the RESEARCHER

IDAHO NSF EPSCoR

April 2023

University of Idaho students Sara Bennett, Kendall Hawley, Michael Youngwirth, and Reagan Raat (clockwise from left closest) sample redband trout from Callahan Creek, a Northern Idaho GEM3 study population. The sampling was during a field trip that was part of an Aquatic Molecular Ecology (AquaMolE) Vertically Integrated Project (VIP) course. Young-of-year trout were collected at night when they can be 'spotlighted' with a headlamp and netted with hand nets. (They are too small to be collected easily during daytime). Photo credit: Chris Caudill

A newsletter publication
of the Idaho EPSCoR Office

the
RESEARCHER

Andy Kliskey
Project Director
akliskey@uidaho.edu | 208-885-6499

Rick Schumaker
Assistant Project Director
rschumak@uidaho.edu | 208-885-5742

Sarah Penney-Jackson
Diversity, Outreach, and
Communication Coordinator
sarahp@uidaho.edu | 208-885-2345

Tami Noble
Finance Director
tnoble@uidaho.edu | 208-885-5842

Dalynne Veeder
Administrative Financial Specialist
dveeder@uidaho.edu | 208-885-7102

Andrew Child
Data Manager
awchild@uidaho.edu | 208-885-7129

Follow us on Twitter
@IdahoEPSCoR

Idaho EPSCoR Website
idahoepscor.org

Track 1 GEM3 Website
idahogem3.org

Track 1 MILES Website
idahoecosystems.org

LETTER FROM THE DIRECTOR

Andy Kliskey

This issue of *the Researcher* presents a wealth of work demonstrating the interconnections among teaching, research, outreach, and workforce development – and the key role that undergraduate and graduate students play in making these connections happen. Each article in this issue represents the outcomes from the capacity built and being built by Idaho EPSCoR through the GEM3 project.

You will read about the collaborations among Jon Masingale, Anna Ringelman, and Ben Kline and their faculty and postdoctoral supervisors to assess the adaptive capacity in redband trout from genomic to landscape scales. Then the work on Yellowstone cutthroat trout hybridization that builds from Lizzie Jossie's Masters research. There is an excellent example of outreach through regional and national training on genomic approaches for wildlife conservation by Molly Garrett, Stacey Nerkowski, and team. Undergraduate students Cayden Whipkey, Amy Johnson, and Cana Foncannon team up with graduate student Andrii Zaiats and team to extend the sagebrush common garden experiments. And it is exciting to see the results from ID EPSCoR Seed grant awardees with: graduate student Mosope Abanikannda's work on Jake Bledsoe's seed award; Trey Harris' work on Josh Grinath's sagebrush establishment research; Cadre Francis' graduate research on David Estrada's seed project on wireless sensors for detecting chemical phenotypes in sagebrush, that includes undergraduate teams (Alex Naderman, Jonathan Ryan, Nick Irwin, Sam Mark, Riley Mark and Jaelyn Friberg). And finally the inspiring Summer Authentic Research Experience of CWI undergraduate Cayden Whipkey.

I commend the effort and insight provided by each of these students. Enjoy reading the details of each of these in this Newsletter.

This material is based in part upon work supported by: The National Science Foundation under grant number OIA-1757324. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

Unless otherwise noted in feature byline, articles and features in this publication are written by Sarah Penney-Jackson with editing and content contributions by EPSCoR administrative team.

GEM3 Research

Weaving it all together: assessing adaptive capacity across scales from genomes to landscapes in native redband trout populations in Idaho

By Chris Caudill, *Associate Professor of Fisheries, University of Idaho*

(with major contributions from ***T. Seaborn, Z. Chen, J. Masingale, S. Narum, A. Ringleman, E. Keeley, L. Huang, K. Andrews, T. Link, E. Du, K. Griswold, B. Kline, P. Hohenlohe, L. Waits, D. Pradhan, A. Wooding,*** *and* ***B. Small)***

Assessing ecological and evolutionary effects across multiple scales remains a key challenge to predicting the response of populations to environmental change, including climate change. Addressing this gap using redband trout and sagebrush as model species is a central goal of the GEM3 project. During the final year of the GEM3 project, we (the Trout Mechanisms team) are working toward synthesizing and integrating results for trout studies across scales and disciplines with the aim of discovering which scale or population attributes have the greatest influence on trout population dynamics as their environments shift.

