SEEDS: The CFAES Research Competitive Grants Program

2018 Report of Progress
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For more information, visit the SEEDS website (oardc.osu.edu/seeds) or email us at seeds@osu.edu.

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SEEDS: THE CFAES RESEARCH COMPETITIVE GRANTS PROGRAM

The Ohio State University College of Food, Agricultural, and Environmental Sciences (CFAES) employs nearly 650 scientists and staff members who support CFAES’ research mission across the state. With a presence throughout the state of Ohio, including Columbus, Wooster, and nine research stations, the Ohio Agricultural Research and Development Center (OARDC) is CFAES’ comprehensive research enterprise. CFAES scientists work closely with researchers in Ohio State’s Colleges of Education and Human Ecology, Medicine, Public Health, Veterinary Medicine, Biological Sciences, and Engineering.

At any given time, CFAES researchers are engaged in more than 400 research projects. These research projects are centered around three grand challenges:

- **Food Security, Production, and Environmental Sustainability**
- **One Health**
- **Rural Urban Interface**

Addressing the differing challenges and vast opportunities of Ohio’s agricultural industry is the ultimate goal of SEEDS: The CFAES Research Competitive Grants Program. SEEDS encourages excellence in research by promoting exploration that is consistent with the mission and vision of CFAES and by encouraging connections across disciplines, with industry, and with other external partners.

Established in 1996, SEEDS is unique among U.S. state-assisted universities. By fostering high-quality research among scientists supported by CFAES, SEEDS enables those scientists to collect the preliminary data needed to give them a competitive edge in national programs. It also provides them with leverage to attract industry support. Due to the changing nature of economic and societal trends, the agriculture, food, and green industries depend on innovators and researchers to generate new processes and products. Ohio’s largest industry increasingly links with other industries to take on common challenges and opportunities in key areas such as food production and security, energy and the environment, and health and wellness. CFAES’ SEEDS program is just one of the many ways in which Ohio State’s innovative research and development connect to industry and the community on a global scale.

The following pages provide a quick glance at the SEEDS objectives and successes. Each faculty project completed in 2018 is included along with a brief explanation of the problem being addressed, its importance, and the impact of the results. Also included is a sampling of graduate and undergraduate projects, and a listing of our industry partners.

For specific information regarding these projects, please contact the faculty members directly or contact SEEDS at seeds@osu.edu.
OBJECTIVES

Increase the competitiveness of scientists in extramural grant programs.

- **$26,770,504** total CFAES funds awarded
- **$150,781,643** extramural/matching/agency funds generated
- **$6.48 : $1.00** return on investment (1998–2018)

Encourage the development of interdisciplinary teams.

- **10** colleges
- **31** departments
- **$9M** SEEDS funding
- **$30M** extramural funding

Encourage partnerships with industry and other stakeholders.

- Invested **$6 million** in projects requiring matching funds, generating **$9.4 million** in industry matches.

Encourage international collaborations.

- Provide undergraduate students with research experience.
  - Funded 73 undergraduate student projects out of 128 submissions.

- Provide graduate students with the opportunity to take part in the grant-writing/review process.
  - Funded 339 graduate student projects out of 844 submissions.
2018 IN REVIEW

The grants completed in 2018 represent:

- $1,002,324 invested by CFAES
- $2,434,139 in extramural funds received
- $143,450 in matching funds from industry partners
  - 19 publications and 18 presentations
  - 12 graduate dissertations/theses
  - 1 patent application
- A return on investment of $6.48 (five-year average)


Published 1,016 peer-reviewed scientific manuscripts, abstracts, popular press articles, bulletins, and/or book chapters.

Made more than 1,698 presentations throughout the world.

Obtained 14 patents, 26 invention disclosures, and 6 licensing agreements.

Funding percentage of 41% for faculty proposals.

Produced 86 doctoral dissertations and 124 master’s theses.
One College. Three Missions. All Ohio.

As a land-grant institution, the College of Food, Agricultural, and Environmental Sciences (CFAES) supports the industry by conducting research, training the next generation of agricultural leaders, and engaging stakeholders via OSU Extension.

One College. Three Campuses.

COLUMBUS
WOOSTER
STATEWIDE

Extension offices in each county. Outlying agricultural research stations.

CONTACT US
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THE OHIO STATE UNIVERSITY
COLLEGE OF FOOD, AGRICULTURAL, AND ENVIRONMENTAL SCIENCES

AWARDS AND SUBMISSIONS

475 Proposals submitted
478 Awards\(^1\) valued at
>$48 MILLION.

In fiscal year 18 CFAES had a total of 897 ACTIVE GRANTS.

RETURN ON INVESTMENT

\$1 \rightarrow \$5

INTELLECTUAL PROPERTY

$217,000 Total Licensing Revenue
5 New Patents Issued
27 Invention Disclosures
40 New Inventors

Agriculture is the \#1 industry in Ohio, contributing more than \$100 BILLION to Ohio's economy and employing 1 in 7 Ohioans. CFAES leverages over \$175 MILLION in grants and contracts from the public and private sectors, having a return on investment greater than \$5 for each state dollar invested.\(^2\)

GRANT EXPENDITURES

Funds spent on personnel, supplies, and services, reflecting the research activity of the college.

$41 MILLION

SPONSORED PROGRAM FUNDING SOURCES

42% Federal
28% State
12% Industry
9% Private Agencies
9% Other

Federal: legislatively authorized monies allocated to each state as a land-grant institution.

\(^1\)Extramural awards, contracts and cooperative agreements

\(^2\)According to the 2017-2018 Legislative Platform for the County Commissioners Association of Ohio.

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\(\text{THE OHIO STATE UNIVERSITY}\)
COLLEGE OF FOOD, AGRICULTURAL, AND ENVIRONMENTAL SCIENCES
ADVANCED BIOENERGY AND BIOBASED PRODUCTS

As the importance of renewable sources for energy and materials increases, research and industry partnerships come together in this area to develop biomass-based advanced energy technologies and value-added biobased products such as fuels, specialty chemicals, and fiber products.
Feasibility Analysis of a Novel Whole-Plant Feedstock Supply System for Co-located Corn Grain and Lignocellulosic Biomass-based Biorefineries

Ajay Shah, Food, Agricultural and Biological Engineering*

It’s a growing field, both literally and figuratively. Plants are increasingly being used to produce sustainable fuels and other materials. While the technology to convert the starch in corn to ethanol or the oil in soybeans to biodiesel is commercially viable, using other parts of plants is more challenging. Lignocellulose, the strong fibers that provide the support structure for most plants, is abundant and U.S. policy has set targets for its use in biofuels. However, lack of an efficient and cost-effective feedstock harvest and post-harvest handling and logistics system have limited its use. CFAES researchers are addressing these challenges.

At the Wooster Campus, CFAES researchers are developing and testing a novel feedstock supply logistics system that will improve the efficiency and costs of harvesting, baling, and transporting lignocellulosic biomass. The system focuses on using the whole corn plant, so that the grain, cobs, and stalks are not separated in the field but treated as a single package all the way to the biorefinery. This system addresses two major challenges of current feedstock supply systems that harvest, collect, and transport corn plant components separately. Separating corn grain in the field requires a combine, which is expensive and used only a very short time each year. By storing the whole plant on-farm or at centralized storage locations and delivering loads to the biorefinery throughout the year, a stationary grain separator can operate all year, thus reducing farm expenses and increasing equipment efficiency. Current transportation of only corn stover, the lignocellulosic component with low-bulk density, results in trucks meeting their volume capacity well before the weight capacity is met. Transporting bales of higher density whole-plant corn will increase trucks’ payload capacity and reduce costs.

