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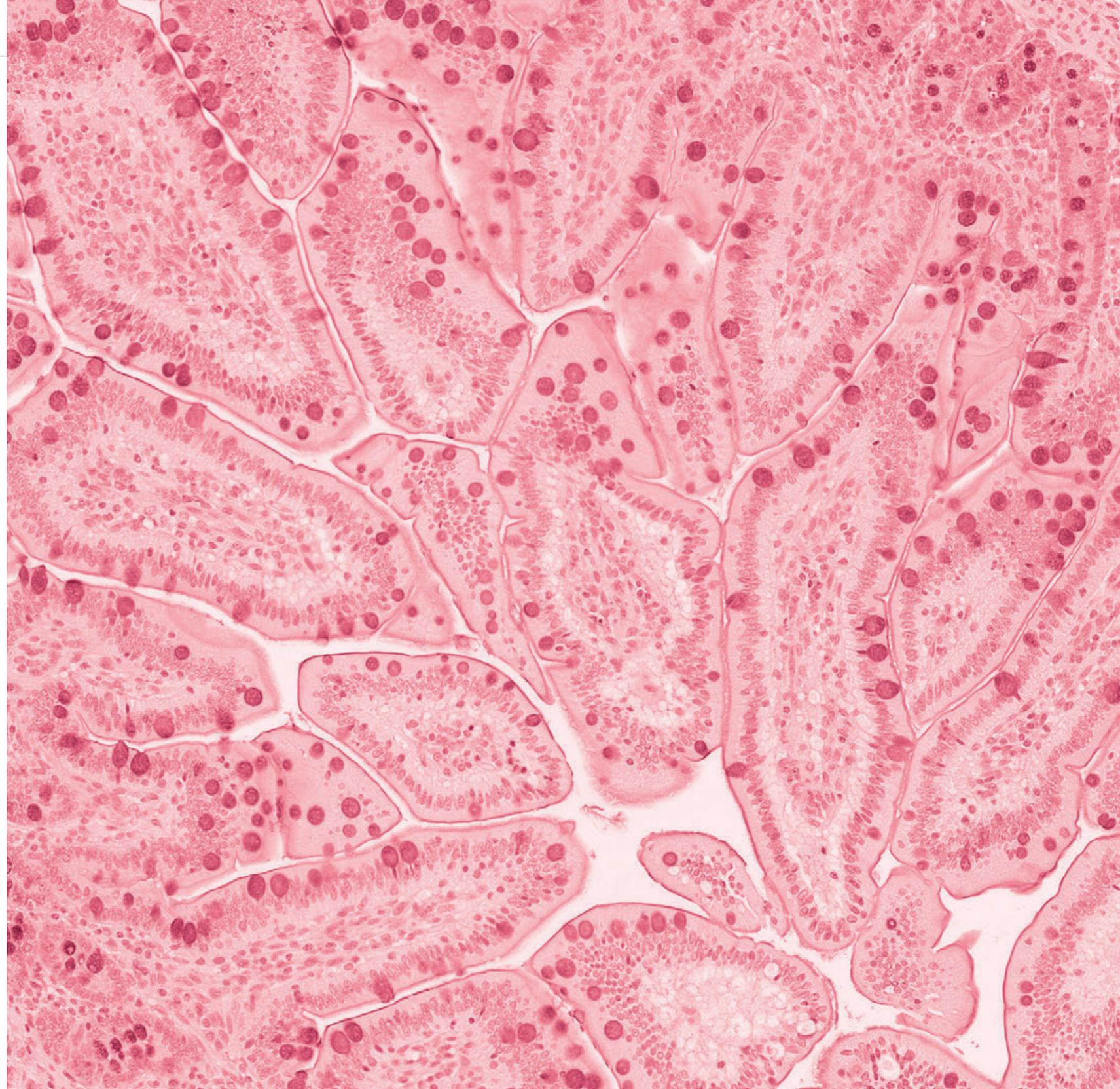
Carl R. Woese Institute for Genomic Biology

ILLINOIS

Where Science Meets Society

New truths become evident when new tools become available.

—Rosalyn Yalow



IGB Themes

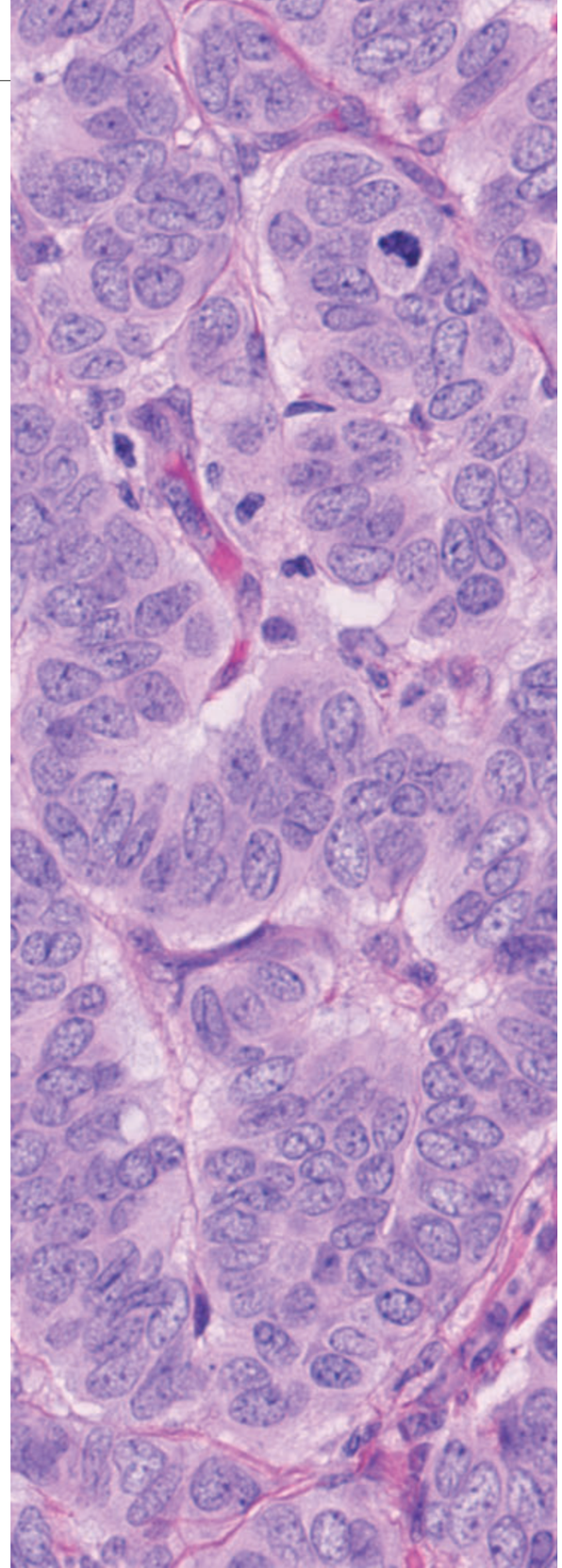
ACPP	Anticancer Discovery from Pets to People
BCXT	Biocomplexity
BSD	Biosystems Design
CGRH	Computing Genomes for Reproductive Health
GEGC	Genomic Ecology of Global Change
GNDP	Gene Networks in Neural & Developmental Plasticity
GSP	Genomic Security and Privacy
IGOH	Infection Genomics for One Health
MME	Microbiome Metabolic Engineering
MMG	Mining Microbial Genomes
ONC-PM	Omics Nanotechnology for Cancer Precision Medicine
RBTE	Regenerative Biology & Tissue Engineering

IGB Strategic Partnerships

CABBI	Center for Advanced Bioenergy and Bioproducts Innovation
CNLM	Center for Nutrition, Learning, and Memory
EBI	Energy Biosciences Institute

IGB Funding Agencies

DOE	United States Department of Energy
HHMI	Howard Hughes Medical Institute
NASA	National Aeronautics and Space Administration
NCSA	National Center for Supercomputing Applications
NIH	National Institutes of Health
NSF	National Science Foundation
USDA	United States Department of Agriculture



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Director's Message

> "By acknowledging and embracing the true complexity of biology, we can strengthen our science and our society."

Gene E. Robinson

DIRECTOR, CARL R. WOESE
INSTITUTE FOR GENOMIC BIOLOGY

THE STRANDS THAT HOLD US TOGETHER

The structure of a genome reflects two apparently contrasting ideas: unity and diversity. The basic chemical composition of DNA and the genetic code that enables its entwined strands to convey information across space and time are shared across all life on Earth. This universality is key to the success of our efforts to explore and innovate in the world of genomics. Yet the motivation to understand genomes is driven by their endless differences, and how those differences translate into phenotypic variation from the smallest to the largest scales.

As we have assembled this year's edition of *Biomarker*, one side of this coin has been uppermost in our minds. Our society is undergoing a period of intense public dialogue about the way we consider and value human diversity. In the realm of genomic research, this movement has the potential to immensely strengthen the science of medicine and to rectify longstanding biases in how genomic research is applied in health care settings. By acknowledging and embracing the true complexity of biology, we can strengthen our science and our society.

We are proud that existing and new members of the IGB are contributing to this movement. In these pages, we report how researchers are participating in efforts to reshape the demographics of genomic research at the NIH; innovating ways to safeguard the privacies of all human genomic research participants; and learning about the implications of molecular anthropology research through dialogue with Indigenous researchers and scholars.

As the field of precision medicine continues to accelerate, we have also highlighted IGB research that seeks to describe diverse presentations and outcomes within what traditionally would be described as a single condition or disease. Two separate studies on breast cancer examined how predisposition to disease is influenced by an interaction of multiple biological factors, and how a novel cancer therapy could avert the risk of drug resistance.

The philosophical framework for these types of initiatives in genomic research are built into the field: since the beginning, the study of genomes has also been the study of biodiversity. The IGB continues this tradition, with recent breakthroughs describing ways to leverage plant diversity to increase crop yield; the cellular mechanisms underlying sexual plasticity in anemonefish; the horizontal transfer of genetic material across microbiota within the human body; and the possibility of improving estimates of global climate history using the mineral record of coral skeletons.

Finally, we continue to be mindful of the pervasive influence of genomic technologies on every aspect of life—the food we eat, the fuel we use to power our activities, our knowledge of the environments we inhabit, the decisions we make about healthcare. Through outreach events, symposia, and other formal and informal interactions, we remain dedicated to open communication with stakeholders in genomic research from every part of our society.

IGB is a young institution. Even as we play our part in addressing social justice issues in the sciences, we are humbled by how much we have to learn, the long history of such work and how much remains to be done. We continue to be inspired by the symbolism that can be found in the structure of the genome—diversity represented through a unifying language. We face great challenges as a society: if we embrace the full diversity of nature and of human minds, we can solve them together.

Participants in the SING conference

Nurturing the human element of genomics

THE STUDY OF HUMAN GENOMICS IS inextricably linked to larger societal practices: how well diversity is represented in those who direct and conduct scientific research, how we balance data access with individual privacy, and the ways we group and describe both healthy and ill people. Unfortunately, our society's complex and shameful history of prejudice, mistreatment of minorities, and ongoing institutional bias has resulted in weaknesses in genomic health research—weaknesses that can and must be rectified.

IGB members are establishing and expanding efforts to address issues of bias and representation in all arenas of genomic research: subject matter, stakeholders, and the scientific workforce.

Respecting and fostering diversity in research and in communities

IGB's tagline, "where science meets society," offers a pathway to healing systemic weaknesses in genomic research. This September, the IGB had the privilege of collaborating with the National Human Genome Research Institute (NHGRI) to host a workshop examining these issues.

The workshop, "Equity, Diversity, and Genomic Data Science," featured presentations and discussions offered by University of Illinois faculty and invited experts from institutions across the U.S. Attendees were drawn from academia, industry, government, professional societies, advocacy groups, community-based organizations, and education groups. During the workshop, those present worked together to draft recommendations for the NHGRI's forthcoming strategic plan, which is currently under development.

"Genomics research is conducted in a very rigid manner that does not allow for community feedback or what community members feel are their problems (health, justice or otherwise)," said Ripan Malhi (CGRH/GNDP/GSP/IGOH/RBTE), a professor of anthropology. "Genomic research is conducted using concepts that trace back to colonial ideas that are not representative of human diversity we see in the world today."

Malhi co-facilitates the annual Summer internship for INdigenous peoples in Genomics (SING) Workshop, which aims to empower indigenous people with knowledge and access that enables them to determine best practices surrounding genomic science in indigenous communities. This program provides a strong example of how thoughtfully created opportunities for dialogue among scientists and other community members can improve communication, strengthen science, and increase the diversity of participation in genomic research.

Malhi also pointed to gender bias and other diversity issues within STEM pipelines, and in genomic research in particular, as issues to be addressed within the workshop. Conclusions from the workshop will be reflected in the NHGRI's updated strategic plan, anticipated to be published in October 2020 to coincide with the 30th anniversary of the inception of the Human Genome Project.

Protecting the privacy of research participants and consumers

Another part of the effort to democratize access to genomic research and innovation is finding new ways to secure individual genomic data. Genomic technologies have the power to transform individual healthcare for the better. But with that power comes responsibility—the responsibility to protect the privacy of the individual and to make ethical choices that respect the rights of communities and populations.

A newly established research theme at the IGB will address these and related issues. The new theme, Genomic Security and Privacy (GSP), will be led by Professor of Computer Science Carl Gunter. Assistant Professor of Political Science Aleksander Ksiazkiewicz will lead policy-based work within the theme.

"As the methods get cheaper to produce sequencing data . . . people are going to be a lot more concerned," Gunter said. "Going back ten years ago when it cost hundreds of millions of dollars to sequence something, it wasn't really that much of a concern, whether the data might be captured . . . but now, it seems like every time you turn around, there's some new security- or privacy-related concern."

Gunter and Ksiazkiewicz represent the two-pronged approach that the theme will take, simultaneously pursuing the identification of privacy concerns and development of strategies in the arenas of technology and policy. For example, genomic data collected in a medical setting could be vulnerable to the same cybersecurity risks that threaten other forms of personal data; however, unique formats for genomic data storage could lend themselves to unique, optimal data security solutions. Similarly, well-designed policy surrounding genomic data privacy should take into account the unique societal implications of such data, including genomic information that is shared across related individuals.

The theme's work will be strengthened by the interdisciplinarity of its research team, which already includes researchers with backgrounds in computational genomics, electrical and computer engineering, nutrition, anthropology, business, and law.

"One of the things I'm most excited about, having people from so many different disciplines, is being able to draw on the expertise that they have . . . finding interesting intersections that we wouldn't find if we were just holed up in our own offices, distributed around campus," Ksiazkiewicz said.

As the new theme ramps up activities, Gunter and other members have continued to play a role in related events around campus, including the recent NIH workshop and a TEDxUIUC talk by Gunter highlighting the urgency and everyday relevance of genomic privacy and security issues.

"The Golden State Killer is a pretty good example of what's in the wind. These direct to consumer [sequencing services] collect millions of data points, and those data points are enough that you can triangulate from them to find the name associated with anybody's DNA if they're of European descent," Gunter said. "Big attention will need to be paid to the security and privacy of genomic data." ■

The Kleinmuntzes at the St. Louis Science Center World of Genomics event

Kleinmuntz Center provides a kick-start to IGB innovation

SINCE ITS INCEPTION, THE IGB HAS aimed to provide a research environment that facilitates the kind of cross-discipline communication and collaboration on which genomic research thrives. As ideas for new technologies grow into new business ventures, they need extra support. The launch of the Catherine and Don Kleinmuntz Center for Genomics in Business and Society, announced this February, is providing the resources that genomic innovations need to branch out into everyday applications.

In its first year, the Kleinmuntz Center is already providing unique opportunities for economic development, public engagement and social impact.

Drs. Catherine and Don Kleinmuntz are the co-founders of Strata Decision Technology, a healthcare analytics software company that was an early tenant of the University of Illinois Research Park. Their generous donation funded the center and is providing researchers with proof-of-concept and pre-commercialization support that will help them bring technologies and innovations to market.

"I was introduced to IGB when I was invited to come speak to the students and faculty about entrepreneurship and building a start-up business. It is easy to see that IGB is a very special place, because of the scientific talent gathered under one roof and because of the importance of the problems being addressed," said Catherine Kleinmuntz.

"Looking at IGB from my perspective as a former University of Illinois faculty member, what stands out is the interdisciplinary, team-based nature of IGB's research," Don Kleinmuntz said. "Solving these truly difficult problems requires breaking out of traditional academic silos, drawing together the best minds from across campus, and giving them the resources they need to devise unique solutions."

