All 2020 PRL Stories

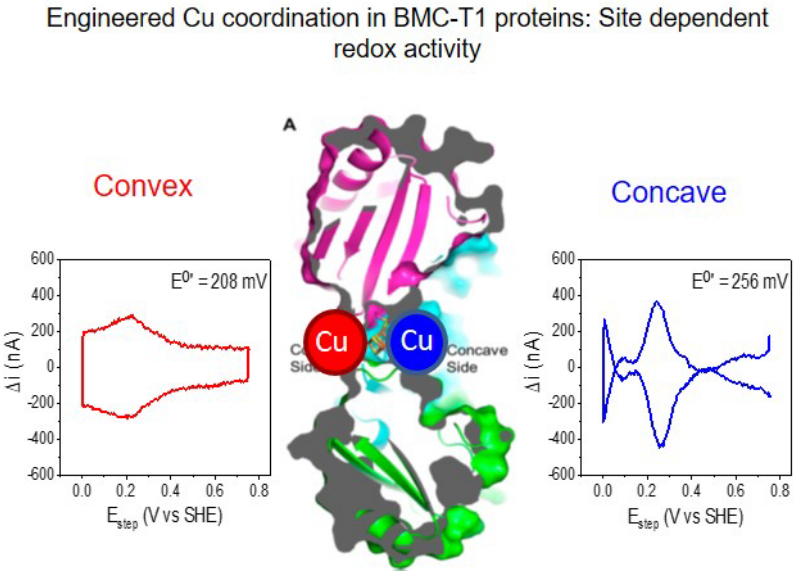
Research Highlights

Stories

Modifying a bacterial microcompartment shell proteins to bind metal ions for electron transfer with electrodes

1/28/20

The Kerfeld lab, in collaboration with the Naval Research Lab, has engineered a bacterial shell protein to incorporate copper for redox activity.



Electrode bound BMCs T1 proteins showed good electrochemical interactions when bound to an electrode, which could provide an infinite source/sink of electrons to the BMC as these structures continued to be developed for biotechnological applications.

Scientific Achievement

Engineered a shell protein to incorporate copper for redox activity with an electrode surface.

Significance and Impact

Demonstrates the ability to expand the functionality of engineered bacterial microcompartments to non-native applications. Harnessing natural biological processes to synthesize new materials are key for developing future functional bioreactors and biomaterials.

Research Details

- We designed, synthesized, and characterized a bacterial microcompartment shell protein for redox reactions by engineering either a Cu or [4Fe-4S] binding site.
- Protein film voltammetry demonstrates tunable redox activity when the protein is attached to an electrode surface, which is preferable to solution state reactivity for many biomaterials applications.

Related people: Jefferson Plegaria, Matthew Yates, Sarah Glaven, **Cheryl A. Kerfeld (CA)**

DOI: **10.1021/acsabm.9b01023**

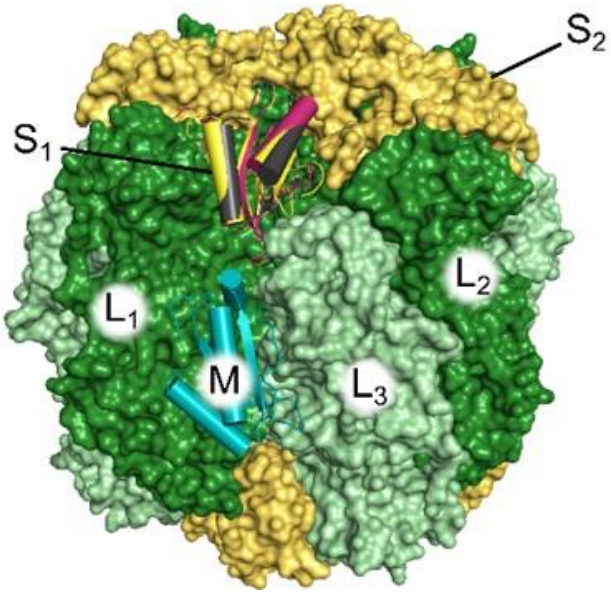
Download the highlight

This work was primarily funded by the **US Department of Energy, Office of Basic Energy**, with additional funding by the Naval Research Laboratory and the US Department of Defense.

Considering multiple binding sites for proteins with domain similar to the small subunit of rubisco

3/2/20

Protein modeling in cyanobacteria predicts binding interactions between rubisco and proteins with homology to the small subunit of rubisco.



L8S8 rubisco is shown with 8 large (RbcL, green) and 8 small (RbcS, yellow) subunits. Small subunit-like domains (SSLDs) have been shown to bind to the equatorial M position (blue), but when considering an open S1 position, an SSLD could form favorable interactions (black). These are improved when considering the linker region (burgundy) that was absent in all experiments showing binding at the M position.

Scientific Achievement

Protein homology modeling in cyanobacteria predicts binding interactions, at two sites, between rubisco and proteins with a domain (SSLD) similar to the small subunit of rubisco.

Significance and Impact

Rubisco fixes carbon dioxide (CO2) during the process of photosynthesis. The study suggests that SSLDs could bind at additional rubisco sites than previously shown. This variety suggests dynamic regulatory mechanisms to be explored regarding these protein-protein interactions.

Research Details

- The small subunit-like domain is found in two proteins in cyanobacteria and is important for their interaction with rubisco.
- They may bind in the same location as the rubisco small subunit, since they are homologous to the small subunit of rubisco, though recent studies suggest that the binding is at a different site.

- Modeling of the full small subunit-like domains in an additional organism supports a view that considers binding at both sites.
- The small subunit-like domain is not expected to bind the S1 position as well as RbcS, but it still forms favorable interactions at this site and maintains many important interactions, especially when considering residues that were absent in published experimental studies.
- Previous work studied environments that would favor the new M binding site, but other conditions, species, and post-translational modifications could allow for binding at the small subunit site as well.

Related people: Brandon Rohnke, Cheryl Kerfeld, **Beronda Montgomery (CA)**

DOI: **10.3389/fmicb.2020.00187**

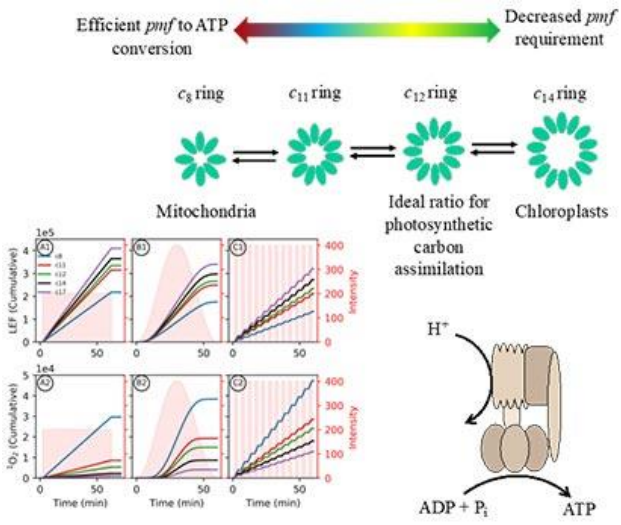
Download the highlight

This work was primarily funded by the **US Department of Energy, Office of Basic Energy Sciences**.

The limits of photosynthetic efficiency

3/5/20

Increasing the efficiency of the ATP synthase could lead to ROS production. This has important implications for synthetic biology efforts to alter photosynthetic efficiency by engineering the ATP synthase.



Scientific Achievement

Experimental and computational studies demonstrated that increasing the efficiency of one energy storing reaction in photosynthesis will likely lead to production of deleterious reactive oxygen species in others. To cope with these trade-offs, Nature has tuned photosynthesis to balance the needs for efficient and safe energy storage.

Significance and Impact

It has been proposed that genetically modifying the protein subunit stoichiometry for the chloroplast ATP synthase could lead to substantial increases in the efficiency of photosynthesis. We show that this strategy will likely fail because it leads to photodamage and loss of yield. Instead, our work suggests a new engineering approach that increases efficiency while avoiding deleterious side reactions.

Research Details

- Photosynthesis uses light to store energy in a redox gradient and an electrochemical proton gradient (proton motive force, *pmf*), which drives the synthesis of ATP through the thylakoid F_oF_1-ATP synthase. ATP synthase structure and function are conserved across biological kingdoms, but the number of ion–binding *c* subunits varies between organisms, which alters the proton/ATP ratio, with implications for metabolism. Essentially, the *c*-ring size sets the "gear ratio" of photosynthesis, and it has been suggested that decreasing their size, or increasing the gear ratio, could improve photosynthetic efficiency.
- However our experiments and simulations predict that the change in energy storage will cause large increases in *pmf*, destabilizing charge separated states in photosystem II, leading to

production of reactive oxygen species. Thus, the large *c*-ring size may be optimized to prevent photodamage. This has important implications for the evolution and regulation of photosynthesis as well as for synthetic biology efforts to alter photosynthetic efficiency by engineering the ATP synthase.

- We propose that engineering efforts be focused instead on adjusting the storage of *pmf* and the energy storing reactions of PSII to prevent recombination.

Related people: Geoffry Davis, **David M. Kramer (CA)**

DOI: **10.3389/fpls.2019.01778**

Download the highlight

This work was primarily funded by the **US Department of Energy, Office of Basic Energy Sciences**.

A new method to reveal the molecular landscapes of photosynthetic membranes inside green algae cells

5/14/20

A collaboration with Max Planck Institutes in Germany has led to a new visualization approach that produces a topological view of these native membranes.

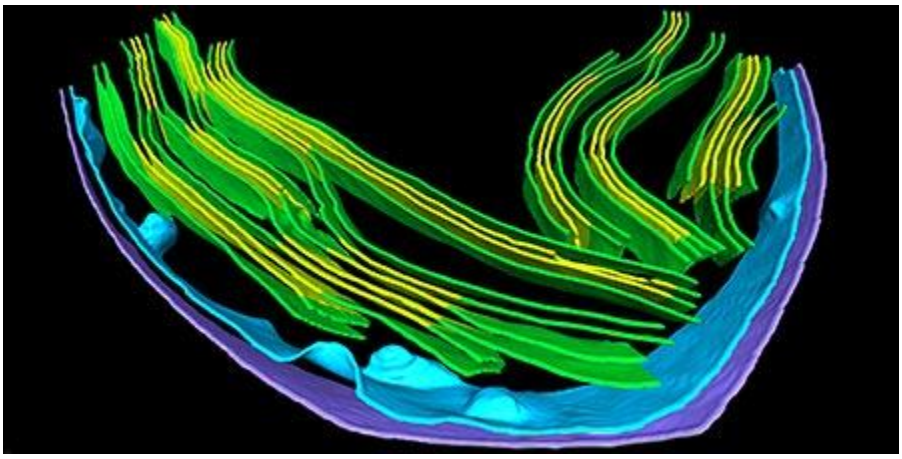


Image of photosynthetic membranes produced by the new visualization method.

Scientific Achievement

The latest advances in cryo-electron tomography were used to image photosynthetic protein complexes embedded within native thylakoid membranes inside the cell.

Significance and Impact

This high-resolution imaging revealed how the intricate network of thylakoid membranes sorts protein complexes into distinct regions to tune the photosynthetic reactions. A surprising discovery shows how large Photosystem II supercomplexes may be able to move fluidly through the crowded membranes, maintaining efficient capture of light energy and transfer of electrons to other complexes.

Research Details

- A new visualization approach called a 'membranogram' projects tomographic images of the proteins onto the surface of the segmented membrane, producing a molecular view of native membrane topology.
- PSII were mostly found in the appressed region, whereas PSI, ATP synthase and ribosomes were restricted to the non-appressed region, and Cyt*b6f* were found with equal abundance in both regions.
- PSII supercomplexes randomly overwrap between appressed membranes, apparently not maintaining stacking.

Related people: Wojciech Wietrzynski, Miroslava Schaffer, Dimitry Tegunov, Sahradha Albert, **Atsuko Kanazawa**, Jürgen M Plitzko, Wolfgang Baumeister, Benjamin D Engel (CA)

DOI: **10.7554/eLife.53740**

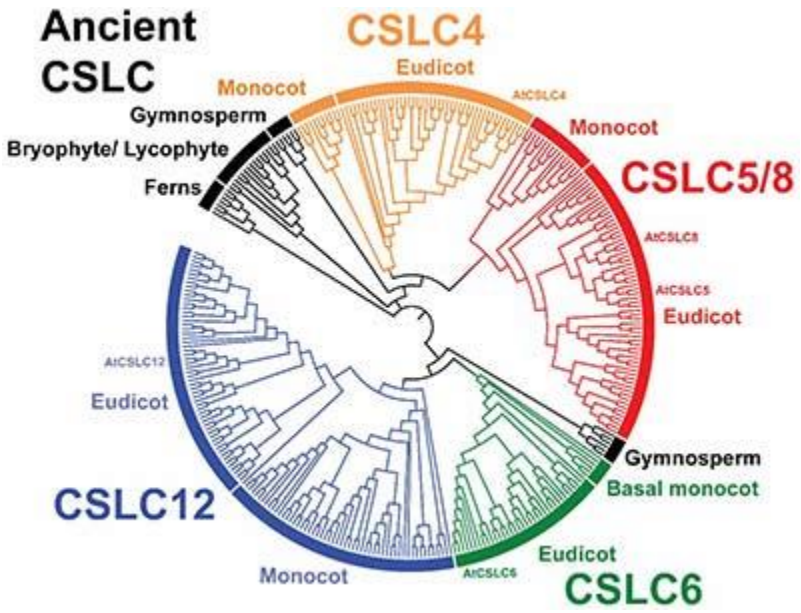
Download the highlight

This work was partially funded by the **US Department of Energy, Office of Basic Energy Sciences**. Contributions from Dr. Kanazawa, from the MSU-DOE Plant Research Laboratory, include: Data curation, Formal analysis, Investigation, and 77K measurements

Investigation of a protein family that generates plant cell walls

8/3/20

A new study increases our understanding of the biosynthesis of xyloglucan, one of the most common polysaccharides in plant primary cell walls.



Phylogenetic analysis of CSLC protein family: A total of 325 CSLC sequences from various plant groups were used (Bryophytes/ Lycophytes, Ferns, Gymnosperms, Basal angiosperms, Monocots, and Eudicots). Orange, CSLC4 lineage; Red, CSLC5/ 8 lineage; Blue, CSLC12 lineage; Green, CSLC6 lineage; Black, ancient CSLC. From PNAS journal, Copyright 2020 National Academy of Sciences

Scientific Achievement

Reverse genetic studies on Arabidopsis cellulose synthase like-C (CSLC) genes show that these genes synthesize the xyloglucan (XyG) glucan backbone.

Significance and Impact

Plant cells have complex cell walls that are important for maintaining their structural and functional integrity. XyG is one of the most common polysaccharides in the primary cell wall. Although XyG's structure is well known, its biosynthesis is poorly understood. This study identifies the enzymes responsible for XyG synthesis by demonstrating that all 5 members of the CSLC family synthesize the XyG backbone. The evidence provided in the work that deletion of CSLC-function leads to cell walls devoid of XyG raises important questions regarding cell wall reorganization and the role of XyG during plant development. Addressing these questions will provide fruitful means for plant cell wall engineering.

Research Details

- Researchers have generated a variety of mutant combinations to investigate XyG synthesis.

- Biochemical analyses using high-performance anion exchange chromatography (HPAEC) and linkage analysis using GC/MS indicated that the mutant lacking all CSLC genes cannot produce XyG.
- Phenotypic analyses using XyG mutants indicated the organ/tissue specific roles for some of the CSLC genes.
- By generating complementation lines with each CSLC member, the researchers demonstrated that all CSLC members are XyG backbone synthases.
- Phylogenetic analyses support an increased diversification of CSLC genes, including the recent evolution of CSLC4 genes in eudicots, most likely from an ancestral CSLC group.

Related people: **Sang-Jin Kim**, Balakumaran Chandrasekar Anne C. Rea, Linda Danhof, Starla Zemelis-Durfee, Nicholas Thrower, Zachary S. Shepard, Markus Pauly, **Federica Brandizzi (CA)**, and **Kenneth Keegstra (CA)**

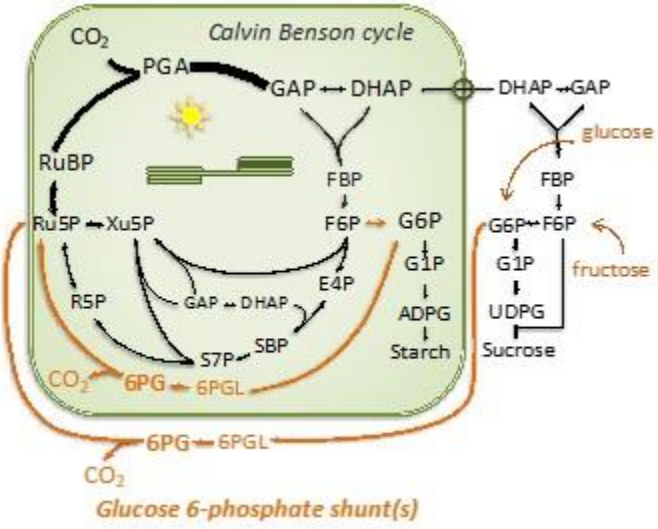
DOI: **10.1073/pnas.2007245117**

Download the highlight

Recycling carbon in photosynthesis

8/25/20

Isoprene and photosynthetic metabolism labeling experiments provided evidence that glucose is recycled back into photosynthetic metabolism.



Glucose and fructose can reenter photosynthetic metabolism (the Calvin Benson cycle) through glucose 6-phosphate shunts (in orange). At normal temperature only the outer (cytosolic) shunt is active. Temperature stress speeds the outer shunt and turns on the inner (chloroplast) shunt.

Scientific Achievement

Discovered evidence that glucose is recycled back into photosynthetic metabolism.

Significance and Impact

The pathway for converting carbon dioxide to starch and sucrose in photosynthesis was discovered by labeling using isotopes of carbon. However, not all carbon in the pathway becomes labeled. A similar phenomenon was known for isoprene emission, not all isoprene is labeled when carbon isotopes are fed. We showed that these observations are linked, isoprene provides a window on photosynthesis.

Research Details

- As much as 40% of isoprene emitted from a leaf fed an isotope of carbon does not become labeled. This varies with stress.
- We showed that this is because photosynthesis metabolites do not label fully.
- Isoprene accurately reflects the labeling of photosynthesis metabolites.
- Modeling showed that this is likely caused by a flow of unlabeled glucose into photosynthetic metabolism through a shunt that bypasses part of photosynthesis.
- The amount of glucose that follows this pathway varies with stress, for example it is much higher at high temperature.
- Isoprene provides a non-destructive method for measuring this flow of carbon.

Related people: **Thomas D. Sharkey (CA)**, Alyssa L. Preiser, **Sarathi M. Weraduwage**, Linus Gog

DOI: **10.1042/BCJ20200480**

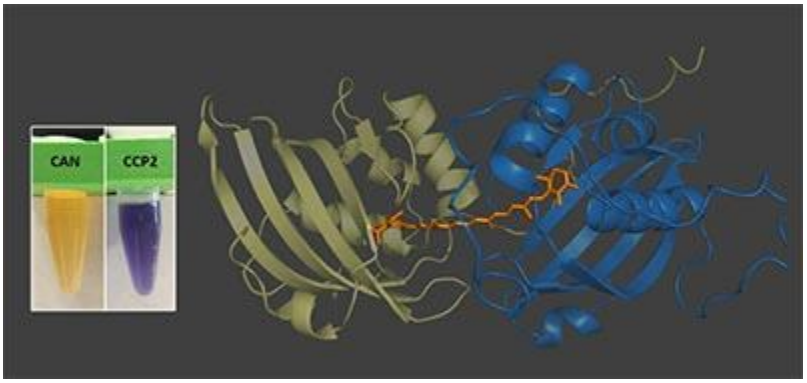
Download the highlight

This work was primarily funded by the **US Department of Energy, Office of Basic Energy Sciences**.