To evaluate the feasibility of the whole-plant feedstock supply systems, CFAES researchers have conducted field-scale tests and systems analyses. They have collected corn plants at two moisture levels and tested different storage methods, including covered, uncovered, and use of preservatives, to determine which method minimizes dry matter loss. The researchers found that treating the bales with 0.5% propionic acid and storing them in anaerobic conditions resulted in less than 4% dry matter loss during nine months of storage. Analyses also showed little to no change in the biomass’ sugar content during storage.

Techno-economic analysis (TEA) of the whole-plant feedstock supply system indicated that it could reduce the number of combine harvesters, tractors, grain carts, and windrowers from current levels due to increased productivity and efficiency. In addition, the system was shown to increase the overall biomass bulk density of bales, thus reducing the number of annual truck trips for transportation, which was shown to potentially reduce the feedstock supply cost by up to 20% from the current level. This system could be used for other energy crops to further reduce the cost of producing biomass-based fuels and products.

*indicates lead investigator
ENVIRONMENTAL QUALITY AND SUSTAINABILITY

Work in this area seeks to understand, protect, and remediate the environment and ecosystems to ensure long-term sustainability. At the core of this effort is the realization that sustaining population and economic growth must be balanced with the preservation of natural resources and environmental assets.
Metabolic Responses of Austrian Pine to an Opportunistic Pathogen Under Drought Stress

Enrico Bonello, Plant Pathology*

A pathosystem is any combination of a living host with a given pathogen. Plant pathologists focus on the interactions between plants and pathogens rather than on one organism or the other in isolation to understand how they work together and figure out how to manage the resulting disease. Tree pathosystems are often made up of opportunistic fungi that develop into highly destructive pathogens only under certain conditions, such as low water availability, which can predispose the tree to infection. However, the molecular and metabolic mechanisms that affect tree susceptibility to pathogens remain poorly understood. This makes it difficult to predict how tree pathosystems will behave and evolve under projected climate change scenarios.

To determine how climate change may affect trees in their interactions with opportunistic fungal pathogens, Austrian pine was subjected to infection by an aggressive opportunistic pathogen, Diplodia sapinea, and a less aggressive sister pathogen, D. scrobiculata, under conditions of combined elevated temperature/drought stress (the climate change treatment). Each tree was sampled at three timepoints (12 and 72 hours, and 14 days), and then the amino acid concentrations, levels of soluble phenolics, and host and pathogen gene expression patterns near infected plant tissues were analyzed.

As expected, under “normal” climate conditions (regular watering; temperature range 15-28°C), D. sapinea was almost twice as damaging on Austrian pine as D. scrobiculata. Under climate change conditions (minimal watering; temperature range 20-33°C), D. sapinea became three times more pathogenic than in the control treatment, and D. scrobiculata became just as pathogenic as D. sapinea. These results suggest that under conditions of climate change, Austrian pine becomes significantly more susceptible to infection in general. Additionally, Austrian pine is susceptible to both aggressive and nonaggressive, closely related fungal pathogens.

While analyses are still ongoing, the data show profound effects in all of the host metabolic compartments, which potentially can explain the conditions of increased susceptibility. Among the most interesting discoveries is that host gene expression patterns in D. scrobiculata-infected trees transition from a state of growth to a state of defense only under conditions of climate change. This highlights a major trade-off in how trees cope with a pathogen under adverse climate conditions. Understanding how pathosystems are affected by climate change is important to ensure the future health of our forest ecosystems.
Ohio once contained a diverse and abundant array of wetland ecosystems including marshes, swamps, fens, and bogs. Peat bog ecosystems in Ohio are of significant conservation concern, as bogs can act as a “canary in the coal mine” for interactions between climate change and human disturbance. Many have been impacted by drainage, disturbance, and nutrient inputs from surrounding human land use, and less than 2% of Ohio’s bogs remain intact today. Unfortunately, we have little detailed knowledge of their status, history, or current condition. This is an issue, as the restoration of remnant peat bogs could help improve water quality, protect rare biodiversity, and control climate change.

The researchers’ broad aim was to understand how disturbance to bog ecosystems (from drainage, fire, peat mining, surrounding agricultural land-use, etc.) affects their ecological and environmental conditions. The project consisted of three main tasks:

1) assessing the differences in the environmental conditions (e.g., soil and water chemistry) found within and between different peat bogs with different levels of disturbance;
2) examining whether plants could be used as indicators of the environmental conditions found in bogs; and
3) testing whether populations of soil microorganisms and the greenhouse gases they produce (carbon dioxide and methane) differ between intact and degraded parts of a bog.

Researchers studied bog vegetation and soils on-site and in the lab. Results show that considerable variation in environmental conditions exists both within and between different bogs. The researchers observed strong influences from runoff and ground water at the edges of bogs, while the interior tended to be more nutrient-poor and acidic. Variation in water levels on the bogs showed similar trends across sites and seasons but was also influenced by the shape of the surrounding landscape.

Data also show that populations of soil microorganisms differed between bogs. There were big differences in the rate at which microbes produced greenhouse gases. Production varied with depth down through the bogs’ peat soils and between drained and preserved bogs. Excitedly, the researchers observed signatures suggesting that microbes were able to turn methane into carbon dioxide where no oxygen was present. This is a topic of considerable research interest at present and radically changes our understanding of how wetlands work. The field monitoring of greenhouse gases showed that disturbances, such as drainage, tend to reduce methane emissions. In the absence of disturbance, methane release was strongly tied to water depth and to the balance between methane-producing and methane-consuming organisms.

This work also showed that mosses make particularly good indicators of environmental conditions and could be used to help managers assess the condition of a bog. Many bogs showed consistent vegetation patterns from their edges to interior, and these were linked to differences in water table and water chemistry. Next, the researchers would like to gain a better understanding of the stocks of ancient carbon held by these ecosystems and to investigate in detail the mechanisms by which this is released to the atmosphere. Understanding how bogs hold (and release) carbon could help us learn how to harness these ecosystems to reduce global warming.
Evaluating Trade-Offs Between Improving Water Quality and Maintaining Biodiversity in Coastal Wetlands in the Western Lake Erie Basin

Lauren Pintor, School of Environment and Natural Resources*

Historically, wetlands have often been drained or filled for agricultural use or development of housing. In Ohio, most remaining coastal wetlands on the western Lake Erie basin are diked to control the water flow; however, this also limits important ecosystem functions such as water quality improvement and biodiversity support. Growing concern about the frequency and intensity of harmful algal blooms (HABs) has prompted the reconnection of coastal wetlands as one way to improve Lake Erie’s water quality. Great Lakes Restoration Initiative collaborations aim to restore and reconnect protected, diked wetlands in and adjacent to the Ottawa National Wildlife Refuge (ONWR). Reconnecting coastal wetlands to Maumee River and Lake Erie is expected to reduce nutrient inputs into the Maumee Area of Concern (AOC), reduce HABs, and benefit economically important fish and wildlife by increasing spawning, nesting, nursery habitat, and prey resources.

The goal of this project was to evaluate the changes in nutrient dynamics, macroinvertebrate biodiversity (indicators of water quality), and community structure following the reconnection of six coastal wetlands in the ONWR. Specifically, researchers compared the nutrient dynamics, macroinvertebrate diversity, and community structure between six restored and six unrestored (diked) wetlands in the ONWR. Current results suggest that unrestored wetlands had higher nutrient concentrations and lower diversity of macroinvertebrates, on average, than restored wetlands. However, increases in macroinvertebrate biodiversity and shifts in community structure were associated with higher nutrient concentrations across both restored and unrestored wetlands. Specifically, wetlands that had higher nutrient concentrations had a higher percentage of macroinvertebrate groups that are more tolerant of nutrient pollution than other species.

