BIOMARKER magazine

winter 2017, vol. 11

10 Year Anniversary Issue

Carl R. Woese
Institute for Genomic Biology

Where Science Meets Society

CARL R. WOESE INSTITUTE
FOR GENOMIC BIOLOGY
1206 WEST GREGORY DRIVE
URBANA, IL 61801
WWW.IGB.ILLINOIS.EDU

ILLINOIS

"Science and everyday life cannot and should not be separated."

-Rosalind Franklin

IGB Themes

ACPP	Anticancer Discovery from Pets to People
BCXT	Biocomplexity
BSD	Biosystems Design
CGRH	Computing Genomes for Reproductive Health
GNDP	Gene Networks in Neural & Developmental Plasticity
GEGC	Genomic Ecology of Global Change
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
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

CONTENTS

BIOMARKER

Director: Gene Robinson
Associate Director: Jennifer Quirk
Director of Communications & Engagement: Nicholas Vasi

Writers

Steph Adams
Sarah Banducci
Claire Benjamin
Courtney Fenlon
Rachael Geiger
Kim Gudeman
Leanne Lucas
Claudia Lutz
Kathryne Metcalf
Laura Schmitt
Emily Scott
Gregory Toreev
Diana Yates
Lois Yoksoulian

Design
Jillian Nickell

Images
Scott Areman, Kathryn Faith, Ken Graham, Jillian Nickell, Steve Shattuck, L. Brian Stauffer

Biomarker is published by the Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign

1206 West Gregory Drive, Urbana, IL 61801

Research Articles

Director's Message

Features

Briefs

Honors

Director's Message

"The scale of our goals is lofty, but they are grounded in real and pressing challenges faced by our society—the need for greater knowledge and continued innovation."

Gene E. Robinson

DIRECTOR, CARL R. WOESE
INSTITUTE FOR GENOMIC BIOLOGY

TEN YEARS IN AND STILL CLIMBING

"The opportunity to position the Urbana campus as a major center for genomic biology turns on the linchpin of the PGI."

-Carl Woese, in a 2003 letter to university officials to voice support for construction of the Post Genomic Institute (PGI), which would eventually become the Carl R. Woese Institute for Genomic Biology.

Anniversaries can be a time for reflection and for inspiration. This year is the 10th anniversary of the establishment of the Carl R. Woese Institute for Genomic Biology (IGB), an exciting milestone for the Institute; our panoply of celebratory events this year have provided many opportunities to evaluate our progress and our goals. In particular, this is a natural time for us to assess how well the IGB has lived up to the vision that led to its formation, and what our own vision is for the coming years.

The ideas that grew into the physical reality of the IGB were far-reaching ones. With the first major scientific advances of the genomic era came a recognition that the new field was one in which the University of Illinois could excel if the various strands of related research on campus could be unified by a common mission or shared space. By enabling the establishment of the IGB, funding from the state of Illinois made all three possible and promised to help position the university as a leader in biotechnological research.

Today, we can say with confidence that the IGB has lived up to that early promise, thanks to the faculty, students and staff who have worked to make it a truly transdisciplinary environment. So far, our adaptive system of faculty-proposed themes has ensured that our research portfolio remains cutting-edge. Our community of researchers is vibrant, collaborative, and diverse. The scale of our goals is lofty, but they are grounded in real and pressing challenges faced by our society—the need for greater knowledge and continued innovation.

This connection to the larger community is another central element of IGB's mission. We were conceived as an institution positioned "where science meets society," with an emphasis placed on fostering true dialogue between scientific researchers and the general public. A highlight of our 10th anniversary celebrations occurred in May, when we had the privilege of sharing the science of genomes at the Field Museum of Natural History in Chicago during a three-day visit that spanned two Members' Nights and visits by over 10,000 museum-goers. The enthusiasm for science that permeated the event was an inspiration for presenters and attendees alike.

In this issue of *Biomarker*, we have shared a few highlights from this year's festivities, as well as our traditional selection of exciting research developments. When we consider what is now possible—engineering cellular environments to foster stem cell development, developing effective and efficient genome-editing strategies for diverse organisms and a multitude of potential uses, creating new yeast strains to revolutionize the biofuel production process—we appreciate the consistent progress of genomic research, and see even grander possibilities in its future.