Identifying a new family of carotenoid-binding proteins in cyanobacteria

10/2/20

In a study published in Scientific Reports, scientists describe a new family of carotenoid binding proteins.



Visible appearance of the canthaxanthin (CAN, *left tube in yellow*) in organic solvent and bound to CCP2 (right). Structural model of the CCP2 dimer. Figure from **Dominguez-Martin, M.A. *et al.*, *Sci Rep* CC BY 4.0**

Scientific Achievement

The work is the first structural description of a carotenoid binding protein called C-terminal domain-like carotenoid protein (CCP2).

Significance and Impact

CCP2 is a cyanobacterial protein that is a member of the widespread NTF2-like superfamily of proteins. Our structural analysis is the first insight into how such a protein allocates the carotenoid pigment, which usually plays a protective role within the host organism. Given the ubiquity of NTF2-like proteins across all domains of life, perhaps other organisms, such as photosynthetic algae and plants, have members of this carotenoprotein family that await discovery.

Research Details

- Bioinformatic analysis has revealed the existence of a new family of proteins, homologs to the C-terminal domain of the Orange Carotenoid Protein (OCP), the C-terminal domain-like carotenoid proteins (CCPs).
- In this study, we purified holo-CCP2 directly from *Fremyella diplosiphon* and determined that it natively binds canthaxanthin.
- Structural analysis using small-angel X-ray scattering (SAXS) characterized the structure of this protein in its two main oligomeric states: dimer and tetramer. A single carotenoid spans the two CCPs that form the dimer. In addition, analysis with X-ray footprinting-mass spectrometry identifies residues for carotenoid binding within the CCP2.
- The unusual spectroscopic properties of this protein, an extreme red shift (ca. 80 nm) of the absorption maximum of the carotenoid bound by the CCP2 dimer is also discussed. These data

provide the first structural description of carotenoid binding a protein consisting of only an NTF2 domain.

Related people: Maria Agustina Dominguez-Martin, Michal Hammel, Sayan Gupta, **Sigal Lechno-Yossef**, Markus Sutter, Daniel J. Rosenberg, Yan Chen, Christopher J. Petzold, Corie Y. Ralston, Tomáš Polívka, **Cheryl A. Kerfeld (CA)**

DOI: **10.1038/s41598-020-72383-y**

Download the highlight

Identifying transcription factor networks that protect maize when its main cellular biofactory is under stress

10/26/20

Scientists have identified new transcription factor networks and their dynamic activities that protect the endoplasmic reticulum in situations requiring the production of large quantities of proteins.

A maize plant. Courtesy of Dae Kwan Ko.

Scientific Achievement

Plant biomass accumulation largely depends on protein biosynthesis in the endoplasmic reticulum, a conserved organelle across eukaryotes. Using a high-throughput protein-DNA interaction assay and transcriptome analyses, we identified new transcription factor networks and their dynamic activities that protect the endoplasmic reticulum in situations requiring the production of large quantities of proteins.

Significance and Impact

When plants undergo stressful situations, like drought or high heat, the endoplasmic reticulum can accumulate unfolded or misfolded proteins, leading to cell death and crop loss. A conserved signaling pathway, the unfolded protein response (UPR), functions to restore the balance between protein folding capacity and demand through transcriptional mechanisms that are not fully understood. This study identified new transcriptional factors controlling the activity of the UPR in maize. These results are foundational for understanding transcription regulatory mechanisms in the stress responses and crop improvement.

Research Details

- A potentially lethal condition, known as endoplasmic reticulum (ER) stress, is buffered by the unfolded protein response (UPR), a set of signaling pathways designed to either recover ER functionality or ignite programmed cell death. The regulatory transcriptional landscape underpinning ER stress management is largely unmapped, especially in crops.
- To address this knowledge gap, we performed a large-scale systems-level analysis of protein-DNA interaction (PDI) network in maize (*Zea mays*). Using 23 promoter fragments of six UPR marker genes in a high-throughput enhanced yeast one-hybrid (eY1H) assay, we identified a highly interconnected network of 262 transcription factors (TFs) associated with significant biological traits and 831 PDIs underlying the UPR.
- We established a temporal hierarchy of TF binding to gene promoters within the same family as well as across different families of TFs.
- Cistrome analysis revealed the dynamic activities of a variety of *cis*-regulatory elements (CREs) in ER stress-responsive gene promoters. By integrating the cistrome results into a TF network analysis, we mapped a subnetwork of TFs associated with a CRE that may contribute to the UPR management.
- Finally, we validated the role of a predicted network hub gene using the Arabidopsis system.

Related people: Dae Kwan Ko and **Federica Brandizzi (CA)**

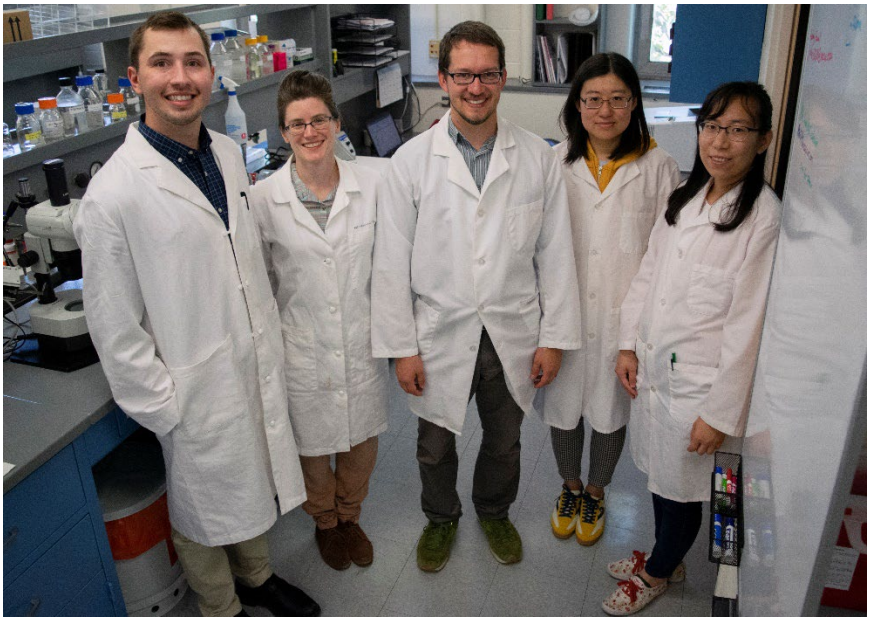
DOI: **10.1111/tpj.15044**

Download the highlight

Berkley Walker: trying to improve bioenergy crops with 'big picture' math models

1/8/20

Igor Houwat, Berkley Walker



Victor DiRita, NatSci Photographer

Berkley Walker's DNA synthesis proposal has been selected by the **U.S. Department of Energy (DOE) Joint Genome Institute (JGI)**, a DOE Office of Science User Facility, to study how high temperatures impact plant enzymes that support photosynthesis.

The big picture push behind the proposal: to understand and quantify that process, called photorespiration, in order to improve crop efficiency, with a focus on enhancing bioenergy crops.

Photorespiration, an important process that works alongside photosynthesis. expand iconPhotosynthesis uses the sun's energy to capture carbon dioxide (CO_2) from the atmosphere and fix it into stable carbon bonds. These bonds become the sugars and starches that power life on the planet.

But **photosynthesis is not as efficient** at capturing the sun's energy as one might think. It often achieves about a quarter the conversion efficiency of a low-cost solar cell. One major inefficiency happens when the when the first expand iconenzymes to capture CO_2, expand iconrubisco , takes oxygen instead of CO_2.

This reaction produces a toxic compound that the plant has to recycle, which is what photorespiration does. Recycling costs are high, however, and they consume a hefty 30-40% of leaf energy. Moreover, the process releases CO_2 back into the atmosphere at about 25% the rate of net fixation under field conditions, in most bioenergy and food crops.

Photorespiration will be greatly impacted by changing climates in ways we don't fully understand. On one hand, higher CO_2 levels provide more CO_2 for plants to capture, instead of oxygen. So, plants are more efficient at photosynthesis and photorespiration rates decrease.

On the other hand, as temperature levels rise, rubisco gets more 'sloppy' and might capture more oxygen, which increases photorespiration rates.

So far, we know quite a bit about how changing temperature and CO_2 levels change how much rubisco captures oxygen.

"What we don't know as much is how photorespiration deals with that captured oxygen under high temperatures," says **Berkley Walker**, Assistant Professor at the **MSU-DOE Plant Research Laboratory**. "We need to understand and quantify how photorespiration itself responds to increased temperature in order to enhance crop efficiency. This critical to improve bioenergy crops and to better understand global carbon cycles."

Systems-level math models of photorespiration

Working with the JGI will provide the Walker lab with the DNA needed to synthesize enzymes that they can measure in the laboratory. The measurements will improve the accuracy of their systems-level mathematical model of photorespiration.

Berkley Walker (center) with Han Bao (left)
By Victor Di Rita, NatSci Photographer, 2019

"We have what we think is a good model of photorespiration, but the model is only as good as the data we give it about the enzymes…you know, garbage-in, garbage-out, "Berkley says. "The numbers available today were measured in many different labs across different species over the last 40 years. We need to get more consistent data, across the same species, to have more confidence in the model's results."

The lab has selected nine photorespiratory enzymes from seven important bioenergy crops and species adapted to high temperatures.

“We will be studying their properties and temperature responses, Berkley adds. “The model will help us identify the ‘choke’ points that prevent photorespiration from being more efficient.”

Another benefit of improving the model is that it would examine how photorespiratory enzymes work together as a network. This holistic approach should allow for future predictions on how photorespiration works in line with temperature changes.

And with the power to predict performance, the dream, futuristic goal would be to try and engineer better performing plants.

“Once we identify photorespiratory ‘choke points,’ we could mix and match enzymes across species to remove those blockages. For example, some species we are looking at can do photorespiration well at high temperatures – 10 degrees Celcius above normal growing conditions. They have obviously adapted to hot surroundings. Perhaps their enzymes can useful to other plants.”

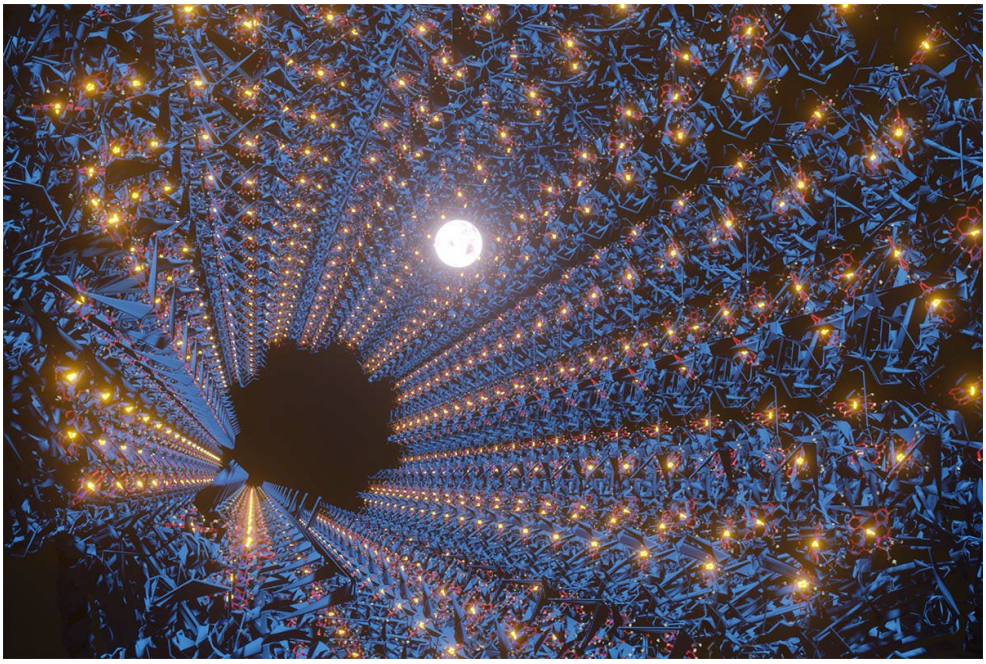
The grant is set to be in collaboration with Dr. Aaron Liepman, a former MSU-DOE Plant Research Laboratory postdoc who is now faculty at Eastern Michigan University.

Banner image, from left to right: Luke Gregory, Audrey Johnson, Berkley Walker, Han Bao, and Xinyu Fu.

Taming electrons with bacteria parts and a little 'blood' - a new synthetic biology system [VIDEO]

1/15/20

Igor Houwat, Jingcheng Huang



VIDEO SUMMARY IN 90 SECS

https://youtu.be/ROvnjvbzf80

Electrons are tough to pin down in biology. Trying to guide one to go where you want it is as unpredictable as **tipping a bean machine** over and guessing where individual beans will end up.

Learning how to harness electrons is no fool's errand, though. Because, when electrons move, they are the electricity that powers life.

Electrons power the production of fuel and medicine. Electron movement is behind expand iconphotosynthesis, our main source of food, and combustion. Moving electrons are the definition of an electric current, which is why you can read this story.

In a **new study**, scientists at the MSU-DOE Plant Research Laboratory report a new synthetic system that could guide electron transfer over long distances. The new system is made up of two components plucked from nature. One is a expand iconprotein from bacteria and the other a molecule found in our blood.

Iron-containing molecules that make your blood red

Nature has figured out how to tame electrons. The trick is to split up their journeys into short pit stops that are easier to manage. Electrons then hop between stops as they are guided towards some final destination.

One of these natural pit stops is the heme, a molecule that contains iron. It is what gives our blood its color, and it is found in many other biological molecules.

"In nature, multiple hemes have to be closely positioned and angled precisely to allow for fast electron hops. The hemes are fixed in place by attaching to protein structures," says Jingcheng Huang, a former graduate student in the labs of **Danny Ducat** and **David Kramer**. "Otherwise, if the distances between hemes become to large, an electron will hop out of control. It is lost."

Artificial pit stops

Since hemes are found in almost all living beings, they can associate with many types of proteins. So the science team used the protein BMC-H, from expand iconbacteria, to build their artificial electron pit stops.

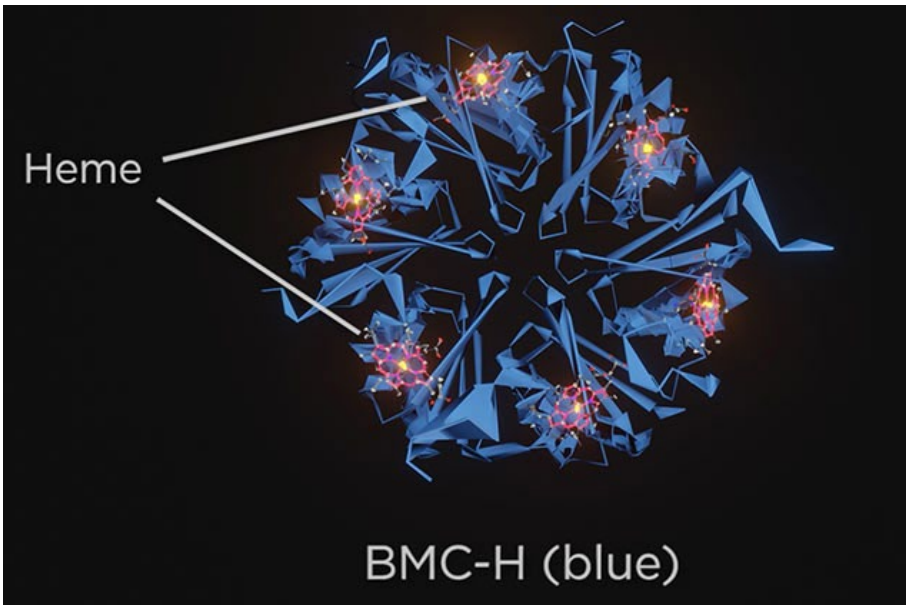


Figure 1 Concept drawing of BMC-H protein with hemes fixed onto it. By MSU-DOE Plant Research Laboratory, 2020

The team identified four possible locations the heme can dock into. Specifically, the alpha helical region was the most promising host area.

"We didn't have to modify the BMC-H protein much," Jingcheng says. "With only three amino acid substitutions, we can get a heme binding tightly to it. Because the modification is minimal, the protein's shape and functions remain intact."

Why BMC-H?

“It is known to assemble with other proteins of its type into large and defined structures. Groups of BMC-H have been seen to cluster into flat sheets, tunnels, or swiss roll shapes. So if we find an easy way

to attach hemes to these large structures, we could facilitate electron transfer over long distances," Jingcheng says.

The scientists have managed to produce these larger structures with hemes attached to them. Moreover, they can produce them 'naturally' inside of bacteria cells, which saves resources.

"We'd like to optimize this system into a functional 'nanowire'," Jingcheng, adds. "Someday, it could funnel electrons to power the production of new medicines, or biofuels or electronic devices made of biogoo. The possibilities are endless."

"The exciting part is that we played with what nature has already figured out. We took a protein that self-assembles into large structures but doesn't bind hemes and functionalized it so that it hosts them," Jingcheng muses. "Otherwise, if we had created a system from scratch, we would have add extra layers of difficulty. That's the essence of synthetic biology, taking natural ingredients and re-configuring them in new, unseen ways."

The study is published in **Frontiers in Bioengineering and Biotechnology**.

This work was funded by a **National Science Foundation Emerging Frontiers grant** and the **US Department of Energy, Office of Basic Energy Sciences**. Collaborators included members of the **Kerfeld** and **Kramer** labs at the **MSU-DOE Plant Research Laboratory**.

Insect bites + Warmer climate = Double trouble for plants [VIDEO]

1/20/20

Igor Houwat, Nathan Havko, Gregg Howe

Figure 1 Banner image by Nathan Havko

VIDEO SUMMARY IN 90 SECS

https://youtu.be/zYdbbZIEwkE

Recent models are telling us that, as our climate warms up, herbivores and pests will cause more damage to agricultural crops. **One study** predicted that crop losses to insects increase 10 to 25 percent for every 1 degree Celsius increase.

Michigan State University scientists think that these models are incomplete and that we may be underestimating the losses. A new study shows that infested tomato plants, in their efforts to fight off caterpillars, don't adapt well to rising temperatures. This double whammy worsens their productivity losses.

According to the study, two factors are at play. The first is rising temperatures. Insect metabolism speeds up with heat, and they eat more. Also, warmer temperatures could open up a wider range of hospitable habitats to insects.

Second – and this is what current models ignore – is how the *infested* plants react to the heat.

"We know that there are constraints that prevent plants from dealing with two stresses simultaneously," says **Dr. Gregg Howe**, University Distinguished Professor at the MSU-DOE Plant Research Laboratory. "In this case, little is known about how plants cope with increased temperature and insect attack at the same time. So we wanted to try and fill that gap."

Sometimes, it's too much to handle

Plants have systems to deal with different threats.

Caterpillar attack? There is a system for that. When a caterpillar takes a bite off a leaf, the plant produces a expand iconhormone , called Jasmonate (JA). JA tells the plant to quickly produce defense compounds to thwart the caterpillar.

Temperatures too hot? Overheated crops have another bag of tricks to cool themselves down. (Obviously, they can't make a run for the inviting shade under a tree.) They lift their leaves away from the hot soil. They also 'sweat' by opening up their stomata – think like skin pores – so that water can evaporate to cool the leaves.