Monitoring water quality and wetland biodiversity post-restoration was an appropriate first step and goal, but it has been modest. Furthermore, the monitoring protocol was not designed to measure whether restoration and reconnection resulted in the increased ability to capture and retain nutrients. While this study provided a first step toward understanding how wetland restorations can be used as a management tool to reduce HABs in the Maumee AOC, more comprehensive and longer-term monitoring of wetlands within the ONWR is needed.
Climate change is expected to negatively impact the productivity of many agricultural plants worldwide. We must understand the degree to which crops are adapted or well-suited to the environments they presently occupy (and the genetic basis for that adaptation) in order to anticipate their fate with climate change. Areas of crop diversity, where landraces (or traditional varieties) and wild relatives of our cultivated crops thrive, are particularly important for this research. These places can provide genes that could be useful for adapting agriculture to a changing climate. However, they also act as living laboratories because genetic variation has been, and continues to be, shaped by natural and human-mediated evolution.

CFAES researchers planned to study the adaptation of the chile pepper to drought in southern Mexico, which is an important center of its diversity, where moisture availability varies over a diverse landscape. Researchers are trying to identify a genetic basis of drought tolerance in chile by combining observations of plant responses to drought with a molecular genetic analysis of diverse chile collections from known climatic conditions.

First, the researchers investigated how drought response varied among diverse chile landraces. Controlled laboratory and greenhouse experiments were done where researchers manipulated the moisture availability, then measuring seed, seedling, and mature plant responses. Preliminary analyses have confirmed the number of fruits produced in the greenhouse was dramatically affected by the drought treatment in some lines, but not all. Seeds of chile collected from different ecozones (geographical regions with distinct biodiversities of plants and animals) across southern Mexico exhibited different germination patterns under control and drought-simulating conditions. Specifically, chile seeds collected from drier ecozones were more likely to have slower germination under drought conditions than those from wetter ecozones. These results indicate that chile possesses drought-related adaptations at both the seed and mature plant stages.

The second step was to determine regions of the chile pepper genome that might encode drought tolerance. Researchers related variation in the environment of origin of the chile collections with genetic variants at thousands of points along the genome. In preliminary analyses, researchers identified many significant genetic variants, some of which were confirmed to also relate to variation in plant performance in the greenhouse when challenged with drought. Thus, these genetic variants could play a role in abiotic stress tolerance.

Drought Tolerance in Chile Pepper (*Capsicum annuum*): The Genetic Basis of Adaptation to Drought in a Center of Crop Diversity

Kristin Mercer, Horticulture and Crop Science*
FOOD SECURITY, PRODUCTION, AND HUMAN HEALTH

This area focuses on improving agricultural production; enhancing the quality of food and feed; ensuring an adequate, affordable, and safe food supply; and maintaining agrosecurity to ensure food security and the basics of nutritional health for a growing global population.
Genetic and Nutritional Strategies to Enhance Yellow Perch (*Perca flavescens*)

Performance on Soy Protein-based Diets

Konrad Dabrowski, School of Environment and Natural Resources*

Michael Davis, Animal Sciences

Macdonald Wick, Animal Sciences

Richard Bruno, Human Nutrition

The global demand for seafood continues to increase. While wild-caught fish production has remained stagnant since 1985, aquaculture (fish farming) production has grown rapidly. In 2014, aquaculture production rose to around 81 million tons of fish, compared to 28 million tons in 1995. However, the aquaculture industry still struggles to meet the demand of consumers due to the high cost of fishmeal (FM), the major protein source in fish feed. The primary solution to reduce costs has been to replace dietary FM with plant proteins.

One CFAES laboratory has been looking for an alternative, low-cost diet formulation that allows for the optimal growth and health of yellow perch by using soybean meal (SBM), one of the most promising plant-based protein sources. First, researchers nutritionally programmed with an SBM-based diet juvenile yellow perch (F1 generation), whose parents (F0) were also programmed with the same diet. Nutritional programming was done by feeding juveniles an SBM-based diet as their initial formulated feed for 60 days. Fish were then fed an FM-based diet for nine months, and were then transferred back to the SBM-based diet for another nine months. Growth and survival were then measured. By exposing the fish to the SBM-based diet as their first feed, it is hypothesized that the fish create a “memory” to this diet, thus being nutritionally programmed.

Previous literature has shown that SBM can cause inflammation in the intestines of fish, ultimately hindering their health and growth. Therefore, the second goal was to determine the molecular changes in the juvenile yellow perch after their initial exposure to formulated diets (FM or SBM). Using RNA sequencing, which takes a molecular snapshot of a specific tissue, the researchers were able to compare the expression differences of over 15,000 genes in fish intestines after being fed FM- or SBM-based diets.

From the RNA-sequencing data, researchers were able to focus on 65 of the top genes that were differentially expressed between the FM- and SBM-fed fish. Of these genes, 40 were up-regulated in fish fed SBM, with most of the genes found to be associated with the cholesterol biosynthesis pathway. Other genes with up-regulated expression (function) were found to be involved in fat metabolism and transport, glycoprotein metabolism, and cellular transport. Genes that were down-regulated in the SBM-fed fish were those involved in inhibitory regulation of the inflammatory immune response, cellular growth and division, and cell death.

The results generated in this study have brought researchers closer to replacing the majority of FM with SBM in aquafeeds, while still maintaining a high-quality fish with similar (if not better) growth than FM-fed fish. Additionally, the nutritional programming phases can be used as a model for other fish species to incorporate higher levels of SBM or other plant proteins into diets. This would result in a more sustainable, less expensive way to produce fish in aquaculture.
Process to Eliminate the Allergenicity of Milk Proteins by Combination With Phospholipids Using Supercritical CO2 Environment

Rafael Jimenez-Flores, Food Science and Technology*
Balasubramaniam, V.M., Food Science and Technology

Over 50 million Americans suffer from allergy symptoms each year, ranging from sneezing, itching, and watery eyes to death in rare cases. Allergies occur when the body’s immune system overreacts to a foreign substance, such as pollen, leading to these nuisance symptoms. Food allergies are among the most common, with milk allergies at the top of this list. Discovering new methods to reduce allergic reactions would be beneficial to consumers and would have applications across the food industry.

The goal of this project was to develop a process to eliminate allergic reactions caused by milk proteins. The main allergen in milk, Beta-lactoglobulin (bLG), has been extensively studied, so researchers know how and when it denatures (loses its structure). However, little information is known on its antigenic properties or about protein denaturation in substances other than water. Supercritical CO2 (pressurized carbon dioxide that behaves like a liquid) offers a novel method to treat and denature proteins. In addition, the media is highly hydrophobic, meaning that it does not mix with water, which makes the reactions highly different from those in water. Therefore, the researchers sought to explore this novel processing method to determine its viability in buttermilk.

The researchers detected a remarkable change in bLG after processing with supercritical CO2: Its molecular weight had changed dramatically, which indicated a profound change in structure. This structural change due to complex oligosaccharides (sugars) being added to the protein seems to be extremely important in reducing the reaction of the protein with the antibody. This is an important link between food and health, with great potential to reduce allergic reactions to food. Since an allergic reaction is caused by the interaction of an antibody (made by the living organism) and the antigen (the protein/food that is the cause of allergic reaction), this processing method could lead to a reduction in or eliminate some allergic reactions that many people experience.
Characterization of Avian Enteric Inflammation Models to Further Facilitate Study of Host-Microbiome Interactions
Lisa Bielke, Animal Sciences*

The gastrointestinal (GIT) microbiome is a dynamic population, well known for its influence on enteric inflammation and integrity. Immunization of the GIT with microbes begins at birth. Emerging evidence suggests that microbial populations can influence the ability of GIT tissue to maintain itself. This may play a major role in the control of infectious diseases, allergies, autoimmune diseases, type 1 diabetes, asthma, and chronic gastrointestinal inflammatory disorders.