To aid commercialization efforts, the Kleinmuntz Center has created a new pre-commercialization Proof-of-Concept (POC) program named the "Mikashi Awards." The Mikashi Awards fund IGB projects that demonstrate market viability, to help those projects succeed. This year, the labs of Donald Biggar Willett Professor of Engineering Brian Cunningham (ONC-PM leader/MMG) and Kenneth L. Rinehart Jr. Endowed Chair in Natural Products Chemistry Paul Hergenrother (ACPP leader/MMG) received awards for their development of revolutionary disease diagnostic tools and a novel liver cancer treatment, respectively.

"Great scientific discoveries do not simply leap out of the laboratory and into the real world," Don Kleinmuntz said. "We see an opportunity to encourage and facilitate the process of translating great science into applications that will benefit business and society."

"Part of the solution is to help scientists understand what it takes to make the transition to commercial applications," Catherine Kleinmuntz said. "But we also want to make sure that individuals in business, government, and society at large understand the immense potential that these scientific advances have to impact their health, wealth, and well-being."

"We are very excited to be able to launch the Kleinmuntz Center, and deeply grateful to Catherine and Don for their generosity and confidence in the IGB," said Swanlund Professor of Entomology and IGB Director Gene Robinson (GNDP). "This center will enable us to take our commercialization and social impact efforts to the next level, and help further develop the reputation of the IGB as one of the leading genomics institutes in the country."

The Kleinmuntz Center is also broadening the Genomics For™ program, which teaches basic concepts in genomics to specific demographic or professional groups, helping them understand the full impact of genomics both in their professions and in society. Since the Center's establishment, the program hosted a workshop for journalists, and is exploring future workshops for investors and government agencies.

The IGB's World of Genomics at the National Academy of Sciences (see sidebar) received support from the Kleinmuntz Center, delivering the impact of genomic research to a broader audience.

These initiatives assist the IGB in its goal of reaching young students, especially those in underserved and underrepresented communities, through its varied outreach programs. The Kleinmuntz Center is bringing together economic development and societal advancement, proving that genomic research has the ability to make a difference in all areas of life.

"The IGB is already a crown jewel of the University of Illinois System, advancing the frontiers of knowledge and solving critical problems," Catherine Kleinmuntz said. "Don and I want the Kleinmuntz Center to accelerate and leverage the impact of these advances, for the benefit of the people of Illinois and the entire world." ■

"We see an opportunity to encourage and facilitate the process of translating great science into applications that will benefit business and society."

The IGB partnered with the National Academies of Sciences, Engineering, and Medicine (NASEM) to present Family Science Day at the NAS Building: DecisionTown in the World of Genomics, combining the IGB's largest outreach event, World of Genomics, with NASEM's engaging DecisionTown interactive public experience.

Over 3000 people from the Washington, D.C. area and across the country visited DecisionTown in the World of Genomics in the NAS Building this April. Visitors were invited to visit DecisionTown to see how the decisions they make every day are influenced by science, engineering, and medicine.

DecisionTown in the World of Genomics featured more than 17 interactive spaces, each offering a different activity centered on an issue facing DecisionTown as it plans for the future. Activities included a health-themed food court, an interactive weather station, a courtroom hearing eyewitness testimony, a medical center explaining DNA sequencing and personalized health, and much more. Visitors rounded out their experience by completing DecisionTown's ballot, expressing their choices on science-informed policy choices linked to each learning station's content.

"The IGB was proud to co-host this with the NAS in their debut open house event to the public, and we saw thousands of D.C. families, visitors, and tourists come through their doors to experience first-hand our dynamic and diverse research portfolio," said Swanlund Professor of Entomology and IGB Director Gene Robinson (GNDP). "We received numerous compliments about the excellent abilities of our volunteers to engage with and explain the science to the attendees . . . because of their enthusiasm, warmth, and aptitude we were able to demonstrate the strength of Illinois' public engagement to an entirely new audience."

Carl R. Woese Undergraduate Research Scholar Monika Ziogaite

Woese Undergraduate Scholars experience a summer of science

TWO OF THE MOST BASIC MOTIVATIONS that drive scientific research—exploration of the unknown and the desire to solve a pressing problem—were represented by this year's Carl R. Woese Undergraduate Research Scholars. Allison Narlock spent her summer investigating the mechanics of archaeal cell division; Monika Ziogaite worked to identify genetic variants that contribute to the metastatic potential of breast cancers.

Both Narlock, a sophomore majoring in molecular and cellular biology, and Ziogaite, a senior majoring in interdisciplinary health sciences, were awarded support for 10 weeks of independent research at the IGB.

"I had always found cancer to be this incredibly frightful entity. Its ability to take over and multiply with such ease were attributes that I thought were rather daunting," said Ziogaite, who works in the laboratory of Assistant Professor of Nutrition Zeynep Madak-Erdogan (GSP/ONC-PM). "Growing up and experiencing this powerful impact on my own family, I ultimately knew that in order to reduce my fear of cancer and all that it entails, I had to better understand it."

"I ultimately knew that in order to reduce my fear of cancer . . . I had to better understand it."

Since the ground-breaking discovery of a link between predisposition to breast cancer and specific variants of the human gene *BRCA1*, the identification of additional genetic variants associated with breast cancer and other cancers has improved early detection, diagnosis and treatment.

There are many diverse genes that are involved in the metastasis of breast cancer such as the *BRCA1* and *BRCA2* genes," Ziogaite said. "Over the summer, I hope to identify other potential genes that may be associated with an increase in metastatic potential, specifically in breast cancer cells that metastasize and respond to the female hormone estrogen."

Ziogaite intends to pursue a career in medicine after completing her undergraduate degree, and sees research as an important part of her pre-medical education.

Carl R. Woese Undergraduate Research Scholar Allison Narlock

Narlock, who became involved in research while still in high school, also sees her experience as a Woese Undergraduate Scholar as an opportunity to explore aspects of a future career in science.

"My career dream is to be a professor at a university to both teach and pursue research and I hope this summer gives me the opportunity to experience what a career in research would be like," she said. "I am hoping this summer experience helps me decide where I might want to focus on."

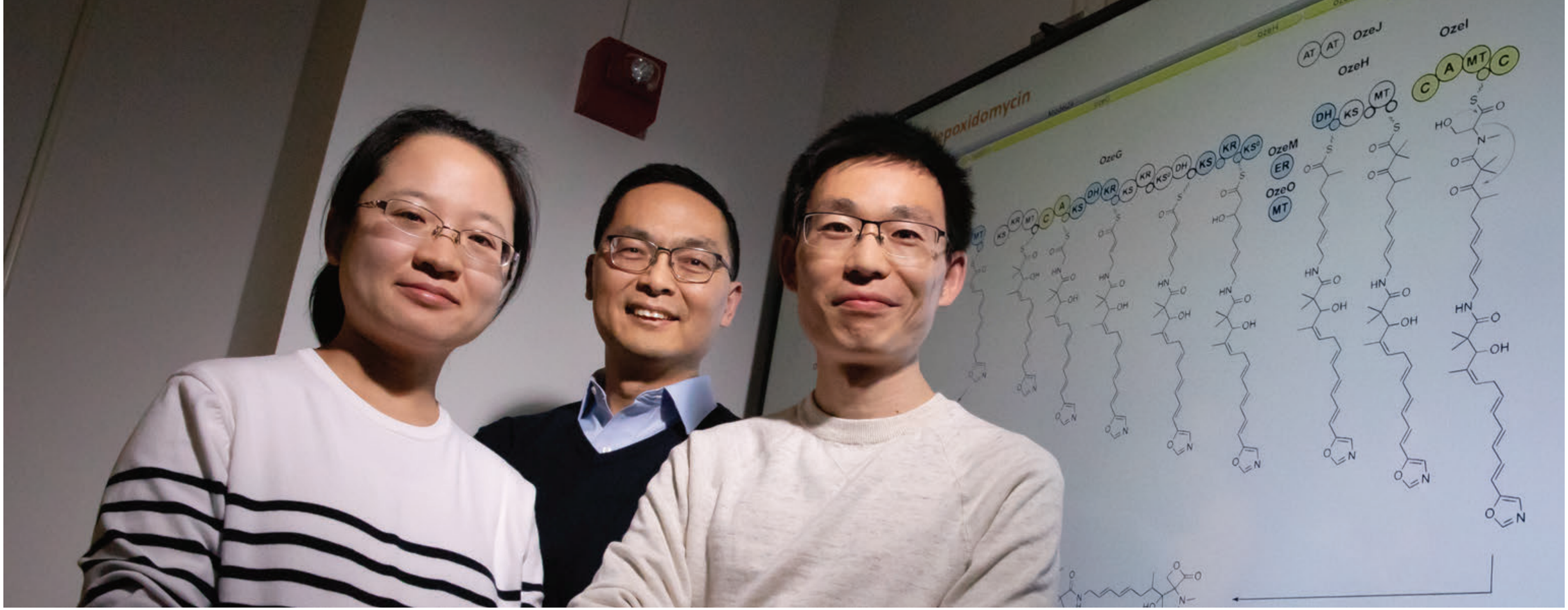
Narlock joined the laboratory of Professor of Microbiology Rachel Whitaker (IGOH leader/BCXT) after a description of the lab's work on microbial ecology piqued her interest. She spent the spring learning to use imaging techniques that will help her examine a mechanism of cell division in the archaeon *Sulfolobus islandicus*.

The cells of *S. islandicus* and related archaeal species are protected by a protein layer called the S-layer. When one of the genes encoding a component protein of this enveloping material is mutated, the cells appear enlarged and clump together, suggesting that something has gone awry with the cell division process.

"Are the cells fusing together to form larger ones or are the cells growing and simply not dividing?" Narlock said. "By being able to accurately stain and image the DNA and the membrane, I will take a step towards answering if the cell size has any relation to the amount and or location of the DNA within the cell, or even if these cells have DNA at all."

Narlock is thrilled to be contributing to research addressing such a fundamental biological question.

"I chose to transfer to Illinois for the research opportunities and this is definitely the experience I was hoping to get," she said. ■



From left: Fang Guo, postdoctoral fellow; Steven L. Miller Chair Professor of Chemical and Biomolecular Engineering Huimin Zhao; and Bin Wang, postdoctoral fellow

Unmuting large silent genes produces new molecules, potential drugs

BY ENTICING AWAY THE REPRESSORS dampening unexpressed, silent genes in *Streptomyces* bacteria, researchers have unlocked several large gene clusters for new natural products, according to a study published in the journal *Nature Chemical Biology*.

Since many antibiotics, anti-cancer agents and other drugs have been derived from genes readily expressed in *Streptomyces*, the researchers hope that unsilencing genes that have not previously been expressed in the lab will yield additional candidates in the search for new antimicrobial drugs, said study leader and Steven L. Miller Chair Professor of Chemical and Biomolecular Engineering Huimin Zhao (BSD leader/CABBI/MMG).

"There are so many undiscovered natural products lying unexpressed in genomes. We think of them as the dark matter of the cell," Zhao said. "Anti-microbial resistance has become a global challenge, so clearly there's an urgent need for tools to aid the discovery of novel natural products. In this work, we found new compounds by activating silent gene clusters that have not been explored before."

The researchers previously demonstrated a technique to activate small silent gene clusters using CRISPR technology. However, large silent gene clusters have remained difficult to unmute. Those larger genes are of great interest to Zhao's group, since a number of them have sequences similar to regions that code for existing classes of antibiotics, such as tetracycline.

To unlock the large gene clusters of greatest interest, Zhao's group created clones of the DNA fragments they wanted to express and injected them into the bacteria in hopes of luring away the repressor molecules that were preventing gene expression. They called these clones transcription factor decoys.

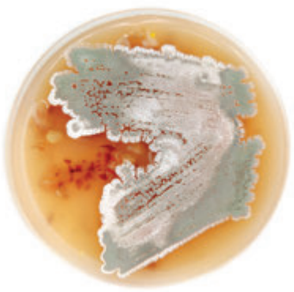
"Others have used this similar kind of decoys for therapeutic applications in mammalian cells, but we show here for the first time that it can be used for drug discovery by activating silent genes in bacteria," Zhao said.

To prove that the molecules they coded for were being expressed, researchers tested the decoy method first on two known gene clusters that synthesize natural products. Next, they created decoys for eight silent gene clusters that had been previously unexplored. In bacteria injected with the decoys, the targeted silent genes were expressed and the researchers harvested new products.

"We saw that the method works well for these large clusters that are hard to target by other methods," Zhao said. "It also has the advantage that it does not disturb the genome; it's just pulling away the repressors. Then the genes are expressed naturally from the native DNA."

In the search for drug candidates, each product needs to be isolated and then studied to determine what it does. Of the eight new molecules produced, the researchers purified and determined the structure of two molecules, and described one in detail in the study—a novel type of oxazole, a class of molecules often used in drugs.

The researchers plan next to characterize the rest of the eight compounds and run various assays to find out whether they have any anti-microbial, anti-fungal, anti-cancer or other biological activities. The NIH supported this work. ■



Streptomyces *bacteria, which aids in the research for new antimicrobial drugs*

Tagatose, an alternative low-calorie sweetener, could be produced by more efficiently produced by yeast

Low-calorie lactose sweetener gets manufacturing boost from yeast

THE QUEST TO SATISFY THE SWEET tooth without adding to the waistline has a new weapon in its arsenal: a strain of yeast that can metabolize lactose, the sugar in dairy products, into tagatose, a natural sweetener with less than half the calories of table sugar.

Yong-Su Jin (BSD/CABBI/MME), a professor of food science and human nutrition, led the research team that engineered the yeast strain, which produces tagatose in much larger quantities than traditional enzymatic manufacturing techniques and could help make tagatose a cost-effective alternative to sugar or high-fructose corn syrup.

The researchers published their work, which was supported by the EBI and the U.S. DOE, in the journal *Nature Communications*.

"Tagatose is a sweetener that exhibits almost identical tastes and textures of sucrose, or table sugar. However, tagatose has many fewer calories than sucrose," Jin said. "In addition, it does not increase blood glucose levels as much as sucrose or fructose. The glycemic index of tagatose is three, which is much lower than that of sucrose, 68, and fructose, 24. As such, tagatose carries a lower risk for developing Type 2 diabetes and other diseases caused by rapid and repeating glucose increases in blood."

In spite of its benefits, tagatose has a high manufacturing cost that has kept it from wide commercial use, Jin said. Although it is naturally present in fruits and dairy products, the concentrations are too low to isolate tagatose effectively. The traditional manufacturing method involves a multi-step enzymatic process that turns galactose—a component of lactose—into tagatose.

> **"Tagatose is a sweetener that exhibits almost identical tastes and textures of sucrose, or table sugar. However, tagatose has many fewer calories than sucrose."**

Unfortunately, the enzyme reaction is so inefficient that only 30 percent of galactose is converted into tagatose, forcing manufacturers to use an expensive process to remove the tagatose from the galactose mixture.

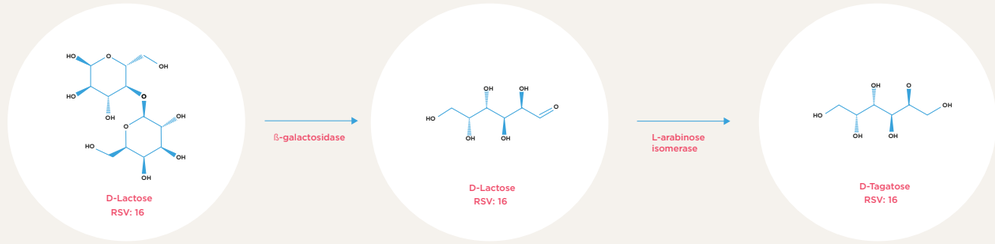
Jin's team used the internal machinery of yeast cells as tiny tagatose factories, much like the way ethanol manufacturers use yeast to produce fuel from corn. The researchers engineered a strain of yeast that produces tagatose from lactose by making two genetic tweaks. First, they took out a gene that let the yeast use galactose as cellular fuel during lactose metabolism. Second, they added two genes that convert galactose into tagatose.

Thus, when the yeast is fed lactose, its own metabolism drives it to produce a solution that is 90 percent tagatose, much higher than the 30 percent yield from traditional manufacturing. Yeast reactors also operate on much larger scales than enzyme-based ones, which could allow for efficient mass production of tagatose, Jin said.

