intensity of tornadoes in the northeastern U.S., increasing the need to understand these ecological processes conservation and management.

Session1/Poster-3

Arthropod Community Assembly Response to Microclimates Caused by Wind-throw Disturbance Event

Isabella Miller (Environmental Science)

Bonfim Lab | Ambler

Climate change intensifies storm events causing environmental disturbances that leaving cascading effects on biodiversity. Arthropods play a central role in forest recovery as health indicators. We examined how arthropod communities respond a disturbance gradient at the

Temple Forest Observatory (TFO) that experienced a tornado event in 2021, and nearby Robbin's Park (RBP), as a control. To investigate whether variable microclimates alter arthropod diversity, we used pitfall traps across low-, intermediate-, and high-disturbance plots in TFO and RBP to collected ground-dwelling arthropods. Disturbance levels were classified by canopy loss from pre- and post-tornado remote sensing imagery. We collected over 1,900 specimens, with peak collections in the summer, as expected with seasonal shifts. Our findings highlight arthropod community resilience following a disturbance. As climate-driven disturbances continue, understanding these dynamics is essential for guiding forest management.

Session1/Poster-4

Glow Under Stress: Measuring Cellular Stress Responses Using Fluorescent Yeast

Emmanuel Ikeh (Neuroscience)

No lab affiliation

Environmental stresses can have substantial effects on cell growth and development. This experiment used baker's yeast (Saccharomyces cerevisiae) as the test organism to evaluate the effects of different environments on yeast growth characteristics. Test cultures were subjected to various environmental stresses such as elevated temperature, higher salt levels, and increased sugar content, while the controls were cultured under standard conditions. Growth of cells was measured throughout the experiment based on changes in culture density. The hypothesis proposed is that yeast exposed to environmental stress will show slower growth than the control group, and the magnitude of the effect will be dependent on the level of stress exposure. Through the execution of this experiment, valuable information could be derived concerning the cellular reaction to external stimuli in eukaryotes.

Session1/Poster-5

Role of Prelimbic Cortex Cav1.2 Channels in Regulating Social Behavior and Their Rescue via ISRIB

Sanjana Khandeshi (Molecular and Cellular Neuroscience)

Rajadhyaksha Lab | LKSOM

Voltage-gated calcium channels, particularly L-type calcium channel Cav1.2 , play a very important role in regulating neuronal excitability and synaptic plasticity. The prelimbic cortex, a subregion of the medial prefrontal cortex, is known for its importance in higher-order cognitive functions such as decision-making, executive control, and social interaction. Altered Cav1.2 signaling in the prelimbic cortex has been associated with psychiatric disorders including autism spectrum disorder, schizophrenia, and anxiety, all of which involve deficits in social and decision-making behaviors. Small molecule inhibitor ISRIB that targets downstream Cav1.2 signaling pathways, and may have therapeutic potential to reverse Cav1.2-associated dysfunction. The goal of this project is to recapitulate behavioral and neuronal dysfunction resulting from Cav1.2 loss in the prelimbic cortex (PrL) and rescue these dysfunctions via ISRIB administration.

Session1/Poster-6

Characterizing the Relative Strengths of Gain and Loss of Function Mechanisms for Dosage Balance Duplicate Gene Retention

Anna Duffy (Biochemistry)

Liberles Lab | BioLife

Gene duplication is an important process leading to the lineage-specific diversification of genomes. Whole genome duplication is a process in which every gene in an organism is duplicate, and after this occurrence, individuals may lose a copy of a gene while its partner remains duplicated, leading to significant stoichiometric imbalances in protein complexes. The selective pressure caused by the imbalance can act in two potential ways that have both been discussed in the literature. A chemical thermodynamic model has been developed that describes the change in concentration of functional heteromultimeric complex formed (loss of function model) and the change in concentration of exposed hydrophobic surface area available for deleterious misinteraction (gain of function model). These are dependent on an equilibrium constant Keq, concentration of hydrophobic surface area exposed to the environment [hp], expression levels of both protein subunits A and B, and the fitness effects for the change of function and formation of the deleterious complex. The goal of modeling and comparing the effects of these two effects is to determine the magnitude of the phenotypic effects themselves under different combinations of underlying biochemistry.

Session1/Poster-7

Interrogating Sex Differences of Neuropsychiatric Risk Genes CACNA1C and CACNA1D Deficiency in Prelimbic-Accumbens Pathway Underlying Sociability

Westley Le (Molecular and Cellular Neuroscience)

Rajadhyaksha Lab | LKSOM

L-type calcium channels (LTCCs), Cav1.2 and Cav1.3, are consistently associated genetic risk factors across many neuropsychiatric disorders. However, it remains unclear how altered LTCC function in neurons translates to behavioral deficits. Prior work demonstrated that Cav1.2 projection-specific knockout (KO) in the nucleus accumbens to prelimbic cortex circuit reduces social preference in male mice. Given evidence for sex-dependent differences and the potential role of Cav1.3 channels, it is critical to investigate potential differences in LTCC loss. Here, we show Cav1.2 KO in female mice similarly reduces social preference, suggesting little sex-dependent effects. In contrast, pilot data indicate Cav1.3 KO does not show the same decrease in sociability as Cav1.2 KO mice, suggesting a limited role of Cav1.3 in social preference. These findings refine understanding of LTCC contributions to social deficits and may inform targeted treatments in neuropsychiatric disorders.

Session1/Poster-8

Heart Rate and Striatal Cholinergic Activity During Fear Learning Induced Prosocial-Like Behaviors in Mice

Lucy Martin (Molecular and Cellular Neuroscience)

Kutlu Lab | LKSOM

Mice demonstrate social learning and fear responses when exposed to distressed conspecifics. We used observational fear conditioning to investigate if mice forgo rewards to prevent conspecifics from receiving aversive stimuli, exhibiting prosocial behavior. In a two-chamber operant box, observer mice were conditioned to associate an active nose poke (RNP) with reward. In fear conditioning, an RNP triggered a 0.70 mV foot shock to a conspecific on the opposite side of the chamber. RNP's and lick counts reduced significantly. We aim to make the connection between Acetylcholine (ACh) release in the dorsal lateral striatum (DLS) and heart rate (HR). A Neurolux nVital system and fiber photometry were

combined to colocally monitor HR, respiratory rate, and ACh dynamics. Coupling analyses reveal HR as the “leader” and ACh as the “follower”. This link provides a framework for understanding how bodily states can shape learning, behavior, and pathological responses.

Session1/Poster-9

Intercellular Trafficking of Oligodendrocyte-Expressed APOE to Neurons

Samar Oubarri (Molecular and Cellular Neuroscience)
Kang Lab | LKSOM

Apolipoprotein E (APOE) regulates lipid transport and has three major human isoforms (E2, E3, E4). APOE4 confers the greatest genetic risk for Alzheimer’s disease. Though astrocytes are the main source of APOE in the brain, oligodendrocytes (OLs) increase APOE expression with age. However, the functional role of OL-derived APOE is unclear. To study APOE trafficking from OLs, we generated AAVs encoding HA-tagged APOE3 or APOE4 and mCherry under Cre control. AAVs were delivered to MOBP-iCre;EGFP mice for OL-specific expression. Two weeks post-injection, mCherry localized to OLs, whereas HA-APOE3 and HA-APOE4 were also detected in neurons. No transfer was detected when AAVs were delivered to astrocytes, suggesting rapid trafficking to neurons is unique to OLs. For both APOE3 and APOE4, transfer increased between 2 and 4 weeks. At 2 weeks, APOE4 showed greater neuronal transfer than APOE3. These results show a previously unrecognized mechanism of OL-neuron communication mediated by APOE.