CFAES researchers used a chicken model to determine how microbes impact GIT and immune system development. Birds offer a unique opportunity to control intestinal microbial populations through in ovo (in egg) delivery because the GIT of a prenatal chick is essentially free of bacteria. Additionally, eggs are nearly sterile and it is possible to introduce bacteria to promote overwhelming colonization with specific bacteria just before hatch. First, multiple tests were performed to determine the best inoculation procedures. Then, researchers completed a study during which chicken embryos were exposed to various types of bacteria just before hatching. GIT were collected from chicks on the day of hatch, three days later, and at 10 days of age to determine changes in the microbiome and GIT tissue development.

The greatest microbiome differences between samples were observed on the day of hatch and were heavily influenced by the bacteria with which the researchers inoculated the egg. For example, chicks exposed to Lactobacillus had high levels of this genus in their gut at the time of hatch. However, by three days of age, those differences were eliminated. Concurrent GIT tissue samples revealed that this bacterial inoculation did alter the development of the immune system. Antioxidant activity was increased, and inflammation was decreased in chicks inoculated with Lactobacillus, and some gram-negative, bacteria-treated chicks experienced increased inflammation. This indicated that pioneer colonization of the GIT impacted immune system development.

Continued plans for this research involve evaluating tissue samples for changes that might aid in digestion. These results will assist in developing methods to select different types of probiotics that can promote proper immune system development in young humans and animals. They also provide the groundwork for scientists to continue studying the role of the microbiome in health and well-being. These research strategies might provide a means by which to investigate the role of the microbiome in the development of food allergies and GIT disorders such as Crohn’s disease and irritable bowel disease, which affect millions of people worldwide.
Partial and Total Replacement of Fish Oil With Fatty Acid Ethyl Esters in the Diet of Rainbow Trout

Konrad Dabrowski, School of Environment and Natural Resources*

Fish oil is a necessary dietary ingredient for meeting the polyunsaturated fatty acid (PUFA) requirements for fish diets. Most of the global supply of fish oil comes from marine forage fish, with 85% of all fish oil produced used in aquaculture feeds. Many marine fish populations used to supply fish oil are harvested at or above their sustainable limit, leading to a decline in population and a rise in fish oil prices. This has created a strong interest in finding a replacement for the PUFA source in aquaculture feeds. Fatty acid ethyl esters (FAEE) are a lipid form created for the production of concentrated PUFA oils, and FAEE byproducts could be used to replace fish oil in animal feeds. This research project investigated the replacement of fish oil with FAEE oil in the starter feeds of rainbow trout fry.

In order to study the viability of FAEE oil, five experimental diets were formulated using Alaskan pollock oil, FAEE oil, or graded levels of both products as the lipid (fat) source. The fatty acid concentrations were very similar between the diets. Rainbow trout (144 mg/fish) were added to tanks with an initial density of 60 fish per tank. Three tanks were assigned to each experimental diet, then fish were weighed and sampled after 31, 62, and 70–76 days of feeding. Afterward, researchers analyzed body lipids and gut tissues to better understand how the diets affect fish performance (growth rate, survival).

The replacement of fish oil with FAEE oil did not have a significant effect on fish survival, body lipid levels, or body fatty acid concentrations at the end of the feeding period. The replacement of fish oil with FAEE oil at 50% or higher caused slower growth during the first 31 days of feeding, but this trend was diminished in the 31–62 day feeding period. Analysis of fish intestines and livers showed lower lipid accumulation when fish were fed the high FAEE diet, which suggests that this lipid form is not as digestible as whole fish oil. The results suggest that FAEE oil can be used to replace 25% of fish oil within experimental diets without having a significant effect on fish growth.

Future studies should examine fish growth at different life stages and should analyze digestive enzyme activity associated with high FAEE diets. In addition, diets should be tested that include more phospholipids, as they have been shown to increase the digestibility of other lipid forms. Aquaculture feed producers can use this study to make more informed decisions about replacing fish oil with FAEE products in their feeds. Future research plans include using FAEE products in larval and juvenile yellow perch as part of live food enrichment. This replacement would reduce feeds costs and decrease reliance on wild fish to meet aquaculture needs.
Understanding the Role of Abscisic Acid on the Acquisition of Freezing Tolerance in Grapevines

Imed Dami, Horticulture and Crop Science*
Joshua Blakeslee, Horticulture and Crop Science

The grape-wine industry is a fast-growing sector of Ohio agriculture, contributing $1.3 billion to the economy each year. However, the sustainability of this industry is limited by climatic constraints, primarily seasonal freezing temperatures. In the United States, cold damage is by far the most devastating weather event to fruit production, including grapes. In recent years, cold damage has accounted for about $250 million per year of insurance payments for crop loss to grape and fruit growers. For example, in 2014, the “polar vortex” event caused unprecedented crop and vine losses valued at $12 million in Ohio.

The long-term goal of this research is to develop novel strategies to increase freezing tolerance (FT) and reduce freezing damage in grapevines. In this project, we investigated the role of the plant hormone, abscisic acid (ABA), on FT in grapes. Greenhouse-grown grape varieties were sprayed with ABA and compared to untreated (control) vines over time. Vines sprayed with ABA closed their stomates (openings on leaves) within hours, and they remained partially closed for nearly two weeks. This stress response is typical in plants and resulted in a cascade of responses in treated vines, including increased expression levels of genes responsible for ABA and sugar biosynthesis. These results suggest that externally applied ABA might positively regulate internally produced ABA biosynthesis. ABA-treated vines entered dormancy earlier, had a lower bud water content, and had a higher FT than control vines. Total sugars increased over time in both control and treated vines, but some individual sugars were higher in treated vines. A group of sugars, called raffinose oligosaccharides (RFO), were higher in ABA-treated vines than in the control group. It is known that tissue dehydration and RFO accumulation lead to increased FT. Based on these results, it appears that the increase of total sugars is a general vine response and that ABA might regulate tissue dehydration via RFO accumulation. The findings from this research have increased the knowledge of the regulatory roles of ABA and sugars on the early cold acclimation responses and will ultimately help develop new strategies to reduce freezing damage, thus enhancing the economic and environmental sustainability of grape production in cold regions.
Evaluation of Jersey Crossbreeding Opportunities for a New, High-Value Beef Market Product for Domestic and Export Markets

Francis Fluharty, Animal Sciences*
Jerad Jaborek, Animal Sciences

Jersey bull calves are a byproduct of the dairy industry. They are a desired breed because their milk has a high butterfat content; however, they tend to be small-framed, slow-growing, and finely-muscled. This makes them undesirable to the commercial feedlot industry, meaning that Jersey producers receive little to no income for selling their bull calves at market. While Jersey cattle numbers continue to rise in the United States, fed dairy steers and cull cows contribute approximately 25% of the U.S. beef supply. Therefore, CFAES researchers saw an opportunity to implement a crossbreeding strategy between Jersey cows and beef-breed bulls to try to improve the feedlot performance and carcass quality of the resulting calves. The experiment compared the use of a Jersey sire versus a sire from one of three different beef cattle breeds: Angus, SimAngus, and Wagyu. Calves produced by terminal beef sire were expected to have a faster rate of body weight gain, more muscling, heavier carcass weights, and greater USDA carcass-quality grades compared with the full-blood Jerseys. Creating a high-value beef product is expected to increase the demand (and price) for these calves, creating more income for Jersey producers.

Over the course of two years, Jersey full-blood and crossbred calves were fed diets containing the recommended amount of nutrients for optimum growth based on their age. Calves were started on a receiving diet at 30 days, switched to a growing diet at 70 days, switched to a finishing diet containing corn silage at 100 days, and switched to a final finishing diet containing soy hulls for the remainder of their time in the feedlot. Each diet change added energy by replacing corn silage with additional corn grain. When the cattle reached an adequate body weight and back-fat thickness based on market requirements, they were removed for harvest. Cattle were harvested at Ohio State's meat lab, and carcass measurements were obtained after chilling in the cooler for seven days. Because Jersey heifers were not a part of the study, as they will be used as replacement females in the dairy herd, two models had to be used to analyze the data. One model compared Jersey-, Angus-, SimAngus-, and Wagyu-sired steers. The second model compared steers and heifers from Angus-, SimAngus-, and Wagyu-sired cattle.