The Trout Mechanisms team includes more than twenty students, post-doctoral researchers, faculty and GEM3 partners. The group has studied a dozen different Idaho trout populations spanning a range of habitats, from those that are colder than optimal for trout growth to desert streams that would be lethal during summer if trout in those streams did not have genetic adaptations to warmer waters. To date we have evaluated (in order of increasing scale): 1) genomic structure and genome-environment associations using whole-genome sequencing; 2) physiologic thermal capacity in a common garden in Hagerman, Idaho; 3) growth and habitat quality of in-field populations using a bioenergetic framework; 4) current and future flow and thermal regimes by integrating climate and hydrological models; and 5) spatially explicit agent-based models (ABMs) for a subset of populations to integrate GEM3 and other data sources. We have produced a major modification to an ABM software platform (CDMetaPop) to include phenotypic plasticity as well as genetic traits, and the software will be used to compare model outcomes for alternative climate, land management, and assisted migration scenarios.

During 2023, members of the Trout Mechanisms team will participate in a series of planned Synthesis and Integration workshops where ABM models will be refined. We will also grapple with how to integrate key GEM3 empirical findings described below into a multi-scale conceptual framework of trout population response to environmental change. Thus far, we have found that trout population genomic structure across the landscape was associated with geography and thermal environmental parameters, including metrics of thermal variability. Different measures of trout performance depended on the temperature the fish had been acclimated to prior to testing and differed by the genetic source population. In other words, both “nature” and “nurture” had effects and these effects differed among important traits such as upper thermal limit, maximum heart rate and growth rate. Field habitat surveys and drift foraging models revealed higher productivity in desert streams, but predicted warming will decrease habitat capacity, especially for larger fish. Hydrologic modeling results revealed riparian vegetation and fire management were unlikely to buffer effects of climate warming on modeled montane thermal regimes. ABM models accounting for warming predicted that trout abundance decreased (desert) or was neutral/increased (montane), that the relative importance of plasticity and genetic adaptation depends on the strength of natural selection and nature of the plastic response, and that dispersal strongly affects demo-genetic dynamics, or the integration of genetics with demographic data.

Weaving cont.

In combination, we are evaluating the contribution of genetic and plastic traits to adaptive capacity (i.e., persistence), identifying key scale(s) and uncertainties affecting the reciprocal interactions between ecological and evolutionary processes, and evaluating the relative potential for management actions to mitigate impacts. We also plan to compare our findings for sagebrush, and we anticipate contrasts in the ecology and life histories between the two species will illuminate processes affecting adaptive capacity in terrestrial vs. aquatic habitats. Overall, this multi-scale and interdisciplinary approach can be applied in other systems to evaluate population responses to environmental change, including complex effects of demo-genetic feedbacks, and to identify management and conservation options.

GEM3 Research

Understanding the dynamics of Yellowstone cutthroat trout hybridization and connectivity within the Teton River system

By Travis Seaborn, *Assistant Professor, School of Natural Resource Sciences, North Dakota State University (previously Postdoctoral Scholar at University of Idaho);* **Alexandra Fraik,** *Research Biologist, United States Forest Service;* **Paul Hohenlohe,** *Associate Professor, Department of Biological Sciences, University of Idaho*

Stream connectivity restoration efforts are an important management action for increasing the prevalence of migratory fish within stream networks, which can have domino effects on population dynamics. For example, in Yellowstone cutthroat trout, some individuals who migrate can become very large and produce a larger number of eggs compared to non-migratory fish. Thus, one unintended outcome of increasing connectivity may be negative impacts from invasive species, including increasing hybridization rates, also known as interbreeding of species.

Paul Hohenlohe with a Yellowstone cutthroat trout in the Teton River drainage. A small clip of the adipose fin allows researchers to learn about the fish population through their genetics.