Session1/Poster-10

Sex-Dependent Effects of GPR55 Antagonism on Glutamatergic Gene Expression in Opioid Tolerance and Withdrawal

Yashvi Patel (Molecular and Cellular Neuroscience)
Ward Lab | LKSOM

Opioid use disorder is characterized by tolerance and withdrawal, processes linked to dysregulated glutamatergic signaling. Prior work in rodents demonstrated that KLS-13019, a GPR55 receptor antagonist, reduces morphine tolerance and naloxone-precipitated withdrawal, with greater efficacy in males. These effects were associated with decreased expression of the glutamate-producing enzyme GCPII and increased expression of the glutamate transporter GLT1, suggesting reduced excitatory signaling. This study investigates whether sex-dependent differences in gene expression underlie these effects. Brain regions, including the nucleus accumbens, prefrontal cortex, ventral tegmental area, and bed nucleus of the stria terminalis, were collected from male and female mice treated with vehicle, cannabidiol, or KLS-13019. RNA was extracted and quantified, and qRT-PCR will assess the expression of GPR55, GCPII, GLT1, and GAD.

Session1/Poster-11

PDE4B Inhibition and Psilocybin as Promising Approaches for Treating Methamphetamine Use Disorder: Preclinical Evidence from Rat Models

Satoria Ayer Zagorski (Molecular and Cellular Neuroscience)
Ward Lab | LKSOM

A significant hurdle in methamphetamine use disorder (MUD) is relapsing to METH use, with no current FDA-approved treatments. This study tested two drug candidates – 11H, a PDE4B inhibitor, and psilocybin – on relapse-like behavior in rats trained to self-administer

methamphetamine. After, rats either experienced three weeks of abstinence with cue re-exposure or extinction followed by cue-induced reinstatement; responses on the meth-paired lever were measured. 11H reduced lever pressing during cue re-exposure, while psilocybin reduced responses in both paradigms. These results suggest that both compounds may help reduce meth craving and cue-driven relapse through different mechanisms.

Session1/Poster-12

Endoscopic Neurotomy Provides Superior Pain Relief Compared to Radiofrequency Ablation for Facet- and Sacroiliac Joint–Mediated Chronic Low Back Pain: A Systematic Review and Meta-Analysis

Yusuf-Zain A Ansari (Genomic Medicine)

Hasan Lab | LKSON

Chronic low back pain (CLBP) due to lumbar facet joint (LFJ) and sacroiliac joint (SIJ) dysfunction remains a major source of disability. Radiofrequency ablation (RFA) is widely used, while endoscopic neurotomy (EN) enables direct visualization and targeted denervation. This systematic review and meta-analysis evaluated comparative outcomes. Seven studies (n=345) were included. EN demonstrated greater pain reduction (VAS: MD −1.72, 95% CI −2.72 to −0.72; $p<0.01$), with significant benefit at 12 months but not longer follow-up. Functional outcomes (ODI) trended in favor of EN but were not statistically significant. EN required longer operative time (+24.86 minutes; $p<0.01$) but had low complication rates in both groups. EN offers superior short- to mid-term pain relief with comparable safety, though further studies are needed to assess long-term durability.

Session1/Poster-13

Malaria as driver of global patterns of human genetic variation in blood

Abhi Bolisetti (Genomic Medicine)

Kulathinal Lab | BioLife

Certain variants in hemoglobin genes are associated with hemoglobinopathies, a diverse group of blood disorders. The most well-known example is sickle cell anemia, a disease prevalent in tropical regions where malaria is endemic, and positive selection has been observed in the sickle-cell variant in malaria-prone populations. However, a comprehensive understanding of the global distribution of hemoglobin-related genetic variation remains limited. The study leverages population-scale genomic datasets such as the 1000 Genomes Project to investigate genetic variation in a comprehensive set of hemoglobin genes across global populations by estimating FST, a measure of population genetic differentiation, relative to malaria incidence. We identified variants in select hemoglobin genes that exhibit high differentiation relative to malaria incidence, providing insight into how modern human populations have adapted to their environments. Using blood as a model for human evolution these findings have implications for personalized diagnostics and preventative medicine.

Session1/Poster-14

Reconciling Known Mutational Effects Over Short-Term and Long-Term Timescales in Gene Expression Evolution

Mia Elkind (Genomic Medicine)

Liberles Lab | BioLife

The expression level of a given gene has been shaped by natural selection acting on regulatory units over evolutionary time. As a result, gene expression levels are typically higher than those expected from random regulatory sequences. However, experimental studies have shown that mutations that randomize regulatory regions produce, on average, symmetrical effects on gene expression levels. These two observations appear contradictory. This project aims to reconcile them through a mechanistic, process-based framework. To address this question, mock genes and their regulatory environments have been generated and evolved in a Wright-Fisher style forward time simulation to characterize what scenarios give rise to the contradictory short-term and long-term effects of mutation.

Session1/Poster-15

Assessment of Intracellular Bacterial Presence in Widely-Used Colorectal Cancer Cell Lines

Darien Reyes (Genomic Medicine)

Sun Lab | BioLife

Recent studies suggest that invasive bacteria such as Klebsiella pneumoniae can reside within colorectal cancer (CRC) cells and affect tumor invasion and immune responses. However, commercial CRC cell lines have not been well characterized for endogenous invasive bacterial populations, raising concerns about the validity of experiments using these models. In this study, gDNA was extracted from three commercial CRC cell lines (HT-29, DLD-1, and Caco-2), and RT-PCR was performed using short and long primers targeting bacterial 16S rRNA genes. Preliminary results detected bacterial signal in these cell lines, with K. pneumoniae gDNA as a positive control and nuclease-free water as a negative control. Future validation using FISH is needed to confirm intracellular localization and quantify bacterial burden per human cell.

Session1/Poster-16

The Potential of Deep-Sea Corals and Sponges within the Current Biomedical Context

Muhammad-Safwaan B Ahmer (Biology)

Cordes Lab | BioLife

The Ocean is one of the Earth's most majestic and mysterious wonders, and there is evidence to make a compelling argument that it may hold a value towards human physiology. Based on a dive analysis of multiple studies, there's enough evidence to indicate a valuable correlation between deep-sea coral biology and human health applications [3]. Scholars such as Shirley Pomponi and collaborators argue that deep-sea coral ecosystems are not simply passive habitats, but dynamic biological events producing metabolites and frameworks capable of influencing human physiology. Much of the research remains pre-clinical, and considerable work remains to chart the durability, scalability, and safety of coral-derived medicines. And before we can properly explore this potential, understanding the health of these coral systems is a necessity to understand whether extraction is in the marine ecosystem's best interests as well as ours.