Results show that the carcasses from terminal beef breed calves had larger ribeye areas and generally produced higher marbling scores and USDA-quality grades when compared to Jersey-sired carcasses. Carcasses from Angus-sired steers produced the highest quality, with Wagyu- and SimAngus-sired steer carcasses being intermediate. Thus, researchers determined that the use of all three terminal sires could be used to improve upon the value of Jersey bull calves to be fed in the feedlot to produce high-quality beef when compared to purebred Jersey bull calves. Jersey cow producers can use these findings to increase the value of their Jersey cows.
Optimizing Nutritional Support to Maintain Gut Barrier Function in the Developing Neonate

Sheila Jacobi, Animal Sciences*

Mortality in pigs suffering from intestinal diseases is high. It is estimated that diarrheal diseases cause 10% of deaths of preweaned pigs, and 83% of U.S. swine producers surveyed have significant problems with diarrheal diseases. Dietary nutrients play a significant role in enhancing health and preventing diseases in animals. Therefore, getting young animals started with a healthy intestinal environment is key to optimizing early production efficiency. The goal of this research was to understand how specific dietary nutrients and their interactions enhance healthy intestinal development in young pigs. In addition, the researchers wanted to determine how dietary nutrients affect the development of intestinal diseases and progression, and if specific nutrients could be used to reduce the impact of intestinal diseases, thereby enhancing the production efficiency and welfare of domestic livestock.

Many studies have shown how individual nutrients can impact intestinal health, but understanding how multiple nutrients interact to impact intestinal and overall animal health has not been as closely studied. This research looked at how dietary fatty acids (long-chain polyunsaturated fatty acids) and prebiotics affect the impact and reaction of pathogenic bacteria that cause diarrhea in swine. Specifically, researchers looked at the intestinal barrier's form and function after exposure to a pathogen when treated with dietary fatty acids and prebiotics.

Researchers determined that long-chain polyunsaturated fatty acids and prebiotics have independent, possibly additive, effects on intestinal barrier function proteins involved in maintaining a healthy intestine when used prior to pathogenic infection. This piglet intestinal model has allowed us to understand the concentration of individual nutrients in the intestine, which are effective in the maintenance of the intestinal barrier function.

The next step is to further investigate the interaction of long-chain polyunsaturated fatty acids and prebiotics in production and then determine the impact on intestinal health, the developing intestinal microbiome, and the animal’s immune system development. The researchers will repeat the in vitro experiments from this project to verify their results in the model system, as well as move into small, on-farm pilot studies to determine the efficiency of protective effects of the nutrients on piglet intestinal diseases. If successful, this could prove to be a highly beneficial solution, increasing the production efficiency and welfare of the animals.
Bacteriophage-Driven Emergence of Shiga Toxin-Producing *E. coli* Strains

Jeffrey LeJeune, Food Animal Health Research Program

The bacteria *Escherichia coli*, or *E. coli*, are commonly present in the intestines of people and other warm-blooded animals. Typically, *E. coli* strains play an important role in health, but occasionally, this group of bacteria can cause serious illness and even death. Shiga toxin-producing *E. coli* (STEC) are a particularly dangerous group of *E. coli* that causes an estimated 250,000 cases of illnesses annually in the United States. An organism can cause symptoms ranging from diarrhea and vomiting, to life-threatening kidney failure and death in rare cases. Prior to 1982, STEC-causing human illnesses were rarely found; however, over time, more cases have been identified. It is hypothesized that the emergence of STEC as an important foodborne pathogen is in part due to nonpathogenic strains of *E. coli* acquiring the Shiga toxin gene (*stx*). Previous research has shown that bacteriophages can carry this gene and transfer it when infecting *E. coli*, creating a new strain of *E. coli* that now produces the toxin.

Understanding where foodborne pathogens come from provides insights about how to prevent and control food contamination. In this context, the researchers set out to determine the extent that *stx*-encoding bacteriophages were present in the food chain. These data would provide clues as to how likely and where new pathogenic strains of *E. coli* might emerge.

STEC bacteria were discovered in several samples of beef and herbs. Often, many different strains of *E. coli* with *stx* can be found in the same sample. In addition to STEC bacteria, we also found bacteriophages encoding *stx* in these same samples. This provides evidence that the virus containing *stx* is responsible for spreading the *stx* gene among *E. coli* strains in foods. During the course of this research, we also identified new bacteriophages that were responsible for spreading genes that make *E. coli* resistant to antibiotics. Additional research, including DNA sequencing, is required to further substantiate this hypothesis of bacteriophages being responsible for the emergence of new strains of STECs in food animals. This information is critically important because it will allow us to develop or change food production and processing methods in such a way that this type of new pathogen emergence is minimized, making food safer for all.
Development and Validation of Biomarkers for Bull Fertility

Kichoon Lee, Animal Sciences*

Beef and dairy farmers are facing monetary losses due to infertility and poor fertility. Reproduction at cattle farms is regularly performed by artificial insemination (AI), and the success of AI often depends on semen qualities. Quality indicators can be found in a group of genes found among various tissues in the testis. However, no background information is available on testis-specific genes and their expression patterns in the cattle.

CFAES researchers focused on identifying testis-specific genes by analyzing gene expression databases for humans and mice, because they are similar to the genes in cattle. Throughout the project, gene expression databases, combined with confirmatory measurements, were used to investigate testis-enriched genes, protein localization in the testis, developmental regulation of gene expression, gene expression profiles of testicular disease, and signaling pathways to develop reliable biomarkers for high fertility in male bulls.

A comparative analysis of gene expression databases revealed that 24 genes are predominantly expressed in the testis. Cellular locations of 15 testis-enriched proteins in the human testis have been identified. Further analysis revealed that expressions of these 15 genes are significantly increased during testis development. It also indicated that expressions of these 15 genes were significantly decreased in teratozoospermic—sperm with abnormal morphology affecting fertility—patients, suggesting their involvement in normal testis development. Pathway analysis revealed that most of those 15 genes are implicated in various sperm-related cell processes and disease conditions. This approach paves the way for future characterization of gene functions regarding infertility and providing new biomarkers for specific stages of spermatogenesis.

Researchers recently created knockout mice—mice that have been genetically modified to not express a certain gene—to investigate their role in spermatogenesis and male fertility. They believe that several of these new testis-specific genes will be eventually selected and serve as reliable biomarkers for male fertility in the bull. This would ultimately create a more effective way to test for bull fertility and increase success of cattle reproduction.
Assessing the Impact of Ohio Wheat Viruses
Pierce Paul, Plant Pathology
Lucy Stewart, Plant Pathology

Ohio is one of the leading producers in the United States of soft red winter wheat (SRWW); however, low profitability due to environmental and biological stresses has led to a decline in the number of acres of wheat planted. This decline has not only impacted the wheat industry, but it has also impacted corn and soybean production because having wheat in the rotation helps improve soil quality and minimizes pest and disease problems. Viruses can cause yield-reducing stresses, and the impact is often underestimated because virus-related problems in wheat are often not diagnosed or are misdiagnosed as abiotic stresses such as nutrient deficiency. Regionally, virus diseases cause an estimated 7–10% yield reduction in wheat every year, though some viruses may reduce yields over 60%. Results from surveys of Ohio wheat fields showed that viruses were detected in 32–95% of fields sampled, but their impacts on wheat growth, grain yield, and quality are largely unknown.

An understanding of which viruses are most prevalent in the state, and how they spread and impact wheat is important for developing effective strategies to minimize losses caused by these pathogens. This study aimed to conduct a comprehensive survey of Ohio wheat fields to determine the prevalence and distribution of wheat viruses in the state; screen Ohio-grown SRWW cultivars for susceptibility to several of the viruses detected in the survey; and evaluate the effects of the most prevalent viruses on wheat development, grain yield, and yield components.