Within the Teton River Basin, stakeholder interviews and fish movement simulation models combined stakeholder-informed connectivity scenarios, Yellowstone cutthroat trout life history variation, and hybridization with Rainbow trout to better understand these issues. However, these previous models and simulations are very sensitive to the existing rates of hybridization and how strongly individuals may prefer to mate with their own species.

Yellowstone cont.

Electrofishing crews catching Yellowstone cutthroat trout, Rainbow trout, and hybrid (interbred) individuals. Crews included people from University of Idaho, Friends of the Teton River, and local volunteers.

To fill in this gap and better understand potential outcomes, a team of researchers led by Travis Seaborn, Alexandra Fraik, and Paul Hohenlohe are sequencing Yellowstone cutthroat trout, Rainbow trout, and hybrid individuals across the riverscape to quantify these processes.

> *The genomic data from fish located across the landscape will help generate more refined models and simulations to understand the role of genomics as stakeholders consider restoration and other management efforts.*

This is especially important for the benefit of the Yellowstone cutthroat trout, which is a species of conservation concern (meaning, there is concern about its ability to remain on the landscape in the future).

Last year as part of an NSF EPSCoR GEM3 sequencing effort, scientists kicked off the project with two sets of field work to collect fin clips. This research is ongoing, with the DNA sequence data actively being developed, both for fish collected in the field and fish previously collected by Idaho Fish and Game and Friends of the Teton River.

This research is part of a larger series of studies focused on understanding the Teton watershed as a social-ecological system across multiple species. This system approach focuses on the shared impacts of humans on natural systems and of natural systems on humans.

This work builds off of the modeling efforts by Elizabeth Jossie, an Idaho State University (ISU) graduate student in the GEM3 project, as part of her work with ISU professors, Colden Baxter and Morey Burnham.

Additional collaborators during both the previous research work and this new genomic work include Friends of the Teton River, U.S. Forest Service, and Idaho Fish and Game. All organizations participated in field work, including additional field work with University of Idaho (U of I) Associate Professor Chris Caudill.

The fin clips collected in the field were sent to U of I for DNA lab analysis along with previously collected samples, with those data now being analyzed by researchers from the U.S. Forest Service, North Dakota State University, and U of I.

The results of this study will have both local, regional, and national impacts. These results will fill the gap of missing genetic and morphological (physical form) data from the Teton region, which is an area of active social-ecological research within GEM3.

We hope that significant outcomes will include a better understanding of the spatial distribution of hybridization, the preference of mating with a fish's own species, and predictions of the impacts that different stream connectivity restoration actions may have on these fish species.

The Teton region Stakeholder Advisory Group and stakeholders interviewed by the ISU team have shown a strong interest in Yellowstone cutthroat trout conservation. In addition, stakeholders have

Yellowstone cont.

Michael Youngwirth, University of Idaho (U of I) SARE undergraduate student, and Alexandra Fraik, Research Biologist with the United States Forest Service, working on on processing collected fish.
Photo credit: Travis Seaborn

expressed interest in specific stream tributaries with research questions that they classify as important to address with these data.

Beyond the local system, Yellowstone cutthroat trout are a species of conservation concern, and similar questions about connectivity and hybridization exist regionally. Even beyond the region, this research also serves as an example to link social, human-dimension research with genomics of fish and wildlife. This unique research approach will hopefully expand the field of social-ecological system research.

Communications

Workshops provide an overview of genomic approaches for wildlife conservation and management

An Idaho NSF EPSCoR GEM3 team conducted multiple genomics workshops in the Pacific Northwest in the last few months as part of regional and national conferences for the Wildlife Society. The Wildlife Society is a large international non-profit association of wildlife management, science, and conservation specialists.

The workshops, titled, "An overview of genomic approaches for wildlife conservation and management," took place at Wildlife Society Conferences in both Spokane, WA and Boise, ID. Workshops were led by a team including Lisette Waits, Molly Garrett, Paul Hohenlohe, and Stacey Nerkowski, University of Idaho, and Stephanie Galla, Boise State University.