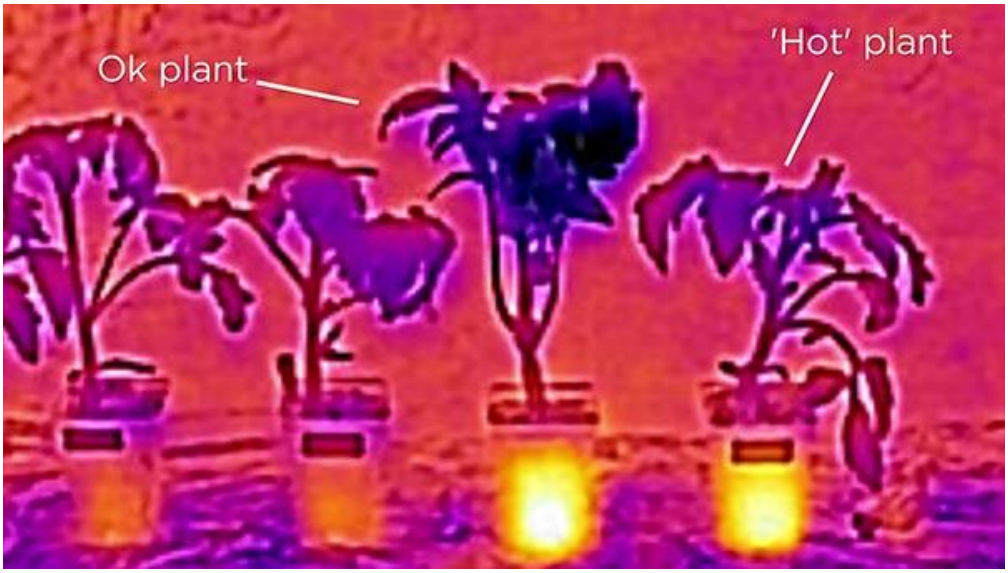


Figure 2 Heat map of infested plants. Once they are infested by caterpillars, the plants suffer. By Nathan Havko, Howe lab, 2020.

But then, Nathan Havko, a postdoc in the Howe lab, grew tomato plants in 'hot' growth chambers (38 degrees Celsius). He also let loose hungry caterpillars on them.

"I was shocked when I opened the doors to the growth chamber where the two sets of plants were growing at 'normal' and 'high' temperatures," Howe says. "The caterpillars in the warmer space were much bigger. They had almost wiped the plant out."

"When temperatures are higher, a wounded tomato plant cranks out even more Jasmonate, leading to a stronger defense response. Somehow, that does not deter the caterpillars," says Havko. "Moreover, we found that Jasmonate blocks the plant's ability to cool itself down. It can't lift its leaves or 'sweat'."

Perhaps, the plants close their pores to stop losing water from the wounded sites. But they end up suffering the equivalent of a 'heat stroke.' It's even possible that the caterpillars are crafty and do extra damage to keep the leaf pores closed and leaf temperatures elevated, which will speed up the insect's growth and development.

And, there are consequences.

“We see expand iconphotosynthesis – which is how crops produce biomass – is strongly impaired in these plants,” Havko adds. “The resources to produce biomass are there, but somehow they aren’t used properly. Crop productivity decreases.”

There are many open questions to be resolved. But, the study suggests that, as global temperatures rise, plants might have too many balls to juggle.

“I think we have yet to appreciate the unexpected tradeoffs between defense responses and plant productivity, especially when other types of environmental stress are present,” Howe says. “Turning on the defense response may do more harm than good if the plants face high temperatures or other stresses.”

*The study is **published in the journal Proceedings of the National Academy of Sciences**.*

The research team at the **MSU-DOE Plant Research Laboratory** includes Michael Das, George Kapali, Nathan Havko, and Gregg Howe from the Howe lab. Research on photosynthesis was done with the support of Alan McClain and Thomas. D. Sharkey from the **Sharkey** lab. It was funded by the Plant Resilience Institute at Michigan State University and by the **US Department of Energy, Office of Basic Energy Sciences**.

A protein lulls algae to 'sleep', and what that means for making green fuels

2/3/20

Igor Houwat, Tomomi Takeuchi

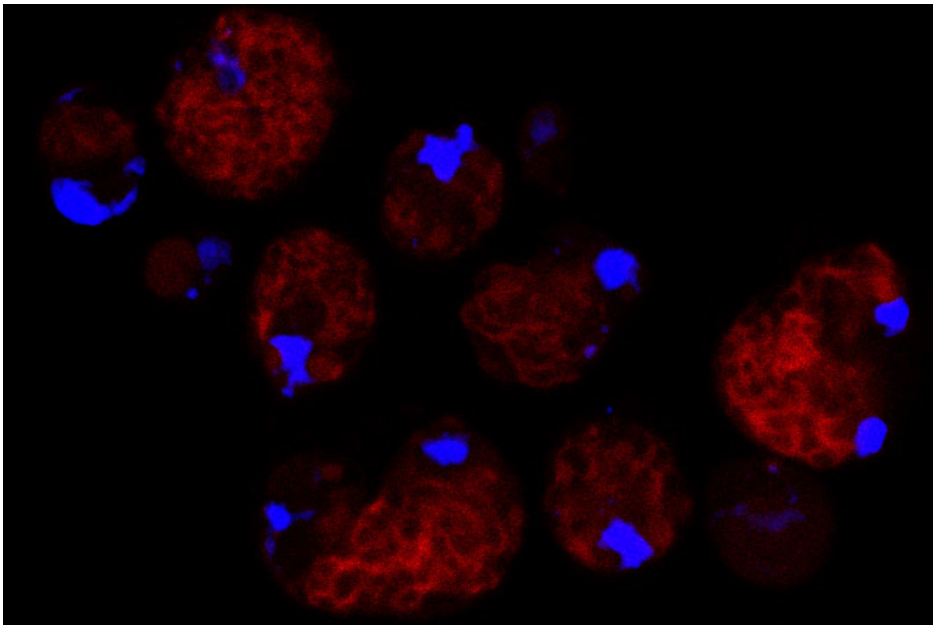


Figure 1 Banner image of mutated algal cells by Tomomi Takeuchi

Algae have the potential to become a sustainable source of high value biofuels and oils. A big hurdle that holds us back from mass producing algae feedstocks is that they make more oil when stressed out, like during starvation.

When stressed, algae need to save energy. They go into a resting state, or 'hibernation', and stop growth and cell division functions. They store energy reserves in the form of starch and triacylglycerols (TAGs), and **TAGs are the raw material for biofuels**.

When the stress passes, the algae get out of hibernation. They consume their energy reserves so that they can resume cell growth and division.

The dilemma for making biofuels is this: stressed algae make more TAG but grow poorly. Unstressed algae don't produce enough of it. The economics don't add up, one way or the other. Understanding how stress controls hibernation cycles would help us develop new ways to overcome the dilemma.

The **lab of Christoph Benning** at the **MSU-DOE Plant Research Laboratory** is trying to understand the biological reasons behind this dilemma. In their latest study, they look at a protein that helps the algae manage hibernation. The study is **published in The Plant Cell**.

A glimpse into algal hibernation

The team is studying a mutant algal strain that degrades TAGs, slower than usual, as algae try to exit from hibernation. Somehow, the algal mutant does not manage the hibernation process in a normal way.

Figure 2 Tomomi Takeuchi. By MSU-DOE Plant Research Laboratory, 2020

The responsible protein, missing due to the mutation, is called Compromised Hydrolysis of Triacylglycerols 7 (CHT7). It is part of a system that helps algae enter hibernation or wake up from it.

“When we remove CHT7 from algal cells, the cells can’t go into hibernation properly. They can’t resume normal cell division during the exit from hibernation,” says **Tomomi Takeuchi**, a recent graduate from the Benning lab. “CHT7 itself doesn’t generate the energy reserves, including TAG.”

There mutant cells suffer other problems:

- **They can't stop their cell cycle genes during hibernation**. They keep growing and are bigger than usual, and many cells die. In comparison, normal cells stop growth once they enter hibernation.
- **They continue dividing during hibernation, even when they shouldn’t.** Their offspring are not equally sized and have disorganized organelles. The situation is like out of control human cancer cells that keep dividing when they shouldn’t, hence forming tumors.
- **They are slower to resume growth functions when they try to exit hibernation**.

Tomomi says that these are extreme, damaging changes to the algal cell.

And there is mounting evidence that CHT7 doesn’t work alone.

“We think it is part of a bigger protein complex that controls hibernation. We need to examine how CHT7 integrates into and works with the larger complex,” Tomomi says.

They started by chopping CHT7 into smaller parts and reinserting these into the mutant to see which parts reverse the defects. This helped zoom into the parts that are critical for hibernation and might interact with other proteins. The next step will be to examine the other proteins in the complex.

Richard Cyr, the grant program manager at the National Science Foundation remarks, “Production of biofuels from higher plants suffers from two drawbacks: a significant period of growth is required before seeds can be harvested, and specific types of farmland are required for optimal production.”

“Algae promise the production of biofuel precursors throughout their growth and can be cultured in ponds, ditches, and bioreactors. Before the promise of algae for biofuel production is realized, several hurdles need to be overcome. This work provides a significant advance by which biofuels precursors might be produced.”

“This paper represents a deep dive into the inner workings of an important cellular process. It was beautifully choreographed and drafted by Tomomi Takeuchi as part of her recently defended PhD thesis,” says Dr. Christoph Benning, her PhD supervisor. “Credit also goes also to the other students involved and Professor Emerita, Barb B. Sears, who’s expertise on the algal organism has been invaluable.”

Leaf under attack from bacteria? One way plants stop the spread of infection

2/11/20

Igor Houwat, Yong Sig Kim, Michael Thomashow

A new study from MSU-DOE Plant Research Laboratory (PRL) scientists shows how the protein, CAMTA, helps trigger whole-plant immunity against bacteria. The study is published in the **journal Molecular Plant**.

Unlike us humans, plants can't pack up and run when things go bad. Instead, they have evolved molecular tricks to survive different threats.

These tricks are very complex and not a simple matter of 'bunkering down' till a threat passes. Instead, plants take an 'all-hands' approach to survival.

Take the **CAMTA protein system**. One of its major roles is to fortify plants in anticipation of long periods of cold. Bone-chilling temperatures can cause freezing injury that limits crop productivity. The CAMTA proteins control the activation of genes that impart tolerance to freezing.

But years of research shows that CAMTA has another important job. A **2017 study** from the **Thomashow lab** showed that it readies cold-affected plants to protect themselves from bacterial invasions. The idea is that plants will still get injured upon freezing, however well they prepare for the cold. And those injury sites are vulnerable to bacterial infection.

The new study suggests that CAMTA takes this protective role even further. **When bacteria breach a leaf, CAMTA helps warn neighboring, unaffected leaves to prepare for possible invasion**.

Warning beacon: Systemic acquired resistance

When a leaf is infected by a pathogen, the plant makes a chemical called salicylic acid (SA). An increase in SA levels tells the plant to activate hundreds of defense genes to counter the threat.

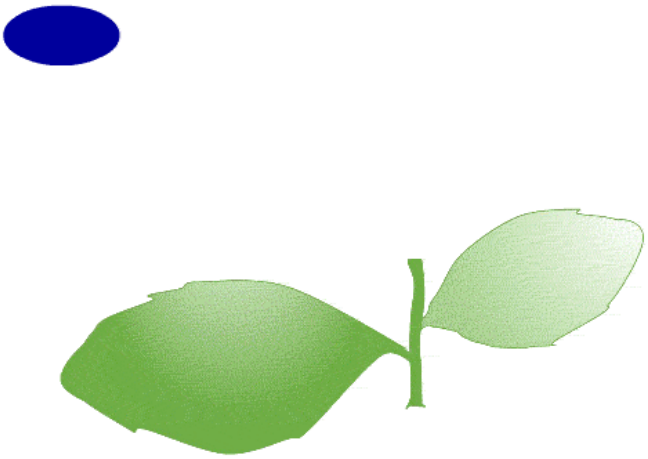
There is more. An infected plant also produces another chemical that takes on the role of messenger of doom. The chemical is called pipecolic acid (Pip).

"PIP, and another compound derived from it, travel to distant, unaffected leaves," says **Yong Sig Kim**, a postdoc in the Thomashow lab. "They prime the pathogen defense response. If the unaffected leaves are infected, they can put up a strong defense response quickly."

This warning system, called systemic acquired resistance (SAR), helps the whole plant become hypersensitive to pathogen attack. It is one way the plant tries to stop the spread of infection.

Playing a wider role

"We found that the CAMTA system also has a role in regulating this systemic acquired resistance," says **Michael Thomashow**, University Distinguished Professor at the MSU-DOE Plant Research Laboratory. "Under normal conditions, CAMTA represses the production of Pip. When a pathogen is sensed, CAMTA repression is lifted, and Pip levels rise."



GIF of how CAMTA helps warn neighboring leaves of impending bacterial invasion
By MSU-DOE Plant Research Laboratory, 2020

When Pip reaches the unaffected leaves, its message of doom causes the activation of those defense genes that usually respond to the primary defense signal, SA.

“We have proposed that Pip causes the distant leaf to become sensitive to the low levels of SA that are already present on site, resulting in the activation of systemic acquired resistance,” says Thomashow.

Work on CAMTA began back in 2008, and it is the scientist’s gift that keeps on giving.

"It keeps yielding new functions!” Kim says. “We started working on CAMTA due to our interest in cold stress. We then found this intimate connection to biotic stress. We are always asking ourselves: what else can CAMTA do?”

"Our big clue is that these proteins are huge and have fascinating gene profiles,” Kim says. “For example, CAMTA 3, the main protein we focus on, has around 1000 amino acids with many domains. Each domain may unlock a specific function."

Banner image of an Arabidopsis plant by **INRA, Jean Weber**, **CC BY 2.0**

Anne Rea starts Assistant Features Editor position at The Plant Cell

2/17/20

Igor Houwat, Anne Rea

Anne Rea, a postdoctoral research associate in **Jianping Hu's lab** at the **MSU-DOE Plant Research Laboratory** (PRL), has started a position as an Assistant Features Editor (AFE) with the journal *The Plant Cell*.

She will primarily write In Brief articles that highlight recently published papers in the journal. The In Briefs are targeted at scientists who browse the journal and want to read a summarized version of a study. They are also a way to draw them in to reading the full manuscripts.

Anne will continue her postdoc work while she works with *The Plant Cell*.

She shared her thoughts in an interview. Here are the highlights:

What attracted you to this position?

I've always liked writing, and I am particularly interested in science writing and editing. Some of my favorite parts about research are the thinking, designing and analyzing of experiments, and the writing that culminates in a cohesive story. June Nasrallah, my Ph.D. mentor, is one of the best writers that I know, and I aspire to be as proficient a writer as she!

I always thought to myself, "What if there were a job out there where someone could hire me to write their manuscripts?" It would seem to address an area that many people in science suffer through: the writing!

So how do you qualify for an AFE position?

Most are postdocs working in the plant biology field, with good writing skills and interest in communicating plant biology. These positions give us postdocs more writing experience, with an eye towards developing our future careers – whether having our own labs at a university, or becoming journal editors or science communications writers.

Whatever the goal, this position gives us the experience to write in the scientific field. It exposes us even further to the literature, and it also demands some creativity. We don't just write summaries; we are encouraged to put an interesting spin on our stories, and we have to be able to capture the reader's attention.

Anne Rea
By MSU-DOE Plant Research Laboratory, 2020

How did you find out about this job opening?

Danve Castroverde, a former member of Sheng Yang He's lab at the PRL, is a good friend. We share a love for words, language, and writing. He once told me that he had a position as an AFE and that I would enjoy doing it.

A few months later, he shared an announcement about the opening for this position. A couple of my PRL friends, **Giovanni Stefano** and Kyaw (Joe) Aung, told me that it would be a good fit for me. So I sent in my application, which included a mock In Brief article – and the rest was history!

Can you walk us through how you write an In Brief article?

We work with the Senior Features Editor, Nan Eckardt, who alerts us to upcoming papers. It is a first-come-first-serve situation. I really appreciate working with Nan – she is a great writer with an excellent work ethic, and she always wants to help!

Once the assignment is official, I get access to all of the manuscript documents. I usually read carefully through the manuscript, take notes, and look for connections to other things I have heard or read about. Sometimes, you can find an interesting angle that the authors might not have had the opportunity or space to include in their paper.

Then I write up a draft and send it to the editors and manuscript authors for comments and edits.

I also choose a figure that represents the story. It's usually one from the paper. And, I even have to cite my own sources.

I heard that you even got to write one up for a former PRL member!

Yes! Joe Aung. He used to work in both Jianping Hu's and **Sheng Yang He's** labs at the PRL, and now **he is an Assistant Professor at Iowa State University**.

When Joe mentioned that he may publish his most recent paper in *The Plant Cell*, I told him, "Wouldn't it be cool if you do, and I write up an In Brief article based on it?!" He was very excited about that possibility.

And then, months later, after he had moved on to Iowa State, he texted me one day to tell me that his manuscript got accepted into *The Plant Cell*.

I really wanted to write this one up, so I immediately contacted Nan, and mentioned that I knew Joe. She liked the idea, and it just happened, like that!

Has your postdoc mentor been supportive of your new position? One issue that might come up is that it might suck time away from your postdoc work.

Jianping Hu, my postdoc mentor, was so supportive of the AFE position. I really appreciated that. In general, she strikes a good balance between coming up with projects that I might enjoy and stretching me beyond my comfort zone.

When I joined her lab, the first thing she asked me was, "What do you want to do in your career, and how can I help?" When I shared my ideas about teaching and research, and writing and editing, she came up with some career ideas and grants to which I could apply.

I am very grateful to Jianping for her genuine mentoring and collegiality that she extends to me and her other current and former lab members. I am happy to be a part of her lab!

Plant protein helps control both chloroplast's chemistry and lipid membrane

2/18/20

Igor Houwat, Patrick Horn, Montgomery Smith

Figure 1 Banner image by Victor DiRita, NatSci photographer

A new Michigan State University study shows how a protein, called peroxiredoxin Q (PRXQ), connects two biochemical pathways that are vital for plant chloroplast health.

Chloroplasts are the power houses of plants. They are the site of photosynthesis, the process that uses sunlight and carbon dioxide to produce the energy that powers life on Earth.

The protein PRXQ seems to bridge two systems that keep chloroplasts (and by extension, plants) healthy.

The first system relates to chloroplast redox states, or how chloroplasts keep a healthy balance of chemicals and energy. PRXQ's role in this context is well known. It sits in the photosynthetic tissue of plants, where it protects the chloroplast from damage by the chemical, peroxide. (Think of the peroxide in 'hydrogen peroxide').

"Peroxides are potentially toxic byproducts of photosynthesis. We think PRXQ helps regulate these byproducts by transforming them into less toxic molecules," says Patrick Horn, a former postdoc in the

lab of Christoph Benning at the **MSU-DOE Plant Research Laboratory**. Patrick is currently **Assistant Professor at East Carolina University (ECU)**. “Limiting this damage is a constant battle in plants, especially under stress conditions.”

The new research shows PRXQ impacts a second system that produces chloroplast membranes. These membranes are made of lipids, small molecules found in fats, oils, and waxes. And one reason researchers study lipids is that they are great at storing energy. Scientists are targeting them to produce renewable sources for industrial (ex: biofuels) and nutritional (ex: healthy fat) applications.

How do lipids and redox states connect?

When scientists removed PRXQ from a plant, the amounts of one type of lipid (containing the fatty acid, 16:1t) dropped. Interestingly, this molecule is found in all plants, except for orchids, for reasons the lab would love to know.

The team saw that PRXQ affects a protein, called FAD4, which produces that same molecule.

"We designed various experiments to confirm the lipid and redox pathways are related," Patrick says. "We made genetic complementation tests, we mutated parts of the proteins. We also tested this relationship in a non-plant system."

Enter **Montgomery Smith**, an undergrad who supported Patrick’s work on the project.

"We placed both proteins in yeast," Montgomery says. "Since they are not naturally found in yeast, it would be powerful to show that they interact in a ‘foreign’ environment. We did see production of a similar unusual lipid, not normally present in yeast."