"Another advantage is that our yeast-based process can use whey indirectly. Whey is an inevitable byproduct of the cheese and Greek yogurt manufacturing processes as a raw material," Jin said. "As our yeast fermentation-based approach allows a higher product ratio and the direct use of inexpensive dairy waste, we expect that the production cost of tagatose can be significantly reduced."

Next, the researchers will explore using their yeast-based approach to manufacture other products from lactose.

"We showed that lactose can be efficiently and rapidly utilized by engineered yeast. With further metabolic engineering, we can produce other valuable products from the lactose abundant in whey, using our engineered yeast strain," Jin said. ■



Chemical steps in tagatose production

Fettucini may be most obvious sign of life on Mars

A ROVER SCANNING THE SURFACE OF MARS FOR evidence of life might want to check for rocks that look like pasta, researchers report in the journal *Astrobiology*.

The bacterium that controls the formation of such rocks on Earth is ancient and thrives in harsh environments that are similar to conditions on Mars, said Professor of Geology and Microbiology Bruce Fouke (BCXT), who led the NASA-funded study.

"It has an unusual name, *Sulfurihydrogenibium yellowstonense*," he said. "We just call it 'Sulfuri.'"

> **"If we see the deposition of this kind of extensive filamentous rock on other planets, we would know it's a fingerprint of life."**

The bacterium belongs to a lineage that evolved prior to the oxygenation of Earth roughly 2.35 billion years ago, Fouke said. It can survive in extremely hot, fast-flowing water bubbling up from underground hot springs. It can withstand exposure to ultraviolet light and survives only in environments with extremely low oxygen levels, using sulfur and carbon dioxide as energy sources.

"Taken together, these traits make it a prime candidate for colonizing Mars and other planets," Fouke said.

And because it catalyzes the formation of crystalline rock formations that look like layers of pasta, it would be a relatively easy life form to detect on other planets, he said.

The unique shape and structure of rocks associated with Sulfuri result from its unusual lifestyle, Fouke said. In fast-flowing water, Sulfuri bacteria latch onto one another "and hang on for dear life," he said.

"They form tightly wound cables that wave like a flag that is fixed on one end," he said. The waving cables keep other microbes from attaching. Sulfuri also defends itself by oozing a slippery mucus.

"These Sulfuri cables look amazingly like fettuccine pasta, while further downstream they look more like capellini pasta," Fouke said. The researchers used sterilized pasta forks to collect their samples from Mammoth Hot Springs in Yellowstone National Park.

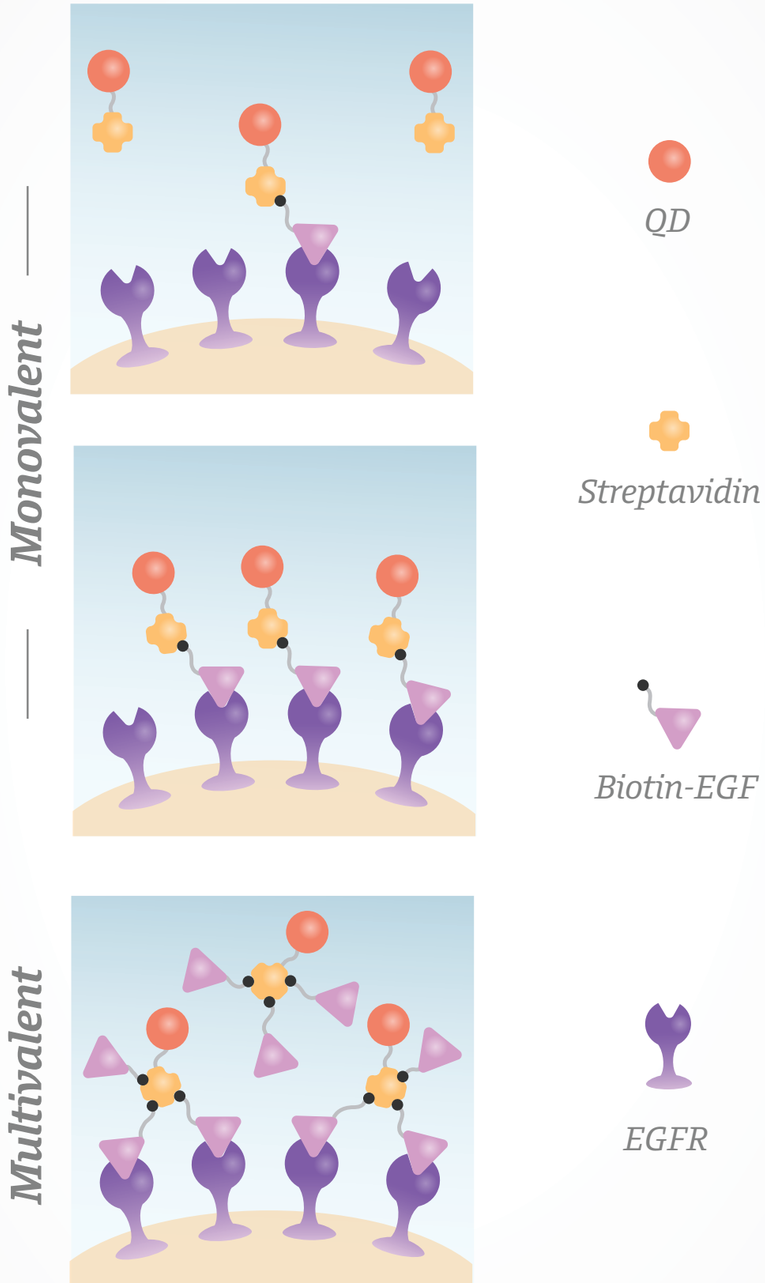
The team analyzed the microbial genomes, evaluated which genes were being actively translated into proteins and deciphered the organism's metabolic needs, Fouke said.

The team also looked at Sulfuri's rock-building capabilities, finding that proteins on the bacterial surface speed up the rate at which calcium carbonate—also called travertine—crystallizes in and around the cables "1 billion times faster than in any other natural environment on Earth," Fouke said. The result is the deposition of broad swaths of hardened rock with an undulating, filamentous texture.

"This should be an easy form of fossilized life for a rover to detect on other planets," Fouke said.

"If we see the deposition of this kind of extensive filamentous rock on other planets, we would know it's a fingerprint of life," Fouke said. "It's big and it's unique. No other rocks look like this. It would be definitive evidence of the presence of alien microbes." ■

Fettucini rocks created from bacteria growing in a hotspring at Yellowstone National Park



In the platform, each growth factor (EGF) is tagged with a fluorescent quantum dot (QD), allowing it to be counted.

Illinois researchers are first to count growth factors in single cells

WHETHER HEALTHY OR DISEASED, human cells exhibit behaviors and processes that are largely dictated by growth factor molecules, which bind to receptors on the cells. For example, growth factors tell the cells to divide, move, and when to die—a process known as apoptosis.

When growth factor levels are too high or too low, or when cells respond irregularly to their directions, many diseases can result, including cancer. "It is believed that cells respond to growth factors at extreme levels of sensitivity," said Associate Professor of Bioengineering Andrew Smith (ONC-PM). "For example, a single molecule will result in a major change in cell behavior."

In a recent paper published in *Nature Communications*, Smith reported the invention of a new technology platform that digitally counts, for the first time ever, the amount of growth factor entering an individual cell. Prior to this, researchers inferred growth factor binding based on how the receiving cells responded when the growth factor molecules were introduced.

"We showed the first direct cause-and-effect relationships of growth factors in single cells," he said. "We expect the outcomes to lead to a new understanding of cell signaling, how cells respond to drugs, and why cell populations become resistant to drugs, particularly toward improved treatments for cancer."

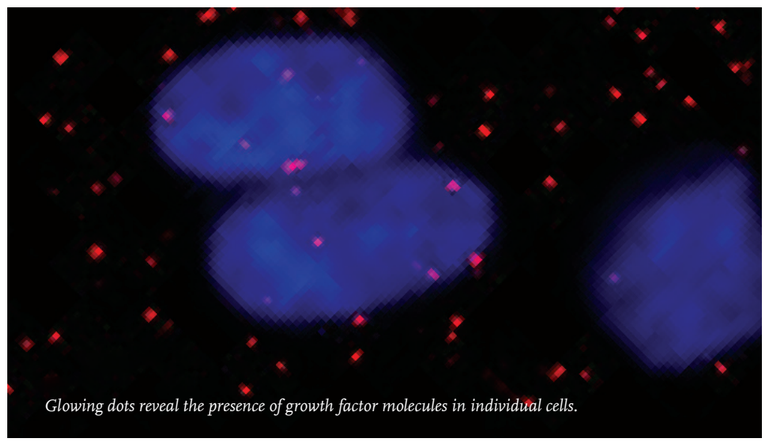
Smith's technology platform tags each growth factor with a single engineered infrared fluorescent quantum dot, just 10 nanometers across, which can then be viewed using a three-dimensional microscope. In this study, the team counted how many epidermal growth factor (EGF) molecules bound to human breast cancer cells that were pre-patterned on island-like surfaces.

EGF molecules typically signal cell division and lead to tissue growth. Numerous cancers have mutations in their EGF receptors.

"We used quantum dots as the fluorescent probe because they emit a lot more light compared to other conventional fluorescent probes such as organic dyes, and we can tune their wavelengths by changing their chemical composition," said bioengineering doctoral student Phuong Le, the lead author of the paper. "In our study, we demonstrated that quantum dots emitting light in the near-infrared wavelength allowed the most accurate counting of growth factors binding to cells."

The team also treated the breast cancer cells with quantum dot-tagged EGF in the absence and presence of pharmaceutical drugs that inhibit EGF signaling in cells. "We found that the amount of EGF binding is inversely proportional to drug efficacy," Le said. "This finding is significant as it means that signaling molecules present in the cancer cells' tumor—a place where signaling molecules are often misregulated—can enhance the cancer cells' resistance to pharmaceutical agents."

This work was funded by the NIH and the University of Illinois. Recently, Smith and Assistant Professor of Bioengineering Pablo Perez-Pinera (ACPP) received more than $1 million in funding from the NIH to further expand Smith's novel technology with new cell engineering tools and image analysis software. The goal of their project is to develop a quantitative analysis platform for single-cell signaling through growth factors and cytokines. ■



Glowing dots reveal the presence of growth factor molecules in individual cells.

Mount Mutnowsky, an area where archael cells thrive in high temperatures

Study of archaeal cells could teach us more about ourselves

FORTY-TWO YEARS AFTER CARL WOESE defined Archaea as the third domain of life, scientists are still learning about these ancient organisms in ways that could help us learn more about eukaryotes.

"Everybody's interested in the origin of eukaryotic cells because we're eukaryotes," said Professor of Microbiology Rachel Whitaker (IGOH leader/BCXT). "The more we can learn about archaea, the more we'll understand about our own cells and what makes us unique."

Whitaker and Changyi Zhang, a research scientist in her research group, wanted to better understand the archaeal cell by studying *Sulfolobus islandicus*, a microorganism found in geothermal hot springs. Their work was supported by NASA, the NSF, and the University of Illinois.

Their results, published in *Nature Communications*, give insight into archaea's shared ancestry with eukaryotes and the evolutionary history of cells. Their research also overturns previously held beliefs about what *S. islandicus* requires for growth.

The researchers determined which genes in the *S. islandicus* genome are essential for its survival, and then compared them to the essential genes of bacteria and eukaryotes to look for commonalities. In particular, they wanted to see if eukaryotes shared any essential genes with *S. islandicus*, as this could give insight into the origin of eukaryotes.

All the overlapping genes they identified had been described previously, but they did find a novel set of genes that are both unique to archaea and essential for their growth. Now, they want to understand whether these genes are unique to archaea or whether they were present in a common ancestor of archaea and eukaryotes. If they can understand this better, they can further understand how archaea and eukaryotes diverged, and just how that process of evolution took place within the cell.

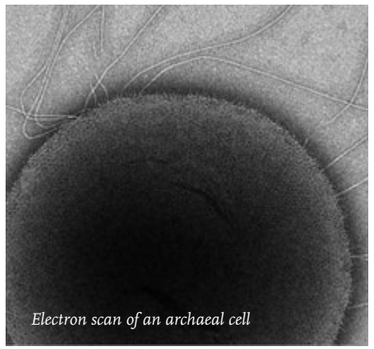
"There are two options. Either they were once shared by a common ancestor and lost by eukaryotes as they diverge from a common ancestor," Whitaker said. "Or they're new, and they're innovations that happened in the archaeal cell that didn't happen in the eukaryotic cell." To study *S. islandicus*, a unique organism that grows in high temperatures, Zhang had to develop new tools to analyze its genome. These tools allowed him to make an unexpected discovery about the surface (S-) layer, the outer shell of archaeal cells that provides protection.

"It only has an S-layer surrounding the cell," Zhang said. "If the cell loses the S-layer, it loses its protection against a lot of environmental stress."

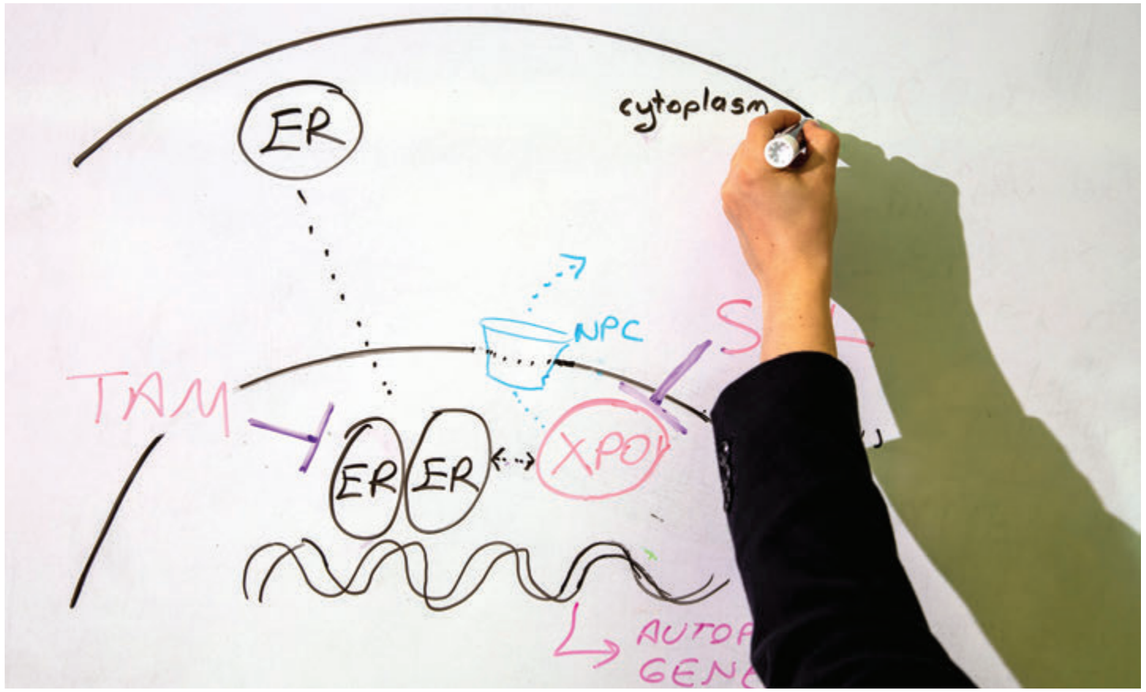
The consensus among scientists was that the S-layer was essential to *Sulfolobus*, but Zhang confirmed that it's not. He said this came as a surprise, but they now have the tools to test how the archaeal cell functions with and without this outer shell.

A better understanding of archaeal cells could help the scientific community learn more about functions of eukaryotic cells, many of which are not well understood.