Because the field of wildlife genetics is being transformed by new genomic methods, the workshop provided an overview of genomic methods that can be used to address research questions in wildlife ecology, conservation and management. The workshop included examples of how these new methods are being used to identify conservation and management units; assess genetic diversity and gene flow; monitor biodiversity; estimate population size; monitor survival, reproduction and population growth in reintroduced species; evaluate diet; detect invasive species; and better understand adaptation and fitness.

Over 75 participants took part in the workshops and included a combination of students, faculty, post-docs and wildlife professionals. The workshop provided participants with the tools to be better prepared to collaborate with genomics experts or lead a project using genomic methods. It also provided a greater understanding of the ways that new genomic methods can be used to gather critical information about wildlife populations.

GEM3 Research

Plants get crowded too: Improving the design of common garden studies

By Andrii Zaiats, ***PhD candidate, Department of Biological Sciences, Boise State University*****; Trevor Caughlin,** ***Associate Professor, Department of Biological Sciences, Boise State University***

Undergraduate researchers collect field data on sagebrush growth and survival in Castle Rocks State Park, Idaho. From left to right, Cayden Whipkey, Amy Johnson, and Cana Foncannon. Photo credit: Andrii Zaiats

Conservation programs, including those that seek to respond to climate change, heavily rely on understanding how plant species adapt to local environmental conditions. However, in natural landscapes, plants grow together with other plants, and how they interact can determine whether the plant lives or dies.

NSF EPSCoR GEM3 scientists have taken the well-recognized idea, that plants interact with each other, and begun to test interactions in a previously unexplored setting - a common garden.

> *Common gardens are experimental plots where many plants grow in an open space together, in a garden.*

This type of experiment is considered a gold standard for measuring how populations of the same species differ genetically.

In our study, we demonstrate how the results of research intended to focus on genetics may reflect not only genetic differences due to climate but also differences due to how competitive plants may be with each other. This can be undesirable because competitive interactions can bias the conclusions from common garden research.

Our collaborative effort crossed many disciplinary boundaries, from plant genetics and physiology to population models and large-scale ecosystem processes. Equally important was the partnership between universities (Boise State University and the University of Almeria) and federal agencies (U.S. Forest Service and U.S. Geological Survey). This partnership allowed us to use legacy data (from the common garden established more than 10 years ago) through the lens of demographic changes in big sagebrush that play out over long periods of time.

The outcomes from the research provide several options for how the risk of bias can be minimized. But we also see this as an opportunity to ask novel questions. Novel statistical methods allow us to quantify how one plant affects its neighbor, including in a common garden. For example, researchers can use this knowledge to design common gardens that minimize neighbor interactions.

A common garden experiment near Orchard, Idaho, where each plant represents a genetically distinct population. While differences in genes could be one reason for different growth and survival, plants can also compete for water and other soil resources when they grow together. Photo credit: Andrii Zaiats

Garden cont.

Study authors, Andrii Zaiats (left) and Juan Miguel Requena Mullor (right), on a field trip to measure plant growth and survival in a common garden near Boise, Idaho. Photo credit: Andrii Zaiats

Alternatively, suppose competition does play out in the common garden. In that case, it could be used as an opportunity to incorporate it as an experimental treatment and test how environment (abiotic) and competition (biotic) shape the genetic diversity of a species.

Our research shows that this information can be readily incorporated into studies of species adaptation and, ultimately, into conservation programs.

The team recently had their research published in Ecology and Evolution in December, 2022. See full journal citation below. Since the investigation of plant competition in a common garden, starting in 2019 within the scope of the GEM3 project, we have expanded the scale of our research to better understand how sagebrush and other shrub species respond to local and landscape factors after a wildfire.

Using drone technology, we can retain our focus on individual shrubs and expand the survey horizon to continuously map and measure plants and environmental variability. We aim to incorporate this knowledge into our understanding of wildfire disturbances and landscape resilience.