Surveys were conducted in March and April of 2016 and 2017 across 20 Ohio counties in the main wheat-growing regions of the state. Wheat leaves and leaves from grassy weeds adjacent to wheat fields were brought back to the lab and tested for viruses. Then, 18 of the most commonly-grown SRWW cultivars were tested for susceptibility to several of the viruses found in the survey, including barley streak mosaic virus (BSMV), brome mosaic virus (BMV), and wheat streak mosaic virus (WSMV). Finally, the effects of BMV infection at early and late growth stages on wheat growth and grain yield were quantified in field experiments in 2016 and 2017. Greenhouse experiments were also conducted to evaluate the effects of WSMV and BSMV on yield components.

At least five viruses that are new to the state of Ohio were detected, including cereal yellow dwarf virus, barley yellow dwarf virus, wheat spindle streak mosaic virus, and wheat streak mosaic virus. All tested SRWW cultivars were susceptible to infection by WSMV, BSMV, and BMV; however, disease severity and impact was variable depending on the virus and the cultivar. Results from the field experiments showed that BMV reduced grain yield by up to 61% when infections occurred in the fall, and by as much as 25–36% when infections occurred in the spring. The magnitude of the yield reduction varied among cultivars and was associated with reductions in grain size and weight or plant population. These findings suggest that WSMV, BSMV, and BMV could impact wheat productivity in Ohio. The results will also serve as the basis for more large-scale investigations of the effects of these viruses in commercial fields.
Flavor Molecules in the Fight Against Stress

Christopher Simons, Food Science and Technology*

In the United States, stress levels are higher than what is believed to be healthy, and many individuals are ill-equipped to effectively reduce daily stress. One leading cause of stress is linked to the challenges of balancing too many responsibilities and activities associated with daily living. Multitasking causes stress when demand exceeds abilities. With increasingly demanding lifestyles, there is a need for additional methods to control stress. Various agricultural products have anti-stress properties, leading to the potential development of innovative and novel functional foods to combat the growing effects associated with stress from multitasking. However, before functional foods can be made, an experimental framework needs to be developed that can be used to assess the stress-relieving properties of agricultural products.

Lavender aroma has shown to be effective at reducing stress, so CFAES researchers assessed whether linalool, the active compound in lavender aroma, can reduce stress if consumed as part of a flavored beverage. The researchers developed a test that requires a volunteer to play two video games simultaneously. This task increases the feelings of stress (caused by multitasking) and leads to measurable physiological indicators such as heart rate, skin conductance, and salivary-amylase (a protein found in saliva). The researchers measured stress-related feelings and physiological indicators while either (1) simultaneously inhaling linalool or (2) after consuming a linalool-flavored beverage.

Researchers found that linalool entered the blood and was metabolized more quickly when inhaled (20 minutes) compared to when ingested as a beverage (37 minutes). Inhaled linalool had significant effects on physiological stress markers, although reported stress-related feelings were unaffected. When ingested in a beverage, linalool had only modest effects on physiological indicators of stress.

This lack of reported effect could reflect linalool blood plasma concentration differences resulting from different delivery routes (oral or nasal) or the different way linalool is metabolized. It may also reflect non-optimal timing between the ingestion of the beverage and the onset of the stressor.

These results provide evidence that linalool affords stress-relieving properties when inhaled. The development of anti-stress functional foods will require further effort to optimize delivery and timing conditions relative to the stressor. Nevertheless, researchers have validated the experimental framework to assess the anti-stress properties of agricultural products related to a multitasking stressor. This framework is convenient, low-cost, and works in a laboratory setting. Future studies will look to assess the impact of other natural compounds reported to have anti-stress properties, such as apigenin (from chamomile) and ligustilide (from angelica root or celery seed).
Impact of Frozen Storage on the Quality of Poultry Meat

Macdonald Wick, Animal Sciences*

Warehouse operators and consumers can benefit from reducing energy consumption throughout the supply chain of foods that must be frozen. Reduced costs along the supply chain can lead to a less expensive end product. Energy consumption can be reduced by 3% for each 1°C increase in temperature; however, it is uncertain how this might affect meat quality.

To determine the effects of an increased storage temperature on meat quality, chicken breasts were placed into one of nine freezers, each set to one of three temperatures. Over one year, CFAES researchers randomly analyzed the breasts for processing and quality characteristics, from each freezer. Statistical analysis focused on the differences among the temperature groups, as well as the relationships among the analytics to gain a better understanding of the observed phenomena.

Results of the study primarily revolved around changes in each chicken breast’s water component. The maximum drip loss volume—a measurement of water holding formed during the thawing process—was dependent on the storage temperature, where the warmest condition produced the most water loss. The ability of the chicken breast to be able to pick up brine increased with warmer storage. The hardness of the cooked breasts increased more rapidly at the warmer storage temperatures. Lastly, the measure of rancidity was unchanged throughout the study likely because the fat content is extremely low in chicken breast.

These data supported the hypothesis that raising the temperature of frozen meat storage would save energy with little or no negative impact on meat quality. Experimentally executing continuous and consistent testing protocols became one of the most significant achievements throughout this project. These testing strategies and protocols will be used in future studies. A similar study, focused on ground beef, obtained more success due to the experience gained here. Other areas of interest lie in refrigerated and frozen egg protein quality, as well as plant-based and mycoproteins as they enter into the mainstream food market.
One of the biggest challenges for agriculture is increasing food production to feed the world population, which is predicted to approach 10 billion by 2050. Plant diseases caused by diverse pathogens can significantly reduce food quality and production and lead to huge economic losses. For example, the bacterial pathogen *Pseudomonas syringae* and the fungal pathogen *Botrytis cinerea* infect a large variety of plants, are very difficult to control, and can result in significant economic losses. Additionally, the applications of chemicals to control the related diseases can be harmful to the environment and human health. One powerful approach to secure the plant production and meanwhile reduce the risk to the environment is to develop the broad and long-lasting plant disease resistance against diverse pathogens. This project focuses on members of the Acyl Carrier Protein (ACP) family of the model plant Arabidopsis, including ACP4 and ACP1. The goal is to gain a detailed, mechanistic understanding how these proteins function in disease resistance against diverse pathogens such as *P. syringae* and *B. cinerea*.

CFAES researchers discovered that a gene encoding an adenosine diphosphate (ADP) ribosylation factor (ARF) guanine nucleotide exchange factor (GEF) protein is involved in plant cuticle formation. The plant cuticle is the outermost layer of a plant that interacts with the environment and protects the plant from water loss and various biotic and abiotic stresses. However, its active roles and related mechanisms are not well-studied. Researchers identified that function of this ARF-GEF gene and ACP4 function cooperatively in plant disease resistance against both bacterial and fungal pathogens. This novel genetic linkage will facilitate the development of the strategies to enhance plant health and yield through genetic manipulation of the plant cuticle. CFAES researchers also identified and characterized ACP1 as a novel, negative regulator of plant defense. The ACP1 protein was shown to play a critical role in broad-spectrum disease resistance and to interact with a previously unstudied protein. The function of this novel complex in regulating plant disease resistance will be the topic of further investigation.

Thus, the current results and future studies will provide insight into the mechanisms of how ACP and associated proteins contribute to disease resistance. This study has great potential to inform strategies for controlling diverse plant diseases, initially in Arabidopsis. Subsequent translation of the findings into other plant systems, such as tomatoes, will contribute to disease control, thus reducing chemical application and benefitting the environment and human health.
The brown marmorated stinkbug (BMSB) is a serious invasive insect pest in North America that was first detected in Ohio in 2009. It feeds on a wide range of agricultural commodities including fruits, vegetables, and field crops (such as corn and soybean). Crop producers lack suitable options for control, and only a limited number of chemicals can be used across all crops. This can accelerate pesticide resistance by increasing stinkbug exposure to the pesticide, making the pesticides less effective. Therefore, new control strategies are necessary to ensure a safe and productive food supply.