Session1/Poster-17

Placental DNA Methylation Differences in Assisted Reproductive Technology

Anila Awal (Biology)

Ghosh Lab | LKSOM

Assisted reproductive technology (ART) has been associated with epigenetic differences in children conceived in vitro compared with those conceived in vivo. In this project, I am exploring how DNA methylation patterns in placental tissue differ between these groups and whether these differences are linked to ART procedures themselves rather than infertility alone. Prior work from the Ghosh lab and collaborators compared fertile controls, infertile ART cases and donor oocyte ART cases, showing that many methylation differences were more strongly associated with ART protocols. This research highlights the role of epigenetics in developmental biology and personalized medicine and may help improve understanding of how reproductive technologies influence early gene regulation.

Session1/Poster-18

Investigating Androgen Effects on Liver Metabolism in Polycystic Ovary Syndrome (PCOS)

Selin Gunaydin (Biology)

Wu Lab | LKSOM

Androgen-induced metabolic dysfunction occurs in states of elevated androgen in females. However, the mechanisms by which androgens in the liver/brain/ovary/pituitary contribute to metabolic dysfunction and/or fatty liver, and to reproductive function in states of androgen excess, such as polycystic ovary syndrome (PCOS), remain unknown. Hyperandrogenemia is one of the defining features of PCOS and is often accompanied by hyperinsulinemia and obesity. A model that isolates the pathophysiological effects of hyperandrogenemia from obesity-related metabolic changes is warranted. The project focuses on the role of pathophysiological androgen levels on the liver, brain, pituitary, and ovary. Methods included genetic deletion of AR developmentally or acutely (adenovirus-associated Cre) in vivo or ex vivo in tissues in elevated androgen, which were treated with or without a Western diet-induced obesity mouse model.

Session1/Poster-19

Taste Perception and Intensity in Human Oral Cavity

Daniel Lee (Biology)

Smutzer Lab| BioLife

The main goal of this study was to identify oral taste perception of tannic acid and to minimize its bitter off-taste with addition neotame. Sweet taste stimuli generally decrease bitter taste perception in humans. Rapidly dissolving films were prepared that uniformly incorporated four micromoles of tannic acid within a hexagonally shaped film. To achieve uniformity of tannic acid in films, melted coconut oil was added to the stock film solution. These edible films contained either 4 µmoles of tannic acid or 4 µmoles of tannic acid and neotame. Taste intensity (and taste quality) was evaluated using the general Labeled Magnitude Scale (gLMS). Hedonics scale (-100 to +100) was used to measure overall pleasantness of each film. This study contributes to taste interactions in the oral cavity and is the first to examine astringency with edible film formulations. The results demonstrated that neotame significantly diminished the bitter off-taste of tannic acid in edible films.

Session1/Poster-20

BioLens: Temporal Filtering Software for Camera Trap Observations

Henry McNaughton (Computer Science)

Bonfim Lab | Ambler

Camera trap networks are widely used to monitor wildlife presence, behavior, and biodiversity across space and time. While data from these projects are stored in platforms like Wildlife Insights, they lack flexible, interactive tools for meaningful exploration and visualization. Existing work emphasizes centralized storage and machine learning–based identification, but not user-friendly data visualization, leaving valuable metadata underutilized. This project addresses that gap by developing a Python-based desktop application for interactive data exploration. Using open-source libraries including Pandas, Plotly, Dash, and PySide, the tool dynamically parses and visualizes data through interactive graphs. It enables analysis of biodiversity trends, seasonal activity, and species presence over time, while providing a foundation for expanded visualization capabilities.

Session1/Poster-21

Adaptive genomic landscapes: Divergence, selection, and functionalization across primate lineages

Shrihith Gologula (Integrative Genetics & Genomics)

Kulathinal Lab| BioLife

Both positive Darwinian selection on conserved orthologs and the functionalization of new gene duplicates are major drivers of evolutionary innovation. Here, we utilize a comprehensive comparative genomic framework to investigate patterns of protein divergence and selection in orthologous genes as well as tissue diversification of duplicated gene families across eight representative primate genomes. We performed codon-aware alignments and phylogeny-informed selection analyses on 13,074 high-confidence 1:1 orthologs using HyPhy to detect gene-wide, branch-wide, and site-specific signals of protein evolution. Selection analyses revealed ample evidence of episodic diversifying selection across each of the primate lineages and functional enrichment tests highlight the overrepresentation of adaptively evolving genes in immune, reproductive, and sensory pathways. We then complemented this study of protein divergence and adaptation by examining functionalization patterns of gene duplicates in these lineages through the analysis of tissue-specific expression shifts in gene families exhibiting 1:2:1 copy number changes. Gene tree species tree reconciliation uncovered 1,105 duplication events across the primate phylogeny and, when mapped to a common set of tissues, a trend towards neofunctionalization was observed. Together, these results provide a divergence landscape in primates where positive selection is pervasive across the primate proteins and where gene duplication provides a substrate for innovation with selection driving functional diversification across lineages.

Session1/Poster-22

Assessing NAS Incidence and Severity at Temple Hospital Over Two Years

Richard Regan (Biology)

Daws Lab | LKSOM

In the United States, the ongoing opioid epidemic has become a major problem for hospitals and other healthcare systems. Pregnant women with opioid use disorder subsequently have infants who were exposed to opioids during pregnancy, badly threatening maternal and child health. Since the start of the 21st century, rates of prenatal opioid exposure and diagnosis of Neonatal Abstinence disorder have increased by more than fivefold, presenting a major problem for healthcare systems and NICUs. In newborns, NAS is characterized by a range of withdrawal symptoms, including tremors, feeding difficulties, and respiratory complications, often making hospitalizations longer.Despite established guidelines from the organizations

such as the American College of Obstetricians and Gynecologists (ACOG) and the American Academy of Pediatrics, (AAP) inequalities persist in care quality, consistency, and the implementation of universal screening in today's healthcare environment. Furthermore, socioeconomic factors further influence access to patient care for Mothers with OUD, as well as the outcomes of infants with NAS. Our study seeks to track and address these gaps through a retrospective review of Electronic Medical Record (EMRs) from Temple University Hospital. Our goal is to audit the incidence, severity and clinical management of perinatal opioid use, as well as Neonatal Abstinence Syndrome. Through this, we will be able to see maternal opioid use patterns, diagnoses of NAS, and patient treatment, along with inpatient outpatient audits, and the duration of NICU and hospital stays. In future goals, we seek to examine the influence of environmental factors such as community trauma, social vulnerability, and economic status on healthcare utilization as well as outcomes among mothers and their infants. Key outcomes of this study are the identification of factors affecting the outcomes for both Mother and Child. We hypothesize that Temple Hospital has a higher incidence of opioid withdrawal and neonatal abstinence syndrome compared to the national average, due to the high rates of opioid use in the community surrounding the hospital. Secondly, we hypothesize that the severity of opioid withdrawal symptoms are associated with increased hospital stay and complications for opioid-exposed infants. This study is significant, as it addresses a critical public health issue which involves substance abuse, maternal health, and neonatal outcomes. Ultimately, findings from this study will support future healthcare improvement initiatives and research aimed at enhancing care for mothers with OUD and their infants.