"Our hope is that, in better understanding the core pieces of those functions, we might be able to better understand those systems, and in doing that, better understand our own selves," Whitaker said. ■



Electron scan of an archaeal cell



Cancer therapies shift the dynamics of a complex network of signaling molecules within tumor cells

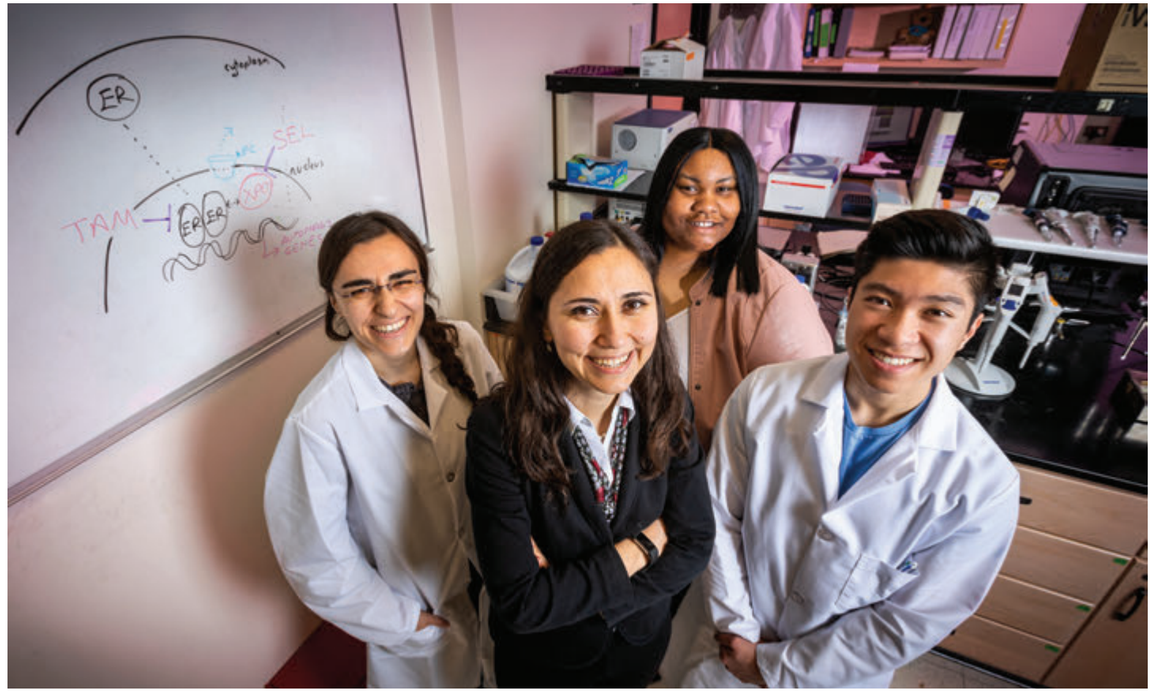
Drugs reprogram genes in breast tumors to prevent endocrine resistance

TREATING BREAST TUMORS WITH TWO cancer drugs simultaneously may prevent endocrine resistance by attacking the disease along two separate gene pathways, scientists have found in a recent study.

The two drugs used in the study, selinexor and 4-OHT, caused the cancer cells to die and tumors to regress for prolonged periods, said Assistant Professor of Food Science and Human Nutrition Zeynep Madak-Erdogan (GSP/ONC-PM), the principal investigator on the study.

The study, published recently in the journal *Cancers*, involved human breast cancer cells that were implanted in mice and analyses of the genes expressed by endocrine-resistant breast tumors.

While endocrine therapy currently is the most effective form of treatment for hormone-responsive breast cancer, some patients will either not respond or will develop resistance to the drugs over time. This condition, called endocrine resistance, causes metastases and is responsible for a majority of women's deaths from hormone-responsive breast cancer.



Zeynep Madak-Erdogan, center, joined by her research team, graduate students Eylem Kulkoyluoglu-Cotul, far left, Brandi Patrice Smith, back, and undergraduate student Kevin Duong, right

"They found that the combination of 4-OHT and selinexor caused the tumors to regress faster and more completely than either drug alone—effects that continued for several weeks after treatment ended."

Based upon the team's prior research, the researchers hypothesized that two elements might work together to cause endocrine resistance—the hormone receptor ERα, which is responsive to estrogen and is expressed in 70 percent of all breast cancers, and the nuclear transport gene XPO1, which removes foreign materials from cells' nuclei.

Combining the drugs selinexor, which prevents XPO1 anti-cancer proteins from functioning, and 4-OHT, which inhibits estrogen receptors from responding to the hormone, might be more effective than either drug alone, the researchers hypothesized. They treated endocrine-resistant tumor cells with 4-OHT or selinexor alone, or with a combination of both drugs to determine how each of these treatment protocols affected the tumors' survival and functioning.

The drug combination was more effective at reducing the tumor cells' viability than either drug by itself. When they tested the three treatments on human breast tumor cells implanted in mice, they found that the combination of 4-OHT and selinexor caused the tumors to regress faster and more completely than either drug alone—effects that continued for several weeks after treatment ended.

In analyzing genetic activity in human endocrine-resistant breast tumors, the researchers found that the drug combination decreased the activity of genes that were associated with endocrine resistance and metastasis, possibly explaining the increased efficacy of this treatment. Among these were sets of genes regulated by the protein Akt that control cells' survival, proliferation and migration.

The research was supported by the USDA, a Karyopharm Investigator grant, the University of Illinois, an Arnold O. Beckman Award, and private donors. ■

Cystic fibrosis treatment uses ‘molecular prosthetic’ for lung protein

Martin Burke, right, at work in his lab with Katrina Muraglia, foreground, who just completed her PhD in biochemistry, and research grad student Rajeev Chorghade

AN APPROVED DRUG NORMALLY USED to treat fungal infections may also be able to substitute for a protein channel that is missing or defective in the lungs of people with cystic fibrosis, operating as a prosthesis on the molecular scale.

Cystic fibrosis is a lifelong disease that makes patients vulnerable to lung infections. There are treatments for some but not all patients, and there is no cure. The drug restored infection-fighting properties in lung tissue donated by human patients as well as in pigs with cystic fibrosis. It has potential to become the first treatment to address all types of cystic fibrosis, regardless of the genetic mutation that causes the protein deficiency.

The researchers who discovered the drug’s potential published their findings in *Nature*. The study was funded by the HHMI and NIH.

“Instead of trying to do gene therapy, which is not yet effective in the lung, or to correct the protein, our approach is different. We use a small molecule surrogate that can perform the channel function of the missing protein, which we call a molecular prosthetic,” said Professor of Chemistry Martin Burke (MMG), who led the study.

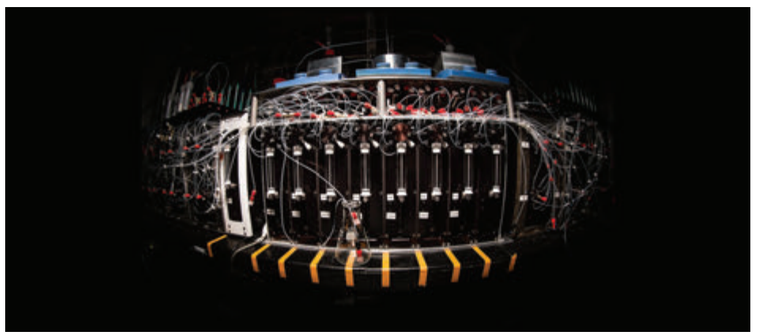
Healthy lungs have a layer of mucus on the surface of the airways that helps protect against infection. Cells in the lining of the lung secrete mucus, as well as a mixture of salts and other compounds that keep mucus flowing and discourage invading bacteria. However, in people with cystic fibrosis, one of the proteins in the cell membrane that helps facilitate the transport of salts and regulate the flow of mucus, called CFTR, is defective or missing altogether.

“Losing CFTR channel function makes airway surface liquid more acidic and disrupts salt secretion. These defects cripple two important lung defenses: the antibiotic activity of airway liquid and the clearance of mucus. As a result, people become vulnerable to infection,” said study co-author Dr. Michael J. Welsh, a professor of internal medicine at the University of Iowa Carver College of Medicine and an HHMI Investigator. This loss of function is caused by one of several possible mutations in the gene encoding CFTR.

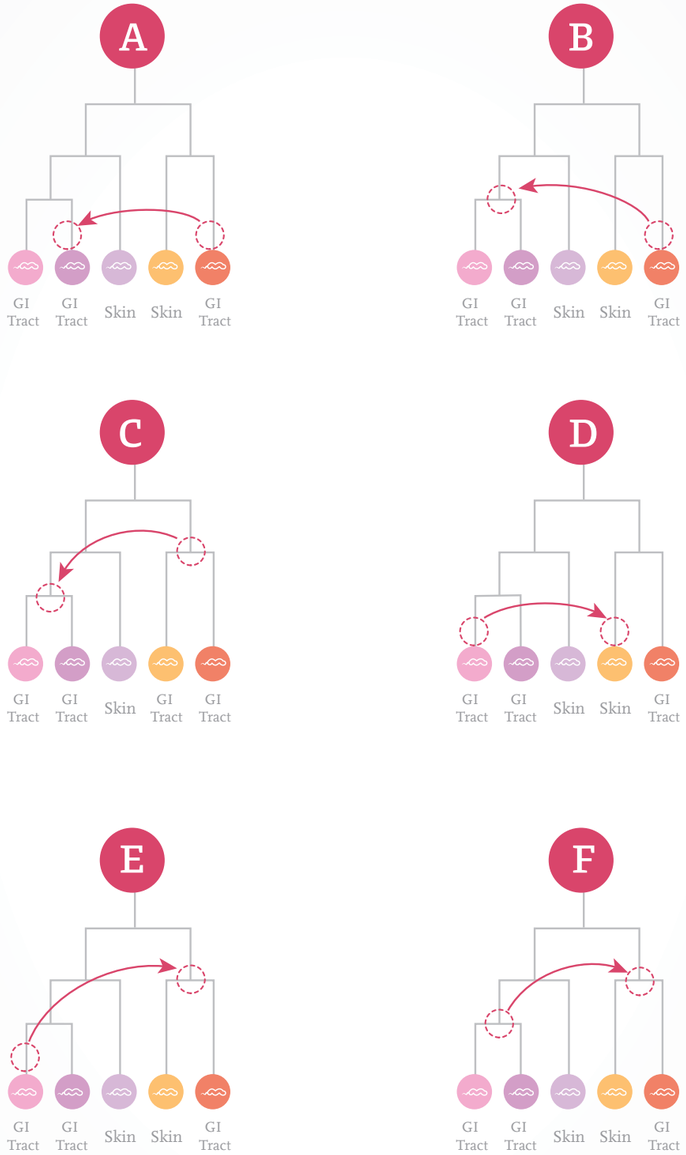
“We use a small molecule surrogate that can perform the channel function of the missing protein, which we call a molecular prosthetic.”

The researchers found that a drug used to treat fungal infections, amphotericin, can form channels in the surface membrane of lung tissue donated by people with cystic fibrosis. The channels released bicarbonate that had built up in cells and brought the pH and thickness of the airway surface liquid back within normal range. When pigs with cystic fibrosis were treated with the drug, the researchers saw a restoration of the infection-fighting properties in the liquid lining the lung surfaces.

Next, the joint Illinois-Iowa research team will conduct clinical trials to see whether amphotericin delivered to the lungs is effective in humans with cystic fibrosis.



“Since amphotericin is an already approved drug, the path to clinical translation is more direct. It’s already been shown to be safe when delivered directly to the lung, and it doesn’t get into the rest of the body, so we can avoid the negative side effects that the drug is known for,” Burke said. “We are hoping to conduct clinical trials soon.” ■



The majority of gene sharing among bacteria living within the human body occurs across tissue boundaries.

Microbes in human body swap genes, even across tissue boundaries

BACTERIA IN THE HUMAN BODY ARE sharing genes with one another at a higher rate than is typically seen in nature, and some of those genes appear to be traveling—independent of their microbial hosts—from one part of the body to another. Researchers described this phenomenon in the journal *Scientific Reports*.

The findings are the result of a molecular data-mining method initially conceptualized by Kyung Mo Kim, a senior research scientist at the Korea Polar Research Institute. Professor of Crop Sciences Gustavo Caetano-Anollés (GEGC) developed the approach with his former student Arshan Nasir, now a postdoctoral fellow at the Los Alamos National Laboratory in New Mexico. The NSF supported the international collaboration that made this work possible.

This computationally challenging method allowed them to identify instances of "horizontal gene transfer," the direct transfer of genes between organisms outside of sexual or asexual reproduction.

"Horizontal gene transfer is a major force of exchange of genetic information on Earth," Caetano-Anollés said. "These exchanges allow microorganisms to adapt and thrive, but they are likely also important for human health. There are some bacteria that cannot live outside our bodies and some without which we cannot live."

For the new analysis, the scientists used genomic information to build tens of thousands of "family trees" of bacteria that colonize the human body. Reconciling those with trees of microbial genes allowed the team to tease out which genes had been inherited and which were present as the result of horizontal gene transfer.

"Most current methods for determining horizontal gene transfer compare DNA features or statistical similarity between genomes to identify foreign genes," Nasir said. "This works fairly well for relatively recent gene transfers, but often fails to identify transfer events that occurred millions or billions of years ago."

The more labor-intensive approach enabled the team to surmount this barrier, he said.

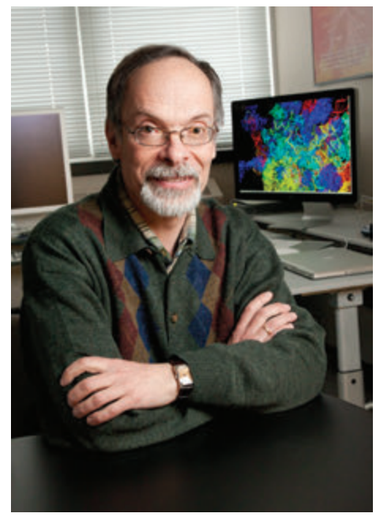
"We studied human-associated microorganisms, since they are known to be key players in maintaining human health and metabolism," Nasir said. "We calculated gene-transfer rates and direction—who transferred what to whom—for more than 1,000 reference bacterial genomes sampled by the NIH Human Microbiome Project."

The researchers found evidence to support earlier findings that human-associated bacteria are quite promiscuous with their genes, Caetano-Anollés said.

"The horizontal exchange between microbes in our bodies is about 30 percent higher than what you'll find on the rest of the planet," he said. "This implies that our bodies provide a niche that is unique and facilitates innovation at the microbe level."

About 40 percent of gene swapping occurred among bacteria living in the same body sites. The other 60 percent involved gene sharing among bacteria in different tissues, for example between organisms in the gut and in blood. Gene transfer was most common among closely related organisms, regardless of whether they occupied the same or different bodily tissues. In fact, gene sharing among organisms in different body sites occurred at a higher rate than gene sharing among distantly related bacteria living at the same sites.

The researchers say other scientists can use the tool they developed for this work, HGTree, to more accurately predict which genes were inherited "vertically," through the process of reproduction, and which were picked up from other microbes through horizontal gene transfer. This will lead to an improved understanding of both microbial and human evolution, the researchers said. ■



Gustavo Caetano-Anollés, Professor of Crop Sciences

Researchers study bacterial immunity to understand infectious disease

PATIENTS WITH CYSTIC FIBROSIS ARE OFTEN INFECTED by *Pseudomonas aeruginosa*, a bacterium that infects the lungs and prevents breathing; for these patients, infections are usually chronic and may be deadly.

P. aeruginosa itself can also be infected by viruses, which can affect the clinical outcomes of cystic fibrosis patients. Research published in *mSystems* has provided insight into this bacterium's diversity and immune system. The work was supported by the Cystic Fibrosis Foundation, the University of Illinois, the Allen Institute, and the NIH.

"Just like humans get infected by bacteria, the bacteria get infected by viruses," said Rachel Whitaker (IGOH leader/BCXT), a professor of microbiology. "There's this nested, layered set of ecosystems and interactions of infection."

Whitaker and her graduate students, Whitney England and Ted Kim, chose *P. aeruginosa* as a model system for understanding how bacterial interactions with viruses may affect human health, in part because of the significant role it plays in the disease progression of cystic fibrosis. Most serious infections of the bacterium happen in hospitals.

"There are lots of efforts to prevent children (with cystic fibrosis) from getting that infection, but that initial infection almost always happens," Whitaker said. "The strain that you get is the strain that you pretty much have for the rest of your life."

"The strain that you get is the strain that you pretty much have for the rest of your life."

The specific strain that a patient is infected with affects their treatment. Some strains are resistant to antibiotics, while others contain genes that make the infection more harmful to the patient.

The bacterial immune system, called the CRISPR/Cas system, wards off viral infections. The researchers analyzed this immune system within *P. aeruginosa* in a group of cystic fibrosis patients at a clinic in Copenhagen, Denmark. They found that the bacterial immune profiles were diverse.

"The bacterial population in Copenhagen looks like the global diversity," Whitaker said. "Within a person it's not diverse, but within this community, within this one hospital, it is."

From there, the research team wanted to see if they could determine which viruses had a chance of infecting that population of bacteria. They compared the bacterial population to known viruses of *P. aeruginosa*, and found that some viruses were highly targeted by the bacteria's immune system, while others were not.