As we conclude our year, the future promise of our work is what matters most. The true spirit of the original vision for the IGB lies not only in metrics, but in our ability to continue to adapt and innovate. We take pride in how far we have come already, but even more in how our work has led to new goals set and new challenges undertaken. The power of the genomic approach still has much more to offer, and so do we.

A decade of IGB inspires growth and discovery

IN 2003, THE IGB'S FUTURE NAMESAKE, CARL WOESE, COULD ALREADY SEE HOW THE creation of the IGB would impact genomic research.

It was the dawn of the genomic area. The Human Genome Project would confirm that the human genome contains over 20,000 genes, opening up a world of possibilities.

Plans for the IGB had been laid, but state budgetary concerns had brought the construction schedule to a halt. Woese decided to write a letter to James Stukel, who was then the president of the University of Illinois, to voice his concern.

"I have been a member of the University of Illinois faculty for 40 years. Never once in this time have I contacted the President of the University or members of the higher administration regarding matters of University policy," he wrote. "Please, then, take the fact that I now address you on such an issue as a measure of the extreme importance I assign it."

Woese emphasized the IGB's potential to make the University of Illinois campus "a major center for genomic biology" that would stimulate the bio-based economy in central Illinois.

"The community, the campus and many of the faculty are looking to the [IGB] to provide the infrastructure that will enable development of new technologies that can be licensed to local business or faculty start-up companies," Woese continued. "If we fail in this mission, we will fail the people of the state and put ourselves at a decisive disadvantage in recruiting the best young scientific minds."

> **"We attract the best and brightest faculty on the campus because they want to come here and work on the unique problems we're working on."**

Four years and two days after Woese wrote this letter, the IGB was officially dedicated on March 29, 2007.

But the IGB wasn't always the institute that it is today. Ten years ago, it was built from the ground up by a team that included Jennifer Quirk, who has been with the IGB since it began and is now its Associate Director.

"It was pretty fun when it was new," Quirk said. "There were so few people doing things that everything seemed sort of monumental."

With Harris Lewin, the founding director of the IGB, Quirk played a part in creating a staff and figuring out what worked and what did not work for the institute's unique structure.

"In the beginning I built up the staff and it was all new," she said. "Now it's basically a mature building and a mature institute."

Over time, Quirk has seen the IGB gain faculty members who are now tackling large-scale research problems.

"We attract the best and brightest faculty on the campus because they want to come here and work on the unique problems we're working on here," she said. "So we attract the best and brightest faculty, which in turn, I would argue, attract the best and brightest students and postdocs."

Quirk has always felt that the faculty's dedication to the mission of the IGB has made a difference.

"They want what's best for the institution, not what's best for them personally," she said.

She believes this is also true of the IGB's administrative staff.

"I really do think that we have the best administrative support staff on campus," Quirk said. "We have this incredible staff that's committed to the place."

Together, she sees the faculty and staff of the IGB as creating an environment that inspires innovative research.

A decade after IGB began, the building now houses 11 research themes that address challenges in environmental conservation, food security, energy, health, and technology. The newest themes are discovering new anticancer drugs and working to better understand infection biology.

Recent research from the IGB has modified photosynthesis to increase crop yield, identified important mechanisms in bacteria, given us a look into our molecular heritage, and much more.

"Our faculty, research staff and students are changing the world by using genomics in many different ways to tackle some of the most pressing grand challenges in fundamental and applied science," said IGB Director and Swanlund Professor of Entomology, Gene Robinson. "Fueling this, our cutting-edge research has secured some of the most prestigious and largest grants the campus has ever seen."

Recently, the IGB-affiliated Realizing Increased Photosynthetic Efficiency research project received a $45 million reinvestment from the Bill & Melinda Gates Foundation, the Foundation for Food and Agriculture Research, and the U.K. Department for International Development.

The DOE also recently funded the $115 million Center for Advanced Bioenergy and Bioproducts Innovation, a collaboration between the IGB and the Institute for Sustainability, Energy, and Environment.