Session1/Poster-23

Antibiotic resistance of E.faecalis microaggregate biofilms

Aryan Pasyar (Biology)

Buttaro Lab | LKSOM

Enterococcus faecalis is a gut commensal, but strains carrying mobile genetic elements can cause hospital-acquired infections, including endocarditis. The conjugative plasmid pCF10 remodels biofilms into complex aggregate structures linked to antibiotic resistance. Under flow, we observed free-floating microaggregate biofilms above surface-attached biofilms. Aggregates were isolated from microfluidic devices, stained with SYTO9, and imaged to visualize cells and extracellular DNA. Multiple morphologies were identified, including open complexes, collapsed thread-like structures, and a hyperchaining phenotype of long tangled chains lacking defined aggregates. Quantitative analysis using MorphographX and a MATLAB Connections Algorithm showed remodeling, with increased overall structure volume and increased numbers of smaller structures. These findings suggest that pCF10 promotes diverse free-floating biofilms that may enhance persistence under antibiotic stress.

Session1/Poster-24

A Cost-Effective Strategy for Building Gene-Specific Neurogenetic Tools in Drosophila

Katelyn Rose Porrecca (Biology)

Chen Lab | BioLife

Understanding how genes shape neural development and function is central to neuroscience. Drosophila melanogaster is an ideal model due to its well-characterized genetics, short life cycle, and conserved neural pathways. However, many advanced genetic

tools remain costly and resource-intensive, limiting functional studies. This project aims to develop a cost-effective, scalable pipeline for generating gene-specific reporter lines using recombination-mediated cassette exchange (RMCE). Donor plasmids targeting 49 neurotransmission-related genes will be constructed to generate split-GAL4 reporter lines via precise insertion into transgenic flies with attP docking sites. This approach expands the genetic toolkit for mapping and manipulating neuronal populations, enabling efficient cell-type-specific studies of brain development and circuit function.

Session1/Poster-25

TDG as a Potential Epigenetic Target in Uveal Melanoma

Emily Mae Seaman (Biology)

Bellacosa Lab | Fox Chase Cancer Center

Uveal melanoma (UM) is the most aggressive subtype of ocular melanoma. UM responds poorly to both chemotherapy and immune checkpoint inhibitors. Methylation clusters are heavily concentrated in several profiles of UM, pointing to a strong link between methylation and UM progression. This connection suggests that targeting DNA methylation could be a promising therapeutic approach. Thymine DNA Glycosylase (TDG) is a dual-function enzyme that plays a critical role in active DNA demethylation and in repairing G/T mismatches. Our findings show that knockdown of TDG in UM cells induces cell cycle arrest and senescence, while treatment with the small-molecule inhibitor closely mimics these effects both in vitro and at the biochemical level. These observations underscore that aberrant methylation not only shapes UM progression but also positions TDG as a central regulator whose disruption reveals therapeutic vulnerabilities.

Session1/Poster-26

Assessment of Intracellular Bacterial Presence in Widely-Used Colorectal Cancer Cell Lines

Monuay L. Torh (Biology)

Sun Lab | BioLife

Recent studies suggest that invasive bacteria such as Klebsiella pneumoniae can reside within colorectal cancer (CRC) cells and affect tumor invasion and immune responses. However, commercial CRC cell lines have not been well characterized for endogenous invasive bacterial populations, raising concerns about the validity of experiments using these models. In this study, gDNA was extracted from three commercial CRC cell lines (HT-29, DLD-1, and Caco-2), and RT-PCR was performed using short and long primers targeting bacterial 16S rRNA genes. Preliminary results detected bacterial signal in these cell lines, with K. pneumoniae gDNA as a positive control and nuclease-free water as a negative control. Future validation using FISH is needed to confirm intracellular localization and quantify bacterial burden per human cell.

Session1/Poster-27

Bottle Effect and Mixotrophic Protist Physiology

Lauren Tran (Biology)

Grattepanche Lab | BioLife

Mixotrophs obtain carbon through both photosynthesis and by consuming bacteria. “Bottle effect” is where the physiology of microorganisms are affected differently in function of the

incubation volume. However, it is unclear whether mixotrophic mode is driven by carbon demand or nutrient limitation, and how “bottle effect” influences mixotrophic algae. In previous studies, growth rates of temperate freshwater chrysophyte tended to be higher when protists were cultivated in smaller volumes, suggesting a role of the bacterial abundance. Here, we studied the impact of bottle effect on the polar marine chrysophyte Dinobryon faculiferum. We hypothesized that larger culture volumes may positively influence growth rates. Results showed that all cultures exhibited similar growth trends regardless of bottle size, indicating that bottle volume did not significantly affect Dinobryon growth. Future studies may investigate the role of phototrophy and phagotrophy by manipulating light availability.

Session1/Poster-28

Post-COVID Increases in Stress and Disordered Eating in Pre-Healthcare Students

Ginger Uhlfelder (Biology)

Bonfim Lab | BioLife

Eating disorders (EDs) are prevalent mental health conditions and major contributors to morbidity and mortality, yet risk patterns in high-pressure student populations remain underexplored, especially after large-scale behavioral disruptions such as the COVID-19 pandemic. This study combined literature review and survey data from pre-healthcare students at Temple University to examine how stress-related factors relate to ED behaviors before and after the COVID-19 pandemic. Results suggest substantial increases in anxiety and academic stress after the pandemic, alongside smaller increases in restrictive and binge-like ED behaviors. Moderate positive correlations were identified between anxiety and ED behaviors, with weaker positive correlations between academic stress and ED behaviors, and weaker negative correlations with protective factors. These findings suggest that sustained stress impacts personal and academic well-being, underscoring the need for accessible mental health support.

Session 2 (11am–12:30pm, SERC Lobby)

Session2/Poster-1

Wineberry's Effect on Understory Species Diversity and Sapling Resilience in a Post-Disturbance Deciduous Forest Ecosystem

Aidan Chapin (Environmental Studies + Biology Minor)

Bonfim Lab | Ambler

Disturbance is a key driver of community assembly, yet rare, high-intensity events can exceed the adaptive capacity of regenerating communities. In September 2021, an EF2 tornado struck Temple University's Ambler campus, creating a large-scale disturbance within the Temple Forest Observatory and a natural experiment in forest recovery. Since then, Rubus phoenicolasius (wineberry) has rapidly expanded and now dominates parts of the understory. This study evaluates whether wineberry alters woody sapling survival and understory diversity during early regeneration. We test whether wineberry presence is linked to increased sapling mortality and reduced diversity across post-disturbance years. Using repeated surveys in 90 1 × 1 m plots from May–August 2023–2025, we quantify patterns in survival and community composition. This work provides insight into how invasive species may constrain recovery when regeneration capacity is limited.

Session2/Poster-2

How does a novel ecological disturbance impact bat activity in an eastern deciduous forest?