"That's kind of a surprise, because you would think that maybe there'd be one virus or something that would be the focus of immunity," Whitaker said. "But really there's a diverse immune profile to a diversity of viruses."

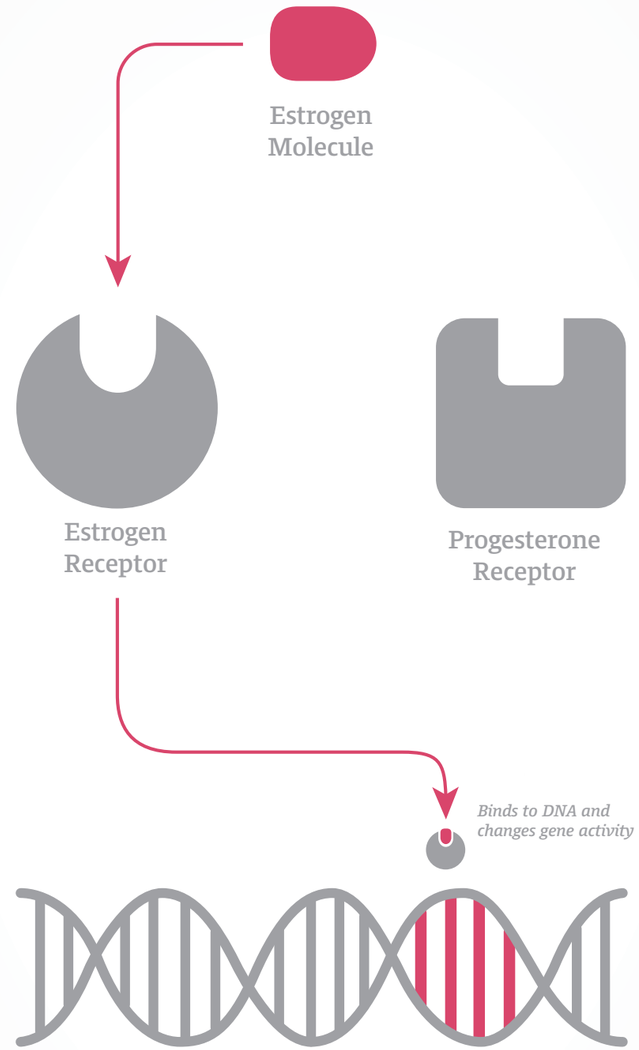
Whitaker said this knowledge could be used to target—or at least be cautious of—certain viruses that could invade bacterial populations in specific hospitals.

"It kind of gets to community medicine ideas . . . can we predict how this epidemic is going to spread in this bacterial population?" she said. "These data can be used to do that."

For now, the research is at more of a predictive stage until scientists figure out where these viruses come from.

"Until we know that, it would be hard to design a strategy to stop transmission," Whitaker said. "There are some other pieces of the puzzle that we need before we can really design strategies to prevent this transmission. This is sort of the first step." ■

A Petri dish with a growing culture of Pseudomonas aeruginosa



Estrogen fuels the growth and division of breast cancer cells

Fatty acids rewire cells to promote obesity-related breast cancer

SCIENTISTS HAVE FOUND THAT FREE fatty acids in the blood appear to boost proliferation and growth of breast cancer cells. The finding could help explain obese women's elevated risk of developing breast cancer after menopause.

"When taken up by estrogen receptor-positive breast cancer cells, these fatty acids activated pathways that increased tumor cell growth, survival and proliferation," said Assistant Professor of Food Science and Human Nutrition Zeynep Madak-Erdogan (GSP/ONC-PM), who led the study. "Our clinical data provide a more complete understanding of the mechanisms that connect obesity with breast cancer, and provide an opportunity to assess the ability of pathway-preferential estrogens to decrease breast cancer risk in obese postmenopausal women."

The findings were published in the journal *Cancer Research*.

Scientists have long known that excess body weight increases women's risks of breast cancer after menopause, but the specific metabolic pathways and genetic processes that trigger the disease have been less clear. Many of these breast cancers are estrogen receptor-positive; the cancer cells exhibit high production of estrogen-responsive protein.

To explore associations of body mass index with breast cancer risk, Madak-Erdogan's group obtained blood samples from the Susan G. Komen Tissue Bank and compared those of healthy women to those of women who developed breast cancer after the study began. The team looked for the presence of various metabolites, biomarkers of inflammation and cancer-related proteins.

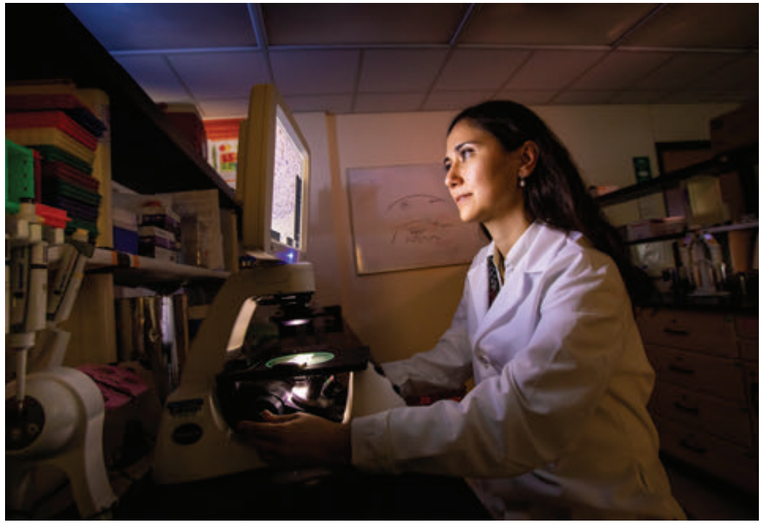
Women who developed breast cancer and women who were overweight or obese had significantly higher blood concentrations of five free fatty acids and glycerol, which are released as byproducts when fat tissue breaks down triglycerides.

Madak-Erdogan's research group analyzed additional blood samples from nonobese and obese postmenopausal women, as well as samples from 21 postmenopausal women who previously were obese but lost weight. They found that obese women's levels of free fatty acids were significantly higher; however, blood levels of all the fatty acids fell significantly in women who were obese at the outset of the study but later lost a significant amount of weight.

To explore the impact that obesity has on estrogen receptor-positive cancer cells, the researchers treated several lines of primary tumor and metastatic cancer cells with the blood of obese women. They found that the cancer cells became more viable and multiplied—effects that increased as the fatty acid levels in the women's blood samples increased. Exposure to the fatty acids in the women's blood also appeared to make the disease more aggressive.

To examine how estrogen would affect gene activity, Madak-Erdogan and her coauthors treated one group of breast cancer cells with oleic acid, a fatty acid, and another group of cells with a combination of oleic acid and estrogen. Among other effects, oleic acid increased the activity of genes involved in cell proliferation. However, these effects were greatly reduced in cells that were treated with the estrogen and oleic acid combination, the research team found.

The research was supported by grants from the University of Illinois and the USDA. ■



Zeynep Madak-Erdogan, Assistant Professor of Food Science and Human Nutrition

Scientists engineer shortcut for photosynthetic glitch, boost crop growth 40%

PLANTS CONVERT SUNLIGHT INTO ENERGY THROUGH photosynthesis, but this biological superpower is plagued by a key weakness. To deal with it, many plants rely on an energy-expensive process called photorespiration that drastically suppresses their yield potential.

Now, researchers from the University of Illinois and USDA Agricultural Research Service have reported in the journal *Science* that crops engineered with a photorespiratory shortcut are 40 percent more productive in real-world agronomic conditions.

> **"We could feed up to 200 million additional people with the calories lost to photorespiration in the Midwestern U.S. each year."**

"We could feed up to 200 million additional people with the calories lost to photorespiration in the Midwestern U.S. each year," said principal investigator Donald Ort (GEGC leader/BSD/CABBI), Robert Emerson Professor of Plant Science and Crop Sciences. "Reclaiming even a portion of these calories across the world would go a long way to meeting the 21st Century's rapidly expanding food demands—driven by population growth and more affluent high-calorie diets."

This landmark study is part of RIPE, supported by the Bill & Melinda Gates Foundation, the Foundation for Food and Agriculture Research, and the U.K. Government's Department for International Development.

Photosynthesis uses the enzyme Rubisco—the planet's most abundant protein—and sunlight energy to turn carbon dioxide and water into sugars that fuel plant growth and yield. Over millennia, Rubisco has become a victim of its own success, creating an oxygen-rich atmosphere. Unable to reliably distinguish between the two molecules, Rubisco grabs oxygen instead of carbon dioxide about 20 percent of the time, resulting in a plant-toxic compound that must be recycled through the process of photorespiration.

"Photorespiration is anti-photosynthesis," said lead author Paul South, a research molecular biologist with the Agricultural Research Service. "It costs the plant precious energy and resources that it could have invested in photosynthesis to produce more growth and yield."

Photorespiration normally takes a complicated route through three compartments in the plant cell. Scientists engineered alternate pathways to reroute the process, drastically shortening the trip and saving enough resources to boost plant growth by 40 percent. This is the first time that an engineered photorespiration fix has been tested in real-world agronomic conditions.

The team tested their hypotheses in tobacco: an ideal model plant for crop research because it is easier to modify and test than food crops, yet unlike alternative plant models, it develops a leaf canopy and can be tested in the field. The team is translating these findings to boost the yield of soybean, cowpea, rice, potato, tomato, and eggplant.

"Rubisco has even more trouble picking out carbon dioxide from oxygen as it gets hotter, causing more photorespiration," said co-author Amanda Cavanagh, a postdoctoral researcher working on the RIPE project. "Our goal is to build better plants that can take the heat today and in the future, to help equip farmers with the technology they need to feed the world."

While it will likely take more than a decade for this technology to be translated into food crops and achieve regulatory approval, RIPE and its sponsors are committed to ensuring that smallholder farmers, particularly in sub-Saharan Africa and Southeast Asia, will have royalty-free access to all of the project's breakthroughs. ■

Scientist Paul South collects samples to analyze how well tobacco plants modified to shortcut photorespiration perform beside unmodified plants in real-world conditions

Great Barrier Reef coral provides correction factor to global climate

Professor of Geology / Microbiology Bruce Fouke, front center, is joined by research teammates, including from far left, Mayandi Sivaguru,Kaitlyn Fouke, Kyle Fouke, and Lauren Todorov, far right

NEWLY DEVELOPED GEOLOGICAL techniques help uncover the most accurate and high-resolution climate records to date, according to a new study. The research finds that the standard practice of using modern and fossil coral to measure sea-surface temperatures may not be as straightforward as originally thought. By combining high-resolution microscopic techniques and geochemical modeling, researchers are using the formational history of Porites coral skeletons to fine-tune the records used to make global climate predictions.

"We can ground truth coral-based sea-surface temperature records against records made using temperature probes."

The new findings are reported in the journal *Frontiers in Marine Science*.

For over 500 million years, the natural history of corals has passively created a record of changing sea-surface temperature, the researchers said. Coral skeletons, which are made of calcium carbonate mineral, grow layers like tree rings with mineral compositions that vary with the season. Climate scientists use layer density to estimate sea surface temperature through time.

However, this climate-tracking technique is not without its flaws, said Professor of Geology and Microbiology Bruce Fouke (BCXT), who led the new research.

"We can ground truth coral-based sea-surface temperature records against records made using temperature probes," Fouke said, "Remarkably, the coral records are accurate most of the time, but there are instances where measurements have been off by as much as nine degrees Celsius, and this needs to be rectified."

Coral skeletons contain a mineral called aragonite, deposited by coral polyps. However, the mineral also crystalizes from seawater, the researchers said, and that can cause problems when analyzing the original coral skeleton chemistry. As seawater flows through the porous coral structure, it deposits newly crystalized aragonite on top of skeletons. That new aragonite, which may reflect sea-surface temperature different from that in which the different layers originally formed, alters skeletal chemistry through a process called diagenesis, Fouke said.

"It is difficult to tell the diagenetic aragonite from the original coral skeleton without using high-powered microscopes," said Kyle Fouke, a Bucknell University undergraduate student and co-author of the study. "It is also challenging to know exactly when the diagenetic alteration took place—days or decades after the skeletons were formed. Unless you are using the newest microscopy techniques to help select your samples, you could be collecting and measuring a mix of the two very different temperature records."

The team collected drill cores from the skeletons of living Porites coral heads at 10 to 100 feet water depth on the Great Barrier Reef off the coast of Australia. These large coral heads reach nearly 10 feet in diameter, and some have been growing for hundreds of years.Using microscopy techniques developed by coauthor Mayandi Sivaguru, Associate Director of the IGB's Core Facilities, the team uncovered a multitude of different aragonite crystallization histories.

The refined aragonite data were then integrated with chemical-mixing models for calcium, strontium and oxygen isotopes from geochemical studies of Porites from Papua New Guinea. From these models, the team created the first reliable and reproducible correction factor that estimates the magnitude of error that diagenetic alteration introduces into sea-surface temperature calculations.

"Additionally, because this has been achieved using the carbonate mineral aragonite, which is ubiquitous among marine life, this same correction factor can be used with other sea creatures that secrete carbonate skeletons and shells," Bruce Fouke said.

The NASA Astrobiology Institute, Office of Naval Research and the Australian Research Council supported this study. ■

Coral skeletons could help researchers learn more about past climates

Outreach

Indigenous scholars confront the power, limitations of genomics

Participants in the 2019 Summer internship for INdigenous peoples in Genomics (SING) workshop spent a week together in the classroom and the lab, learning not only how to amplify and sequence a fragment of their own DNA, but also discussing the implications of genomics research involving their ancestors and communities.

This was the seventh SING workshop. It is offered most summers and moves to different sites in North America. This year, SING came back to its birthplace in the IGB.

The workshop is part of a broader effort to support Indigenous community members, scientists and students who want to improve their genomics education and bring that knowledge back to their own institutions and communities. Indigenous and non-Indigenous scientists, scholars and students led the sessions and participated in the workshop.

"When I was coming along in genomics, I found it really lonely," said Justin Lund, a Diné (Navajo) PhD candidate at the University of Oklahoma who studies molecular anthropology and bioethics. Lund said the SING workshop offers a safe space where he and other Indigenous scholars can sort through the issues "better as a group, as a collective, rather than alone in your home institution."

Professor of Anthropology Ripan Malhi (CGRH/GNDP/GSP/IGOH/RBTE), one of the originators of SING and a member of its advisory board, said the workshops are part of a larger effort to build relationships and develop better policies and protocols for anthropologists, clinicians, Indigenous scholars and others seeking to work in Indigenous communities. SING and similar initiatives build networks and knowledge among Indigenous scholars and community leaders, Malhi said, "making it that much easier for them not only to participate and collaborate, but also to take the lead in scientific research on initiatives important to the community."

Summer heats up with a week of science at Pollen Power camp

Pollen Power camp, offered this July for the seventh consecutive year by the IGB, is a quirky blend of plant science, technological exploration, and summer fun. The camp aims to introduce middle school girls to the world of plant biology research and provide strong female role models in STEM fields; this year's attendees appreciated the full breadth of the camp's offerings.

Seventh grader Lauren Payton, a fellow camper, enjoyed making new friends. "But I like succulents a lot, I love them so much, especially cacti. So when we went to the greenhouse earlier and we went into the room with all the succulents, I was in love," she said.

Highlights of the camp's activities include imaging, modeling, and 3D printing representations of individual grains of pollen; pollinating research plants in the field; and constructing an evolutionary timeline of Earth's flora. Campers also script, plan, and film newscasts on the past, present, and future climate.

The camp is co-organized by USDA Agricultural Research Service scientist Lisa Ainsworth (CABBI/GEGC) and Professor of Plant Biology Andrew Leakey (CABBI/GEGC), working with IGB Core Facilities and Outreach staff. Funding is provided in part by the NSF and the IGB. Outreach and Communication Specialist Adrienne Gulley directs the week-long camp, and female researchers in plant sciences, entomology, crop sciences, and related fields are recruited as counselors.

"On the last day of camp after the prizes are given away . . . the girls come up to me and say 'thank you' or 'I had a really good time,'" Gulley said. "They give hugs and smiles and tell me how they were glad they were able to attend the camp because they made new friends throughout the week."

IGB and SciLine host Genomics for Journalists

Imagined as a sort of science "boot camp" for reporters, Genomics for Journalists, a multi-day workshop co-hosted by the IGB and the AAAS, was designed to arm journalists with the knowledge and context they need to cover newsworthy science, health, and environment issues with confidence. Genomics—the study of collections of genes, their structure and function, and how they work together within organisms—is increasingly central to advances in health, agriculture, and environmental science, as well as law enforcement and criminal justice.