"We're delighted to be celebrating our 10th anniversary and look forward to many more years of path-breaking, genome-powered team science." Robinson said. "Genomic technology changes so rapidly, we can only imagine the array of new tools that will be available to accomplish these goals, and we look to the future with great anticipation."

World of Genomics brings IGB research to Chicago

FROM MAY 18TH TO 20TH, 2017 IN CHICAGO, OVER 10,000 VISITORS EXPERIENCED the World of Genomics at the Field Museum of Natural History, a three-day event presented by the IGB. A large, blue-lit funnel presented an artistic interpretation of the tree of life; beneath it, the world's smallest sequencer read out the genomes of never-before-sequenced organisms.

With six learning stations distributed across Stanley Field Hall, the main floor of the museum where famous *T. rex* Sue is displayed, World of Genomics represented the full scope of IGB research in health, technology, and the environment, with hands-on activities and exhibits for all ages.

The scale and scope of the event was made possible by numerous partners and sponsors, including Abbott, AbbVie, ZEISS Microscopy, Elanco, the Illinois Soybean Association Checkoff Program, NASA, Opentrons Pacific Biosciences, and the University of Illinois Sesquicentennial celebration.

"In all of the outreach events I've been a part of, I've never experienced such an engaged audience that asked so many excellent, relevant questions about our research," said Beryl Jones, one of the over 60 volunteers from the IGB who staffed the event. "World of Genomics was truly one of the most rewarding experiences of my PhD, and I feel honored to have been a part of an event that reached so many people."

> **"I've done outreach before, but it usually focuses on just one group—kids or adults. WOG really engaged with everyone."**

Jones was one of the volunteers tasked with running the Brains and Behavior learning station, which focused on the shared genomic underpinnings of behavior between humans, honey bees, and other animals. To bring their work to life, researchers presented explorable brain models in virtual reality as well as an observation hive with live bees.

"It was an amazing experience," said Michelle Goettge. She was a volunteer with the DNA to Drugs learning station, which presented information and activities based on antibiotic resistance, the development of new therapeutics, and high-throughput screening. "I've done outreach before, but it usually focuses on just one group—kids or adults. World of Genomics really engaged with everyone, and people were so excited to learn about the science, it was unbelievable."

Other learning stations included Food and Fuel, where visitors could control a miniature agricultural robot through plants demonstrating different phenotypic traits while the larger TERRA-MEPP rover looked on, and Personalized Health, which presented a suite of activities demonstrating differences between bodies of individuals as well as their commensal microbial communities to explain concepts in human health and development.

A fifth station, the sprawling Emergence of Life, partnered with ZEISS to bring high-end microscopy to the Field. There, visitors viewed the intricacies of coral and travertine at the nanoscale; remote microscopy from IGB Core Facilities scanning electron microscope was also on hand to image human kidney stones at an even higher resolution. ZEISS also provided several other instruments to other stations, offering a closer look at a variety of biological specimens.

In all, the event represented IGB's largest outreach effort to date, and perhaps its most successful, not only in the number of people reached, but in the quality of the interactions between scientists and guests.

Members' Nights attendees responded with high praise, with comments such as "The World of Genomics was absolutely amazing," "Loved the virtual reality experience by the bees," and "More research information booths like U of I. Those were amazing." The volunteers especially made a lasting impression, with responses including "The U of I people explaining the exhibits were all very enthusiastic, patient, and knowledgeable."

One attendee elaborated, "I enjoyed the exhibits by the university students. First of all, they were interesting. Even more importantly, they gave us a vision of the future—the next generation of scientists." When asked for favorites, attendees responded "Crop robot and talk on GMO vs other, viewing the 3D printer, virtual reality" and, simply, "Bees."

"We reached everyone from young children to their grandparents, from those who had never heard of us to Chicago alumni, friends of the university, even the University of Illinois President," IGB Director and Swanlund Professor of Entomology Gene Robinson said of the event. "The entire floor was abuzz with rapt and engaged visitors, who immersed themselves into each exhibit, learning about our research, talking to our people, and gaining a new understanding of how fundamental genomics is to their lives."