Rachel Linhart (Ecology, Evolution & Biodiversity)

Sewall Lab | Ambler/BioLife

As novel disturbances increase in frequency due to our changing global climate, it becomes even more vital to study their consequences as ecological communities recover from these novel events. Bats play vital roles in ecosystems; studies show that bats frequently use temperate forests as roosting sites in addition to controlling insect populations. Our study looked at bat presence in a forest recovering from a severe windthrow disturbance. We used acoustic monitors in 24 plots. We hypothesized that bats with more maneuverability will be more active at sites with higher structural complexity, or sites with less disturbance, while straight-flying bats will have higher activity at sites with less structural complexity, or sites with higher disturbance. Our results indicate that disturbance does play a role in the presence and activity of bats across our 24 sampling plots. Our results also indicate that disturbance plays a role in the species which are present at a given site.

Session2/Poster-3

When Fire Brings Life: How Burn Seasonality Shapes Violet Abundance for Eastern Regal Fritillary Restoration

Miriam Amelia Parrucci (Ecology, Evolution & Biodiversity)

Sewall Lab | Ambler/BioLife

Argynnis idalia idalia is a rare eastern grassland butterfly whose primary host plant is Viola sagittata. Eastern grasslands have declined mainly because of wildfire suppression.

Consequently, the A. i. idalia population is now found solely on the Fort Indiantown Gap military base in south-central Pennsylvania. This suggests that frequent disturbance associated with military activity may mimic natural fire regimes that sustain host plant communities. To examine how seasonal fire regimes affect grassland composition, we surveyed plants in 4 m2 plots across multiple sites on the military base, which were subjected to different burn regimes. We quantified the abundance of V. sagittata. to assess post-burn abundance. We aim to clarify how seasonal fire regimes influence the availability of V. sagittata. These findings may help grassland management practices aimed at restoring fire-dependent habitats and supporting the recovery of A. i. idalia.

Session2/Poster-4

Identifying the Neural Circuits Coordinating Food Preference across Dietary Fats in Mice

Ashlynn Daniel (Molecular and Cellular Neuroscience)

Sutton-Hickey Lab | Weiss Hall

Diets enriched with fat (HFD), known for their palatability, represent a key driver of the overconsumption that can often lead to obesity. Its overwhelming influence can result in maladaptive feeding behaviors and standard diet devaluation (SD) during prolonged exposure, even in the presence of more nutritious options. However, patterns in the hypothalamus responsible for this shift in preference are underexplored. This study leverages targeted recombination of active populations (TRAP) and c-Fos immunohistochemistry (IHC) to compare active cell populations in mice that have been exposed to vegetable (vHFD) and animal based (aHFD). The timeline begins with one day of vHFD, aHFD, or SD exposure, followed by five days of only SD, and completed with a second day of alternate HFD exposure. We hypothesize agouti-related peptide (AgRP) neurons within the arcuate nucleus (ARC) initiate different pathways depending on ingestion of vHFD or aHFD and their interaction with the mesolimbic system.

Session2/Poster-5

Effects of Psilocybin on Neuroinflammatory Gene Expression and Anxiety-Related Behaviors in Mice

Farris Eihab Elazazy (Molecular and Cellular Neuroscience)

Rawls Lab | LKSOM

Psilocybin has emerged as a potential therapeutic agent for neuropsychiatric disorders, possibly through modulation of neuroinflammatory pathways. This study examined the effects of psilocybin on anxiety-like behavior and inflammatory gene expression in mice. Adult male C57BL/6J mice received saline, 0.3 mg/kg, or 1.0 mg/kg psilocybin and were assessed using the elevated plus maze (EPM). Brain regions including the prefrontal cortex (PFC), hippocampus (HPC), and amygdala (AMG) were analyzed using qPCR to measure cytokine expression. Psilocybin-treated mice showed increased time in the open arms of the EPM, indicating reduced anxiety-like behavior. Molecular analysis revealed significant reductions in IL-1β and TNF-α expression in the PFC, particularly at 1.0 mg/kg. These findings suggest that psilocybin may reduce anxiety-like behavior through region-specific anti-inflammatory effects in the PFC, supporting its potential as a therapeutic agent for neuroinflammatory disorders.

Session2/Poster-6

Investigating the Role of the Mycobacterial Potassium Channel MycK in Tuberculosis Drug Sensitivity

Emily Lasalla (Molecular and Cellular Neuroscience)

Rothberg Lab | LKSOM

Mycobacterial pathogens cause infectious diseases like tuberculosis (TB) and remain a leading cause of death worldwide. To better understand the role of the mycobacterial potassium ion channel as it pertains to TB virulence, we have conducted a series of bactericidal assays to determine whether MycK inhibitors used in conjunction with existing anti-TB drugs will enhance the potency or efficacy of these drugs. Our work focuses on testing different concentrations of etbambutol or hydrogen peroxide in a 24-hour culture system using wild-type and Myck-Rv3200c-knock-out mycobacterium smegmatis to measure the difference in bacterial growth upon removal of the Rv3200c gene. Drug-dose response curves used a Hill equation to estimate the concentration of antibiotic required to reduce the growth by 50% to determine if Rv3200c removal impacts antibiotic efficacy. Preliminary results show a decrease in IC50 values in KO cultures compared to WT.

Session2/Poster-7

Pathogenic Mechanisms of microcephaly driven by the overexpression of P53 and Myosin light chain

Anais Chloe Morlet (Molecular and Cellular Neuroscience)

Kim Lab | LKSOM

Microcephaly, or reduced cortical size, is caused by various genetic mutations. Deletion of apical polarity protein, Pals1, is known to cause microcephaly due to mitotic defects and entosis of cells. In this case, the deletion of Pals1 causes an overactivation of P53 and Rho ROCK signaling. Both of these components are likely to contribute to the onset of entosis and resulting microcephaly. In this study, we characterize the impact of P53 and myosin light chain overactivation, independent of Pals1 deletion. We found that activation of P53 and myosin light chain cause microcephaly and are currently working towards understanding the mechanism driving the condition. The findings from this study will provide a novel understanding of pathogenic mechanisms driving microcephaly.

Session2/Poster-8

Automated tracking of different population densities and sex ratios reveal trends in density-dependent courtship behavior in Drosophila melanogaster

Finnian Tate Mousseau (Molecular and Cellular Neuroscience)

Kulathinal Lab | BioLife

Quantifying how social context shapes courtship behavior requires controlled experimental design and scalable analysis. Here, we combined multi-condition assays of population density and sex ratio with an automated pipeline to study courtship in Drosophila melanogaster. We tested 24 male–female conditions with five replicates each in standardized arenas (120 videos). Behavioral data were processed through a multi-stage workflow: flies were tracked using FlyTracker (MATLAB), behaviors were classified using JAABA, and custom Python scripts converted outputs into structured datasets for cross-condition analysis. This enabled quantification of interaction frequency, variability, and behavioral complexity.

Courtship activity increased with population density, and male abundance showed a slightly stronger association with behavioral intensity, suggesting a role for male–male competition.