"We think FAD4 experienced some physical change that induced it to produce the lipid,” Patrick says. “Maybe, this happened only when PRXQ was in the vicinity and was interfering with the chloroplast’s chemical balance.”

“We're still not sure exactly yet HOW the relationship works. It is complicated to untangle these two biochemical pathways in a living plant.”

Careers built and science keeps moving

Montgomery joined Patrick’s’s project during her freshman year. She was thrown into the thick of things right away.

“I had to trust it would all make sense,” Montgomery says. “It helped to work with Patrick, who knew what he was doing. I got to experience the intellectual side as well as the ‘tricks’ scientists use to tackle complex scientific problems.”

"I spent a lot of time trying new methods, many of which didn't work out. However, that didn’t hold us back. It was exciting to follow the science wherever it took us, even if we didn’t know what we would find. That's a good lesson for aspiring scientists. Things don't always work perfectly."

"Some of the fun in science is to 'see what happens', despite the perceived failures - which are all learning experiences," Patrick agrees.

Now, Montgomery is a budding scientist with a solid and practical knowledge base. (Patrick credits her for always being up to a challenge and quick to the task).

Patrick's career has also evolved, having recently started his first tenure-track position at ECU. The PRXQ work fits with his new lab's research direction.

"We study how redox reactions and states are broadly involved in lipid metabolism," he says. "We now know a bit more about how lipids work within plant cells. But the more we investigate, the more new roles and traits we find associated with lipids."

The importance of mentorship is not lost on **Dr. Christoph Benning**, lead investigator for the study. He adds, "Mentoring future mentors is an important mission of the academic enterprise. Seeing it all come together, as it did in this case, was very gratifying."

This work was primarily funded by the **US Department of Energy, Office of Basic Energy Sciences**. It is published in **The Plant Journal**.

How plants tune their greenness to light quality in their surroundings

3/5/20

Igor Houwat, Hussien Alameldin

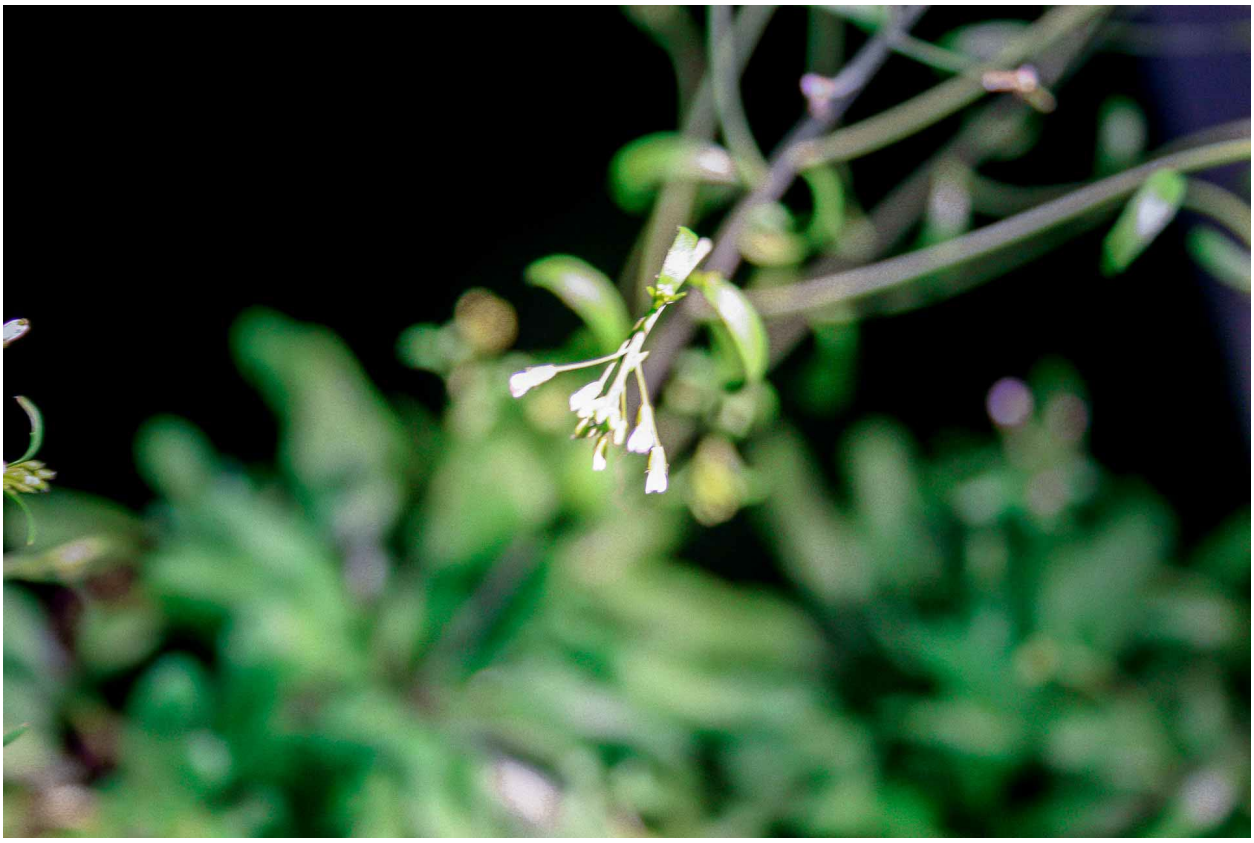


Figure 1 Banner image of Arabidopsis by Igor Houwat

MSU-DOE Plant Research Laboratory scientists are refining our understanding of how light wavelengths impact how plants develop their chloroplasts.

Chloroplasts are the 'engines' of plants. They use light from the sun and carbon dioxide to produce energy compounds, through the process of photosynthesis. Chloroplasts are full of, chlorophyll, a pigment that absorbs sunlight to kick off that process. (Chlorophyll is what gives plants their green color.)

Scientists know the major players that build chloroplasts and fill them with chlorophyll. But they don't know enough about how a plant's environment can affect this process.

Take light. It has many qualities, like strength of emission or wavelength. Each variable can hinder or improve a plant's health.

"One big aim behind studying chloroplasts, and photosynthesis, is to grow more productive crops. We already know much about the major processes that happen inside a plant. Now, the field is trying to

understand the many roles played by a plant's environment. And light is one of many factors that challenge plants daily," says Hussien Alameldin, a post-doc in the **lab of Beronda Montgomery**.

In a new study, the Montgomery lab examines how far-red light impacts chloroplast development in seedlings. The protein Sigma factor 6 (SIG6), already known to contribute to chloroplast development, plays a big role in these early stages of a plant's life. The study is **published in the American Journal of Botany**.

A network of light detectors

Far-red is at the extreme end of the visible light spectrum, just before infra-red. Plants have light-absorbing signaling proteins, called phytochromes, to detect that wavelength.

It turns out too much exposure to far-red is harmful to plants.

"If we expose wild plants to excessive amounts of far-red at an early stage, and then transfer them to normal, white light, they do not 'green.' In other words, the chloroplasts don't accumulate enough chlorophyll pigments and are thus less healthy and productive," says Hussien.

"The phytochromes' ability to detect far-red somehow leads to this block of 'greening'."

To understand why, the Montgomery lab tested lab plants under extreme far-red exposure.

They grew mutant plants, each missing a gene related to chloroplast development or light detection. They exposed the plants to far-red light over the first five days of growth– a much higher exposure level compared to plants' experience in nature. The team then transferred the plants back to normal white light to examine how each mutant fared.

Enter the SIG6 protein

"The plants without the SIG6 protein stood out. These plants developed green leaves, even under these extreme conditions. This indicates SIG6 plays a role in regulating this block of greening mechanism," Hussien says.

Next, the science team explored SIG6's influence on other proteins related to chloroplast development. The mutants lacking *SIG6* gene had higher levels of expression of other genes that encode:

- proteins that help accumulate chlorophyll (PORA)
- proteins that play a role in the very last step of chlorophyll production (HEMA1), when exposed to far-red light.

"There are a lot of connections to explore in this network. But we have tried to create a molecular model for SIG6," Hussien says. "SIG6 might work on its own to control the chlorophyll-producing proteins under far-red. As for the connection with the light detecting phytochromes, we are still exploring how that relationship works."

A common metabolic currency tunes growth-defense balance in plants

4/7/20

Igor Houwat, Ian Major

When plants defend against a threat, their growth slows to a crawl. In their efforts to understand why, the Howe lab is constantly pushing the limits: how high can one tune plant defenses before a plant goes belly up?

Their new study, **published in Plant Physiology** (**and featured on the journal's June 2020 issue cover**), suggests a new metabolism-sensing mechanism that may mediate between growth and defense functions.

Plant defense is controlled in part by a collection of genes, called JAZ. When all is well, JAZs are the car brakes that keep defense mechanisms from speeding out of control. Once danger arises – say attack from hungry caterpillars – the JAZs are broken down, the brakes released. Plant defense responses are put into gear.

There is a catch. Plants in defense mode slow down their growth. To probe this mystery, the lab of **Gregg Howe** at the MSU-DOE Plant Research Laboratory has been gradually removing the genetic brakes from the model plant, Arabidopsis. There are 13 JAZ genes in Arabidopsis, and with each extra gene removed, the plants get smaller.

'Seeing' the light vs. defense mode

In 2016, the lab made a breakthrough towards understanding the defense vs growth dynamic.

"**We grew a plant missing 5 of the 13 JAZ genes**. It was better defended but smaller in size," says **Ian Major**, a post-doc in the Howe lab. "We showed that its defense system conflicts with a light detection system. This light detection system receives cues – about neighboring plant competitors and other factors that affect surrounding light conditions – to control how plants grow and develop."

When the team removed a key light detector – called Phytochrome B – growth and defense were no longer at odds.

"Our plant recovered normal growth patterns and kept its strong defenses," Ian says. "We found a sweet spot, a plant that defends and grows at the same time."

Caterpillar on an Arabidopsis plant
By Kurt Stepnitz, © 2006 University Relations - Michigan State University

Fast forward to 2020. **The Howe lab has to date removed 10 of the 13 JAZ braking components**. The result is a relatively healthy and well defended plant – albeit much smaller – called *jazD*.

"With fewer JAZ proteins left, *jazD* plants have stronger defenses. It is more resistant to caterpillars. It is also more resistant to some pathogens, which we didn't see before," Ian says. "When we remove the phytochrome B light detection system, *jazD* also retains a strong defense capability. "

"But, unlike what we saw in 2016, *jazD* does not recover its growth."

A Sensing mechanism that slows growth?

This new study reveals a potential sensing mechanism – other than light detection – that is integrated with the defense system.

One possibility is that the flood of extra defense compounds produced by *jazD* are taxing on metabolism. The concept itself is not new: defended plants restrict the flow of resources to growth so that the high-speed defense production doesn't deplete its energy reserves.

"The new information about *jazD* plants show us is that plants might shape their metabolism towards making defenses," Ian says. "One of these metabolic changes is higher levels of a key amino acid nutrient, tryptophan."

“We see higher tryptophan levels before and after removing the light detection gene. This might be the clue linking growth and defense processes in Arabidopsis. We think the plant senses these metabolic changes to adjust growth accordingly.”

The sensing mechanism itself remains unknown. However, unpublished data on *jazD* has revealed other genetic mutations that actually improve its growth.

“Hopefully, one of these new genes will indicate how metabolism is sensed,” Ian adds. “Regardless, this study indicates that current models to explain how elevated defense inhibits plant growth need to be refined and further tested.”

This work was primarily funded by the **US Department of Energy, Office of Basic Energy Sciences**, with additional funding from the MSU Plant Resilience Institute and Michigan AgBioResearch.

Plants control microbiome diversity inside leaves to promote health [VIDEO]

4/9/20

Igor Houwat, Sheng Yang He

Figure 1 Banner image credit: Shutterstock/Sinitar

In a **new study**, published in the journal Nature, Michigan State University scientists show how plant genes select which microbes get to live inside their leaves in order stay healthy.

This is the first study to show a causal relationship between plant health and assembly of the microbial community in the phyllosphere — the total above-ground portions of plants. The work suggests that organisms, from plants to animals, may share a similar strategy to control their microbiomes.

Microbiome studies are a hot topic in human health science. When scientists mention that human 'gut bacteria' should be well balanced, they refer to the gut microbiome, the genetic material of all the microbes living in human digestive systems.

"The field of large-scale plant microbiome study is only about a decade old," said **Sheng Yang He**, lead co-author of the study, a member of the **MSU-DOE Plant Research Laboratory** and a **Howard Hughes Medical Institute Investigator**. "We want to know if plants need a properly assembled phyllosphere microbiome.

https://youtu.be/vVeUI-DeJ-0

Plant genes: gatekeepers of microbes

“In nature, plants are bombarded by zillions of microbes,” He said. “If everything is allowed to grow in the plants, it would probably be a mess. We want to know if the numbers and types of microbes matter, if there is a perfect composition of microbes. If so, do plants have a genetic system to host and nurture the right microbiome?”

It seems plants do. The newly discovered mechanism involves two genetic networks. One involves the plant immune system and the other controls hydration levels inside leaves. Both networks work together to select which microbes survive inside of plant leaves.

“When we remove both networks from a plant, the microbiome composition inside the leaves changes,” He said. “The numbers and mix of bacteria types are abnormal, and our team sees symptoms of tissue damage in plants.”

“The symptoms are conceptually like those associated with inflammatory bowel disease in humans,” he said. “This is probably because the genes involved are ancient, in evolutionary terms. These genes are found in most plants, while some even have similarities to those involved in animal immunity. “

According to the scientists in the He lab, this may be the first time dysbiosis-associated sickness is formally described in the plant kingdom. The fact it seems conceptually similar to human health suggests a fundamental process in life.

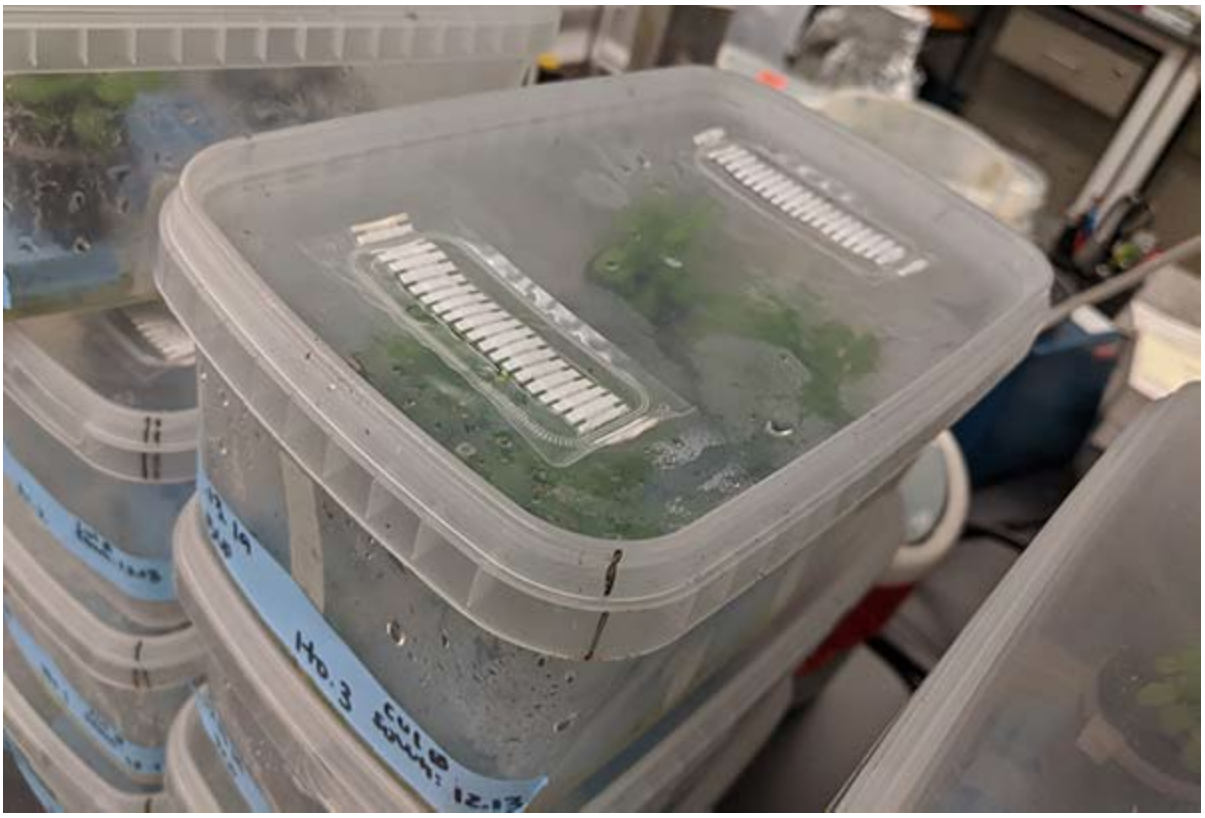
Developing new tech to determine causality

The reason it is difficult to find causality in microbiome studies is because it is practically impossible to cut through the noise of zillions of microbes.

The He lab has worked around this problem by developing a germ-free growth chamber they call the gnotobiotic system – an environment for rearing organisms in which all the microorganisms are either known or excluded.

“Very few people have grown a sterile plant in sterile, organic-rich material,” He said. “Our system uses a peat-based soil-like substrate, basically greenhouse potting soil. We use heat and pressure to kill all the germs in the soil, and the plants can grow under this germ-free condition.”

Researchers can then introduce microbes in a controlled fashion, into this environment.



Gnotobiotic chambers stacked on top of each other
By MSU-DOE Plant Research Laboratory, 2020

“You can add one, two, or even a community of bacteria,” He said. “In our study, we extracted a community of bacteria from dysbiotic, or sick, plants and introduced them to our healthy plants, and vice-versa. We found that both the microbiome composition and the plant genetic systems are required for plant health.”

For example, a plant with defective genetics could not take advantage of a microbiome transplanted from a healthy plant. The microbiome slowly reverted to the state that caused sickness.

On the other end, a healthy plant exposed to a sick plant’s microbiome also suffered. Although it had the genetic tools to select the right microbes, microbe availability was limited and abnormal. The plant couldn’t fix the situation.

Microbe levels and composition matter

It turns out that increased microbiome diversity correlates with plant health. Somehow, plant genes are gatekeepers that encourage this diversity.

The sick plants in the study had 100 times more microbes in a leaf, compared to a healthy plant. But the population was less diverse. To figure out why, the scientists did thousands of one-on-one bacteria face-offs to tease out which strains were aggressive.


A sick plant (left) has 100 times more microbes in its leaves, but the population is less diverse.
By Kinya Nomura, He lab

In the sick plants, proteobacteria strains – many of which are harmful to plants – jumped from two-thirds the composition of a healthy microbiome to 96% in the abnormal population. Fermicutes strains, many which may be helpful to plants, went down in numbers.

“Perhaps, when the population of microbiome is abnormally higher in that sick plant, the microbes are physically too close to each other,” He said. “Suddenly, they fight over resources, and the aggressive – in this case harmful – ones unfortunately win. Healthy plants seem to prevent this takeover from happening.”

The big picture: supporting plant health

The study is yet another example of how diversity is important to support healthy living systems. Each type of microbe might impart different benefits to plants, like increased immunity, stress tolerance, or nutrient absorption.

Scientists such as He want to be able to manipulate the plant genetic system to reconfigure the plant microbiome. Plants could become more efficient at selecting their microbial partners and experience improved plant health, resilience, and productivity.

“Our field is still young,” He said. “Microbiome research tends to focus on human gut bacteria. But many more bacteria live on plant leaves, the lungs of our planet. It would be wonderful to understand how microbes impact the health of the phyllosphere in natural ecosystems and crop fields.”