In order to develop more effective and specific pest control, CFAES researchers focused on gut bacteria in the BMSB, specifically the primary bacterial symbiont, Candidatus "Pantoea carbekii" (hereafter P. carbekii). Using electron and fluorescence microscopy approaches, the researchers found that adult female BMSBs smear a solution of P. carbekii on the surfaces of eggs. When the nymphs hatch, they feed on the eggs and solution to obtain P. carbekii.

Then researchers wanted to determine how P. carbekii affected the BMSB, so they selectively removed the symbiont from some insects. Researchers determined that BMSB mass increased without P. carbekii and the amount of certain amino acids differed when the symbiont was removed, suggesting a nutrition imbalance. This supports the hypothesis that the bacterial symbiont P. carbekii provides nutrients to the BMSB. Researchers also sequenced gene expression from the BMSB with and without P. carbekii to see if both species coordinated to produce important amino acids. In the absence of P. carbekii, certain amino acids were not as highly expressed.

Finally, researchers sequenced the complete genome of P. carbekii itself, allowing identification and prediction of physical pathways that might be coordinated between the symbiont and its host. The researchers were able to develop experimental protocols that facilitate testing, using RNA-interference (RNAi). Using this method, three BMSB genes that help in detoxifying chemicals (such as insecticides) were effectively silenced. Although this did not lead to observable changes in P. carbekii, the work confirmed that RNAi can be used to silence BMSB genes. Future methods might include novel mechanisms via plants that can cause RNAi in BMSB.

Currently, the researchers are investigating and validating changes in gene expression when P. carbekii is removed. These will be prime gene candidates to better understand the coordination between BMSB and P. carbekii, and to evaluate for novel targets of control using RNAi in the future.
STUDENT PROJECTS

The CFAES Undergraduate Research Competitive Grants program, funded to a maximum of $3,300 per award, provides undergraduate students with a professional grant-writing, research, and reporting experience. Projects are designed, submitted for review, and carried out with a faculty member.

The Graduate Research Competitive Grants program offers two levels of funding. Single investigators may receive up to $5,000 per award, and team projects up to $10,000. Graduate students who receive awards are asked to serve on a panel to review applications in the following year’s competition. This experience provides students with an opportunity to develop their grant-writing and reviewing skills, which are essential to their careers.

Laura Hopkins  Allison Labyk  Michael Dzakovich

*Alan Coburn Not Pictured
Every day, approximately 23,000 individuals around the world lose their battle with cancer. It is estimated that 30% of all cancers are linked to dietary and nutritional factors. Plants produce an array of compounds known as phytochemicals, which can serve as vitamins, vitamin precursors, or simply be associated with favorable health outcomes. In tomatoes, prominent examples are carotenoids, which give tomatoes their vibrant color, and their consumption is associated with a decreased risk for developing various chronic diseases. After consumption, carotenoids and their breakdown products (apocarotenoids) accumulate in the liver (the primary metabolizing organ). Recent evidence suggests that these compounds might protect against many diseases including liver cancer by altering gene expression. Tangerine tomatoes are a naturally-occurring variant that accumulate unique carotenoids that are absorbed more efficiently from the diet relative to those found in red tomatoes. However, it was unknown 1) what apocarotenoids these tomatoes produce and 2) if the chemical landscape and gene expression of the liver are affected as a result of tomato consumption or tomato type.

To address these gaps, mice were fed standardized diets with either 10% red, 10% tangerine, or no tomato powder for 35 weeks. A high-performance liquid chromatography and mass spectrometry method was developed to separate and quantify carotenoids and apocarotenoids from mouse livers. We found that all mice had quantifiable levels of apo-13-carotenone, including the control-fed animals. Based on its chemical structure and its presence when consuming a carotenoid-free diet, it is hypothesized that apo-13-carotenone is derived from Vitamin A. Apo-13-carotenone can act as a retinoid receptor antagonist, which might have metabolic consequences. Additionally, new—not previously described—apocarotenoids were found in tangerine tomatoes, likely formed from the unique carotenoids present in those fruits. Gene expression in response to diet was also examined in the liver. RNA sequencing experiments determined that genes related to metabolizing phytochemicals were upregulated differently depending on whether mice consumed red tomatoes, tangerine tomatoes, or no tomatoes at all.

Moving forward, our team plans to conduct further metabolomics experiments with the mouse liver tissue. Our goal is to gain a more complete picture of the chemical landscape of the liver and how it is changed as a function of tomato type or tomato consumption, in general. Ultimately, the gene expression data and metabolomics data will be integrated to reveal novel gene-diet relationships. The eventual goal is to gain a more comprehensive understanding of how different tomato phytochemicals affect the function of the liver and leverage that information to develop tomatoes and/or tomato products that can prevent certain diseases.
Project SWEAT (Summer Weight and Environmental Assessment Trial): Summer Weight Gain and Learning Loss in Underserved School-Age Children (MASTER’S AND DOCTORAL TEAM)
Laura Hopkins, Human Sciences
Allison Labyk, Human Sciences
Carolyn Gunther, Human Nutrition (Advisor)

There is a notable body of literature documenting unhealthy summer weight gain in school-aged children. Various subpopulations such as children that are already overweight or obese, black children, Hispanic children, or female children might be at an increased risk. It has also been well-documented that summer is a vulnerable time for learning loss, with great disparities existing based on socio-economic status. Summer programming has been suggested to help overcome these disparities and protect these children from both unhealthy weight gain and learning loss. However, if and to what extent there might be a relationship between weight status and academic achievement changes before and after summer has not been explored. Our study was a substudy within a body of larger, multistate, observational research called Project SWEAT, and it was the first to examine this relationship. The specific aims of our study were to:

• determine the relationship of BMI with academic achievement during the summer months among a racially and ethnically diverse sample of underserved, school-aged children.
• determine if and to what extent the relationship between BMI and academic achievement during the summer months is influenced by participation in daily structured programming, such as the USDA’s Summer Food Service Program (SFSP), among a racially and ethnically diverse sample of underserved school-aged children who are and are not engaged in programming.
• examine the underlying dietary factors that might explain the potential protective effect of participation in daily structured programming, such as the USDA’s SFSP, on BMI and academic achievement among a racially and ethnically diverse sample of school-aged children who are and are not engaged in programming.

Project SWEAT was a prospective, observational study. In summer 2017, two elementary schools enrolled in Project SWEAT, and 113 participants took part in the main study. From this main study sample, a subset of participants (62) was invited to take part in a more in-depth Project SWEAT substudy. The relationship between summer weight status and learning outcomes was assessed on the Project SWEAT substudy sample. Data were collected at four timepoints from May/June 2011 through November 2017. These data included height and weight to calculate BMI z-score (zBMI); blood pressure to calculate systolic and diastolic blood pressure z-score (zSBP and zDBP respectively); demographic information including child age, gender, and race/ethnicity; household income; learning outcomes; child attendance at structured programming; and dietary intake.