Zaiats, A., Requena-Mullor, J. M., Germino, M. J., Forbey, J. S., Richardson, B. A., & Caughlin, T. T. (2022). ***Spatial models can improve the experimental design of field-based transplant gardens by preventing bias due to neighborhood crowding****. Ecology and Evolution, 12, e9630. https://doi.org/10.1002/ece3.9630*

GEM3 Seed Awards

Seed Award Projects

The GEM3 Seed Funding program allows the NSF EPSCoR Research Infrastructure Improvement Track-1 project to respond to new opportunities as well as pursue high impact, potentially transformative research and educational projects. Its principal objective is to create a mechanism to catalyze new research on focal species, species interactions, ecosystems, genomics/phenomics, or other emerging areas related to the scope of GEM3. It is intended for groups or individuals that emphasize the collaborative development and testing of important ideas and theories, cutting-edge analysis of recent or existing data and information, and/or investigation of social ecological systems issues.

Since 2018, Idaho EPSCoR GEM3 project has awarded just under $2.0 million to 22 projects around the state. This section highlights a few projects that have taken place and the impacts of their research and education.

GEM3 Seed Awards

Comparing microbial ecology in desert and mountain populations of redband trout to understand how fish genetics, temperature, and the environment influence fish microbiomes

By Jacob Bledsoe, *(PI), Assistant Professor, Hagerman Fish Culture Experiment Station, University of Idaho;* **Mosope Abanikannda,** *PhD candidate, Hagerman Fish Culture Experiment Station, University of Idaho*

University of Idaho assistant professor, Jake Bledsoe, and graduate student, Mosope Abanikannda, collect a swab of skin mucus from a redband trout to identify which microbes are found on trout from different habitats. Photo credit: Chris Caudill

Our research will give us insights into how fish-microbe interactions are influenced by changing water temperatures and whether changes in microbial communities are involved in helping fish adapt to environmental changes. By understanding the microbial communities present in trout, water and sediment samples, we can track changes (seasonal or locational) in these communities and identify potential environmental threats.

More specifically, the research focuses on exploring the microbiome (the collection of all the microorganisms and viruses that live in a given environment) of redband trout populations native to differing Idaho ecotypes (such as cold-montane vs. desert streams). Our project uses DNA sequencing techniques to study the microbial communities that are found in (e.g., gut), on (e.g., skin and gill), and around (e.g., water, sediment, prey/diet) redband trout. In particular, we are interested in how the trout microbiome varies across genetic, environmental, and seasonal gradients in order to understand how these interactions are involved in variation of genetic and observable characteristics.

Furthermore, studying the microbiomes of redband trout and their environment will better our understanding of microbial ecology in varying Idaho aquatic ecosystems to inform environmental monitoring efforts.

> *Together these insights can further inform conservation efforts to protect redband trout and other aquatic resources from environmental threats such as human activities and climate change.*

Our project has benefited from many collaborations with other GEM3 redband trout researchers. For example, we were able to collect microbiome samples from a common-garden experiment conducted by Zhongqi Chen (U of I research scientist) and Jon Masingale (U of I PhD candidate) that will allow us to understand genetic and environmental regulation of fish microbiomes. We were also able to participate in a U of I FISH 204 Aquatic Molecular Ecology Field Sampling Methods course field trip to collect fish, invertebrate, microbial, and environmental samples from Northern Idaho streams.

Outcomes from the research include a greater understanding of the environmental and genetic determinants of redband trout microbiomes. The research will aid in ongoing redband trout conservation efforts as well as other aquatic resources by broadening our understanding of microbial ecology in western-US desert and mountain streams. The research will also provide insights on how host-associated microbes (i.e., microbiomes) are involved in an aquatic organism's ability to adapt to changing environmental conditions.