The workshop was attended by 29 working reporters and science writers from across the country. Sessions covered the basic science of genomics, including exploration of advances in the field that are changing the way diseases are diagnosed and treated, novel crop varieties are developed, forensic evidence is interpreted, and new materials and fuels are being produced.

Workshop activities included faculty presentations, panel discussions, networking opportunities, and hands-on scientific laboratory experiences. Topics covered include such items as genomics, genealogy, and criminal justice; genomic editing in health, medicine, and agriculture; direct-to-consumer genetic testing; diet, microbiome, and health; ecosystems and environmental genomics; and the ethical, legal, and social issues raised by genomic advances. The workshop also held a lab exercise featuring hands-on experience with editing bacterial genomes.

Genomics for Journalists was offered in collaboration with SciLine, an independent, nonpartisan, philanthropically supported service hosted by the nonprofit AAAS. SciLine offers scientific resources to journalists and helps connect them to content experts in academia.

New avenues and new audiences for Art of Science

The IGB's Art of Science program, now in its ninth year, continued to push boundaries this year. Julia Pollack, IGB's Creative Program Manager, explored new art forms, shared exhibits with new communities, and invited researchers into the creative process.

The theme of this year's annual exhibit was "Comparisons." Pieces in Art of Science 9.0, which was displayed at the Springer Cultural Center in Champaign, highlighted parallels and contrasts in different biological structures, endeavors, and research approaches. Pieces from this and previous years were also showcased at the St. Louis Science Center; the offices of the National Institutes of Health in Washington, D.C.; and the Alice Campbell Alumni Center in Urbana.

Art of Science art piece

Awards

Ikenberry Endowed University Chair of Crop Sciences and Plant Biology Steve Long in the field

Stephen Long elected to National Academy of Sciences

Stephen Long (BSD/CABBI/GEGC), Ikenberry Endowed University Chair of Crop Sciences and Plant Biology, has been elected to the National Academy of Sciences, one of the highest professional honors a scientist can receive. He is one of 100 new members and 25 foreign associates recognized for "distinguished and continuing achievements in original research."

"We are very excited and proud," said Swanlund Professor of Entomology and IGB Director Gene Robinson (GNDP). "Steve's accomplishments are monumental, and we are so very fortunate and honored that this member of the departments of crop sciences and plant biology is also a member of the IGB community."

Long uses computational and experimental approaches to improve photosynthetic efficiency, working to address the effects of climate change on crop yield. He was named a Fellow of the Royal Society of London in 2013 and has been recognized by Clarivate Analytics as a highly cited researcher in the field of plant and animal science every year since 2005.

Long directs Realizing Increased Photosynthetic Efficiency, a multinational project supported by the Bill & Melinda Gates Foundation, the Foundation for Food and Agricultural Research and the U.K. Department for International Development.

Long has received many awards, including the Marsh Award for Climate Change Research from the British Ecological Society and the Kettering Award from the American Society of Plant Biologists. He has given briefings on food security and bioenergy to the U.S. president, the Vatican and Bill Gates. He earned a bachelor's in agricultural botany from Reading University and a doctorate in plant environmental physiology from Leeds University, both in the U.K.

Brendan Harley inducted into AIMBE College of Fellows

The American Institute for Medical and Biological Engineering (AIMBE) has announced the induction of Professor of Chemical and Biomolecular Engineering Brendan Harley (RBTE leader) to its College of Fellows.

Election to the AIMBE College of Fellows is among the highest professional distinctions accorded to a medical and biological engineer; the group comprises the top two percent of medical and biological engineers. Membership honors those who have made outstanding contributions to engineering and medicine research, practice, or education and to the pioneering of new and developing fields of technology, making major advancements in traditional fields of medical and biological engineering, or developing/implementing innovative approaches to bioengineering education.

Harley was elected by peers and members of the college of fellows for "innovative and translational contributions to instructive and spatially graded biomaterials for regenerative medicine and for engineering dynamic cell-material interactions." He joined the Illinois faculty in 2008; he received his S.B. from Harvard University in 2000 and SM/ScD from MIT in 2002 and 2006.

Harley has focused his efforts on developing biomaterials that replicate the dynamic, spatially-patterned, and heterogeneous microenvironment found in the tissues and organs of our body. He and members of his lab use this approach to generate insight regarding the design of biomaterials for craniomaxillofacial and musculoskeletal tissue regeneration, hematopoietic stem cell engineering, as 3D models of the glioblastoma tumor microenvironment in the brain, and to replicate dynamic tissues such as the endometrium.

Ainsworth receives 2019 NAS Prize in Food and Agriculture Sciences

Lisa Ainsworth (CABBI/GEGC), a scientist with the USDA Agricultural Research Service, received the 2019 NAS Prize in Food and Agriculture Sciences.

How will the world eat in the face of climate change and other threats? That question dominates Ainsworth's pioneering research, which has helped to reveal how man-made atmospheric changes will affect the physiology and growth of crops around the world.

Ainsworth led the evolution of the SoyFACE Global Change Research Facility, where she serves as lead investigator. There, she has conducted groundbreaking research to show how crops such as maize and soybeans will be affected by increases in atmospheric carbon dioxide and ozone in combination with drought and other environmental stresses, as well as possible solutions. Ainsworth was among the first to use functional genomic and metabolomics approaches to understanding mechanisms of response to global change, and has recently used quantitative genetic approaches to dissect plant responses to these changes.

In addition to her research itself, Ainsworth is also recognized for her tireless advocacy for science, both as a science ambassador and as a role model for the next generation of scientists.

The NAS Prize in Food and Agriculture Sciences recognizes research by a mid-career scientist at a U.S. institution who has made an extraordinary contribution to agriculture or to the understanding of the biology of a species fundamentally important to agriculture or food production. The prize is endowed through generous gifts from the Foundation for Food and Agriculture Research (FFAR) and the Bill & Melinda Gates Foundation. The NAS Prize in Food and Agriculture Sciences is presented with a medal and a monetary award.

Donovan named to 2020 Dietary Guidelines Advisory Committee

Sharon Donovan (MME), a professor of nutrition and the Melissa M. Noel Endowed Chair in Nutrition and Health, has been appointed to the USDA's 2020 Dietary Guidelines Advisory Committee. Donovan is one of 20 nationally recognized scientists serving on the committee to ensure America's dietary guidance reflects the latest science.

The independent advisory committee will review scientific evidence on topics and questions identified by the departments and will provide a report on their findings to the secretaries. Their review, along with public and agency comments, will help inform USDA and the U. S. Department of Health and Human Services' development of the 2020-2025 Dietary Guidelines for Americans (DGAs). These guidelines are updated every five years and serve as the cornerstone of federal nutrition programs and policies, providing food-based recommendations to help prevent diet-related chronic diseases and promote overall health.

Donovan, a registered dietician, conducts basic and translational research in the area of pediatric nutrition. Ongoing work in Donovan's lab is focusing on optimizing intestinal and cognitive development of neonates, development of the gut microbiome, and prevention of childhood obesity and picky eating in children.

"I am excited to serve on the committee, because the 2020 DGA will include recommendations for infants aged 0-2 years and pregnant and lactating women. All previous guidelines started at 2 years of age," Donovan said.

Donovan also serves as principal investigator with the Illinois Transdisciplinary Obesity Prevention Program; a member of the IGB's Microbiome Metabolic Engineering research theme; and an adjunct professor of pediatrics at the University of Illinois at Chicago College of Medicine. In October 2017, Donovan was elected to the National Academy of Medicine.

Research

Scientists transform tobacco into factory for high-value proteins

For thousands of years, plants have produced food for humans; with genetic tweaks, they can also manufacture useful proteins, including antibodies and vaccine components. Now, plants are also being used to produce cellulase, a protein that is used in food processing and to break down crop waste to create biofuel.

A team of researchers from Cornell University and the University of Illinois announced in *Nature Plants* that crops can cheaply manufacture proteins inside their cellular power plants called chloroplasts—allowing the crops to be grown widely in fields rather than restrictive greenhouses—with no cost to yield.

Typically, these proteins are produced using cell cultures of yeast or other microbes. In this study, the team engineered tobacco to produce cellulase proteins in the crop's chloroplasts, intracellular structures that convert sunlight and carbon dioxide into sugar via photosynthesis. Chloroplasts naturally contain many copies of a vestigial genome that can produce an enormous amount of protein.

"Tobacco—as a crop bred to produce large quantities of leaves—could be a factory for good," said Stephen Long (BSD/CABBI/GEGC), the Ikenberry Endowed University Chair of Crop Sciences and Plant Biology who co-led the USDA-funded study. "Chloroplasts are not present in pollen, making it possible to cultivate this engineered tobacco in fields and transform land once used for cigarette and cigar production into protein factories that can improve our health and industrial efficiency."

Biosynthetic pathway in bacteria a recipe for drug discovery and production

Microbes are master chefs of the biomolecular world; collectively, they harbor the ability to produce a vast array of unknown substances, some of which may have therapeutic or other useful properties. In searching for useful products, a team of chemists have discovered a whole new class of microbial recipes.

"The kind of reactions that these enzymes are doing are mind-boggling . . . when we first saw them, we were scratching our heads," said HHMI Investigator Wilfred van der Donk (MMG), who led the study. "Then we had to painstakingly prove that the reactions we thought the enzymes were doing, are indeed carried out."

Van der Donk, who is also the Richard E. Heckert Endowed Chair in Chemistry, and his colleagues at Illinois collaborated with the laboratory of HHMI Investigator and University of California, Los Angeles Professor of Biological Chemistry and Physiology Tamir Gonen to confirm their findings, which were published in *Science*. The work was supported by HHMI and the NIH.

The researchers made their unexpected discovery while examining a cluster of genes found in the bacterium *Pseudomonas syringae,* which infects plants. They had found that their cluster of genes included one that held the information for a peptide made by a ribosome, while another coded for an enzyme that could independently extend the peptide chain. That extension is modified in a series of steps and then broken off to create a desired product, leaving the peptide free to be extended once more. The researchers are excited about finding ways to put this completely novel pathway to use.

Research

Improved model better predicts crop yield, climate change effects

A new computer model incorporates how microscopic pores on leaves may open in response to light—an advance that could help scientists create virtual plants to predict how higher temperatures and rising levels of carbon dioxide will affect food crops, according to a study published in a special issue of the journal *Photosynthesis Research*.

"This is an exciting new computer model that could help us make much more accurate predictions across a wide range of conditions," said Johannes Kromdijk (GEGC), who led the work as part of RIPE, which is supported by the Bill & Melinda Gates Foundation, the U.S. Foundation for Food and Agriculture Research, and the U.K. Government's Department for International Development. Kromdijk is a University Lecturer at the University of Cambridge.

The current work focused on simulating the behavior of what are known as stomata—microscopic pores in leaves that, in response to light, open to allow water, carbon dioxide, and oxygen to enter and exit the plant.

"We've known for decades that photosynthesis and stomatal opening are closely coordinated, but just how this works has remained uncertain," said Stephen Long (BSD/CABBI/GEGC), Ikenberry Endowed University Chair of Crop Sciences and Plant Biology. "With this new computer model, we have a much better tool for calculating stomatal movements in response to light."

Yield-boosting stay-green gene identified from 118-year-old corn

A corn gene identified from a 118-year-old crop experiment on the University of Illinois campus could boost yields of today's elite hybrids with no added inputs. The gene, identified in a recent *Plant Biotechnology Journal* study, controls a critical piece of senescence, or seasonal die-back, in corn. When the gene is turned off, field-grown elite hybrids yielded 4.6 bushels more per acre on average than standard plants.

Dating back to 1896, the Illinois experiment was designed to test whether corn grain composition could be changed through artificial selection, then a relatively new concept.

"One of the things that was noted as early as the 1930s was that the low-protein line stays greener longer than the high-protein line. It's really obvious," says Stephen Moose, a professor of crop sciences and co-author of the study.

Staying green longer into the season can mean greater yield. The plant continues photosynthesizing and putting energy toward developing grain. But until now, no one knew the specific genes responsible for the stay-green trait in corn. The present work to identify these genes was performed in collaboration with DuPont Pioneer, which is now part of Corteva Agriscience™.

"The stay-green trait is like a 'fountain of youth' for plants because it prolongs photosynthesis and improves yield," says Anne Sylvester, a program director at the NSF, which provided additional funding for this research. "This is a great basic discovery with practical impact."

Research

A warming Midwest increases likelihood that farmers will need to irrigate

If current climate and crop-improvement trends continue into the future, Midwestern corn growers who today rely on rainfall to water their crops will need to irrigate their fields, a new study finds. This could draw down aquifers, disrupt streams and rivers, and set up conflicts between agricultural and other human and ecological needs for water, scientists say.

The study, reported in the journal *Ecosphere*, calculated the extent to which hotter conditions expected by midcentury will draw more moisture out of corn plants, said G. William Arends Professor of Integrative Biology Evan DeLucia (CABBI/GEGC). DeLucia is Baum Family Director of the Institute for Sustainability, Energy, and Environment (iSEE) and Director of CABBI. A push for higher yields will necessitate larger plants and thereby increase water usage.

Some strategies can help counter the drying conditions, DeLucia said. The use of minimum tillage and mulches can reduce the rate of water loss from the soil. Breeding or genetically modifying plants to sequester more chlorophyll in their lower leaves and less in the top will allow photosynthesis to proceed more efficiently closer to the ground, where conditions are more humid. The USDA and NASA supported this research.

Fast, efficient way to build amino acid chains

Scientists often build new protein molecules by stringing groups of amino acids together. These amino acid chains, called polypeptides, are the building blocks needed in drug development and the creation of new biomaterials.

The process for building polypeptides is difficult, however. Researchers report that they have developed a faster, easier and cheaper method for making new polypeptides than was previously available. The new approach purifies the amino acid precursors and builds the polypeptides at the same time, unlike previous methods in which these two processes were separate, laborious and time-consuming.

The method can be used in chemistry, biology and industry, where protein chains are routinely used as building blocks for the assembly of useful molecules, the researcher said.

"Previously, the field required specialized chemists like us to make these building blocks," said Hans Thurnauer Professor of Materials Science and Engineering Jianjun Cheng (RBTE), who led the new research. "Our new protocol allows anyone with basic chemistry skills to build the desired polypeptides in a few hours."

The researchers are investigating how to scale up the process and explore the full range of chemical and biological applications the new approach allows. The researchers reported their findings in the P*roceedings of the National Academy of Sciences*; the NSF and the NIH supported this work.

Scientists stack algorithms to improve predictions of yield-boosting crop traits

To better predict high-yielding crop traits, a team of researchers have stacked together six high-powered machine learning algorithms that are used to interpret high resolution spectral data. They demonstrated that this technique improved the predictive power of a recent study by up to 15 percent, compared to using just one algorithm.

In a publication in *Frontiers in Plant Science*, the team led by Carl Bernacchi (CABBI/GEGC), a RIPE research leader and scientist with the USDA Agricultural Research Service, and Kaiyu Guan (CABBI), an assistant professor of natural resources and environmental sciences, described how they improved their previous predictions of photosynthetic capacity by as much as 15 percent using a method in which computers automatically applied these six algorithms to their dataset.

The work was performed as a part of RIPE, which is supported by the Bill & Melinda Gates Foundation, the Foundation for Food and Agriculture Research, and the U.K. Government's Department for International Development.

"By applying the expertise of data analysts to address the needs of plant physiologists like myself, we ended up refining a technique that is relevant to other hyperspectral datasets," Bernacchi said. "The next step is to test more stacked machine learning algorithms on datasets from many more crop species and explore the utility of this technique to estimate other parameters, such as abiotic stresses from drought or disease."

Breakthrough to measure plant improvements helps boost production

An international team is using advanced tools to develop crops that give farmers more options for sustainably producing more food on less land. To do this, thousands of plant prototypes must be carefully analyzed to figure out which genetic tweaks work best. In a special issue of the journal *Remote Sensing of Environment*, scientists have shown a new technology can more quickly scan an entire field of plants to capture improvements in their natural capacity to harvest energy from the sun.

The traditional method for assessing photosynthesis analyzes the exchange of gases through the leaf; it provides a huge amount of information, but it takes 30 minutes to measure each leaf. A faster, or "higher-throughput" method, called spectral analysis, analyzes the light that is reflected back from leaves to predict photosynthetic capacity in as little as 10 seconds.