Credits: *Scientists in the He lab who contributed to this study include former lab member Xiufang Xin and current lab members Tao Chen and Kinya Nomura. The work was funded by the National Institutes of Health, the Howard Hughes Medical Institute, the MSU Plant Resilience Institute, the U.S. Department of Energy Office of Science, and CAS Center for Excellence in Molecular Plant Sciences/Institute of Plant Physiology and Ecology, Shanghai, China.*

Lumen Chao starts new position at Children's National Hospital

4/20/20

Igor Houwat

Figure 1 Banner image courtesy of Lumen Chao

Lumen Chao, a former postdoc from the **lab of Michael Thomashow**, will join Dr. Wei Li's lab at Children's National Hospital in Washington D.C. as a postdoctoral research fellow.

Lumen will use genome-wide CRISPR screen and Single-cell RNA-seq technology to systematically identify critical genes and potential drug targets in brain tumors.

Dr. Wei Li is an expert on developing computational solutions for efficient CRISPR screens including sgRNA design algorithms, algorithms for processing and modeling of pooled CRISPR screens, and algorithms for modeling single-cell CRISPR screens.

"I have trained as an experimental biologist for more than ten years, and I am highly skilled in genetics, molecular biology, cell biology, and biochemistry," Lumen says. "Dr. Li and I hope to integrate our expertise in both computational biology and experimental biology. My skill set will provide me the ability to quickly establish a fundamental molecular biology lab as well as to master new methods and technologies to conduct research at **Children's National Hospital**."

Lumen has been a research associate in the Thomashow lab since 2017. Her research has focused on genetic and epigenetic regulatory networks of **CAMTA transcription factors**, which are master regulators of cold and immune responses in plants.

"I always feel lucky to have spent my first three years of postdoctoral training at the MSU-DOE Plant Research Laboratory (PRL)," Lumen says. "With a number of leading plant scientists and cutting-edge

research facilities, PRL is the best place to conduct plant science, as well as to prepare for advancing one's career."

Lumen Chao, far left, with Dr. Michael Thomashow, second from right.
Courtesy of Lumen Chao

Lumen reserves some warm words for her lab mentor, saying, "I cherish every single day working with Mike [Thomashow]. He is a real model for how to be the best scientist you can be, one with great passion, critical thinking skills, dedication, open mindedness and a thirst for life-long learning."

"I also really enjoyed the working environment on the MPS 4th floor, where I have been able to freely discuss various topics and share research experiences with my co-workers, as well as colleagues from the He, Day, and Howe labs," Lumen adds. "I have learned all kinds of experimental skills that have helped me to conduct research more efficiently. I feel confident enough to switch to any other molecular biology field."

Mike Thomashow, Lumen's mentor, says, "It has been wonderful having Lumen in the lab. She has made important contributions to our long-term goal of understanding how plants sense low temperature and activate regulatory pathways that contribute to freezing tolerance and pathogen defense. Indeed, Lumen is a highly talented scientist who I think is destined to make important contributions in addressing whatever biological questions she chooses to work on."

Exploring human genome biology, specifically the molecular networks of certain types of cancer, has long been an interest of Lumen's.

"It would be a great honor if I could make any contribution to the improvement of human health in the long term, and I am ready to take on this challenge," Lumen says.

Lumen obtained a bachelor's degree in biology at Nanjing University, China, followed by a Ph.D. in Genetics at the University of Chinese Academy of Sciences (UCAS), China.

MSU's Gregg Howe elected to the National Academy of Sciences

5/7/20

Val Osowski, Igor Houwat

Banner image by Anthony Schilmiller

Michigan State University plant scientist **Gregg Howe** has been elected to the **National Academy of Sciences (NAS**). Founded in 1863, the NAS is one of the oldest and most prestigious scientific membership organizations in the United States.

Howe is among 120 new members and 26 international members elected to the NAS in 2020 in recognition of their distinguished and continuing achievements in original research.

He joins 10 current and emeritus MSU faculty as members of NAS.

“Professor Howe has made important contributions to our understanding of the complex biochemical mechanisms through which plants respond to challenges such as insect attack,” said Stephen Hsu, senior vice president for research and innovation at MSU. “His work informs fundamental questions in biology—such as the evolutionary trade-off between defense and growth—that are relevant to all organisms, and also has applications to practical problems such as sustainable agriculture. Michigan State University is very proud of his accomplishments.”


Gregg Howe

By Kurt Stepnitz, MSU University Photographer

Howe, a University Distinguished Professor, MSU Foundation Professor and a member of both the **MSU-DOE Plant Research Laboratory (PRL)** and the **Plant Resilience Institute**, is an internationally recognized leader in research on plant hormone biology and plant-insect interactions. He uses a combination of genetic, cell biological, molecular and biochemical analyses to study how plants use defensive compounds to protect themselves against herbivorous insects. His many honors and awards include selection as a fellow of American Association for the Advancement of Science and the American Society of Plant Biologists, and being named a Clarivate Analytics Highly Cited Researcher for the past six years.

“I am greatly honored to be elected into the National Academy of Sciences,” said Howe, who also a professor in the **Department of Biochemistry and Molecular Biology** in the **MSU College of Natural Science** and an **MSU AgBioResearch** scientist. “This recognition reflects the combined efforts of many talented students and collaborators over the years. I am also grateful for the very supportive research environment and terrific colleagues at MSU.”

“We are delighted about Gregg Howe’s election to the National Academy of Sciences,” said **Christoph Benning**, PRL director. “He has made outstanding contributions to science and the MSU community since his arrival here in 1997, and I congratulate him on behalf of the entire PRL community.”

This year’s election brings the total number of active NAS members to 2,403 and the total number of international members to 501. International members are nonvoting members of the academy, with citizenship outside the United States.

For a complete list of the 2020 NAS cohort (available in July), visit **http://www.nasonline.org/news-and-multimedia/news/2020-nas-election.html**.

New method tracks cyanobacteria photosynthetic productivity, in real time

5/29/20

Igor Houwat, Brandon Rohnke

MSU-DOE Plant Research Laboratory scientists have established a new method to quantify how much cyanobacteria assimilate carbon in the process of photosynthesis, in real time. The study is **published in mBio**.

Photosynthesis captures energy from sunlight in order to make carbohydrates, energy compounds that power life on Earth. The key ingredient in those compounds is carbon. That is why measuring how much carbon cyanobacteria assimilate is a good indicator of how productive they are.

The new method can assess carbon assimilation over a stretch of time. It also better factors in a wider range of environmental variables. Such variables include changing carbon dioxide (CO_2) levels or varying light intensities.

“Our method was enabled by Dr. David Hanson, whose team pioneered a way of putting aquatic, photosynthetic organisms on semi-wet filter discs. Having a solid disc allows us to measure the photosynthetic rates of algae and cyanobacteria in gas-exchange chambers, typically used for plant leaves,” says **Brandon Rohnke**, post-doc in the **lab of Beronda Montgomery**.

In these gas-exchange chambers, the cyanobacteria are fed set amounts of CO_2. Within minutes, researchers can measure how much CO_2 the organisms take up and assimilate.

Then, researchers develop, in real time, so-called carbon response curves. The curves help measure how much carbon the cyanobacteria can pick up from the air and have available to produce the energy compounds.

“Compared to current established methods, this new system makes it easier to monitor the carbon assimilation rate,” Brandon says. “We also can measure how cyanobacteria respond to shifts in environmental conditions, which is not as possible with the established methods.”

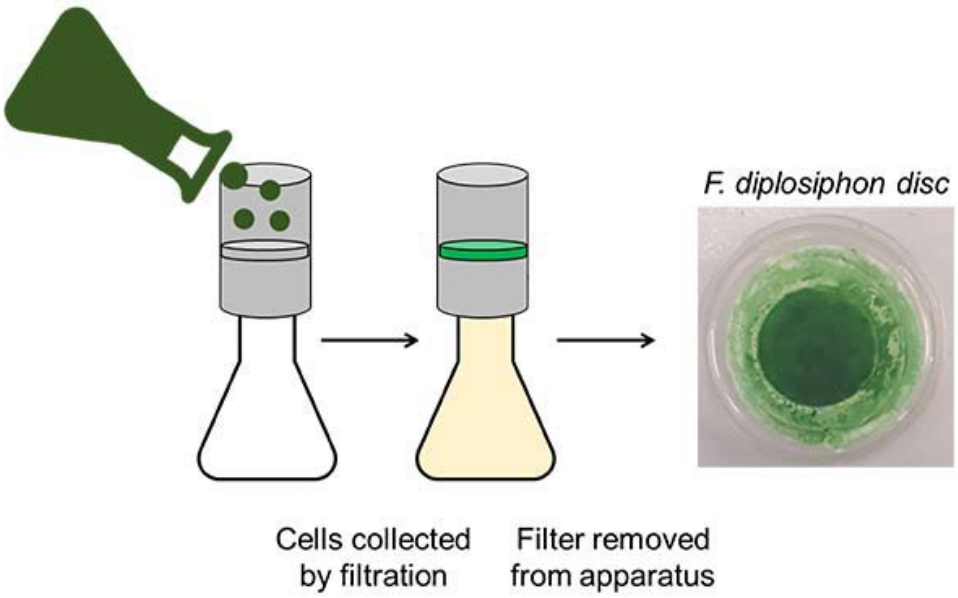


Figure to describe the methodology of the filtered-disc method for cyanobacteria. The disc collected at the end can be inserted in a gas-exchange chamber for carbon response curve analysis.
*By the Montgomery lab, derived from **mBio**, CC BY 4.0*

Improving on previous measuring systems

The Montgomery lab studies how small changes in cyanobacteria's carbon processing system affects their productivity.

"We have a tough time examining minute changes in the carbon concentrating mechanism and determining how relevant they may be to an organism's fitness and survival," Brandon adds. "Even though we have a catalog of cyanobacteria strains that react differently to surrounding environmental conditions, we previously had limited methods to quantify how those changes affect a cell's actual ability to fix carbon."

Established methods take hours to run, generally can only measure the endpoint outcome related to CO_2 uptake and usage, and are challenging.

For example, one standard way is to grow cyanobacteria in a liquid culture. Then scientists measure how quickly the organisms release oxygen into the liquid. Since oxygen is a byproduct of photosynthesis, the measurement infers photosynthetic productivity. But, the result is indirect, a proxy.

Meanwhile, more direct methods can't easily monitor how organisms adapt to changes in their environment. Everytime scientists want to measure the impact of a different concentration of carbon, using endpoint measures, they have to use a new batch of organisms. And liquid cultures take hours to reach a state of equilibrium where scientists can accurately measure CO_2.

Contrastingly, the new method drastically reduces the technical and time challenges.

“The small amount of water on our solid disks allows for much more exposure to air. It takes two to five minutes for cyanobacteria to adjust to the levels of CO_2 we have fed them. We perform the carbon response curves in a matter of minutes and can cover a range of CO_2 levels.”

So, does it work?

The short answer: yes.

The Montgomery lab has tried the method with the cyanobacterium *Fremyella diplosiphon*, which has long-studied, distinct responses to **red or green light availability**.

The method reveals how light color, cell shape, and levels of photosynthetic pigments might impact how *Fremyella* assimilates CO_2.

Specifically, green light encourages slightly higher assimilation levels, compared to red light.

“To test our method, we compared it with the established oxygen release method and managed to uncover novel aspects of carbon uptake versus its usage by cells. Another plus is that our measurements are very reproducible,” Brandon says.

“But we’d like to get to the point where we quantify specific photosynthetic variables.”

In other words, instead of just measuring how much carbon has disappeared from the atmosphere into the organisms, scientists want to discern where that carbon ends up in cyanobacterial cells and where there are any bottlenecks.

“It’ll take a while to get there, and more labs would need to adapt and contribute to developing the method,” Brandon says. “But as a relative measure to compare cyanobacteria strains with mutants, it’s already very effective and complements existing methods in the literature.”

This work was primarily funded by the **US Department of Energy, Office of Basic Energy Sciences**. Hero image: The Grand Prismatic Spring of Yellowstone National Park showing steam rising from hot water, which is surrounded by huge mats of brilliant orange algae and bacteria. By Brocken Inaglory (Own work) [**CC BY-SA 3.0** or **GFDL**], **via Wikimedia Commons**

DOE renews funding for innovative photosynthesis research at MSU-DOE Plant Research Laboratory

5/29/20

Igor Houwat

The U.S. Department of Energy (DOE) has awarded the **Michigan State University-DOE Plant Research Laboratory (PRL)** an $11.25 million DOE Office of Basic Energy Sciences (BES) competitive renewal grant to continue its innovative photosynthesis research.

The three-year grant (2020-2023) will allow PRL scientists to continue investigating how photosynthetic organisms work on the molecular level with an eye toward developing new technologies that improve human lives, particularly in the areas of bioenergy, industry and medicine.

"The PRL has a long and distinguished history at MSU," said Stephen Hsu, senior vice president for research and innovation at MSU. "Continued investment in fundamental and applied research related to photosynthesis will yield important benefits in decades to come."

Photosynthesis is a biological process that uses 'basic' ingredients – carbon dioxide, water, and sunlight – to sustainably make food, fuel and chemicals that power life on Earth.

A team of 11 PRL faculty members will lead a group of exceptional postdocs, students and technicians as they explore the fundamental ways photosynthetic organisms capture sunlight to then convert and store it as usable energy. This talent pool represents a wide range of expertise in molecular, synthetic and cell biology, biophysics, biochemistry, plant and microbial physiology, genomics, and genetics.

"One of the most gratifying aspects of the newly funded work at the PRL is that it is made possible by bringing together a highly diverse group of scientists with complementary expertise," said **Christoph Benning**, PRL director and principal investigator on the grant. "This range of talents gives us a chance to tackle some of the most fundamental biological questions related to photosynthesis."

With the support provided in this new phase of funding, PRL scientists will study photosynthetic processes across various scales that range from basic enzymes and reactions, to how photosynthesis integrates into their host organisms, to how these organisms interact with the environment.The group will also apply biological engineering techniques to improve photosynthetic productivity. More specifically, the grant covers three areas:

- **Understanding how photosynthesis works in the 'real world'**: Natural environments are unpredictable. Light conditions can change in fractions of a second; temperature extremes are common. Photosynthetic productivity (and by extension, crop yield) is limited by these challenges in ways that we do not fully understand.
- **Understanding how organisms integrate the energy harvested from photosynthesis:** Photosynthetic organisms must balance energy supply with metabolic needs such as plant leaf growth or algal reproduction. Maintaining balance is crucial to build healthy organisms and to avoid negative reactions.
- **Using synthetic biology to understand cyanobacterial photosynthesis:** Cyanobacteria are some of the most successful photosynthetic organisms. The team will use engineering principles to

explore the basis of their success and to harvest cyanobacterial parts to build new technologies. These advances could benefit such fields as medicine, bioenergy and industry.

Over the past decade, the PRL – supported by DOE-BES, MSU and **MSU AgBioResearch** – has developed **new technologies** to reposition itself as a leading center for photosynthesis research. The next grant cycle will rely on these tools, which include:

- Growth chambers that recreate external environmental conditions in the lab and quantify measurable signals produced by plant photosynthetic processes
- Hand-held devices that can measure plant photosynthesis and health parameters in the field
- Reactors that enable scientists to study algae in the same conditions found in outdoor ponds, but in the confines of the lab
- New methods to analyze and model plant metabolism and strategies to divert metabolism into useful products
- New tools to engineer cyanobacteria and plants, including devices for introducing custom biochemical reactions inside subcellular compartments that can be powered by photosynthesis

“Advances in basic science will benefit the wider scientific community and align with the long-term mission of DOE-BES,” said Benning, who is also a University Distinguished Professor and MSU Foundation Professor of biochemistry and molecular biology in the **College of Natural Science**. “We will encounter some difficult scientific problems. However, our synergistic approach and collaborations with MSU's vibrant plant science community will be key to our success. We are bringing together scientists from various backgrounds to enable discoveries that would not be otherwise possible.”

Established in 1965, the MSU-DOE Plant Research Laboratory is a joint venture between the U.S. Department of Energy, Division of Chemical Sciences, Geosciences, and Biosciences, Office of Basic Energy Sciences (DOE-BES); and Michigan State University. The PRL marked its 50th anniversary in 2015.

Tomomi Takeuchi and Eric Poliner start new positions at Michigan biotech companies

6/2/20

Igor Houwat

MSU-DOE Plant Research Laboratory (PRL) couple, Tomomi Takeuchi and Eric Poliner, have each joined a Michigan-based biotech company this past month.

Tomomi is employed by Charles River Labs in Mattawan, MI, in the Biomarkers and Investigative Pathology Unit.

Charles River is a drug manufacturer with 90+ facilities in over 20 countries and over 14,000 employees. The company is a contract research organization that offers a range of services that span the **drug discovery and development continuum**. The company's site in Mattwan, MI primarily deals with safety assessments of novel therapeutics.

Tomomi, in her new Scientist position, will tackle developing and validating methods and procedures to test chemical entities or study chemical compounds in vitro or in vivo.

Tomomi Takeuchi
By Igor Houwat, MSU-DOE Plant Research Laboratory, 2020

"Michigan State University and the Benning lab have been a great place for me to develop my skills as a scientist, and I hope I can apply them in my new job in the industry to make positive impacts on people's lives," Tomomi says.

Eric, in turn, is a Laboratory Scientist with Physicians Toxicology in Kalamazoo, MI. **The company specializes** in delivering custom medication monitoring, personalized service, and education. Eric will be developing test protocols for new quality assurance applications.

"I would like to thank and credit PRL for being a great learning environment for me and giving me a lot of opportunity as I move forward with my career," Eric says.

Congrats Eric and Tomomi!

Brandon Rohnke named AAAS Science & Technology Policy Fellow

6/9/20

Igor Houwat

Brandon Rohnke, a postdoc at the MSU-DOE Plant Research Laboratory (PRL), has accepted an offer to be a Science & Technology Policy Fellow with the American Association for the Advancement of Science (AAAS).

AAAS Science & Technology Policy Fellowships (STPF) aim to connect science with policy makers and to foster a network of science and engineering leaders who understand government and policymaking. "[Fellows] learn first-hand about policymaking and contribute their knowledge and analytical skills in the policy realm. Fellows serve yearlong assignments in the federal government... Each year, [the program] adds to a growing corps over 3,400 strong of policy-savvy leaders working across academia, government, nonprofits, and industry.

Brandon, who is currently in the **lab of Beronda Montgomery**, will be placed at the U.S. Department of Energy's Office of Basic Energy Sciences in Washington D.C., where he will contribute to communicating and quantifying the impact of basic research funded by the DOE.

"I'm incredibly excited to use my background in photosynthesis research to be an advocate for the importance of basic science in the energy sphere," Brandon says. "The DOE-BES has done amazing work at Michigan State University through the PRL, so I am very grateful for the opportunity to contribute to the office's work."

A portrait of Brandon Rohnke
Courtesy of Brandon Rohnke

“Since his very first days as a graduate student at MSU, Brandon has expressed an interest in science policy and policy-relevant science communication,” says Beronda Montgomery, Brandon’s mentor and a MSU Foundation Professor at the PRL. “It’s been an absolute pleasure to watch Brandon’s journey at MSU and I’m thrilled that he’s been accepted as a fellow in the highly competitive AAAS STPF program. I look forward to see the contributions that he’ll make in this new adventure.”