Study finds parallels in variation in social responsiveness in bees & humans

HUMANS AND HONEY BEES ARE BOTH SOCIAL CREATURES, AND BOTH have evolved to respond strongly to social cues—the threat of an intruder, the hunger of a relative in need, the appearance of a potential mate. Yet within communities of bees and people, individuals vary in how strongly they respond to each type of cue, or to social cues in general.

A recent study, reported in the *Proceedings of the National Academy of Sciences*, has yielded new insights into the parallels between bees and humans who are less responsive to certain social stimuli. Researchers found that some genes associated with autism spectrum disorders in humans are regulated differently in less responsive honey bees than in their more responsive nest mates.

The study yielded a new view of the molecular heritage shared across animals, the researchers said, and offered tantalizing clues about the evolution of social behavior.

"Some honey bees are more active than others, and some appear indifferent to intruders that threaten the hive. This, in itself, is not unusual," said IGB Director and Swanlund Professor of Entomology Gene Robinson, who led the project. "Honey bees take on different roles at different stages of their lifecycle, and not every bee can—or should—function as a guard," he said.

But when postdoctoral researcher Hagai Shpigler observed that some of those same bees also were unmoved by the presence of a queen larva—a stimulus that typically spurs diligent action in bees involved in caring for young in the hive—it suggested something unusual was going on, said Robinson.

"For any given task, most honey bees fall somewhere in the highly engaged to moderately engaged camp," Robinson said. "Typically, honey bees will respond more robustly to one stimulus than to another." A few bees, though, responded to neither type of stimulus examined in the study.

To explore the biological mechanisms that might drive this behavioral variation, the team analyzed 246 groups of bees from seven genetically distinct honey bee colonies, carefully testing each bee in various social contexts, then analyzing levels of gene expression in their brains. They found that more than 1,000 genes were regulated differently between less responsive bees, nurse bees, and guards.

The researchers found a significant overlap between the less responsive honey bees' gene expression profile and genes associated with autism in humans. Further analyses found no significant overlap with human genes associated with depression, schizophrenia or several other mental disorders.

"Our data are telling us that social unresponsiveness does have some common molecular characteristics in these distantly related species," Robinson said.

"It's important to point out some caveats," he said. "Humans are not big bees and bees are not little humans. The social responsiveness depends on context, and is different in the two cases. Autism spectrum disorder is very complex, and unresponsiveness is not the only behavior associated with it."

While social behavior likely evolved independently in honey bees and humans, Robinson said, "our data reveal that they make use of common toolkits, common building blocks."

The Simons Foundation and the NSF supported this research.

Changing the environment within bone marrow alters blood cell development

Pictured:
Brendan Harley, Associate Professor of Chemical and BiomolecularEngineering

FOR CELLS WITHIN THE HUMAN body, where you grow up influences who you become—physical characteristics of different tissues will help newborn cells follow the right developmental path. Chemical and biomolecular engineering professor Brendan Harley (RBTE Theme Leader) and colleagues have now reported they can alter blood cell development through the use of biomaterials that mimic characteristics of bone marrow.

The findings, reported in the journal *Science Advances*, are a first step toward developing more effective bone marrow treatments for diseases like leukemia and lymphoma. The NSF, NIH, and the American Cancer Society of Illinois supported this research.

Blood cells flow throughout the body delivering life-supporting oxygen and nutrients. As these cells age and die, new ones are generated by bone marrow, the soft tissue inside the body's long and hollow bones.

Harley, who led the research with postdoctoral researcher Ji Sun Choi, explained that certain regions of bone marrow contain hematopoietic stem cells (HSCs), which are the parent cells of all blood and immune cells. "The tissue environment that surrounds these cells in the bone marrow provides a wealth of signals that can alter how these precursor cells behave. This paper looked at the signals provided by the tissue matrix itself," said Harley.

One of the major treatments for leukemia and lymphoma involves transplanting HSCs. The donor stem cells must locate marrow cavities, then nestle there and start producing blood and immune cells. However, there is a limited quantity of available donor HSCs and the success rate of transplantation is low.

"We're interested in this problem from an engineering standpoint," Harley said. "The goal is to create better tools to both expand the number of donor HSCs and improve their capacity to repopulate the bone marrow after transplantation."