Session2/Poster-9

Investigating the effectiveness of split-GAL4 labeling in Lpi3-4 neuron during development in Drosophila Melanogaster

Anastacia Orekhova (Molecular and Cellular Neuroscience)

Chen Lab | BioLife

Different types of neurons express distinct sets of genes, and these molecular identities help shape neuronal morphology, connectivity, and function. Understanding the genetic steps that guide neuronal development can provide important insights into brain disorders, as disruptions at specific stages may lead to abnormal neural circuit formation. We use the visual system of Drosophila melanogaster as a model, which offers a simpler, highly organized system with many identifiable neuron types in the optic lobes. Recent advances in single-cell RNA sequencing allowed to identify CG13287 as an Lpi3-4 cell type-specific marker. This project focuses on CG13287-GAL4 knock-in labeling Lpi3-4 specifically in adults and during development. The future project aims to test the implementation of recombination-mediated cassette exchange (RMCE) to produce split-GAL4 lines targeting the Lpi3-4 cell type with improved specificity.

Session2/Poster-10

Structural Studies of Nucleotide Binding in a Mycobacterial K+ Channel

Cassidy Tower (Molecular and Cellular Neuroscience)

Rothberg Lab | LKSOM

Mycobacterial pathogens cause infectious diseases like tuberculosis, which remains a leading cause of death worldwide. To understand the physiology of mycobacteria, we are determining the structure and function of MycK, a potassium channel encoded by the virulence gene Rv3200c. We have observed that the channel is opened by binding of AMP and closed by binding of ATP to its ligand binding domain (LBD). Studies with ITC demonstrated adenosine dinucleotides Ap3A, Ap4A, and Ap5A bind MycK-LBD with micromolar affinities. To determine the structure of dinucleotide binding, co-crystallization of MycK-LBD with Ap4A and Ap5A was completed, and complexes were solved using X-ray diffraction. The data showed structures of Ap5A at resolution 2.25 Å. In both the MycK-LBD-Ap4A and MycK-LBD-Ap5A complexes, the di-nucelotides were hydrolyzed into AMP, ADP, and/or ATP, at paired binding sites in the LBD. The binding of the hydrolyzed products created a change significant enough to open the channel.

Session2/Poster-11

Xylazine Suppresses Cephalic Regeneration and Defensive Responding in Planaria

Meghana Dachepalli (Genomic Medicine)

Rawls Lab | LKSOM

Xylazine is an alpha2-adrenoceptor agonist found in illicit substances, with peak prevalence in Philadelphia. Injection of opioids adulterated with xylazine causes necrotic tissue injury and a complex withdrawal syndrome. Planarians are flatworms with a simple nervous system, regenerative capacity, and negative phototaxis. In the present study, we investigated the effects of xylazine exposure on cephalic regeneration and anxiety-like behavior. We found

that prolonged exposure suppressed cephalic regeneration at concentrations that did not impair motility in non-decapitated control worms. Acute xylazine exposure reduced defensive responding in whole worms (reduced the time planarians spent on the light side of a closed dish divided into light and dark compartments). Our results with planarians show that chronic xylazine exposure impedes tissue regeneration, indicating the effect was independent of vasoconstriction, and that acute xylazine exposure reduces anxiety-like behaviors.

Session2/Poster-12

Influenza-Staphylococcus aureus Superinfection Induces Systemic Microbiome Dysbiosis and Alters the Gut-Lung Microbiome Axis in Mice

Sami Kazi (Genomic Medicine)

Tam Lab | LKSOM

Secondary bacterial pneumonia following influenza is a leading cause of mortality, yet its impact on the gut microbiome via the gut-lung axis remains poorly understood. Using a mouse model of influenza-S. aureus superinfection, we analyzed 16S rRNA sequencing from lung and fecal samples of C57BL/6 and Ppara–/– mice. Superinfection caused significant gut alpha diversity loss, marked by S. aureus dominance and displacement of commensal Lactobacillales, while pulmonary alpha diversity increased. We observed reduced Lachnospiraceae, butyrate-producing bacteria vital for immune homeostasis, and disrupted microbial co-occurrence networks. These findings highlight systemic dysbiosis as a critical feature of superinfection pathology, implicating the gut-lung axis as a therapeutic target. Restoring butyrate-producing microbes may mitigate immune and metabolic dysfunction associated with secondary bacterial pneumonia mortality.

Session2/Poster-13

Defining the Bioluminescence of Symbiotic Communities Between Individual Reef Fish Hosts

Sanya Ahuja (Biology)

Gould Lab | BioLife

Animals often form symbiotic relationships with bacteria that provide key traits such as bioluminescence. The luminous bacterium Photobacterium mandapamensis inhabits the light organs of the reef fish Siphamia tubifer, where it exists as multi-strain communities. However, how strain composition affects light production remains unclear. In this study, we compared bioluminescence in individual strains and in laboratory-assembled multi-strain communities. We quantified light output from single strains and from mixed communities to assess consistency across strain combinations. We found that strains differed in individual light production, and community-level bioluminescence did not reflect any single strain. Instead, community composition influenced both total light output and its changes over 24 hours. These findings show that bioluminescence is shaped by interactions among coexisting strains, highlighting how microbial community structure influences collective function in symbiosis.

Session2/Poster-14

Investigating the Paracrine and Mechanical Cues Driving Fibroblast Activation in Triple-Negative Breast Cancer.

Elizabeth O Bakare (Biology)

Wang Lab | Bioengineering
Breast cancer is the second leading cause of death among women in the United States. Its progression is strongly influenced by the tumor microenvironment (TME), where biochemical and mechanical cues jointly regulate fibroblast activation. Cancer-associated fibroblasts (CAFs) play a critical role in tumor metastases by remodeling the TME, thereby promoting cancer cell proliferation. This study investigates how ECM stiffness and tumor-derived soluble factors, specifically TGF-β1, drive the transformation of human mammary fibroblasts (HMFs) into CAFs. Using MDA-MB-231 triple-negative breast cancer cells, tumor-conditioned media were collected and analyzed for the presence of TGF-β1, using ELISA. HMFs were cultured on soft (2 kPa) and stiff (20 kPa) polyacrylamide gels to mimic a healthy and tumor-like environment, respectively, and were assessed for matrix assembly. The results indicate that pathological ECM stiffness synergizes with TGF-β1 signaling to promote HMF to CAF activation.

Session2/Poster-15
Pathway to progress: epigenetic profiles in blood and colon tissue illuminate vital pathways in colorectal cancer.
Alisiya Dansberger (Biology)
Ghosh Lab | LKSOM
Colorectal cancer (CRC) is the second leading cause of cancer-related deaths in the U.S. CRC risk is influenced by complex interactions between genetic and environmental factors. These factors shape the epigenome, especially DNA methylation, which may contribute to CRC predisposition and progression. In this study, DNA extracted from blood, normal colon, and tumor biopsy samples from African American and Caucasian individuals across sexes and age groups underwent methylation profiling. Differential methylation analysis identifies CpG sites with significant differences between CRC cases and controls. These sites will be mapped to genes, and pathway analyses could identify pathways linked to CRC progression. Additionally, normal and tumor organoids are being developed for drug testing. Outcomes may reveal molecular pathways involved in CRC progression, advance early pathogenesis understanding, and inform targeted prevention and therapeutic strategies.