University of Idaho PhD student, Mosope Abanikannda, collects eDNA (environmental DNA) samples from a cold-montane stream in Northern Idaho to compare its "microbiome" to that of other stream eco-types. Photo credit: Jacob Bledsoe and Mosope Abanikannda

GEM3 Seed Awards

Challenges to sagebrush establishment: Genome size and resource co-limitation, competition

By Josh Grinath, *(PI), Assistant Professor, Department of Biological Sciences, Idaho State University;* **Trey Harris,** *Graduate Student, Department of Biological Sciences, Idaho State University;* **Kathryn Turner,** *Assistant Professor, Department of Biological Sciences, Idaho State University*

We are studying how an organism's genome size impacts its resource requirements and ability to compete for resources, particularly for plants. Genome size is a measure of how much DNA is packed into each cell of an organism, and we should expect this to be related to resource requirements because DNA is rich in nitrogen and phosphorus. Larger genomes should mean more resources are required to grow, but does it? In most ecosystems, the availability of nitrogen and phosphorus is low, and competition for these nutrients can be fierce.

The situation is further complicated because access to nitrogen and phosphorus depends on the availability of other nutrients and water, and the lack of any one of these resources may limit an organism's ability to grow and reproduce. In our research, we are testing whether plants with larger genome sizes experience greater limitations for nitrogen, phosphorus and water, and how this impacts competition between plants.

To do this, we are conducting a series of greenhouse and field experiments with big sagebrush (*Artemisia tridentata*), which is a great study species because there is a very large amount of variation in genome size among these plants. We are growing sagebrush with small and large genome sizes in different resource conditions and measuring differences in their growth and survival.

Sagebrush cont.

ISU Graduate student, Trey Harris, harvests the experimental sagebrush plants to measure responses to resource and competition treatments. Photo credit: Josh Grinath

We are collaborating with Dr. Donna Delparte in the Department of Geosciences at ISU, Dr. Kathleen Lohse in the Department of Biological Sciences at ISU, Dr. Sven Buerki in the Department of Biological Sciences at Boise State University, and doctoral student Lukas Grossfurthner in the Bioinformatics and Computational Biology program at University of Idaho. Dr. Delparte has used an unmanned aircraft system (UAS) to collect remote sensing data at our field sites, including measurements of temperature and plant productivity. We will pair these measurements with data we are collecting from our experimental plots to investigate differences in sagebrush growth and survival. Dr. Lohse is evaluating differences in soil properties among our field plots, including soil nutrient and water content. Dr. Buerki and Lukas Grossfurthner are helping to source seeds for our experiments and to measure genome size for our plants.

Thus far, we have conducted a greenhouse experiment to test differences in sagebrush growth under high and low water, nitrogen and phosphorus conditions, and we are setting up field experiments to investigate these differences in relation to elevation, recent wildfire, nitrogen pollution, and patches of fertile soils created by shrubs and ants. Data collection for the greenhouse experiment is ongoing, but our preliminary analyses suggest that: 1) sagebrush seedlings needed both high water and nitrogen to grow tall, and 2) competition between sagebrush seedlings was stronger when they had larger genome sizes and there was low availability of water and phosphorus. We will be collecting additional data over the next year to further test our predictions.

Every living thing on Earth has DNA, and the resource demands for constructing DNA are universal. Our

Sagebrush cont.

work will help us to understand whether these demands represent a fundamental constraint for plants, and life more broadly. In addition, our research is increasing our understanding for how changes in resource availability will impact plants, and it may potentially inform restoration efforts for degraded ecosystems as plants with different genome sizes may succeed to different degrees in establishing and growing.

> *Over the last 100 years, many sagebrush steppe ecosystems have been lost and much of what remains has been degraded.*

These ecosystems are widely valued for supporting diverse plants and animals, including wild game species, as well as grazing by livestock. There is great interest in restoring sagebrush ecosystems in Idaho and across western North America, but current restoration efforts frequently have low success. We hope that our work will help to identify sagebrush plants that are well-suited for particular resource conditions and that will enhance the success of restoration efforts.

Sagebrush seedlings were grown under conditions of high and low nitrogen, phosphorus, and water availability, and with competitors with small to large genome sizes. Photo credit: Trey Harris

GEM3 Seed Awards

Wireless sensors for detecting chemical phenotypes: Eavesdropping on sagebrush mechanisms and the environment

By Cadre' Francis, *Graduate Research Assistant in the Micron School of Materials Science & Engineering, Boise State University*

Sagebrush is an aromatic shrub widely distributed across the Western US. It is known to chemically communicate with neighboring plants by sending cues in the form of airborne signals. As humans, we often think of communication as it relates to verbal speech, gestures or written text.

