Idaho State Board of Education
Higher Education Research Council
Undergraduate Research Fellows

Academic Year 24-25
Summary

Institutional Research and Effectiveness
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Introduction

The Office of Institutional Research and Effectiveness, in collaboration with the Office of the Provost & Executive Vice President for Academic Affairs, oversaw the Higher Education Research Council (HERC) undergraduate research fellows' program.

The HERC funds provided undergraduates students with research opportunities in the Science, Technology, Engineering or Math (STEM) fields under the guidance of a faculty mentor. Lewis-Clark State College (LC State) students were selected based on a competitive application process. Eight (8) students received a HERC research fellowship. All participating students presented posters at either the LC State Research Symposium in May 2025 or at the Idaho Conference for Undergraduate Research (ICUR) in Boise, July 2025. Additionally, three students presented at the American Geophysical Union Conference.

Thank you to the Idaho State Board of Education and HERC for their generous allocation of $30,000 in support of advancing STEM student learning. LC State expended the funds as follows:

EXPENSE CATEGORY	AMOUNT
Stipends	$22,672.84
Travel	$9,285.06
Materials and Supplies	$23,899.49*
Miscellaneous Expenses	$1,213.46
TOTAL	$57,070.85

*Received approval to utilize FY24 carryover to purchase computer equipment for student research.

The following are the student project abstracts:

Fellowship Recipient: Stevie Gulman (Fuchs)
Faculty Mentor: Dr. Nancy Johnston, LC State, Division of Physical, Division of Physical Life, Movement & Sport Sciences
Title: *Health Risks Associated with Formaldehyde and Acetaldehyde in Idaho, USA*
Abstract: Air toxics concentrations and corresponding health risks were studied near a paper mill in Lewiston, Idaho at four sampling sites. Hazardous Air Pollutants (HAPs) such as formaldehyde and acetaldehyde can be released via pulp paper processing, in addition to other criteria pollutants like sulfur dioxide (SO2). Since 2016, air samples were collected weekly for one-hour long durations using DNPH-coated cartridges, and were analyzed via US EPA methods TO-11a with liquid-chromatography (LC), and were compared to 2006 values collected by the Nez Perce Tribe. SO2 and Total Reduced Sulfur (TRS) were measured continuously at the LCSC site using a Teledyne T102 analyzer. Aldehyde levels were lower in 2023-24 compared to 2006, while acetaldehyde slightly increased from 2016 to present. The calculated lifetime inhalation exposure cancer risk was calculated via the number of extra cancers per million based on 2023-24 values.

Fellowship Recipients: KC Wahl
Faculty Mentors: Dr. Nancy Johnston, LC State, Division of Physical, Division of Physical Life, Movement & Sport Sciences
Title: *Air Toxics in Communities Near Former Philadelphia Oil Refinery Site*
Abstract: In June of 2019 thousands of pounds of hazardous air pollutants, including volatile organic compounds (VOCs), were released into the air in Philadelphia PA. This tremendous release of toxic gases was the result of an explosion at the East Coast's largest oil refinery. Though the refinery was shut down after the explosion, local communities remain concerned about VOC emissions during remediation and redevelopment at the site. In this study, air samples were collected weekly using Tenax sorbent tubes in multiple locations with close proximity to the former oil refinery site. Samples were analyzed using thermal desorption-gas chromatography-mass spectrometry (TD-GC-MS) to measure levels of benzene, toluene, ethylbenzene, xylenes (BTEX), and other VOCs. Benzene was under 9 $\mu g/m^3$, the EPA action level, during the 2023-2024 sampling period. Residential risk exposure based on benzene concentrations and EPA risk methods estimate an extra seven cancers per million people during the study period.

Fellowship Recipients: Grace Tiegs
Faculty Mentor: Dr. Nancy Johnston, LC State, Division of Physical, Division of Physical Life, Movement & Sport Sciences
Title: *Volatile Organic Compounds in Western U.S. Wildfire Smoke and Associated Health Risks*
Abstract: Wildfires have become increasingly impactful on the land and people in the western United States, with factors like climate change, prolonged droughts, and land-use practices intensifying these events. Emissions associated with wildfire smoke led to important environmental and public health concerns. To better understand and assess these concerns, passive air sampling was conducted at a number of sites across the US West with the use of Tenax sorbent tubes. Samples were analyzed with thermal desorption-gas chromatography-mass spectrometry instrumentation for about fifty volatile organic compounds (VOCs), including aromatic and aliphatic hydrocarbons. Impact of smoke was assessed and correlated with VOCs such as benzene as well as particulate matter. Health risk due to benzene was calculated using EPA methods.