Session2/Poster-16
Title: Mixotrophic Growth Adaptations of Ochromonas and Its Ecological Consequences in a Warming World
Sophia Gordon (Bioengineering)
Grattepanche Lab | BioLife
Ochromonas sp, BG-1 (Chrysophyceae, Stramenopila) is a mixotrophic alga that obtains carbon through both bacterial ingestion and photosynthesis. This study examines the factors influencing growth rates and their implications for aquatic ecosystems under rising climate temperatures. In previous studies, growth rate were assessed using sterile bottles and showed a significant higher growth in small incubation versus larger ones, which was attributed to differences in bacterial abundance. In this study, bottles from the previous experiment were reused, assuming starting bacterial abundance would be high in both treatments. No significant difference in growth rates between small and large incubation volumes was observed. This suggests that the previous assumption is correct, growth of Ochromonas, is most likely enhanced by carbon acquisition through bacterivory.

Session2/Poster-17

Understanding Stable Conditions of Operon Evolution.

Samuel Hill Hartman (Health Science)

Liberles Lab | BioLife

Operons are clusters of genes that function together under the control of a single promoter. Understanding the biological conditions under which operons evolve is important for understanding the regulation of gene expression and how it evolves. This study investigates what conditions allow for the evolution of stable operon gene clusters. To answer this question, we are developing computational models using python in order to simulate operon evolution. This model will test various conditions of operon evolution including, mutation and recombination rates, reproductive mode, effective population size, ploidy, dosage balance constraints of different types, different types of selection on gene expression, and pleiotropic constraints on genes of different types. Currently the foundational model for simulating this evolution is being developed.

Session2/Poster-18

Does bacteria density matter for mixotrophic algae growth?

Roy Huang (Biology)

Grattepanche Lab | BioLife

Mixotrophs are able to perform both photosynthesis as well as consume other organisms. For phytoplankton, it was observed that the culture size (the bottle effect) did not impact their growth rate, but is it the same for mixotrophs? For the marine chlorophyte Micromonas polaris, culture size did not show a significant impact on its growth. In contrast, the experiment carried with the freshwater chrysophyte C. dendrolepidota showed a statistically significant difference, with a greater growth rate observed for the smaller incubation volume. This trend is opposite when the experiment is repeated. It is hypothesized that algae with more bacterial availability tend to graze more on bacteria compared to those with less bacteria abundance. To test this, cultures were grown in 2 bottles, one with a lot of bacteria and one with a lot less. Grazing rate was then assessed using fluorescent beads as bacteria analogs and analyzed by epifluorescence microscopy.

Session2/Poster-19

Enterococcus faecalis–Candida albicans Biofilms Under Low Iron: Hyphal Induction and Computational Quantification

Eleena Suja John (Biology)

Buttaro Lab | LKSOM

Enterococcus faecalis and Candida albicans colonize multiple body sites and are co-isolated from abdominal and periodontal infections. Mobile genetic elements can transform commensal E. faecalis into antibiotic-resistant pathogens, and pheromone-responsive plasmids are common in clinical isolates. C. albicans transitions from yeast to invasive hyphae under high-iron conditions, whereas hyphal formation is reduced under low iron. To determine whether E. faecalis promotes hyphal growth despite iron limitation, OG1RF, OG1RF (pCF10), and a periodontal clinical isolate were co-cultured with C. albicans under low-iron conditions. All strains significantly increased hyphal formation, though OG1RF (pCF10) showed a lower trend. We developed Fungal Labeler with S. Blakely and G. Queisser (Mathematics) to validate against hand-counted data and quantify hyphae in and above the

basal layer. One hypothesis is that pCF10 biofilms elevate hydrogen peroxide and suppress hyphal development.

Session2/Poster-20

Effect of Neotame on the Perceived Astringency of Tannic Acid in Edible Films

Pingwen Lin (Post-Bac Program)

Smutzer Lab | BioLife

Astringency is a tactile sensation associated with polyphenols, producing dryness or puckering sensation through salivary protein precipitation. Since this sensation is often disliked, this study aims to identify agents that might reduce tannic acid astringency. A questionnaire assessed consumption frequency and hedonic responses to astringent foods. The non-caloric sweetener neotame (~8000x sweeter than sugar) was examined as a modifying agent. Rapidly dissolving edible films containing 4 µmol tannic acid were developed using coconut oil for dispersion. The effect of neotame was then examined over time. The general Labeled Magnitude Scale (gLMS) identified perceived astringency, and a bipolar gLMS identified hedonic responses. Results indicated that neotame (150 nmol) significantly reduced astringency and improved the overall hedonic. These findings suggest that neotame effectively masks the astringent perception of tannic acid may enhance the palatability of astringent foods.

Session2/Poster-21

Astrocyte - Neuron microRNA Signatures in Fetal Brain Exosomes as Early Indicators of Fetal Alcohol Spectrum Disorders.

Tina Sa Nguanpho (Biology)

Darbinian Lab | LKSOM

Astrocyte–neuron communication plays a critical role in synaptic development, metabolic support, and neurotrophic signaling during fetal brain maturation. This study investigates microRNAs involved in astrocyte–neuron communication within fetal brain–derived exosomes (FB-Es) isolated from maternal blood as potential early predictors of fetal alcohol spectrum disorders (FASD). FB-Es were isolated using neural-specific immunoaffinity approaches and analyzed for microRNAs regulating neuronal injury, synaptic stability, and neurotrophic pathways (e.g., BDNF, GFAP signaling) using qRT-PCR and ELISA. Preliminary results show significant dysregulation of key microRNAs, including miRNA-9, in alcohol exposed pregnancies. miRNA-9 expression correlated with fetal eye diameter, a characteristic feature of FASD. These findings support FB-E microRNAs as novel, non-invasive biomarkers for early FASD detection and provide insight into disrupted fetal brain development

Session2/Poster-22

Assessment of Intracellular Bacterial Presence in Widely-Used Colorectal Cancer Cell Lines

Jayson Reyes (Biology)

Sun Lab | BioLife

Recent studies suggest that invasive bacteria such as Klebsiella pneumoniae can reside within colorectal cancer (CRC) cells and affect tumor invasion and immune responses. However, commercial CRC cell lines have not been well characterized for endogenous

invasive bacterial populations, raising concerns about the validity of experiments using these models. In this study, gDNA was extracted from three commercial CRC cell lines (HT-29, DLD-1, and Caco-2), and RT-PCR was performed using short and long primers targeting bacterial 16S rRNA genes. Preliminary results detected bacterial signal in these cell lines, with K. pneumoniae gDNA as a positive control and nuclease-free water as a negative control. Future validation using FISH is needed to confirm intracellular localization and quantify bacterial burden per human cell.