> *Just as humans communicate with other humans or animals, plants also communicate in the form of volatiles, which are chemicals responsible for the flavor and aroma we associate with plants such as sagebrush.*

There are monoterpenes that are volatile organic compounds (VOCs) that differentiate sagebrush taxa. Changes in VOCs reflect genome interactions with abiotic (e.g., drought, temperature) and biotic (e.g. herbivores) stressors in their environment. These VOCs represent chemically distinct responses to environmental changes and their impacts on organisms within that environment. Currently, the ability to evaluate the VOCs and their impact on the landscape is lacking.

A collaborative research team is helping to bridge this gap by proposing a new way to eavesdrop on sagebrush. Through GEM3 seed funding, the research team produced a wireless sensor technology capable of sensing VOCs emitted by sagebrush. The use of these sensors will provide new fundamental insights about detecting VOCs from sagebrush under

Sensors cont.

L-R, Riley Mark and Sam Mark, undergraduate engineering students at Northwest Nazarene University (NNU), survey the Soda Fire Site to get a sense of how project team can install the sensor system on a real sagebrush plant.

controlled Genotype by Environment (GxE) conditions established in current greenhouse and common garden experiments within GEM3.

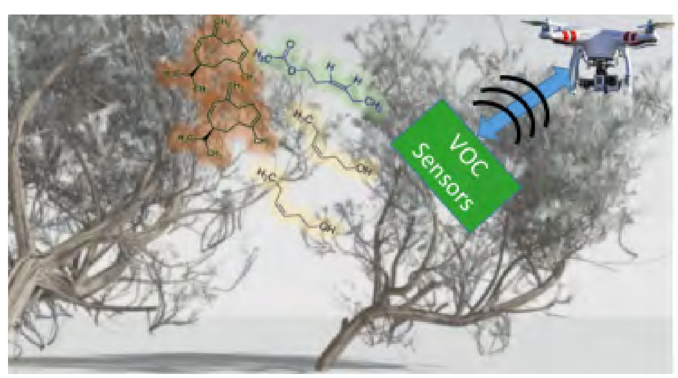
Such sensors will allow us to decode sagebrush volatile communication in response to abiotic and biotic stressors. Real-time data collection on VOCs from genetically distinct populations relative to abiotic and biotic stimuli will provide new phenotypic variables to include in modeling and mapping research objectives.

This collaborative effort is led by Dr. David Estrada, an Associate Professor in the Micron School of Materials Science and Engineering at Boise State University. Dr. Estrada is leading the fabrication of the sensor and providing expertise in nanotechnology and device integration. Dr. Jennifer Forbey, a Professor in the Department of Biological Sciences at Boise State University is a leading researcher on sagebrush ecosystems in Idaho. Dr. Forbey provides expertise in the genetic mechanisms of sagebrush and the effect of environmental conditions on the plants and wider landscape.

The project is also broadening participation through its partnership with Northwest Nazarene University, a primarily undergraduate institution. Project team members include Drs. Joshua Griffin and Ben Pearson, who are both Professors in the Department of Engineering and Physics at Northwest Nazarene University. Dr. Griffin's expertise is in low-power wireless systems and Dr. Pearson contributes to the sensor characterization efforts (his expertise is experimental particle physics).

They are responsible for integrating the laser-induced graphene (LIG) sensor to allow wireless communication of the sensor data. They have led multiple teams of undergraduate students to integrate the LIG sensor into a wireless system and transmit the sensor data from the remote sagebrush measurement site to a convenient location for processing. The first undergraduate team (Alex Naderman, Jonathan Ryan, and Nick Irwin) developed the initial wireless prototype and the second team (Sam Mark, Riley Mark, and Jaelyn Friberg) improved the wireless communication, integrated a preliminary LIG sensor, and experimented with the manufacturing and characterization of the LIG sensor.