"The question we set out to answer is: can we apply spectral techniques to predict photosynthetic capacity when we have genetically altered the photosynthetic machinery," said research leader Carl Bernacchi (CABBI/GEGC), a scientist with the USDA Agricultural Research Service. "Before this study, we didn't know if changing the plant's photosynthetic pathways would change the signal that is detected by spectral measurements."

The research was performed under the umbrella of RIPE, which is supported by the Bill & Melinda Gates Foundation, the Foundation for Food and Agriculture Research, and the U.K. Government's Department for International Development.

Injections, exercise promote muscle regrowth after atrophy in mice

By injecting cells that support blood vessel growth into muscles depleted by inactivity, researchers say they are able to help restore muscle mass lost as a result of immobility. The research is part of a long-term effort to understand the factors that contribute to the loss of muscle mass, in particular as a result of immobility.

The team, led by Associate Professor of Kinesiology and Community Health Marni Boppart (RBTE), reported the new findings in *The FASEB Journal*. The NIH supported this research.

The research, conducted in adult mice, involved injections of cells called pericytes, which are known to promote blood vessel growth and dilation in tissues throughout the body. The injections occurred at the end of a two-week period of immobility. The team also observed that muscle immobility itself led to a significant decline in the abundance of pericytes in the affected muscle tissues. The mice that received the injections had significantly better improvement than those that regained mobility without the injections.

"We know that if you are under a condition of disuse—for example, as a result of long-term bed rest, or the immobilization of a body part in a cast—you lose muscle mass," Boppart said. "We're excited by the new findings because we hope to one day use these cells or biomaterials derived from these cells to help restore lost muscle mass."

Research

Illinois study identifies a key to soybean cyst nematode growth

The soybean cyst nematode, one of the crop's most destructive pests, isn't like most of its wormy relatives. Whereas the vast majority of nematodes exhibit a typical sinuous silhouette, the female soybean cyst nematode shape-shifts into a tiny lemon after feeding on soybean roots. A recent study published in *EvoDevo* explains how it happens and why.

"We think the soybean cyst nematode has evolved this body shape so that they can produce a lot more offspring," says Nathan Schroeder (GNDP), assistant professor in the Department of Crop Sciences and corresponding author of the study. "If you compare the most closely related species that stay long and skinny, they have a lot fewer babies than this lady does."

The research team also investigated the division pattern in other plant-parasitic nematodes and found similar reproductive cell proliferation in several others, despite not being closely related to soybean cyst nematodes. Essentially, they found evidence of convergent evolution, or the appearance of similar traits to meet the same needs in distantly related species. The common example is wings in butterflies and bats, but now nematode body shape can be added to the list.

The discovery could have potential management implications down the road. If researchers could disrupt the proliferation of these reproductive cells at a certain stage, it might be possible to keep female nematodes from becoming quite so round, with room for so many babies. The research was supported by the Schlumberger Foundation, the USDA, and the NIH.

Project aims to revive natural product discovery

An award from NIH is enabling researchers to discover new natural products—compounds produced by microbes that have high potential for medical or industrial use—on a large scale by using synthetic biology and automation.

The project is being led by Steven L. Miller Chair Professor of Chemical and Biomolecular Engineering Huimin Zhao (BSD leader/CABBI/MMG), HHMI Investigator and Richard E. Heckert Endowed Chair in Chemistry Wilfred van der Donk (MMG) and Professor of Chemistry Doug Mitchell (MMG). This interdisciplinary effort will allow them to unlock the potential of a specific class of natural products.

"You can take a package of genes from one organism, stick it in another organism, perhaps optimize it a little bit, and make the molecule in the friendly organism," van der Donk said.

However, they've only been able to do this on a small scale, building a handful of molecules at a time. Now, they want to do this on a large scale using an automated robotic system and synthetic biology tools developed by Zhao's lab, building hundreds of molecules at a time. The robotic system, called iBioFAB, will not only allow them to identify new natural products and create new molecules, but also help determine whether they have medical value.

"In principle, we can discover all the natural products that nature produces," Zhao said. "That's my dream, but with joint and coordinated efforts around the world, this dream is not entirely unrealistic."

Reducing energy required to convert CO2 waste into valuable resources

Surplus industrial carbon dioxide creates an opportunity to convert waste into a valuable commodity, serving as a feedstock for chemicals typically derived from fossil fuels, but the process is energy-intensive and expensive. Chemical engineers have assessed the technical and economic feasibility of a new electrolysis technology that uses a cheap biofuel byproduct to reduce the energy consumption of the waste-to-value process by 53 percent.

The new findings are published in the journal *Nature Energy*. The International Institute for Carbon Neutral Energy Research; Japanese Ministry of Education, Culture, Sports, Science and Technology; Dow Chemical Company; and the Glenn E. and Barbara R. Ullyot graduate fellowship supported this research.

Conversion of CO2 to chemicals like ethylene for plastics is possible through a process called electrochemical reduction. Typically, a stream of CO2 gas and a fluid electrolyte move through an electrolysis cell that breaks the CO2 down into molecules like ethylene on the cathode. The new study proposes glycerol, an organic byproduct of sugarcane biofuel production that requires less energy to oxidize, as an alternative to the energy-intensive step.

"The glycerol-based electrolysis reaction shows a lot of promise. However, we will continue to explore other organic waste materials because even when production rises in the wake of increased biofuel production, it still will not be enough to fully support the need," said Paul Kenis (RBTE), a chemical and biomolecular engineering professor, department chair and study co-author. "The good news is that the chemistry involved is flexible and there are a lot of organic waste products that can do the job."

Smart antioxidant-containing polymer responds to body, environment

Oxidants found within living organisms are byproducts of metabolism and are essential to wound-healing and immunity. However, when their concentrations become too high, inflammation and tissue damage can occur. Engineers have developed and tested a new drug-delivery system that senses high oxidant levels and responds by administering just the right amount of antioxidant to restore this delicate balance.

The findings are published in the journal *Small*. The Korea Institute of Science and Technology-Europe, the DoD, the NSF, and NIH supported this research.

Many pharmaceuticals include specialized polymers and particles that control the timing or concentration of the drug released once administered. However, these additives can hamper crystallization during the manufacturing phase of some drugs, including antioxidants, causing them to dissolve in the body in an uncontrolled manner.

"We saw an opportunity here to develop a different kind of drug-delivery system that could sense the level of oxidant in a system and respond by administering antioxidant as needed," said Professor of Chemical and Biomolecular Engineering and study co-author Hyunjoon Kong (RBTE).

Kong and his team found a way to assemble crystals of catechin, the bright green antioxidant found in green tea, using a polymer that can sense when oxidant concentrations become too high. The researchers tested the responsiveness of the resulting polymer in the common freshwater planktonic crustacean *Daphnia magna*, the water flea. When the team added the new catechin crystal assembled with polymer to the experiment, the water fleas recovered a close-to-normal heart rate.

Research

Archaeologists find 200-year-old African DNA on tobacco pipe

DNA found on tobacco pipe stems from a 200-year-old stone slave quarter at Belvoir, a historic house in Anne Arundel County, Maryland, is most closely related to the Mende people of Sierra Leone. The artifacts were uncovered by archaeologists from the Maryland Department of Transportation State Highway Administration; the slave quarter was discovered as part of the administration's Transportation Enhancement Program project to learn more about the history of the area. The program is partially funded by the Federal Highway Administration.

The excavation yielded thousands of artifacts, including broken dishes, animal bones, and clay tobacco pipes. Four tobacco pipe stems from the slave quarter were sent to Professor of Anthropology Ripan Malhi (CGRH/GNDP/GSP/IGOH/RBTE) for DNA analysis.

"We usually study ancient human skeletal remains, so having the opportunity to recover aDNA from tobacco pipes a few hundred years old was a unique challenge," Dr. Malhi stated. He and then-graduate student Kelsey Witt Dillon successfully identified a woman's aDNA on the pipe stem, but it was too degraded to link to living descendants. The results were published in the *Journal of Archaeological Science*. Dillon is now a postdoctoral researcher at the University of California, Merced.

To learn more, Dr. Malhi contacted Dr. Hannes Schroeder at the University of Copenhagen. Dr. Schroeder found the woman to be most closely related to Mende living in present day Sierra Leone in West Africa.

Rising temperatures may safeguard crop nutrition as climate changes

Recent research has shown that rising carbon dioxide levels will likely boost yields, but at the cost of nutrition. A new study in *The Plant Journal* from the University of Illinois, the USDA Agricultural Research Service (ARS), and the Donald Danforth Plant Science Center suggests that this is an incomplete picture of the complex environmental interactions that will affect crops in the future—and rising temperatures may actually benefit nutrition but at the expense of lower yields.

Two years of field trials show that increasing temperatures by about 3 degrees Celcius may help preserve seed quality, offsetting the effects of carbon dioxide that make food less nutritious. In soybeans, elevated carbon dioxide levels decreased the amount of iron and zinc in the seed by about 8 to 9 percent, but increased temperatures had the opposite effect.

"This study shows that a trade-off between optimizing yields for global change and seed nutritional quality may exist," said co-principal investigator Carl Bernacchi (CABBI/GEGC), a scientist at the USDA-ARS, which funded the research along with the USDA National Institute of Food and Agriculture.

The team tested the soybeans in real-world field conditions at the Soybean Free-Air Concentration Experiment (SoyFACE), an agricultural research facility at Illinois that is equipped to artificially increase carbon dioxide and temperature to futuristic levels. Next, they plan to design experiments to figure out the mechanisms responsible for this effect.

Cell size and cell-cycle states play key decision-making role in HIV

Thanks to the development of antiretroviral drugs, human immunodeficiency virus (HIV) is considered a manageable chronic disease today. However, if left undiagnosed or untreated, HIV can develop into AIDS (acquired immune deficiency syndrome), a disease which led to the deaths of nearly 1 million people worldwide in 2017. The life-saving drugs don't cure HIV, though, because when the virus infects the body, it insidiously targets the very cells required to trigger the body's immune response to any infection.

"Upon infection . . . HIV undergoes one of two fates," said Assistant Professor of Bioengineering Roy Dar (GNDP). "It either integrates into a replicating state, leading to the production of hundreds of infectious virions, or it integrates into a latent state where the provirus lies transcriptionally silent."

In a recent study published in *Cell Reports*, Dar and his research group investigated the reactivation of T-cells that were latently infected with HIV in the lab by using a viral construct that contained a gene for a green fluorescent protein that gets expressed when a cell reactivates. Once they identified the cells that were reactivated, they calculated the cell size and determined the mean cell diameter necessary for reactivation. They discovered that within a latent population, only larger host cells reactivate while the smaller cells remain silent or latent.

These findings may be useful in guiding stochastic design strategies for drug therapies, have applications in synthetic biology, and play a role in advancing HIV diagnostics and treatments. This work was funded by the NIH and the Cancer Center at Illinois.

When temp drops, Siberian Miscanthus plants surpass main bioenergy variety

Photosynthesis drives yields, but in cold conditions, this process that turns sunlight into biomass takes a hit. Miscanthus is a popular, sustainable, perennial feedstock for bioenergy production that thrives on marginal land in temperate regions. A study in *GCB Bioenergy* from the University of Illinois and Aarhus University assessed Miscanthus collected on a Siberian expedition to identify plants with exceptional photosynthetic performance in chilling temperatures that outstrip the industry favorite. The work was funded by the USDA, the DOE, and the Innovation Fund Denmark.

"When an arctic vortex hits, we have the luxury to bundle up and stay indoors," said Stephen Long (BSD/CABBI/GEGC), Ikenberry Endowed University Chair of Crop Sciences and Plant Biology . "Miscanthus stays in the ground year-round, and in the spring, regrows from belowground stems to produce biomass . . . but to survive, it has to withstand and remain productive in a wide range of weather conditions."

Scientists from Illinois, the USDA, and Russia's N.I. Vavilov Research Institute of Plant Industry led an expedition to Eastern Siberia, the coldest region where Miscanthus grows, to find hardy wild populations. The team winnowed down 181 Siberian samples to the top three that photosynthesized better than Illinois' Miscanthus during chilling.

In fact, one cultivar photosynthesized 100 percent more efficiently. Over a two-week period of chilling temperatures, a second cultivar maintained stable photosynthesis, which could make it better adapted to long cold spells. When temperatures were increased after two weeks of chilling, a third cultivar could quickly recover photosynthesis—a trait that could help plants thrive when temperatures fluctuate.

News

Neurobiologist Leslie Vosshall gives IGB Distinguished Public Lecture

Leslie Vosshall, Robin Chemers Neustein Professor, Head of the Laboratory of Neurogenetics and Behavior, and Director of the Kavli Neural Systems Institute at The Rockefeller University, spoke as part of the IGB's Genomics and Society Distinguished Public Lecture series with a talk entitled "Thirst for Blood: Mosquito Neurobiology and Behavior."

Vosshall is a molecular neurobiologist known for her work on the genetic basis of chemosensory behavior in both insects and humans. Her lab studies how complex behaviors are controlled by cues from the environment and modulated by the internal physiological state. Working with the dengue and Zika vector mosquito, *Aedes aegypti*, and human subjects, Vosshall's research has yielded new knowledge about how sensory stimuli are perceived and processed.

Vosshall's lab takes a multidisciplinary approach spanning neurobiology, behavior, genetics, and genomics. Beginning in 2008, the group established a mosquito genetics research program to understand host-seeking and blood-feeding behaviors in the mosquito. The Vosshall lab has also developed genome-editing techniques for targeted mutagenesis in *Ae. aegypti* using the CRISPR-Cas9 system to enable the tracing of neural pathways and functional imaging of circuits activated by sensory cues. They have also expanded their field of research to include olfactory perception in humans. Ongoing work aims to link variation in olfactory perception to genetic polymorphisms, probe the basic perceptual logic of human smell, and develop novel diagnostic tests for patients suffering from olfactory dysfunction.

Crops *in silico* 2.0: Project Extended

The Crops *in silico* (C*is*) project has received a $5 million grant from the Foundation for Food and Agriculture Research (FFAR) to continue building a computational platform that integrates multiple models to study a whole plant virtually.

"Four crops—corn, soybean, sorghum, and wheat—account directly or indirectly for about 60 percent of human calories. Yet they are susceptible to declining yields due to the impending stresses of climate change, including water shortages, elevated carbon dioxide levels, and soil degradation," said Amy Marshall-Colón (CABBI/GEGC), Assistant Professor of Plant Biology and the Principal Investigator for the new four-year grant.

The Institute for Sustainability, Energy, and Environment provided $350,000 in seed funding to establish the original project in 2015 in collaboration with NCSA, which provided $212,000 in seed funding. In 2017, a $274,000 grant from FFAR extended the work.

With the global population increasing and the climate continuing to change, understanding how crops respond and may be adapted to environmental changes is needed to address current and future food insecurity. Developing crops using traditional methods is research, labor and cost intensive. C*is* allows researchers to quickly determine and test characteristics that help crops thrive in specific environments.

Co-investigators on the grant include Illinois' Matthew Turk, Assistant Professor of Astronomy and Research Scientist at NCSA; Stephen P. Long (BSD/CABBI/GEGC), Ikenberry Endowed University Chair of Plant Biology and Crop Sciences; Kaiyu Guan (CABBI), Assistant Professor of Natural Resources and Environmental Sciences; and Meagan Lang, NCSA Research Scientist. The research teams also includes collaborators from Pennsylvania State University, Purdue University, Oxford University, and the University of Nebraska.

Annual meeting explores ways to feed the world in 2050

One of the most significant challenges of the 21st Century is how to sustainably feed a growing and more affluent global population with less water and fertilizers on shrinking acreage, despite stagnating yields, threats of pests and disease, and a changing climate. Recent advances to address hunger through agricultural discovery were discussed early this year at the annual meeting of the AAAS.

"The idea for the session is to highlight research that is transcending scientific and knowledge boundaries, with the ultimate goal to transcend geographic boundaries and reach smallholder farmers in Africa," said Lisa Ainsworth (CABBI/GEGC), a scientist with the USDA Agricultural Research Service. Ainsworth was awarded the 2019 National Academy of Sciences Prize in Food and Agriculture Sciences.

Session speaker Donald Ort (GEGC leader/BSD/CABBI), Robert Emerson Professor of Plant Biology and Crop Sciences, discussed the global food security challenge and a recent breakthrough by RIPE researchers that boosted crop growth by 40 percent by creating a shortcut for a glitch that plagues most food crops.