Session2/Poster-23

Optimization of High-Performance Liquid Chromatography in Drug Metabolism Studies: Investigation of S9 Liver Cells Across Three Species

Sophia Sun (Biology)

Abdulmalik Lab | Children's Hospital of Philadelphia

Traditionally Liquid chromatography-mass spectrometry (LC-MS) is a laboratory method used to analyze the separation of small molecules in a chemical mixture. However, albeit its precision, the mass spectrometry portion of the LC-MS is expensive, time intensive and incapable of being performed in house. To improve the reliability of data collected using high-performance liquid chromatography (HPLC), this project aimed to develop an easy, affordable, reliable, and reproducible HPLC method for detecting investigational molecules during the drug discovery process, including for diseases such as sickle cell disease. I optimized different aspects of the method including the column used, and the concentrations of drugs that would be used to determine the optimal condition for the HPLC run. Ultimately, a reliable and reproducible method was established to measure drug metabolism in vitro, which can also be adapted to evaluate drug concentrations in blood from treated experimental animals.

Session2/Poster-24

Edible Films for Masking the Aversive Taste of Oral Nutritional Supplements

Thomas Tran (Biology)

Smutzer Lab | BioLife

Vitamin D deficiency affects one billion people globally, yet traditional soft gel supplements face low patient compliance due to dysphagia, swallowing anxiety, and aversive oily or bitter tastes. This research independently developed a novel oral delivery system using rapidly dissolving pullulan-based edible films to improve therapeutic accessibility. To overcome loading barriers for water-insoluble Vitamin D3, I engineered a method to complex the supplement with saturated long-chain fatty alcohols, creating solid microparticles for film integration. Sensory evaluation of four wax formulations demonstrated that while pure D3 complexes produce high taste intensity, a combination of sucralose and peppermint oil successfully masks aversive sensations via trigeminal activation. This study validates a stable, palatable prototype for sublingual delivery, offering a viable solution to enhance nutrient compliance in pediatric and geriatric populations

Session2/Poster-25

Bottle effect

Thanh Hao Trinh (Biology)

Grattepanche Lab | BioLife

This study examines factors influencing the growth of the mixotrophic protist Dinobryon, with a focus on the role of the bottle effect. Mixotrophs are organisms capable of both photosynthesis and ingestion of prey, allowing them to adapt to varying environmental conditions. Dinobryon, a polar marine chrysophyte, is an ecologically important genus due to its role in aquatic food webs and carbon cycling. Previous studies on temperate freshwater chrysophytes suggested that smaller culture volumes increased growth rates, potentially due to higher bacterial abundance. In this study, the relationship between Dinobryon growth rate and incubation volume was tested. We hypothesized that larger volumes would promote higher growth rates. Our results suggest that Dinobryon growth is not significantly affected by culture volume sizes, although additional data collection is ongoing. In future studies, we aim to test whether photosynthesis influences Dinobryon growth and grazing behavior.

Session2/Poster-26

The Involvement of PRUNE 1 in the Development of Cancer Under Inflammatory Conditions

Leo E Voet (Biology)

Feitelson Lab | BioLife

Untreated hepatitis B virus (HBV) has been shown to contribute to the development of hepatocellular carcinoma (HCC). When HBV transgenic mice were treated with short chain fatty acids (SCFAs) the progression of HBV into HCC was slowed. Proteomics were conducted on the mice and a list was developed of 150 proteins that were differentially expressed between untreated and treated groups. This review focuses on the protein PRUNE 1, a phosphoesterase that was down regulated 4.35 fold under SCFA conditions. Lit searches were conducted to help understand the effects of the down regulation of PRUNE 1. PRUNE 1 is now shown to be involved in multiple pathways in the progression of cancer where it promotes cell growth, proliferation and motility which are all hallmarks of cancer. The down regulation of PRUNE 1 was also shown to affect other cancers which develop under inflammatory conditions. PRUNE 1 is therefore a potential therapeutic target by SCFAs in the treatment of numerous diseases.

Session2/Poster-27

Action Control Remains Goal-Directed in Both Young and Old Mice

Avery Weidner (Biology)

Giovanniello Lab | LKSOM

It has been suggested that aging may change the transition from goal-directed to stimulus-response behavioral control, which is known to occur during habit formation. This study compares the sensitivity to outcome devaluation in young and old cohorts to investigate age-related differences in habit learning in mice. Outcome devaluation tests were conducted to determine whether behavior had become habitual or remained goal-directed. The devalued reward prompted a lower response, indicating that mice of all ages were still sensitive to outcome devaluation. This suggests that neither age group developed habits. These results imply that the transition from goal-directed to habitual action control was neither promoted nor hindered by aging. Future work should explore whether extended training or stress-based manipulations may be required to induce age-dependent differences in habitual responses.

Session2/Poster-28

Inhibition of TGF-β Signaling by ALK5 Inhibitor BI-4659 Reduces Human Airway Smooth Muscle Cell Proliferation

Mariza Merry (Biology)

Sharma Lab | LKSOM

Asthma is a chronic respiratory disease marked by airway inflammation, bronchoconstriction, and remodeling. A major contributor to remodeling is excessive proliferation of airway smooth muscle (ASM) cells and extracellular matrix deposition, largely driven by transforming growth factor-beta (TGF-β). Activin receptor-like kinase 5 (ALK5), a TGF-β type I receptor, is a key regulator and potential therapeutic target. Human ASM cells were cultured in 12-well plates and serum-starved for 48–72 hours using serum-free medium with 1% ITS. Controls included serum-free and fetal bovine serum (FBS)-containing media. Cells were treated with 1–30 μM BI-4659 in FBS medium. After 48 hours, cells were trypsinized and counted. Higher inhibitor concentrations reduced cell counts, indicating suppressed proliferation. These results suggest ALK5 inhibition disrupts TGF-β signaling and may improve asthma outcomes.

Session2/Poster-29

Exploring MET Overexpression and Drug Target Opportunities in HNSCCs

Sun Ohm (Biology)

Golemis Lab | Fox Chase Cancer Center

Head and Neck Squamous Cell Carcinomas (HNSCCs), the sixth most common cancer worldwide, arise from the mucosal epithelium of the oral cavity, pharynx, and larynx. HNSCCs frequently overexpress Epidermal Growth Factor Receptor (EGFR) and Aurora Kinase A (AURKA), both associated with poor prognosis and therapy resistance. While EGFR is overexpressed in most HNSCC tumors, most patients develop resistance to EGFR inhibition, leading to disease progression. Emerging evidence suggests AURKA supports oncogenic signaling and resistance, though mechanisms remain unclear. This study investigates whether AURKA contributes to EGFR resistance in HNSCCs and validates the functional role of MET in this context. We assess MET-overexpressing cells compared to GFP vector, examining MET activation, while investigating downstream signaling pathways. Finally, we evaluate therapeutic opportunities combining MET, AURKA, and EGFR inhibitors to overcome resistance and improve treatment outcomes in HNSCCs.

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Major Abbreviations
Biology → BIO
Genomic Medicine → GM
Molecular & Cellular Neuroscience → MCN
Integrated Genetics & Genomics → IGG
Ecology/Evolution/Biodiversity → EEB
Environmental Science → ES
Biochemistry → BIOCHEM
Health Sciences → HSCI
Natural Sciences → NATSCI
TUteach → TUTEACH
Computer Science → CS
Bioengineering → BE