The team has also integrated efforts with other educational programs at BSU including the Bridges



Conceptual image of a wireless sensor tag monitoring sagebrush chemical signals emissions to Doctorate Program and the Vertically Integrated Projects (VIP), which will provide undergraduate engineering students the opportunity to gain hands-on experience with additive manufacturing technologies, sensor development, and analytical chemistry preparing them for future internet of things (IoT) industries.

Early outcomes of the research have resulted in synthesized and processed laser-induced graphene sensors that show a response to the presence of sagebrush leaves and also in a demonstrated system that can transmit/receive sensor data. The team has also started to create a dataset showing responses of the sensor to varying VOC concentrations and sagebrush species. Ultimately, this convergent and inclusive research will improve strategies for conservation and management of sagebrush.

A prototype of the LIG sensor-tag created by the original team of NNU undergraduate students (Alex Nadermann, Jonathan Ryan, Nick Irwin, Riley Mark, and Sam Mark) working on the project. The prototype electronics were housed in a plastic tube that could be mounted in close proximity to sagebrush.

Education

Early inspiration and STEM opportunities help shape future for CWI undergraduate

Cayden Whipkey of College of Western Idaho gathering GPS points with survey equipment

Cayden Whipkey, an undergraduate student from College of Western Idaho (CWI), majoring in Biology with an emphasis in Natural Resources, was born and raised in Nampa, ID. Cayden's experiences growing up in the Treasure Valley helped shape his current career aspirations early on. Cayden states, "when I was younger my father used to take me on hikes all up and down southern Idaho. Unfortunately, he passed away when I was young, but he was and remains a great inspiration to me."

Undergraduate cont.

Cayden got an Information Technology job early on and worked there for a few years, but his passion for the outdoors began to take over. Cayden recalls,

> *"I wanted a change in my life from an office-life-future. I decided to quit, as I was tired of staring out the window at the mountains instead of being outside."*

Plans to go on to college began to materialize for Cayden, and he decided to go in a new direction. "If you had asked me before then I would've said that I never would go to college, especially as I did poorly in my previous schooling. I took a leap though, and decided to enroll in higher education at CWI and have been making a point to achieve as much as I can since then."

Research opportunities helped pave the way for Cayden to gain hands-on learning and to network with other students and researchers in his field. In the Spring of 2022, Cayden heard about the Idaho NSF EPSCoR Summer Authentic Research Experience (SARE) program through his advisor, Lindsey Zahller, at CWI, and he decided to apply. During the summer of 2022, he worked under the mentorship of Dr. Trevor Caughlin at BSU on a SARE project focused on *"Investigating the relationship between sagebrush recruitment and early-spring snow patterns."*

In his SARE research, Cayden's work focused on using drone imagery and machine learning to predict which sagebrush plants would flower, which allowed him to do GIS remote sensing work. He also worked with other students and other mentors in the field that helped him to grow his skill-set and network. Cayden notes, "all of these folks were very eager to share their information and passion for their work."

Following his summer SARE research experience, he found out that he could continue working with the Caughlin lab during the semester through the VIP program, so he did just that. The VIP program offers students real-world experience while they earn course credits over multiple semesters working alongside faculty.

His SARE and VIP experiences have helped shape his career aspirations as well. Upon graduating from CWI, Cayden plans on attending the University of Idaho to pursue a four-year degree and then on to graduate school. After graduate school, he also hopes to have a career with the USDA and plans to continue to pursue as many outdoor related opportunities as possible.

> *"I want to keep myself learning in the real world with real experiences," notes Cayden, "I learn best through doing the work and seeing how systems and ideas work in practice."*

To learn more about Cayden's research visit the Idaho GEM3 Student Research Map found at:
www.idahoepscor.org/student-research-map

Photo from: Castle Rocks field site (Almo, ID)

Idaho EPSCoR
University of Idaho
875 Perimeter Drive MS 3029
Moscow, ID 83844-3029

208-885-7102
idahoepscor.org

* 8 7 3 9 1 7 *

Continued from cover: Undergraduate students sample redband trout as part of the Aquatic Molecular Ecology (AquaMolE) Vertically Integrated Project (VIP) course. Photo credit: Chris Caudill