Like cells throughout the body, HSCs are contained in a three-dimensional tissue environment known as the extracellular matrix. Harley and Choi gathered samples of HSCs from mice and then grew them in the laboratory using biomaterials engineered to mimic some of the extracellular matrix properties of the native bone marrow. Their goal was to examine how these engineered systems could alter the HSCs' capacity to proliferate and differentiate to become blood cells.

The researchers examined two main elements of the matrix that regularly interact with HSCs: collagen and fibronectin. They found that the HSCs that were exposed to collagen proliferated more rapidly, but that they had differentiated, meaning they were no longer stem cells. When exposed to fibronectin, they proliferated less rapidly but remained stem cells.

"With the collagen substrates, we got more cells but not useful cells," Harley said. "With the right combination of stiffness in the matrix and the presence of fibronectin, we identified a class of biomaterials that show promise for being able to maintain and eventually expand these stem cells outside of the body. An engineered bone marrow will be of enormous value for treating hematopoietic cancers such as leukemia."

Harley and other researchers in his lab are currently investigating other features of the matrix that can be manipulated to increase the number of stem cells and make them more effective in transplantation.

> **"An engineered bone marrow will be of enormous value for treating hematoietic cancers such as leukemia."**

Study identifies key player in heart enlargement

The heart is a dynamic muscle whose cells have the ability to change size depending on the heart's needs. A new study of mouse hearts reveals a previously unknown mechanism by which heart cells control their size by ramping up or stopping the production of a key protein called PABPC1.

The findings, reported in the journal *eLife*, could assist in the development of therapeutics that promote healthy heart growth and prevent disease.

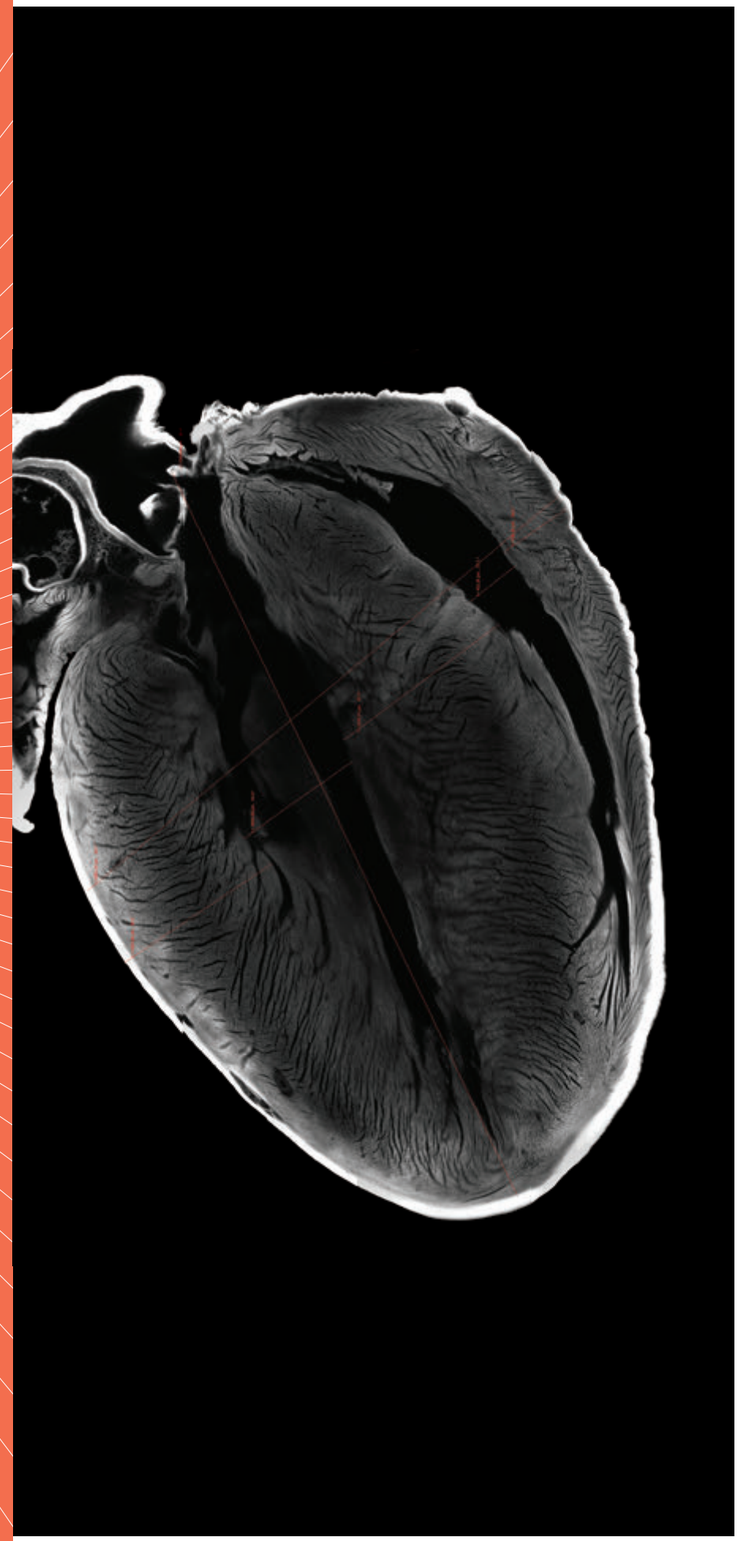
During exercise, the heart beats harder to pump oxygen to the muscles. Heart cells adapt over time by boosting production of specific proteins to increase in size, said biochemistry professor Auinash Kalsotra (GNDP/ONC-PM), who led the study with postdoctoral researcher Sandip Chorghade and graduate student Joseph Seimetz.