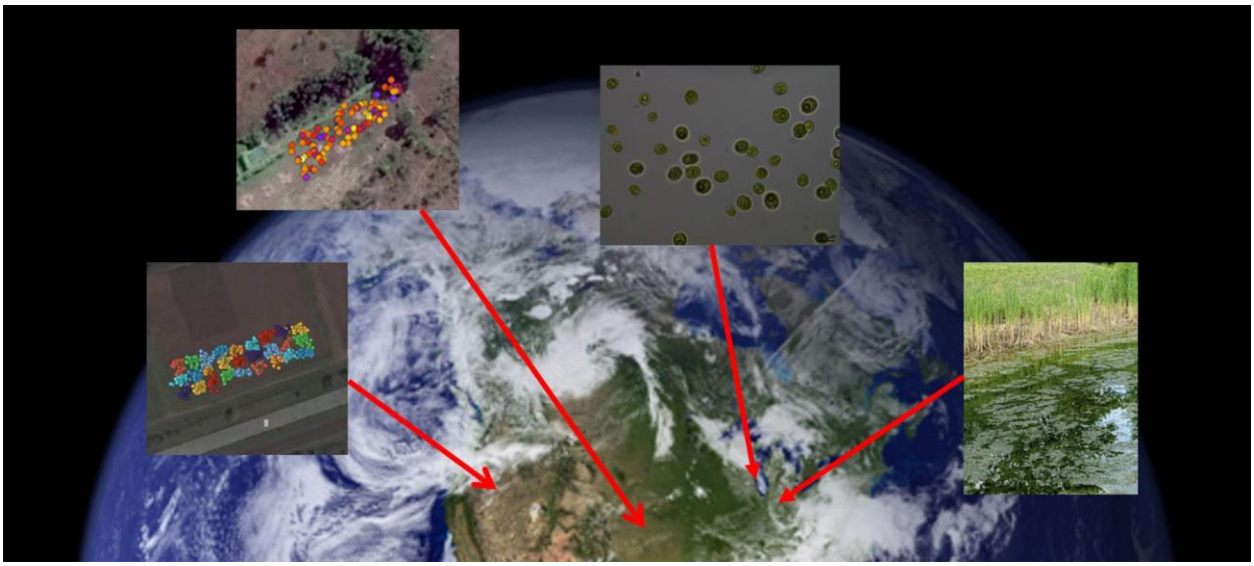
Brandon received BAs in Chemistry and Religion at St. Olaf College in 2014 and, recently, a **PhD in Biochemistry and Molecular Biology at Michigan State University**.

The **AAAS** seeks to "advance science, engineering, and innovation throughout the world for the benefit of all people." The scientific society has individual members in more than 91 countries and is publisher of the *Science* family of journals. The AAAS Science & Technology Policy Fellowships program began in 1973. Today, STPF places more than 250 fellows each year in all branches of federal government.

The diverse ways photosynthesis balances its energy budget

6/24/20

Igor Houwat, Atsuko Kanazawa



Banner image by Kramer lab

Atsuko Kanazawa and members of the lab of David Kramer at the **MSU-DOE Plant Research Laboratory (PRL)** have published a new paper that reveals how nature has come up with diverse solutions for photosynthetic organisms to safely harvest sunlight. The paper is included as a chapter in a new book, Photosynthesis in Algae: Biochemical and Physiological Mechanisms, published by Springer.

The majority of past studies in this area of photosynthesis research have been conducted with two model systems. Those include terrestrial plants, mainly a small plant called Arabidopsis, and a green alga called *Chlamydomonas reinhardtii*.

"It's as if we tried to understand *something* by only looking at two examples…you compare the performance of say, a Ford Mustang and a Lamborghini Huracan, and generalize it to other vehicles. Is it reasonable? How about a motorcycle, a semi-truck or a combine harvester? Or a submarine? They certainly have different kinds of performance abilities," says **Atsuko, who is a Research Assistant Professor at the PRL**.

"Choosing a few so-called 'model systems' for intensive study made a lot of sense in the past, when it was difficult to get genetic information and measure photosynthetic processes. Now, with cheap and rapid genome sequencing and hand-held devices that can probe the inner workings of photosynthesis in great detail, we can expand our studies to include a more diverse set of species."

Atsuko Kanazawa
By Igor Houwat, MSU-DOE Plant Research Laboratory, 2018

In the new review chapter, the authors introduce the basic energy balancing model developed for the higher plant chloroplast system. Then, they compare the model with selected aquatic systems to address how the different systems need to re-balance the energy input and partitioning.

David, Hannah Distinguished Professor at the PRL, says, "The main point is that all organisms have a common problem: photosynthesis is dangerous. If too much energy is taken up and cannot be used, toxic intermediates can build up. Different organisms have found distinct ways to protect themselves from that danger. They all do it by dissipating (getting rid of) excess light energy, but the way they do that is very different, and each way introduces its own set of additional problems that nature has had to fix as well."

The article synthesizes a wide range of recent studies that show how these knock-on effects impact the efficiency and productivity of photosynthesis across species. This body of research provides some clues about how humans can improve the productivity of its crops.

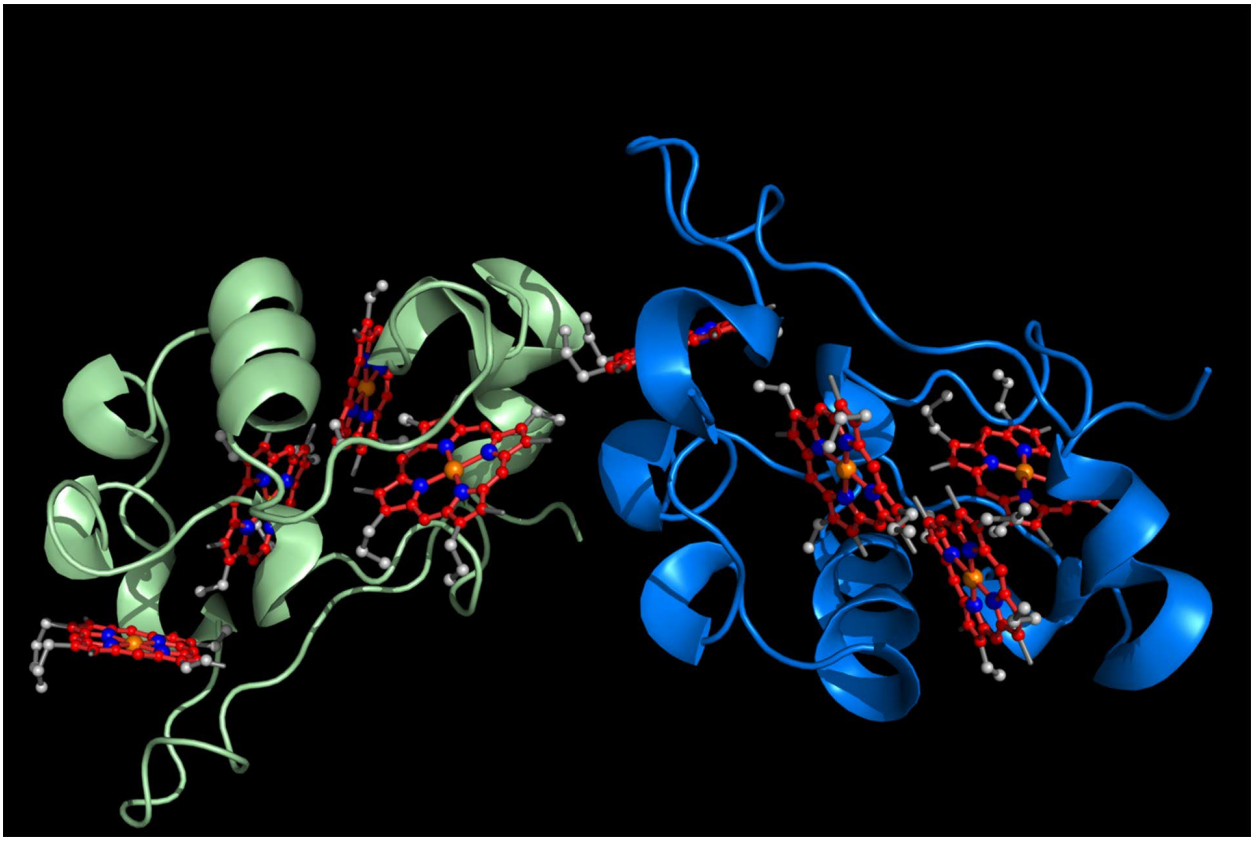
The new book is a unique look at photosynthesis in algae and cyanobacteria. Each chapter is written by authors who are world experts in their fields, which include biofuels, bioenergy and genome sciences. It is aimed at 'researchers, environmentalists, and planners in a range of areas including those of marine resources, nutrient control and pollution of water bodies and that growing body of concerned citizens interested in controlling carbon emissions and global warming.'

*The book chapter is, **Diversity in Photoprotection and Energy Balancing in Terrestrial and Aquatic Phototrophs**. Contributing authors are Atsuko Kanazawa, Peter Neofotis, Geoffry A. Davis, Nicholas Fisher, and David M. Kramer.*

Harnessing the power of biology: Scientists 'go the distance' in electron transfer study

7/6/20

Igor Houwat, Jingcheng Huang, David Kramer, Danny Ducat



In one video, you see a dark, opaque surface, pulsating slowly. All of a sudden, a flash of light streaks across the surface with the intensity of a lightning bolt. The light spreads out, lingers brilliantly for a moment, before it melts away.

We are looking at millions of electrons buzzing within an artificial crystal, made of proteins. The electrons randomly hop between a network of electron carriers.

https://youtu.be/VA_Ix_mi7rw

The video is part of a **new study**, recently published in the Journal of the American Chemical Society, from the labs of **David M. Kramer**, Hannah Distinguished Professor, and **Daniel (Danny) Ducat**, associate professor, in the **MSU-DOE Plant Research Laboratory**. The work explores how electrons can move across long distances within biomaterials, such as proteins.

Electron movement – what scientists call electron transfer – powers many of life's functions. A good deal of the energy we derive from the foods we eat is captured by a process that removes electrons from food molecules, like sugar or fat, and transfers them to the oxygen we breathe.

Scientists are trying to harvest this ‘electricity from biology’ to power our technologies and produce new products, such as high-value medical compounds and hydrogen gas as a clean fuel source. We have a lot of ability to control electron transfer in metals or semiconductors, for example in batteries. Yet our control over electrons in living, biological systems is more limited. Researchers know a lot about electron transfer over very small distances - say, across tens of atoms. But the process of moving electrons over larger distances - even the length of one cell - remains somewhat of a mystery.

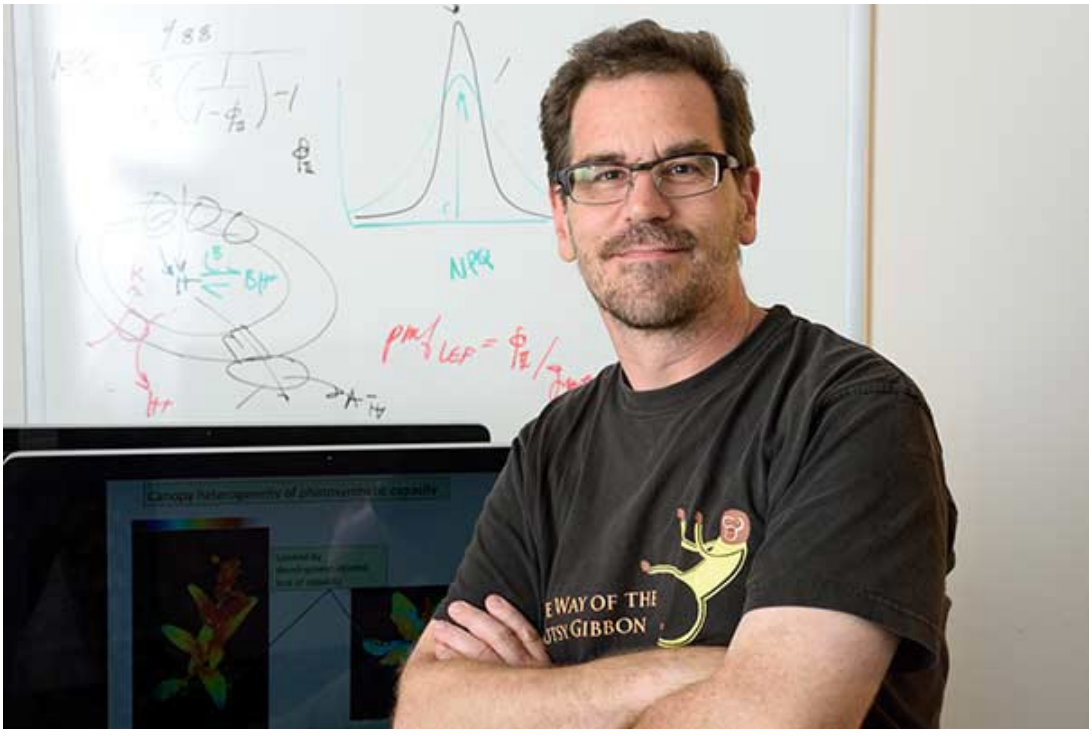
“One common way cells move electrons is to shuttle them around on small protein electron carriers,” Kramer says. “The carriers are ‘docking areas’ that carry the electrons around in a safe way around the cell. But, this method is not very efficient because it is undirected; the electrons move in a random way. Also, if oxygen comes into contact with these proteins, it can hijack the electrons and form toxic reactive oxygen species that can kill the cell.”

These issues have caused scientists to grapple with how to safely target the movement of electrons from one point to another.

Crystal sheets made of proteins

In the study, the labs report a new solid-state system that does just that. It consists of billions of biological electron carriers (cytochromes, named for their vivid red colors) arranged in a 3D crystal so that their electron carrying centers (hemes) are nearly in contact with each other. Electrons added into one part of the crystal rapidly hop from one carrier to another, moving across the entire length of the crystal.

The crystals are long and thin, so that the electrons move large distances. The crystals also protect the electrons from encountering oxygen. This feature could make electron transfer safer and more efficient.



In a new study, David M. Kramer, an expert in bioenergetics and photosynthesis electron and proton transfer

reactions, and his colleagues examine how electron transfer can occur safely and efficiently over long distances.
By Harley J Seeley, 2013

The new system mimics that of one found in some bacteria, like *Shewanella*. These organisms have evolved structures, dubbed “nanowires”, that allow electrons to move over fairly long distances, about as long as a typical bacterial cell. The new crystal “wires” are so much longer in comparison that one can even see them with the naked eye.

The team will use this system to examine the challenges behind long-range electron transfer.

“When a system contains thousands of loose parts, electron transfer is impacted by many factors,” says **Jingcheng Huang**, a postdoc in both the Kramer and Ducat labs. “The larger the system, the more unpredictable the electron transfer, compared to a single point-to-point jump.”

“Without a physical model to work with, like our crystals, it is hard to extrapolate the dynamics of short jumps onto larger surface areas. Our challenge will be to figure out how to efficiently move electrons over long distances, say microns (thousands of nanometers), which is necessary to create this futuristic microbial cell factory or power generation system” Huang adds.

Daniel Ducat (center) is part of a team that are trying to harvest electricity from biology to power our technologies and produce new products, such as high-value medical compounds and hydrogen gas as a clean fuel source.
By Victor DiRita, 2019

Kramer adds, “One very beautiful thing about the crystal wires is that we can make videos of the electrons moving. When an electron is on a heme carrier, the carrier changes its color. We can see electrons moving in real time with a simple video camera. This is allowing us to test whether the theory developed for short distance transfer can work over longer distances. In fact, the work suggests that

some new, and unexpected, factors may become important in these solid-state systems. This new knowledge is pointing the way towards engineering better wires."

The long-range game with these crystalline wires is to harness the electricity for useful applications in fields such as bioenergy and disease.

One idea is to connect two kinds of living cells that would be normally incompatible. For example, a cell that stores energy by photosynthesis could 'wire' the energy to another cell that uses it to make useful products. The wire link would allow both reactions to safely occur in the same space, since photosynthesis makes oxygen, which is toxic to many organisms.

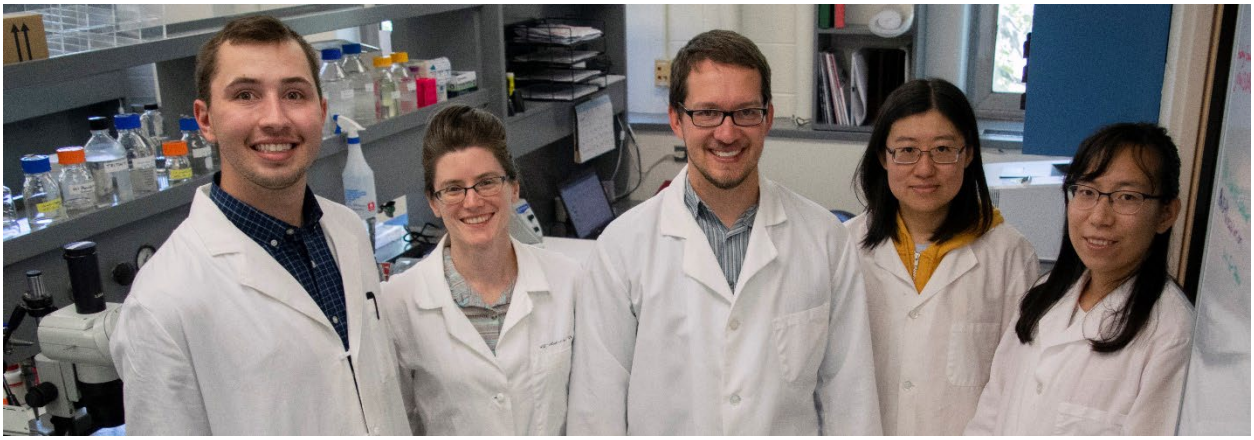
"Indeed, some scientists think that if we can better understand and control the flow of electrons from living organisms, we could build systems where living cells directly communicate with electronic devices," adds Ducat. "This idea may be quite a way off yet. But, such bio-hybrid devices could have a range of applications, from medicines to sustainable energy production."

This work was primarily funded by the **US Department of Energy, Office of Basic Energy Sciences**.
Banner image: One common way cells move electrons is to shuttle them around on small protein electron carriers. This banner image depicts a rendition of electron carrier proteins, with the electron carrying centers in red. By Jingcheng Huang, post-doctoral associate, MSU-DOE Plant Research Laboratory, 2020

NSF-funded project explores plant metabolism links to climate change, human nutrition

7/15/20

Jeff Mason, Berkley Walker, Val Osowski



MSU-DOE Plant Research Laboratory plant biologist **Berkley Walker** is part of a team of scientists that is using a 3-year, $1.4 million National Science Foundation (NSF) Molecular and Cellular Biosciences award to explore the intersection between photorespiration and one-carbon metabolism, two plant biochemical processes that are critical to plant growth and human nutrition.

Photorespiration is a plant process that recycles toxic intermediates produced as a byproduct of photosynthesis and is an essential process needed by the plant to grow. Rates of photorespiration are linked to growing temperature and carbon dioxide concentration, meaning that future rates of photorespiration will change with changing climates. One-carbon metabolism is similarly vital to plant growth and is also the source for essential vitamins such as folate—its deficiency in humans is linked to serious health issues including neural tube defects and heart disease.