"Plants have to do three key things to produce the food we eat: capture sunlight, use that energy to manufacture plant biomass, and divert as much of the biomass as possible into yields like corn kernels or starchy potatoes," Ort said. "In the last century, crop breeders maximized the first and third of these, leaving us with the challenge to improve the process where sunlight and carbon dioxide are fixed, called photosynthesis, to boost crop growth to meet the demands of the 21st Century."

News

NYT columnist and author Carl Zimmer speaks to Urbana-Champaign community on heredity

New York Times columnist and renowned author Carl Zimmer visited the University of Illinois in March to lecture on his newest book, titled *She Has Her Mother's Laugh: The Powers, Perversions, and Potential of Heredity*.

In his lecture, Zimmer redefined heredity, weaving together historical and current scientific research, exemplary original reporting, and his own experience as a parent of two daughters. Introducing audiences to the not-too-distant future, Zimmer explored the ways in which DNA editing with the powerful new tool CRISPR may change our world—and ourselves. He examined controversial topics (Do races actually exist? Is success inherited?) in light of current advances in DNA analysis, and discussed the ways in which heredity has historically been used to justify racism and social inequality.

Zimmer won the National Academies Communication Award and is a three-time winner of the American Association for the Advancement of Science Journalism Award. In addition, he was awarded the Stephen Jay Gould Prize, and the National Association of Biology Teachers gave him their Distinguished Service Award. Zimmer is a columnist for *The New York Times* and writes regularly for magazines such as *National Geographic* and *Wired*. He is the author of thirteen books; his newest, *She Has Her Mother's Laugh*, was named a Notable Book of the Year by the *New York Times* Book Review. It was also selected for *Publisher's Weekly* Best Ten Books of 2018 and the 2018 shortlist for Baillie-Gifford Prize for Nonfiction. *The Guardian* named it the best science book of 2018.

Ethics Center working to develop leadership curriculum for HHMI

Researchers from Illinois' National Center for Professional & Research Ethics (NCPRE) are developing a new curriculum for the HHMI, a nonprofit research organization that employs scientists at more than 60 universities, hospitals, and other research institutions nationwide. The curriculum will support HHMI scientists in creating a culture that encourages the highest levels of excellence and productivity, by coaching them in specific strategies and behaviors for dealing with ethical challenges. The $2.6 million initiative is called "Labs That Work . . . For Everyone."

"The work of science is team-based, yet when faculty are given responsibility for managing laboratories and developing the careers of their students, they are given limited support or preparation for those roles and responsibilities," said Professor Emerita of Business C.K. Gunsalus, director of the NCPRE. "This initiative will address that void by supporting leadership development for lab leaders—and for their lab members, who are the research leaders of the future. It will cover ethical laboratory and scientific practices, improving cultural competence, and helping researchers to work together effectively, including dealing with conflicts, difficult decisions, and interpersonal problems."

NCPRE plans to pilot two modules in 2021 for HHMI, using the IGB as a parallel testbed. The innovative structure of the IGB, which leverages interdisciplinary team science strategies in life science research to tackle grand societal challenges, makes the institute an ideal participant. Their faculty, postdoctoral, and student communities provide a robust environment for the development of these inclusive curriculum goals. Pending the outcome of this early work, a full curriculum for HHMI scientists could follow.

Illinois teams with Anheuser-Busch for bee research

There's plenty of sweetness in a new partnership between Illinois and St. Louis-based Anheuser-Busch, LLC, that will raise money for bee research at the university.

Anheuser-Busch has pledged $5,000 to The Healthy Bee Fund at Illinois. In addition, the company will donate $1 to the fund for every case sold of b, a new alcoholic honey beverage scheduled to go on sale in the Northeast U.S. in March.

Alcoholic beverages might have never been invented in the first place if not for bees. Swanlund Professor of Entomology May Berenbaum (GEGC/IGOH) said very likely the first fermented beverage invented by humans was mead, a fermented honey wine.

Over the years, Illinois has been home to many discoveries regarding these sophisticated creatures. For example, Gene Robinson (GNDP), Swanlund Professor of Entomology and IGB Director, spearheaded the honey bee genome sequencing project completed in 2006, just prior to the first reports of colony collapse disorder. The project has provided valuable insight into the threats facing honey bees. It's appropriate, then, that Anheuser-Busch's new honey beverage will come as a significant boost to bee research at Illinois, where scientists are leading vital research into the threats facing bees across the world.

Berenbaum said that it's too early to know exactly how much will be raised for research by the partnership, but she said it could potentially fund summer assistantships for students, who are essential to collecting data on bees during the critical warm weather months when most bee research is conducted.

AWARDS

Lisa Ainsworth
USDA Agricultural Research Service (CABBI/GEGC); 2019 NAS Prize in Food and Agriculture Sciences

Brian Allan
Associate Professor of Entomology (CGRH/IGOH); University Scholar

Martin Burke
Professor of Chemistry (MMG); 2019 iCON Honoree

Ximing Cai
Professor of Civil and Environmental Engineering (CABBI); Fellow, American Geophysical Union (AGU)

Nigel Goldenfeld
Swanlund Endowed Chair, Center for Advanced Study Professor in Physics (BCXT leader/CGRH/GNDP); Leo P. Kadanoff Award, American Physical Society

Jiawei Han
Abel Bliss Professor of Engineering (GNDP); Michael Aiken Chair

Brendan Harley
Professor, Chemical & Biomolecular Engineering (RBTE leader); American Institute for Medical and Biological Engineering (AIMBE) College of Fellows

Paul Hergenrother
Professor of Chemistry (ACPP leader/MMG); George and Christine Sosnovsky Award for Cancer Research, American Chemical Society

Auinash Kalsotra
Associate Professor of Biochemistry (GNDP/ONC-PM); Provost's Campus Distinguished Promotion Award

Madhu Khanna
ACES Distinguished Professor (CABBI); DOE/USDA's Biomass Research and Development Technical Advisory Committee

Paul Kenis
Elio E. Tarika Endowed Chair; Head, Department of Chemical and Biomolecular Engineering (RBTE); Fellow, Electrochemical Society

Heidemarie Laurent
Associate Professor of Psychology (CGRH/MME); Provost's Campus Distinguished Promotion Award

Stephen Long
Professor of Crop Sciences and Plant Biology (BSD/CABBI/GEGC); National Academy of Sciences

Ting Lu
Associate Professor of Bioengineering (BSD/BCXT/CABBI/MME); Maximizing Investigators' Research Award (MIRA), National Institutes of Health

Zaida Luthey-Schulten
William H. and Janet G. Lycan Professor of Chemistry (BCXT); Murchison-Mallory Endowed Chair in Chemistry

Ripan Malhi
Professor of Anthropology (CGRH/GNDP/GSP/IGOH/RBTE); Director, Undergraduate Studies, Department of Anthropology

Ruby Mendenhall
Associate Professor of Sociology (CGRH/GNDP); Public Voices Fellowship

Jeffrey Moore
Murchison-Mallory Professor of Chemistry, Professor of Materials Science and Engineering (BSD); American Chemical Society Award in Polymer Chemistry

Bruce Schatz
Professor of Computer Science; Head, Department of Medical Information Science (CGRH); Associate Editor, Nature Digital Medicine

Saurabh Sinha
Professor and Willett Faculty Scholar of Computer Science (BSD/CABBI/GNDP/GSP); Maximizing Investigators' Research Award (MIRA), National Institutes of Health

Amy Wagoner Johnson
Professor of Mechanical Science and Engineering (CGRH/RBTE); Public Voices Fellowship

Rachel Whitaker
Professor of Microbiology (IGOH leader/BCXT); Fellow, American Academy of Microbiology

Huimin Zhao
Steven L. Miller Chair in Chemical and Biomolecular Engineering (BSD leader/CABBI/MMG); 2019 Enzyme Engineering Award

GRANTS

Andrew Smith
Brian Cunningham
Rebecca Smith
National Institutes of Health
"Daily Quantification of Cancer-Associated Exosomal miRNA in Patient Blood by Photonic Crystal-Enhanced Quantum Dot Emission (R01)"

Ravishankar Iyer
Mayo Clinic/National Science Foundation
"I/UCRC: Computing and Genomics – An Essential Partnership for Biology Breakthroughs"

Andrew Belmont
National Institutes of Health
"Proposal to Phase Key 4DN Human Cell Lines (Administrative Supplement)"

Ravishankar Iyer
Huimin Zhao
Sandia National Laboratory
"LDRD: Realistic Emulation of Automated Synthetic Biology Facilities to Prevent Risk of Unintended Manufacture"

Xin Li
Sihai (Dave) Zhao
Northwestern University/National Science Foundation
"Computational Reconstruction of Gene-Gene Dynamics in Temporal Patterning of Drosophila Medulla Neuroblasts from Single-Cell RNA-seq"

Isaac Cann
University of CA, Berkeley/Shell Oil
"EBI Director's Research Support"

Stephen Long
Donald Ort
University of Cambridge/Gates Foundation
"Engineering Nitrogen Symbiosis for Africa (ENSA) Phase 2"

Thanh (Helen) Nguyen
Rachel Whitaker
National Science Foundation
"RAPID: Characterization of Pathogens in Water, Soil and Animal Facilities for Resilience Assessment of Civil Infrastructure after Extreme Weather Events"

Matthew Hudson
Neal Cohen
Bryan White
Mayo Clinic
"Automating Genomic Analysis with Cromwell/WDL and Visualization (Supplement)"

Thanh (Helen) Nguyen
Rebecca Smith
Rachel Whitaker
Joanna Shisler
U.S. Department of Agriculture
"Empowering Rural America: Assessment of Risk and Resilience of Livestock and Food Transportation Infrastructure under Extreme Natural Events"

Martin Burke
Douglas Mitchell
Satish Nair
Huimin Zhao
Sfunga Therapeutics
"Developing Hybrid Amphotericin B Derivatives with a Maximized Therapeutic Index"

Brian Cunningham
Rashid Bashir
Minh Do
Ian Brooks
National Institutes of Health
"Smartphone-linked System for Diagnosis and Epidemiological Reporting of Pathogens at the Point of Care (R01)"

Gene Robinson
National Institutes of Health
"NIH Data Science/Community Workshop"

Huimin Zhao
Douglas Mitchell
Wilfred van der Donk
National Institutes of Health
"A Scalable Platform to Discover Antimicrobials of Biosomal Origin (R01)"

Erik Nelson
Stephen Boppart
Wawrzyniek Dobrucki
Benita Katzenellenbogen
David Kranz
Peiyong Qu
National Institutes of Health
"Impact of Cholesterol and its Metabolites on Breast Cancer Progression (R01)"

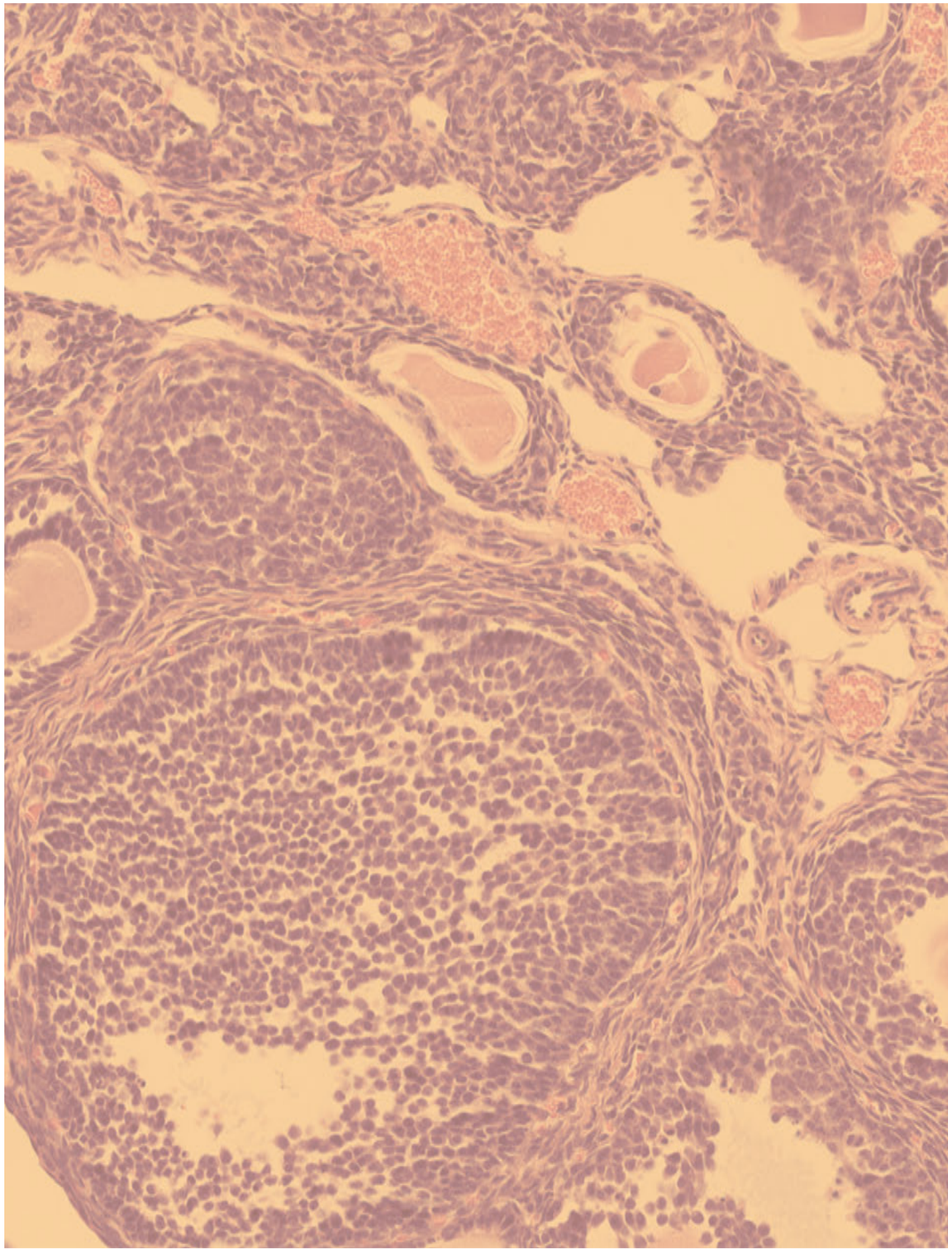
Nathan Schroeder
National Science Foundation
"Collaborative Research: REU Site: Phenotypic Plasticity Research Experience for Community College Students (Supplement)"

Andrew Belmont
National Institutes of Health
"Multimodal, Interactive Data Visualization and Exploration for the 4D Nucleome (Administrative Supplement)"

Andrew Belmont
National Institutes of Health
"Increasing TSA-Seq 4DN Data Set Resolution Through Increased Sequencing Depth (Administrative Supplement)"

Ravishankar Iyer
National Science Foundation
"I/U/CRC: Computing and Genomics – An Essential Partnership for Biology Breakthroughs (Supplement)"

Amy Wagoner Johnson
National Science Foundation
"Convergence: RAISE: Engineering Coral Reef Recovery (Supplement)"



Give to the IGB

The vision of scientific research is limited by the pace of innovation. New technologies let us see the physical world more clearly, in greater detail, in finer scales of space and time. Genomic research, around which the IGB is focused, is particularly tied to advancing technologies.

To continue our record of high-quality research, we need to maintain our position at the forefront of the field. We move past traditional divisions between disciplines of study by constructing a network of collaborations. With your help, we will continue to forge a path toward our vision of a better world.

IGB Annual Fund

Gifts to the IGB help us to foster the collaborative environment that we believe is vital for progress in genomic research. Philanthropy helps us create opportunities for building strong working relationships with intelligent, talented researchers from our own campus, and from across the world. It allows us to provide grants for promising, but risky, research projects that more traditional funding agencies might be hesitant to support. Research needs evolve quickly and unrestricted gifts to the IGB Annual Fund permit us to optimize funds by allocating them for the projects that need them most.

Carl R. Woese Research Fund

Donations may be made to the Carl R. Woese Research Fund to support research on evolution, systems biology, and ecosystem dynamics at the IGB. Professor Woese approved this fund in his name to help the next generation of scientists and to recognize his discoveries and work that spanned nearly half a century at the University of Illinois at Urbana-Champaign.

iGEM Undergraduate Team

The IGB hosts a team of undergraduates from multiple departments to participate in the International Genetically Engineered Machine (iGEM) competition. This opportunity provides students the development of open community and collaboration for the advancement of synthetic biology. Funds for the iGEM team will give undergraduates the chance to present their research to an international audience in Boston.

Stay Connected with the IGB

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