In their NIH-supported study, the researchers focused on PABPC1, a protein that binds to RNA and helps translate RNA into proteins. Scientists had long assumed all cells needed PABPC1 to survive and make new proteins.

But the researchers discovered that the protein is absent in the adult heart, though it is present in all human and mouse cells.

This finding explains why heart cells produce significantly lower levels of new proteins than other tissues in the body—a fact that was known but not understood until now.

"The finding that PABPC1 is usually not present in adult heart cells until needed for growth suggests that if you could control the function of this protein, then you could promote healthy growth and prevent disease," Kalsotra said.



In the developing ears of opossums, echoes of evolutionary history

WHEN WE ARE CONFRONTED with the remarkable diversity and complexity of forms among living things—the lightweight and leathery wings of a bat, the dense networks of genes that work together to produce a functional cell—it can be hard to imagine how chance mutations and selective processes produced them. If we could rewind evolutionary time, what would we see?

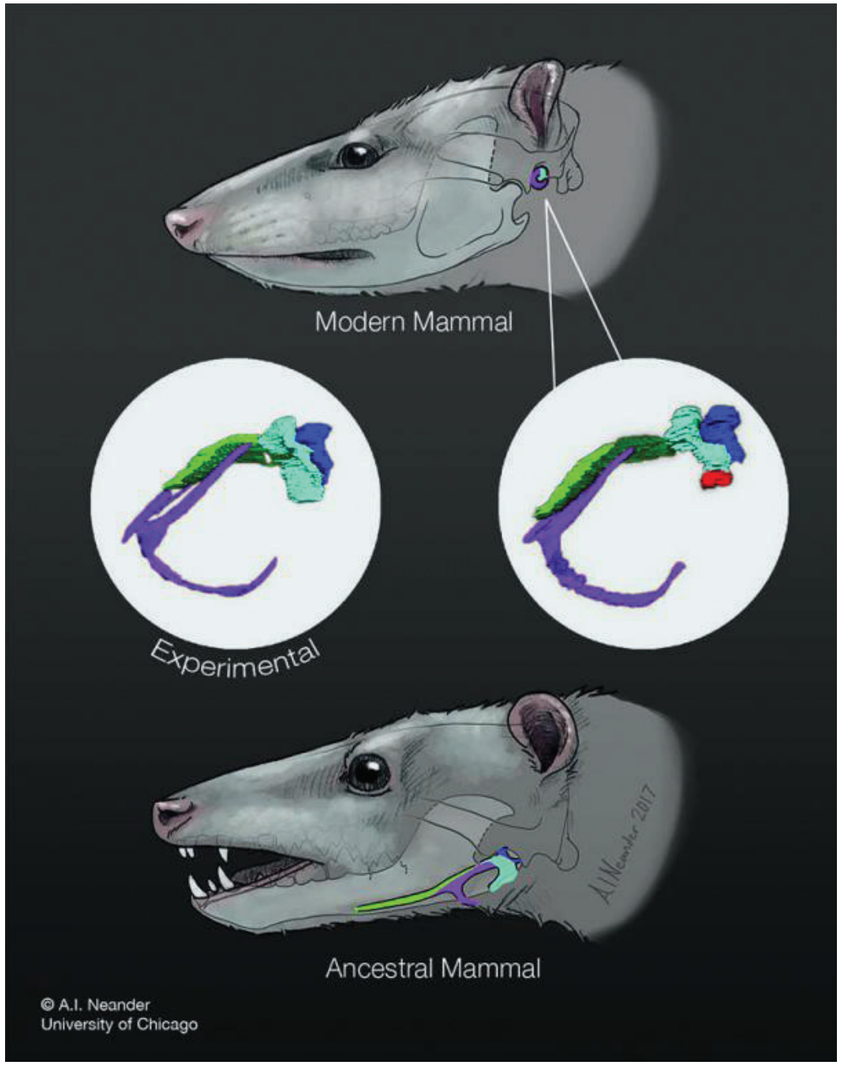
In a new study published in *Proceedings of the Royal Society B* and funded by the NSF, Wellcome Trust, and Leverhulme Trust, animal scientists at Illinois, King's College London, and the University of Chicago have made a discovery that was hidden in the development of opossums. They found one possible version of the evolutionary path that led from the simple ears of reptiles to the more elaborative and sensitive structures of mammals, including humans.