Results found that:
• school-aged children from low-income households experience consistent declines in learning over the summer months.
• significant increases in zBMI were observed, but changes in zBP were inconsistent.
• there are cross-sectional, inverse associations of zDBP with learning, which persist longitudinally (during the summer) in terms of directionality.
Trade-Offs Between Biodiversity and Ecosystem Functions: Exploring the Relationship Between Water Level and Plant Diversity in Restored and Unrestored Coastal Wetlands Along Lake Erie (UNDERGRADUATE)

Alan Coburn, School of Environment and Natural Resources
Lauren Pintor, School of Environment and Natural Resources (Advisor)

Wetlands along the coast of Lake Erie have been dramatically altered by humans since the mid-1900s, which has disrupted important ecosystem functions that include providing habitat for a variety of plant and animal species, containing flood waters, and preventing excess nutrients from flowing into Lake Erie. Concern about the increasing frequency and intensity of harmful algal blooms in Lake Erie has led to recent efforts in the western Lake Erie basin to reconnect coastal wetlands in the Ottawa National Wildlife Refuge (ONWR) to the Crane Creek watershed and Lake Erie. By doing so, the long-term goal is to retain more nutrients in the wetlands, where they will be incorporated into the ecosystem. Ecosystem restoration actions, such as the removal of dikes, aim to restore these natural processes. However, higher-than-optimal water levels and longer inundation periods following dike removal might decrease wetland plant diversity, which could then have a negative impact on the wetlands’ capacity for nutrient retention. Understanding how restoring more natural wetland hydrology affects wetland plant diversity and ecosystem functions will help wetland managers make more informed decisions about restoration actions to maximize ecosystem functioning and minimize losses in diversity.

In order to understand the effects of dike removal on wetland plant diversity, nutrient retention, and primary productivity, CFAES researchers aimed to quantify wetland inundation, plant diversity, nutrient concentrations, and plant biomass. Twelve wetland sites were sampled in the Crane Creek wetland complex located in the ONWR in Oak Harbor, Ohio, from May 2017 to August 2017. Five of the sites have undergone dike removal over the past nine years, and seven of the sites have intact dikes (flow is controlled between the wetlands and the Crane Creek watershed and Lake Erie). In each of the wetland sites, water level was measured and water samples were collected biweekly. A plant diversity survey was conducted in June and July in which nine 0.5 m² plots from each wetland were sampled; each plant within the plots was identified and the relative cover for each species was estimated. In August, peak biomass of above-ground emergent wetland plant material was harvested in three 0.5 m² plots from each wetland, dried, and weighed to estimate primary productivity. The researchers found that mean water depth and its relative changes over time were similar between restored and unrestored wetlands; however, more variation can be seen in the restored wetlands, which reflects the natural variation in the Crane Creek watershed. Taxonomic and functional diversity measures were similar between restored and unrestored wetlands, but taxonomic richness was significantly lower in restored wetlands than in unrestored wetlands. Total phosphorus was similar between restored and unrestored wetlands, but total nitrogen was significantly lower in restored wetlands than in restored wetlands.

Based on comparing the similarities and differences between the restored and unrestored wetland sites, it appears as though dike removal in the ONWR does not seem to have a significant affect on plant diversity or on ecosystem functioning in the short-term. While water levels do vary more in the restored wetlands, they might not be enough to impact the plant species’ life cycles; however, lower species’ richness in restored wetlands but similar biomass levels might mean that some sensitive plant species have been replaced by fewer, more tolerant plant species in restored wetlands. Moving forward, more complex statistical models will be used to look for trends or associations in nutrients, diversity measures, and biomass between one another and other environmental factors.
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Industry Partners

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Lipha Tech Inc.
Lipton Tomato Research Center
Lois Smucker’s Greenhouse
Loveland Industries Inc.
Magical Farms Inc.
Maple Leaf Farms Inc.
Mars Chocolate North America,
LLC
Martek Biosciences Corporation
MBP International Ltd.
M Cellars
Merck Research Laboratories
Merial Limited
M & G Polymers, USA
MicroBio Limited
Mid-America Food Processors
Midfield Cheese
Midori Renewables Inc.
Midtech
Midwest Regional Hosta Society
Ministry of Culture, Education, and Scientific Exchanges, Spain
Monsanto Co.
MTD Products
National All-Jersey Inc.
National Fish and Wildlife Foundation
National Sea Grant Program
National Wildlife Federation
Natural Fiber Composites Corp.
North American Strawberry Growers Research Foundation Inc.
Nourse Farms Inc.
Novartis Crop Protection Inc.
Nunhems USA Inc.
Nursery Growers of Lake County Ohio Inc.
N-Viron International Inc.
Ohio Bioprocessing Research Consortium
Ohio BioProducts Innovation Center
Ohio Corn Marketing Program
Ohio Crafted Malt House LLC
Ohio Dairy Farmers Federation Inc.
Ohio Dairy Producers
Ohio Floriculture Foundation
Ohio Fruit Growers Society
Ohio Lawn Care Association
Ohio Nursery and Landscape Association Inc.
Ohio Pork Producers Council
Ohio Poultry Association
Ohio Seed Improvement Research
Ohio Sheep and Wool Program
Ohio Small Grains Marketing Program
Ohio Soybean Council
Ohio Space Grant Consortium
Ohio Vegetable and Small Fruit Research and Development OHP Inc.
Ontario Greenhouse Vegetable Growers
Optimum Quality Grains LLC
Organic Technologies
Organic Valley
Otterbein College
Outback
PanAridus
Park Foundation
Pennington Seed Inc., Oregon Division
Petroseed
Pfizer
Pharmacia, Wyeth Ayerst Research
Philip Morris Inc., Shared Solutions in Agriculture
Phycotransgenics
PIC USA Inc.
Pig Improvement Co.
Pioneer Hi-bred International Inc.
Polter’s Berry Farm
PolymerOhio Inc.
Protein Technologies International
Purity Foods Inc.
Quality Liquid Feeds
Rainbow Treecare Scientific Advancements
Rainforest Phytoceuticals LLC
Raven
Rhodia Inc.
Roche Vitamins Inc.
Rootella
Satloc
Schillinger Genetics Inc.
Schmack BioEnergy
SCI Protek Inc.
Scotts
Select Sires Inc.
Seminis Vegetable Seeds Inc.
Small Farm Institute
Smithers-Oasis Company
Southwest Research Institute
Standard Process Inc.
Sustane Natural Fertilizers
Syngenta
The Andersons Inc.
The Chef’s Garden Inc.
The Cookie Cop
The Garland Co. Inc.
The HANOR Co. Inc.
The Iams Co.
The Scotts Co. and Subsidiaries
Theis Technology Inc.
Thomas Cook
Toh Products LLC
Top Soil Precision Ag
Tree Research and Education Endowment Fund
Trimble Navigation Unlimited
Tropical Traditions
TruGreen-Chemlawn
University of California, Davis
Valent
Verdesian Life Sciences LLC, Biagro Western Sales
Vermilion Valley Vineyards
Vineland Enterprises LLC
Warner Endowment Grant
Welch’s
West Texas A&M University
Wilmington College
Woori Carbon Co.
Zinpro Corp.
Zoetis
ONE COLLEGE

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The Ohio State University College of Food, Agricultural, and Environmental Sciences (CFAES) is a large, diverse college. We foster economic development through technologies and value-added products. We strive to ensure human, animal, and environmental health. We prepare our future leaders and scientists.

WE SUSTAIN LIFE.

Office for Research and Graduate Education

Grant Development Support Unit

The Grant Development Support Unit is a part of the Office for Research and Graduate Education that is focused on grant related needs. Our mission is to serve CFAES researchers as they conceptualize, develop, write, and submit their proposals to federal agencies and other entities to seek funding. We work across all disciplines with the overarching goal of making the proposal development process as straightforward and streamlined as possible.

To this end, we offer an extensive array of services, which include:

- Identifying appropriate funding opportunities
- Announcing grant opportunities and coordinating internal competitions
- Managing and coordinating the preparation of the proposal
- Drafting non-technical sections of the proposal and some editorial services
- Connecting faculty to appropriate staff and other resources throughout the university
- Offering proposal development and research related training

The GDSU has been successful in obtaining more than $100 million in new extramural funding since its inception in 2010.

The GDSU is a free service provided to all CFAES employees. We are available to assist you with your proposal needs. We have offices on both the Wooster and Columbus campuses. Please contact us if you would like assistance or if you have proposal or research related questions.

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