Fellowship Recipient: Connor Alexander, Jayden Youngren and Ava Hasenoehrl
Contributors: Abigail Brown and Brayden Graves
Faculty Mentor: Dr. Eric Stoffregen, LC State, Division of Physical, Life, Movement and Sport Sciences LC State, Physical, Life, Movement & Sport Sciences
Title: Drosophila *Y chromosome variation impacts survival in Blm-deficient embryos*
Abstract: Blm DNA helicase plays a crucial role in maintaining genome stability during development. Blm females exhibit a significant maternal effect lethality, with most of their embryos failing to survive to the larval stage. Among the few survivors, females (XX) are overrepresented compared to males (XY). This sex-bias correlates with repetitive DNA content, as the XY genotype contains more repetitive DNA content than XX. To test whether Y chromosome variation affects Blm-deficient embryonic survival, we obtained naturally derived lines from global Drosophila populations. We crossed their Y chromosomes into a common genetic background and crossed these males to Blm females. The resulting progeny showed variable female:male ratios. We leveraged the increased meiotic nondisjunction in Blm females to assess Y chromosome-specific lethality by comparing the ratio of sex chromosome aneuploid to euploid survivors (XO:XY males and XXY:XX females). Y chromosomes associated with increased

female:male ratios also showed elevated XO:XY ratios among surviving males, suggesting the exacerbated sex-bias is caused by increased Y-associated lethality. Notably, no XXY females survived, suggesting a repetitive DNA content load that is too high in the absence of Blm. To investigate potential mechanisms for the Y-associated lethality, we used a position effect variegation (PEV) assay to assess relative heterochromatin content of the Y chromosomes, a proxy for chromosome size for the entirely heterochromatic Y chromosome. Surprisingly, we found no correlation between Y chromosome size and Blm-associated male lethality, suggesting that it may be specific types of DNA repeats that require Blm helicase during early development, rather than bulk repetitive content.

A Fellowship Recipients: Ava Hasenoehrl, Jayden Youngren, and Conner Alexander
Contributors: Brayden Graves and Abigail Brown
Faculty Mentor: Dr. Eric Stoffregen, LC State, Division of Physical, Life, Movement & Sport Sciences
Title: *A neurodegenerative phenotype in survivors of Blm-deficient development in Drosophila melanogaster*
Abstract: DNA damage caused by a lack of maternally loaded Blm protein during early embryonic development in Drosophila melanogaster results in significant embryonic lethality. It is unknown, however, how this DNA damage affects normal physiologic processes in the few surviving individuals. We investigated whether this developmental abnormality (Blm-deficiency induced DNA damage) causes neurologic dysfunction in adult survivors. We hypothesized that this DNA damage exposure during early development would cause reduced lifespan, loss of motor function, and disruption of normal sleep patterns and circadian rhythms. To test our hypotheses, we collected adult progeny from Blm– mothers crossed to Blm+ fathers and from the reciprocal cross, Blm+ mothers crossed to Blm– fathers. In both crosses, surviving progeny were heterozygous for Blm, but one set developed with maternally loaded Blm protein (from Blm+ mothers) and one without (from Blm– mothers). We compared lifespan between these sets of progeny, used a climbing assay to measure motor function, and investigated sleep and circadian rhythms using a continuous activity monitor. Progeny that developed without Blm protein exhibit a significant reduction in lifespan, a significant decrease in climbing ability, a significant disruption in sleep condensation, and a significant change in circadian patterns compared to flies that developed with Blm protein. Since these phenotypes are commonly observed in old flies, we are assessing whether there are signs of advanced biological aging in the flies that develop without Blm.