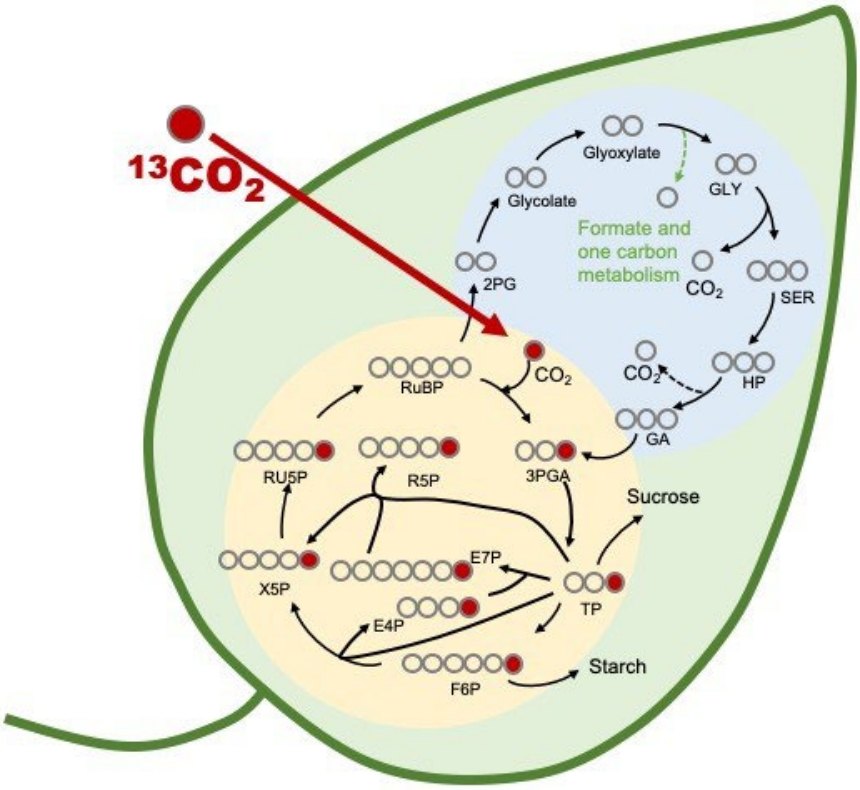
Walker, the MSU principal investigator (PI) on the grant, is teaming up with PI **Sanja Roje** of Washington State University (WSU) to explore novel innovative physiological processes that allow plants to adapt to a variety of environmental conditions, resulting in more resilient crop varieties. Walker and Roje originally met in 2010 when Walker was a graduate student and Roje was a faculty member at WSU, but it wasn't until a chance encounter at last summer's annual American Society of Plant Biologists meeting that they realized their complementary expertise would be perfect to round out this proposal.

Berkley Walker takes samples from leaves in his lab.
By Chelsea Mamott

“This grant gives my lab the resources to look at a question that I have been chasing since I was a graduate student – does photorespiration really look like it does in a textbook, or does it do more for a plant than we currently realize?“ explained Walker, also an assistant professor in the **Department of Plant Biology** in the **MSU College of Natural Science**. “This avenue of research will help us better understand how plants will grow in future climates and how much these climates will effect important pathways for human nutrition.”

The two institutions have each been awarded a separate grant, with Walker’s portion amounting to $681,481. The goal of this project is to help generate models predicting how current and future climatic conditions influence plant performance and yields and inform breeding and engineering approaches to optimize plant productivity and the production of plant compounds important for human nutrition and health.

Walker, with his expertise in photorespiration will chart the course, or flux, of carbon from photorespiration to one-carbon metabolism. This approach combines gas exchange measurements with the use of isotopic tracers that are incorporated into central metabolism and can be measured using mass spectroscopic approaches. These measurements are then interpreted using a structural model of photorespiration and one-carbon metabolism to determine the connections between photorespiration and one-carbon metabolism.



MSU plant biologist Berkley Walker will use labeled carbon molecules to determine how photorespiration and one carbon metabolism are connected.
Graphic by Xinyu Fu

Roje brings a deep understanding of one-carbon metabolism and a group of new mutant plants which have altered concentrations of metabolites shared between photorespiration and one-carbon metabolism. She will lead a deep metabolic characterization of these plants and provide them to Walker to determine exactly how metabolic flux has been altered.

Washington State University molecular plant scientist Sanja Roje will work with Walker to determine how metabolic flux has been altered.
By Anne Mamott

It is expected that the findings will translate to other species, including four of the five most widely cultivated C3 food crops— rice, wheat, potatoes and soybean--because these pathways are conserved among higher plants.

“I’m looking forward to the opportunity to work on an exciting project that may make a meaningful contribution to society,” Roje said. “This project will advance the knowledge of how plants work and add a piece of the puzzle that may be needed in order to grow crops that are better suited to face a broader range of environmental conditions, are more nutrition and are more stress resistant. Also, Berkley has been a lot of fun to work with. He’s very enthusiastic and a good colleague, and that has been an extra bonus.”

In addition to the research, an important component of the project is to communicate the importance of basic plant science to groups that have not historically been exposed to fundamental research. This effort will be pursued through both research- and public-facing activities.

“Research-facing activities at MSU and WSU will include directly engaging these groups in the primary research and recruiting students from underrepresented groups into their laboratories,” said Berkley, who will engage with several MSU-specific programs to recruit undergraduate students into the lab, including the Michigan Louis Stokes Alliance for Minority Participation, the Summer Undergraduate Research Academy and the Leaders Encouraging Academic Development program.

The main public outreach activity of the project is a **Sounds of Science** concert series performance at WSU—a unique collaboration between plant scientists and musicians resulting in a TED-talk style event designed to increase awareness of the importance of plant science.

Sounds of Science started as an unfunded initiative by Walker when he was a postdoctoral researcher at the University of Illinois. With this support, Walker will be able to continue this collaboration with improved scope and production values at not only WSU, but eventually MSU as well.

“While there are a variety of pedagogical strategies employed to communicate and educate the public, music is especially powerful in increasing long-term memory and focus in a variety of contexts,” Walker said. “Additionally, much of the societal importance of plants integrates with the role of photorespiration in plant physiology as investigated in this project.”

Banner image: Berkley Walker (center) poses in the lab with (left to right) graduate student Luke Gregory, lab manager Audrey Johnson, and postdoctoral researchers Han Bao and Xinyu Fu. Photo by Victor Dirita Jr.

PRL alumnus Zhi-Yan Du joins University of Hawaii as assistant professor

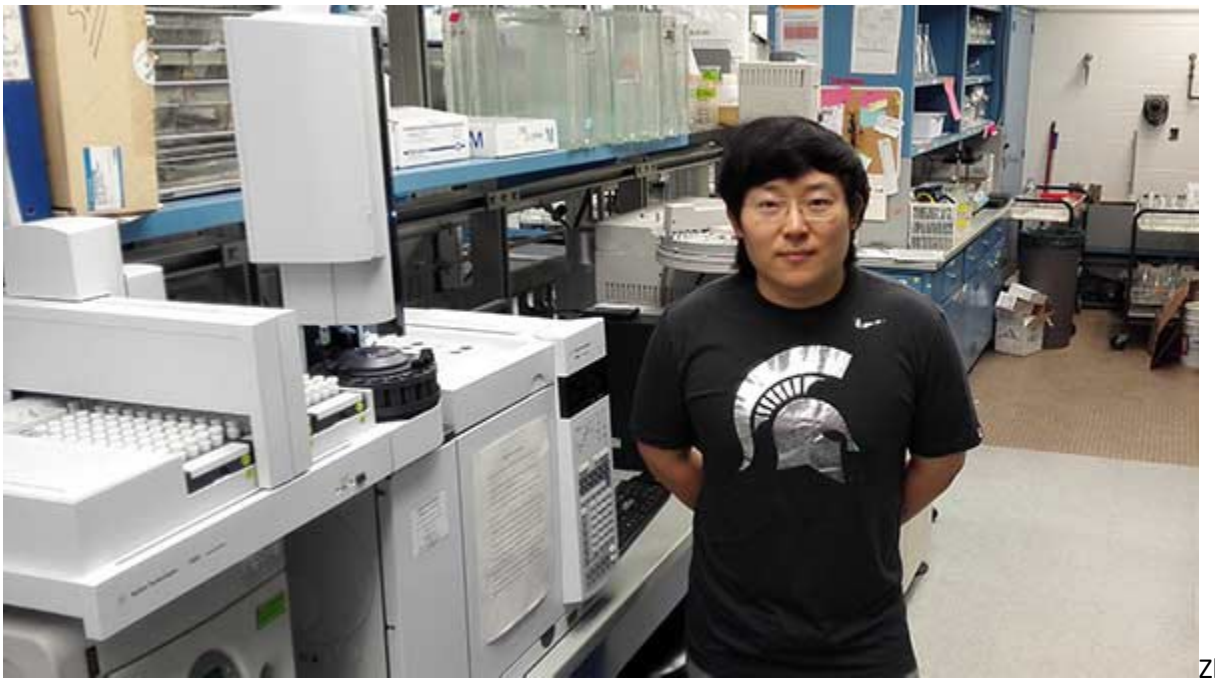
7/23/20

Igor Houwat, Zhi-Yan Du

Zhi-Yan (Rock) Du, a former postdoctoral fellow in the lab of Christoph Benning, will start a new position as Assistant Professor in the **Department of Molecular Biosciences and Bioengineering** at the **University of Hawaii at Mānoa, Honolulu**.

Rock's lab will explore engineering and synthetic approaches to produce valuable bio-products in microalgae and establish co-production systems involving synthetic microbial communities. The lab will also research lipid metabolism in plants, microalgae, fungi, and bacteria, as well as symbiosis among these organisms.

"I enjoyed my experience at the **MSU-DOE Plant Research Laboratory (PRL)** and MSU. It feels like a big family here," Rock says. "I received many great suggestions from the brilliant scientists over here, and I was part of many collaborations that allowed me to further explore my research interests. As I move on in my career, I plan to keep working together with my friends here in the future."



Zhi-Yan Du in the lab
Courtesy of Zhi-Yan Du

Rock joined the **Benning lab** at the MSU-DOE Plant Research Laboratory (PRL) in 2013. He researched how microalgae adapt to stresses in their environments in order to maintain normal activity levels, such as in **photosynthesis**. He also worked on **engineering oleaginous microalgae for fatty acids and other oil products** that are useful for biotech purposes. In that vein, he developed an algae harvesting system

using **oleaginous fungi for valuable bio-products**. This last work was a collaboration between the Benning and **Gregory Bonito** labs at MSU.

In 2018, Rock joined the labs of **Bjoern Hamberger** and Bonito as a research assistant professor. He was awarded with two MTRAC grants to continue his research on the symbiosis between microalgae and fungi. He was the **first to report that eukaryotic microalgae can live inside fungi**. He found that this symbiotic relationship helps both organisms to survive stress conditions and also shows promise for co-production of valuable biomaterials.

“Rock has shown an incredible ability to conceive complex projects and organize a multidisciplinary effort in addressing novel scientific questions with unique outcomes, thereby considerably advancing the field,” says Christoph Benning, his former postdoctoral mentor and PRL Director. “I expect he will hit the ground running in his new position and I wish him the best of luck for his next career move.”

Rock obtained his Ph.D. in Biochemistry and Molecular Biology at the University of Hong Kong, Hong Kong.

Good luck, Rock!

Thomas Sharkey receives NSF grant to study isoprene emission from plants

8/4/20

Igor Houwat, Val Osowski, Thomas D. Sharkey

Building on years of breaktrough research, Michigan State University biochemist **Thomas Sharkey** has received a four-year, $898,946 grant from the National Science Foundation (NSF) to continue his research on isoprene emission from plants. The four-year grant will focus on the evolutionary pattern of the appearance and loss of isoprene emission among various land plants, and the impact of these emissions have on the atmosphere.

Isoprene is a gas molecule given off by many trees, ferns and mosses. The relatively frequent gain and loss of isoprene emissions and its scattered distribution among land plants indicates that the trait is constantly in an evolutionary balancing act, enhancing plant resilience and fitness, but at some cost to the plant. The question facing scientists is: What is it that triggers the coming and going of this trait?

Scientists are yet to fully understand the benefits plants get by making isoprene. What they know so far is that isoprene has been shown to enhance plant tolerance of heat, oxidative stress, and ward off insects that feed on them. Understanding isoprene emission in plants is important for determining if or when it might be useful to engineer crops to make it, or to engineer emitting plants to suppress it.

“We think the benefits and costs to plants of making isoprene are very nearly balanced,” said Sharkey, a University Distinguished Professor at the **MSU-DOE Plant Research Laboratory** and member of the **Department of Biochemistry & Molecular Biology** at the **College of Natural Sciences**. “For some plants, the balance favors isoprene emission, while others are on the cost side of the tipping point. This work will give a much clearer picture of the cost-benefit balance and will help us understand this very important molecule.”

MSU's Thomas Sharkey, front center in this photo of his lab, recently received a 4-year grant from the NSF to continue his research on isoprene emission from plants.
By Victor DiRita, Jr., MSU College of Natural Science

It is also critically important to understand these isoprene emissions because they are a major concern in atmospheric chemistry, contributing to tropospheric ozone formation (the bad ozone, precursor to smog), aerosols and formaldehyde, especially in atmospheres polluted with nitrogen oxide. Plants, particularly trees, emit significant amounts of isoprene into the atmosphere. Because of this, atmospheric modelers need to know how much isoprene is emitted from vegetation and how this may change in the future.

“We believe that a thorough understanding of the forces that shape the evolutionary history of isoprene emission from plants will improve future global emission estimates,” said Sharkey, who also serves as Associate Director with MSU’s **Plant Resilience Institute**.

The study has three primary aims: to investigate the benefits of isoprene emission, the costs of isoprene emission and the genetic mechanisms that isoprene may coopt to relgulate the rate of synthesis and resilience toward plant stress. The overall goal of the research is to determine which specific evolutionary constraints are responsible for selecting for maintenance of isoprene emission in plants and those that favor the loss of the trait.

The scientists will focus on three plants. Two are non isoprene-producing plants, *Arabidopsis thaliana* and tobacco, that have been engineered to make isoprene. The third plant, poplar, makes a lot of isoprene, but has been engineered to stop making the molecule.

Researchers will focus on three plants: Arabidopsis thaliana, tobacco and poplar. A. thaliana (pictured above), is non-isoprene producing plant that will be engineered to make isoprene. Tobacco will also be engineered to produce isoprene. The third plant, poplar, makes a lot of isoprene; it will be engineered to stop making the molecule.
By Igor Houwat, MSU-DOE Plant Research Laboratory

“Information gained from this study will enable us to understand receptors and pathways in plants that facilitate the signaling process of isoprene and how isoprene signaling ‘cross-talks’ with other well-known growth and stress-repsonsive signaling pathways,” Sharkey said. “Knowledge of the dominant evolutionary constraints and factors that enhance the likelihood of isoprene-forming enzymes will enable us to predict the evolutionary trend of isoprene emission in response to climate change.”

Research on isoprene is also of interest to the the biotech industry. A number of projects are aiming to convert it into a source of biofuels or industrial raw materials. New insights from the **Sharkey lab** could help bioengineer better sources of isoprene.

An important component of this research is the inclusion of students participating in the **MSU Plant Genomics REU Program**, which provides high quality research and training programs for underrepresented undergraduate students interested in biochemistry, bioinformatics, biology, biotechnology, chemistry and computational sciences. Several of these students have been involved in isoprene-related projects and have been co-authors on publications from Sharkey’s lab.

“This program is an excellent resource to inspire and train a future workforce that is diverse and globally competitive,” Sharkey said.

Another goal of the program is to improve public scientific literacy. Sharkey and his team will participate in **MSU’s Fascination of Plants Day**—a worldwide event that aims to enthuse the public about the importance of plant science in everyday– and the **MSU Science Festival** to share information on their research.

Banner image: Plants, particularly trees, emit significant amounts of isoprene into the atmosphere. The lab of Thomas Sharkey will study the evolutionary pattern of the appearance and loss of isoprene emission among various land plants and the impact these emissions have on the atmosphere. Image by Diliff, **CC BY-SA 2.5**.

Josh Vermaas joins MSU as assistant professor

8/11/20

Igor Houwat

Josh Vermaas will join Michigan State University on Jan. 1, 2021, as an assistant professor in the field of computational science. He will share his position between the **MSU-DOE Plant Research Laboratory (PRL)** and the **Department of Biochemistry and Molecular Biology (BMB)** in the **College of Natural Science**.

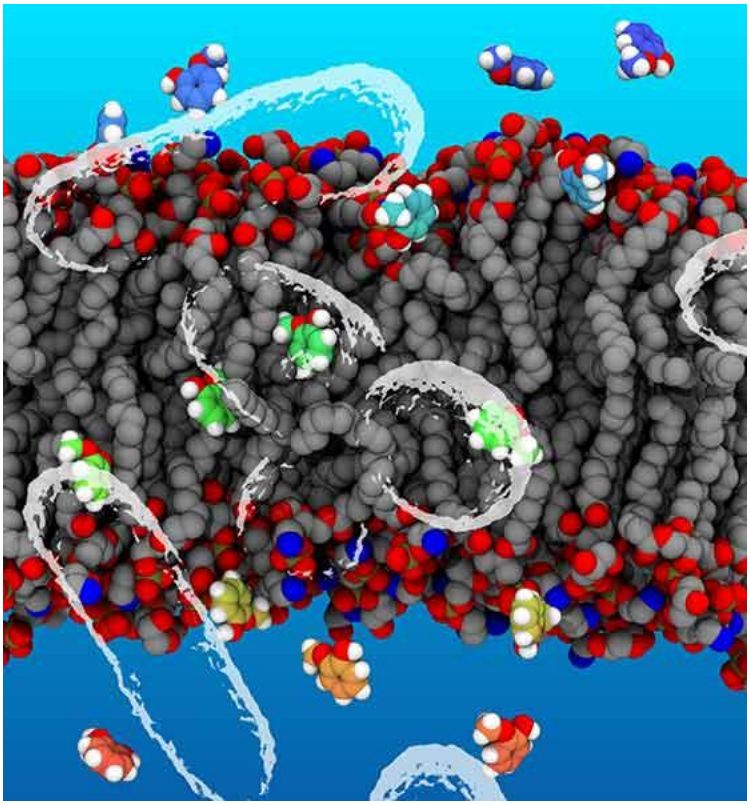
Dr. Vermaas is **currently a computational biophysicist** within the scientific computing group at **Oak Ridge National Laboratory**, where he is investigating adapting molecular dynamics codes to trends in modern high-performing computer systems and enabling advances at the "bleeding edge" of computational science. Beyond recent COVID-19 research, Josh's research interests include developing computational models to better understand membrane processes and plant materials.

Dr. Josh Vermaas
By Carlos Jones, Oak Ridge National Laboratory Communications

"I have always been drawn to renewable energy and sustainability questions, and I am excited to join the larger MSU community committed to tackling the biggest challenges facing society. I look forward to working with my PRL colleagues to develop bioenergy solutions for the 21st century!" says Josh Vermaas.

The Vermaas lab will apply emerging techniques in molecular simulation to study processes associated with photosynthesis and plant metabolism more broadly. A particular focus will be on using machine

learned potential energy functions to model chemical reaction mechanisms on the molecular scale. These new approaches will be coupled with classical simulations using established techniques to determine mechanisms behind biological phenomena.



Computer generated image of small molecules crossing a biological membrane with a foreground from a microscopy image showing the bacteria that the membrane comes from.
By Josh Vermaas

“Josh’s interests in modeling metabolism at multiple levels beautifully complement ongoing research in BMB in metabolism and multiscale models. BMB welcomes Josh to MSU!” says **Erich Grotewold, BMB Chairperson**.

“We are delighted to have Josh Vermaas join the PRL,” says **Christoph Benning, PRL Director**. “Josh is bringing new expertise to the PRL by applying computational simulation to complex biological processes. He will have countless opportunities to contribute to the PRL’s efforts in gaining a mechanistic understanding of plant and bacterial photosynthesis and to develop a successful research program. We are welcoming him as our new colleague and are looking forward to seeing him and his new team succeed in his research endeavors.”

Dr. Vermaas received his bachelor’s degree in physics, biochemistry, and computational math from Arizona State University. He received his Ph.D. in biophysics from the University of Illinois at Urbana-Champaign.

Newly discovered sugar transporter might help beans tolerate hot temperatures

8/31/20

Igor Houwat, James Santiago

MSU-DOE Plant Research Laboratory (PRL) scientists have characterized a sucrose transporter protein found in common beans. The recently discovered protein could help us understand how beans tolerate hot temperatures. The transporter, called PvSUT1.1, is **reported in the journal Plant Direct**.

During photosynthesis, bean leaves capture carbon dioxide from the air and convert it into sugars that fuel their growth and development. Most species transport these sugars throughout the plant in the form of sucrose.