Fellowship Recipient: Ava Hasenoehrl, Conner Alexander, and Jayden Youngren
Contributor: Abigail Brown
Faculty Mentor: Dr. Eric Stoffregen, LC State, Division of Physical, Life, Movement & Sport Sciences
Title: *Metabolic dysfunction following Blm-deficient development in Drosophila melanogaster*
Abstract: Blm DNA helicase is essential for proper DNA replication during early development in Drosophila melanogaster. Blm– mothers, who do not provision their eggs with functional Blm protein, exhibit a maternal-effect lethality. Nearly all progeny from Blm– mothers die before larval hatching; however, a few survive to adulthood (<10% of embryos). These survivors provide a model to study the effects of DNA damage during early development on healthspan. We hypothesized that survivors of Blm-deficient development would display alterations in metabolic function. We first tested whether development without Blm protein affected body mass and determined that Blm-deficient development results in a statistically significant reduction in body mass. Our data also suggests that Blm-deficient development results in decreased energy storage in adult flies, with clear reductions in triglyceride

levels and a possible reduction in glycogen storage as well. These data suggested that the DNA damage sustained by embryos lacking Blm during early cell cycles either affected metabolic processes related to energy storage or affected the feeding behavior of the flies. To test whether these differences in metabolism could be accounted for by food consumption differences, we performed capillary feeder (CAFE) assays and saw no difference in food consumption by flies that survived Blm-deficient development, suggesting instead that these flies exhibit defects in metabolic processes.

Fellowship Recipient: Jayden Youngren, Connor Alexander, Ava Hasenoehrl, Rayana Shah
Contributor: Abigail Brown and Brayden Graves
Faculty Mentor: Dr. Eric Stoffregen, LC State, Division of Physical, Life, Movement & Sport Sciences
Title: *Metabolic dysfunction following Blm-deficient development in Drosophila melanogaster*
Abstract: The absence of maternally provided Blm DNA helicase during early embryonic development leads to severe DNA damage in Drosophila. This damage is lethal to most embryos, and the small percentage that do survive to adulthood are characterized by an extreme sex bias, where ~70-90% of the population is female. This female sex-bias amongst surviving progeny correlates with repetitive genomic DNA content, as the female genotype (XX) contains less repetitive DNA than the male genotype (XY) due to the highly repetitive nature of the Y chromosome in Drosophila. Additionally, embryos from Blm– mothers have a higher probability of aneuploid sex chromosome karyotypes caused by increased meiotic nondisjunction (ndj). These karyotypes include XO, where no second sex chromosome exists and results in a male phenotype. We hypothesized that XO males would exhibit longer lifespans than XY males because of the reduced repetitive DNA content present during Blm-deficient development. To test our hypothesis, we genotyped flies throughout a lifespan assay. In support of our hypothesis, we found that XO males do exhibit longer lifespans than XY males. Additionally, there was a single XO male in our control group (progeny from Blm– males instead of Blm– females) which also exhibited increased survival. This led us to question whether Blm– males also show increased meiotic ndj. We developed a cross scheme to score large numbers of progeny to address this question.

Fellowship Recipient: Erica Stryker
Faculty Mentor: Dr. Leigh C. Latta, LC State, Division of Physical, Life, Movement & Sport Sciences, Dr. Adam G. Jones, University of Idaho, College of Science
Title: *Insights into male pregnancy and its evolution: Patristacin gene family expansion and contraction in Syngnathids.*
Abstract: Seahorses, pipefish, and seadragons are all members of the family Syngnathidae. Syngnathids are characterized by male pregnancy wherein the female deposits eggs into a brood pouch located in or on the male. Structures for male pregnancy range from simple external attachment to an enclosed, internal pregnancy similar to a mammalian uterus. This feature is a relatively unique biological phenomenon that raises questions as to how and why the male brood pouch evolved in Syngnathidae. Patristacins are an astacin metalloprotease found in live-bearing teleosts including Syngnathidae and were likely coopted from a digestive role to support nutrient transfer in the brood pouch. This project seeks to use bioinformatic methods to investigate the expansion and contraction of the patristacin gene family in Syngnathidae in order to shed light on the evolutionary process that led to male pregnancy. Twelve Syngnathidae proteomes were acquired from the NCBI Genome database. OrthoFinder2 was used to identify gene families. CAFE5 was used to analyze expansion and contraction events within these gene families. Analysis showed tail brooding Syngnathids had more patristacin genes than trunk

brooders. Furthermore, there were significant changes in patristacin gene family number in the Syngnathini, Stigmatoporini, and Solegnathini clades. Further analysis including more Syngnathidae species is in our control group (progeny from Blm– males instead of Blm– females) which also exhibited increased survival. This led us to question whether Blm– males also show increased meiotic ndj. We developed a cross scheme to score large numbers of progeny to address this question.