The sucrose travels through a system of vein-like highways, called the phloem, that permeates the entire plant body. A group of helper proteins, aptly called sucrose transporters, load that sucrose from their origin cells into the phloem for transport to growing tissues, such as flowers and fruits.

“In legumes, particularly in common beans, there are very few sucrose transporters functionally identified and studied,” says James Santiago, a post-doc in the lab of **Thomas Sharkey, University Distinguished Professor at the PRL**. “To date, scientists have identified and functionally characterized two transporters in common beans.”

James and the Sharkey lab have now added a third transporter to this small catalogue. The study was made possible after the Lowry lab at Michigan State University **identified the gene that codes for this protein**.

Determining structure and function

PvSUT1.1 is ubiquitous in bean plants where it is found in leaves, stems, flowers, and the bean pods. This suggests a widespread role of the protein within the plants.

To confirm that the protein is a transporter, the team compared its amino acid sequence to that of the other known transporter from common beans. The proteins are 68% similar in sequence, a number which denotes a high degree of resemblence for this type of protein.

Thomas D. Sharkey (left) and James Santiago (right).
By Victor DiRita, Jr., MSU College of Natural Science

“I also did some computer modeling to compare our protein with a known sucrose transporter protein from the model plant, Arabidopsis. The structures highly resembled each other, which reinforces the idea the gene from beans encodes for a sucrose transporter protein,” James adds.

Benchmarking the protein’s performance

PvSUT1.1 activity levels rely on pH, with optimum activity when pH is acidic. The lowest pH level measured, 4.0, showed the highest transport rate.

The protein also has a high affinity for carrying sucrose. In other words, even when sucrose level is low outside the cell, the protein can still pick sucrose up and move it into the phloem cells.

“We also discovered that our protein is located at the plasma membrane, the boundary between the inside and outside of a cell,” James adds. “This is critical. We are putting stock in the idea that this transporter moves sucrose from the outside of cells and into the phloem. To perform this function, its location on the plasma membrane is a must.”

Next, the team will overexpress the new gene in the phloem cells and screen plants for any effects, especially in plant reproduction. Overexpressing the genes should also yield clues on whether a higher number of transporters helps reproductive tissues, such as pollen grains, to better tolerate hot temperatures.

“There are times when sucrose transport or production is reduced, like when plants are stressed by heat,” James says. “The decrease in sucrose transport negatively affects beans’ reproductive capabilities. Perhaps increasing the number of sucrose transporters means the flowers could still get the required amounts of sucrose they need to reproduce.”

The project is primarily funded by the **MSU Plant Resilience Institute** and in collaboration with **Professor John Ward at the University of Minnesota**. Banner image of **assorted colored beans** by **Shelly Pauls**, Unsplash License

2020 Anton Lang Memorial Award winners announced

9/30/20

Igor Houwat

Kellie Walters and Bryan Ferlez have been awarded the 2020 Anton Lang Memorial Award during a ceremony which took place online on Monday, September 21, 2020.

The Anton Lang Memorial Fund was established in honor of the founding director of the **MSU-DOE Plant Research Laboratory (PRL)**, who passed away in 1996. Proceeds from the fund go towards annually supporting the Anton Lang Memorial Lecture and recognizing a graduate student and a postdoctoral research associate who exemplify the research excellence, ideas, dedication, and vision of Anton Lang

This year's lecture, titled "Reflections on a Life in Science," was given by the PRL's own **Dr. Michael Thomashow.**

Kellie, formerly in the **lab of Roberto Lopez** and **currently Assistant Professor of Controlled Environment Vegetable Physiology at the University of Tennessee**, won the graduate student award.

Kellie Walters
Courtesy of Kellie Walters

Kellie's doctoral research focused on controlled environment production impacts on hydroponically grown culinary herb physiology, biochemistry, and consumer preference. She also conducted research on plant growth regulators and photoperiodic responses of ornamental crops.

"It is a great honor to be selected for this award," Kellie says. "I would like to thank the PRL for selecting me, Roberto Lopez, and the Lopez lab for your great support, and the entire plant science research

community at Michigan State. This very knowledgeable, collaborative environment has helped shape me as a scientist, making the research we have accomplished possible!"

Bryan, who is in the **lab of Cheryl Kerfeld**, won the postdoctoral research associate award. He is part of a **team working to understand and engineer protein-based bacterial organelles**, like the carboxysome.

Bryan Ferlez
Courtesy of Bryan Ferlez

Currently, he is investigating how electrons and gases get across the protein shell that surrounds these organelles by characterizing native components that bind redox active metals, and **engineering new parts** to help measure the permeability of shells to oxygen.

"I am incredibly fortunate to be able to work with so many of the brilliant and creative people here at the PRL," Bryan says. "All that I've learned and accomplished as a postdoc, including receiving this incredible award, is in no small way a result of their inspiration, insight, and guidance. I would like to thank the PRL for honoring me with this award, my mentor, Cheryl, for all her support and training, and all my wonderful lab mates and colleagues."

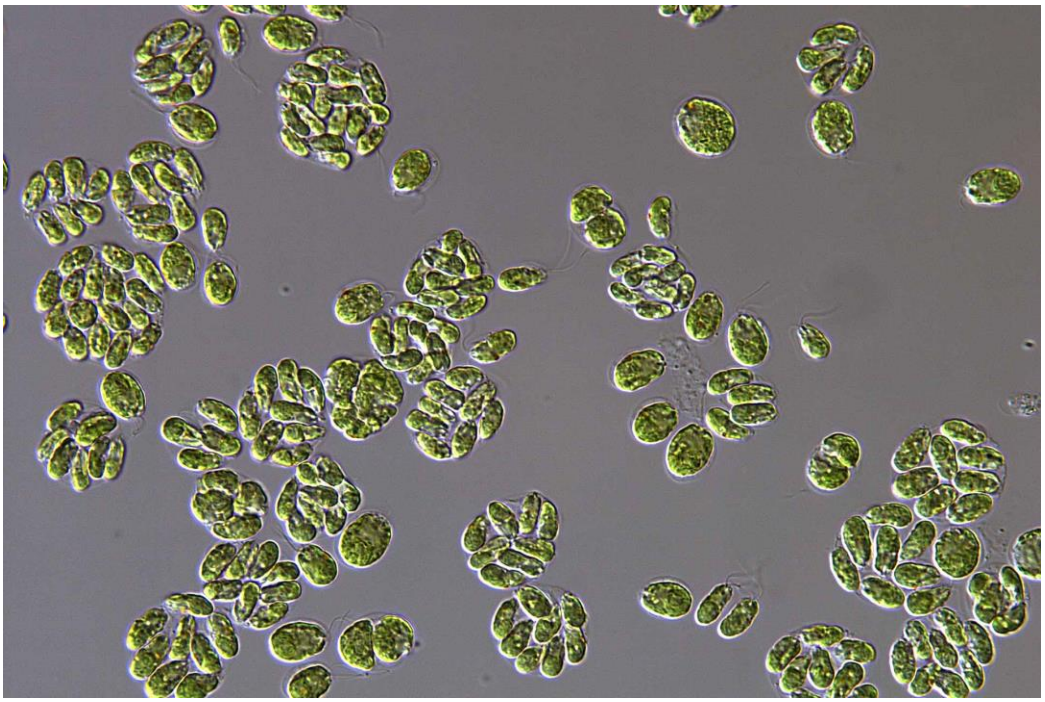
Christoph Benning, PRL Director, says, "This has been an unusual year, to say the least, and I am happy that we were able to have the Awards Seminar by Mike and to recognize Kellie and Bryan in proper fashion by meeting virtually. On behalf of the entire PRL and molecular plant science communities at MSU, I would like to thank Mike for his inspiring talk and to congratulate all three awardees."

The awardees have received an engraved rosewood piano finish clock, a cash reward, and their names have been added to a permanent award plaque located in the Plant Biology Laboratories building.

Understanding how algal cells divide when they are hungry

10/8/20

Igor Houwat, Christoph Benning



Banner image of wild type algal cells by Tomomi Takeuchi

A new study from the **MSU-DOE Plant Research Laboratory** delves into how algae manage cell division processes when they suffer from starvation. The finding has implications for biofuel technologies, given that algae have the potential to become a sustainable source of high value oils.

The key word is 'starvation.' When nutrients are scarce in algae's surroundings, the algae store their energy reserves in the form of oil, which is where the biofuels come from. The issue is that starvation causes the algal cells to stop growing.

"Trying to produce biofuels from stressed algae is not economically viable, as the system is unreliable in case we want to maximize both oil and biomass production," says **Christoph Benning, MSU University Distinguished Professor**. "Scientists are exploring how to engineer algal metabolism so the cells grow and make oil at the same time, leading to more valuable feedstock for biofuel production."

The new study, **published in the journal Plant Physiology**, focuses on the algal protein, CHT7. The work builds on previous research from the Benning lab that showed that **CHT7 stops algal cells from growing and dividing when they are starving for nutrients**. The new research starts to establish how CHT7 interacts with proteins that control cell division in the algal species, Chlamydomonas.

A collaboration of protein complexes

“Cell division in Chlamydomonas is a choreographed cycle,” says Christoph. “The cells grow bigger and bigger during the day, and then cell division occurs at night. The cycle is governed by cell size; the clue for each cell is that, once it has grown to a certain size, it must divide.”

In the new work, the scientists determined that CHT7, which is involved with a cell’s nutritional status, interacts with MAT3, another protein which is part of a large complex of proteins that manages cell division.

The team examined the algal cells in bioreactors, housed in the MSU-DOE Plant Research Laboratory, under conditions where they divide simultaneously.
By G. L. Kohuth, ©2012 Michigan State University-Board of Trustees

“We asked if these two proteins directly interacted within larger protein complexes. By using a sensitive experimental method, we found a small subpopulation of complexes where both proteins coexist,” says Christoph.

The team further examined the cells in bioreactors under conditions where they divide simultaneously. They found that the subcomplexes change during the various stages of the cell cycle, over a 24-hour period.

The scientists think that the protein complexes involving both CHT7 and MAT3 might relate to similar complexes found in animals.

“Animals have a so-called DREAM regulatory complex, which is similar to a related complex in Chlamydomonas. We’re trying to figure out if the algal complex is in fact such a DREAM complex,” Christoph adds. “To do so, we need to identify the other components that work alongside CHT7. We also want to see where exactly in the cell cycle is CHT7 active when algae are starved for nutrients.”

“The ultimate question is: can we understand how nutrient deprivation affects cell division? In addition to possibly improving biofuel production, the algal system can provide fundamental insights into how living cells sense their nutrient status and adapt, by either slowing down or speeding up cell division. For

example, if things go wrong with this process in human cells, these cells can turn cancerous and divide out of control."

This work was part of **Tomomi Takeuchi's** PhD thesis. Additional contributors include Yang-Tsung Lin, PhD student, and Nicholas Fekaris, undergraduate student, both from the Benning lab; MSU Emerita Professor of Plant Biology, Barbara B Sears; and **Jim Umen** at the **Donald Danforth Plant Science Center**. The research was funded by the **National Science Foundation**, **US Department of Energy, Office of Basic Energy Sciences**, **MSU AgBioResearch**, and the **National Institutes of Health**.

MSU and Rajarata University of Sri Lanka awarded Asian Development Bank grant

11/6/20

Igor Houwat

Michigan State University (MSU) and **Rajarata University of Sri Lanka** have been awarded a $250,000 grant by the Asian Development Bank (ADB).

Dr. Chathuranga Bamunurachchige is the project lead on the Rajarata University side, while the MSU team is led by Drs. David M. Kramer, Brad Day, Atsuko Kanazawa, and Saroopa Samaradivakara. Scientists from both universities will together conduct a series of transdisciplinary activities in the area of smart agriculture, ranging from fundamental genomics and chemistry, to student training and curriculum-based activities.

“I’m overwhelmed by the enthusiasm and the involvement of the MSU colleagues, Brad, Dave, Atsuko and especially Saroopa in developing a mere thought into a winning project under this extremely competitive ADB, STHRD grant scheme for collaborations with a renowned university,” says Bamunurachchige. “Hopefully this grant would provide an opportunity to learn from the traditional practices and take the knowledge to the next level through cutting edge technology!”

The grant award is part of the ADB’s **Science and Technology Human Resource Development Project**, which supports Asian and Pacific universities in their efforts to establish partnerships with renowned foreign universities in areas such as, faculty or student exchange programs, innovative teaching and learning at higher education, and joint research activities, especially in industry relevant areas.

Rajarata University students experimenting with the PhotosynQ platform.
By Brad Day.

“I am very excited to not only begin the multidisciplinary research funded by this grant, but I also look forward to continuing my interactions with many great colleagues in Sri Lanka,” says **MSU Foundation Professor, Brad Day**. “We’re looking forward to seeing where this research and collaboration takes us. Sri Lanka has a level of expertise and enthusiasm for applying fundamental research discovers that is second to none!”

One of the new technologies that will be employed on the project is **PhotosynQ**, a cloud-based platform developed in MSU’s Kramer lab that aims to create a global, open access dataset of plant activity. PhotosynQ relies on a hand-held device to measure plant health at a fundamental level in the field and collect data across the world. Collected data is stored in the cloud, where it can be processed through a suite of data analysis tools.

“I am thrilled to be a part of this collaboration between MSU and my home country!” says **Samaradivakara, who is a postdoc in the lab of Brad Day**. “At MSU, we are currently working on the USDA funded project on the development of PhotosynQ platform integrated point of contact pathogen detection method. I look forward to sharing and expanding this platform with the students of Rajarata University.”

Image from the "Smart Agriculture: Logic & New Concepts," conference which took place on March, 2019 in Colombo, Sri Lanka. From left to right: Dr. David Kramer (MSU), Dassana Wijesekera (Director of Solution Architecture, Asia Pacific Regional Head of Technology, WSO2 Inc.) , Dr. Mahanama De Zoysa (Chungnam National University, Korea), Dr. Brad Day (MSU), Dr. Cheol-Hee Kim (Chungnam National University, Korea), Dr. Atsuko Kanazawa (MSU).
By Isuru Sathsara, All rights reserved FASFOCUS UNITY 2019, Media Unit, Rajarata University.

While the current grant represents the first ADB project between MSU in Sri Lanka, it continues a long and successful history of collaboration between MSU and Sri Lankan institutions. In this case, the grant follows the establishment of a memorandum of understanding between MSU and Rajarata University in 2019.

“Some of us at MSU had a rare opportunity to visit Sri Lanka for a conference and a workshop using the PhotosynQ platform,” says **Kanazawa, Research Assistant Professor**. “It was truly impressive to witness

that the students from Rajarata University took the initiative. They ran the show! Now with Saroopa, our native Sri Lankan colleague here, it will be a great exchange of science and education."

"I'd like to add that I am especially impressed with the strength, excitement, and tenacity of these students," adds **Kramer, who is a Hannah Distinguished Professor In Photosynthesis And Bioenergetics**. "They were amazing when we met them, and they have kept this excitement through some difficult political and social situations in Sri Lanka, including the COVID-19 pandemic."

Banner image of Dr. Kramer demonstrating the PhotosynQ platform to students from Rajarata University. Photo by Brad Day.

Learning what it takes to grow a space garden

12/21/20

Igor Houwat, Evan Angelos

As the public buzz continues to build around sending a **human mission to Mars**, even colonizing it someday, scientists are studying what it takes to survive such a long trip. One problem is food. If humans spend long stretches of time out in space, they can't pack all their food before the trip. They'll have to grow some in space, not an easy feat.

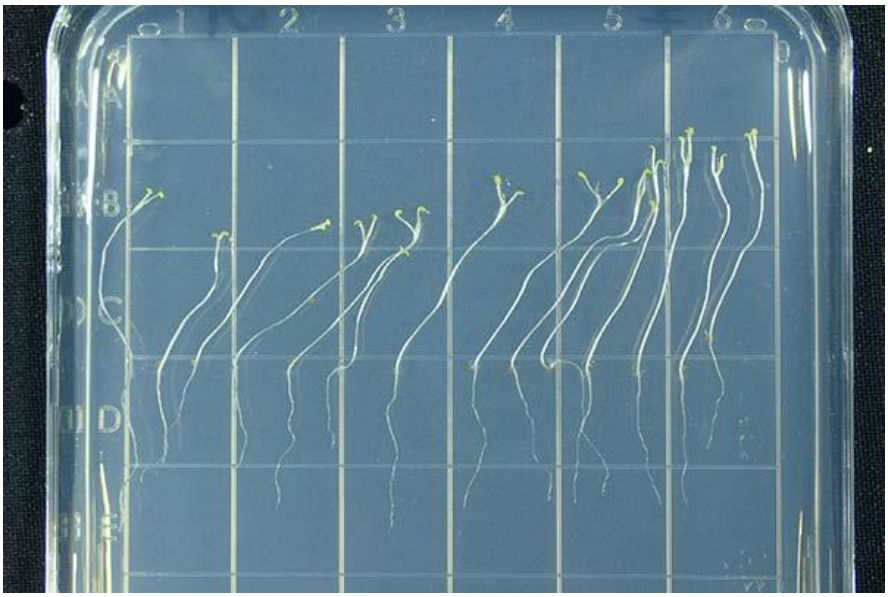
To grow food beyond planet Earth is tricky. Crop plants face unusual conditions for them, like microgravity, radiation, freezing temperatures, and a lack of natural light.

With the **support of NASA**, the lab of **MSU-DOE Plant Research Laboratory** scientist **Federica Brandizzi** has been studying how plants survive in space conditions. In a new study, they start revealing how a plant system – which helps plants manage various types of Earthly stresses, such as extreme heat – might function in space. The study is **published in the journal Astrobiology**.

The survival mechanism is called the **unfolded protein response (UPR)**. When plants are stressed, they produce defective proteins that are harmful and sometimes deadly to these plants. **The UPR kicks in** to tell the plant to dump the faulty proteins and to go back to making good ones.

"We want to see how plant genes, which control how plants react to their environments, work differently during space flight, compared to ground conditions," says **Evan Angelos**, a graduate student in the Brandizzi lab. "Past research has given us an idea of how plants react to stresses in space. But we don't know if or how the UPR plays a role."

In 2017, **the lab sent plant seeds to the International Space Station**, where they **grew in confined containers and in microgravity for two weeks**. The plant seeds were from different genetic backgrounds, including ones defective in UPR. As a control, plant seeds were grown in similar conditions, but on solid ground at the Kennedy Space Center in Florida.



Arabidopsis seedlings grown without light; the stalks grow much longer, the leaves are smaller, and the overall color is paler
By Evan Angelos

“A huge number of genes that were not active in ground samples were expressed in space. Our observations partially overlap with past studies that have been conducted in space, which is a major win for the field. To date, most of the other space studies have not been able to be reproduced. Our ability to replicate some of these findings gives the field more confidence the data is correct,” says Evan.

To the researchers’ surprise, however, the UPR itself was somewhat muted in response to the stressful conditions of space. All plants – some with functioning UPR and others with defective UPR – didn’t react very differently.

In another twist, the similar plants grown at the Kennedy Space Center revealed different reactions, depending on whether they had working UPR or not. The UPR reacted to types of stress that scientists have not associated with it before, including lack of oxygen or water deprivation.

To be fair, the stresses imposed by the special growth chambers used in the study are unusual. These chambers are tiny, sealed, and there is no light for the plants to grow. Yet somehow, these unsual conditions impact ground plants much more than their space counterparts.

One explanation for this disparity could be the effect of gravity, which is lower in space.

Evan Angelos, in the lab, preparing his flight samples
Courtesy of Evan Angelos

“Still, no one has tested whether UPR reacts to some of these stresses to date,” Evan says. “Putting these plants in this highly weird situation opened our eyes to the possibility that the UPR may play a wider role in protecting plants on Earth than previously known.”

Back to space, the science team has yet to draw any conclusions about the importance of the UPR beyond Earth. More testing needs to be done on more plants and in more kinds of growth chambers. The investigation to grow the perfect space salad continues.