Three tiny bones in the middle ear of mammals form a mechanism that converts the air vibrations of sound into the electrical impulses understood by the brain. In the simpler ears of reptiles, as well as the shared ancestors of both groups, only one of these bones is found in the middle ear, while the other two form part of the jaw. This contrastdrew the attention of Associate Professor of Animal Biology Karen Sears (RBTE) and IGB Fellow Daniel Urban, who led the study and have since moved on to positions at University of California, Los Angeles.

"We came at this project through the approach of evolutionary developmental biology (evo-devo), which looks at the development of an organism ... to help understand its evolutionary history," said Urban, explaining their experimental approach.

To get a better idea of how the mammalian ear might have evolved, Sears, Urban and their colleagues chose to study the gray short-tailed opossum, a small and charismatic South American marsupial whose key stages of jaw and ear development take place gradually and after birth.

The group first detailed the anatomical progression of middle ear development in their opossums, capturing images that revealed the changing architecture of cartilage and bone. They observed that the progression of structures in the developing opossum jaw and ear appeared to re-enact the evolutionary progression of these structures in the mammalian fossil record.



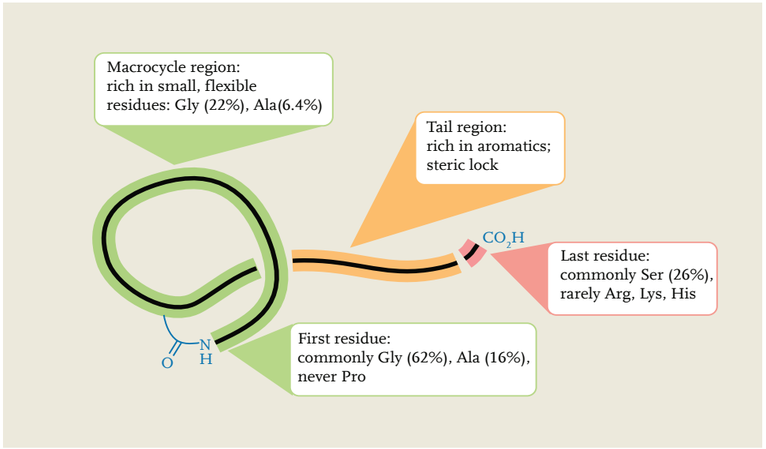
"It was truly remarkable how well the developmental stages of our extant opossum model organism matched up with the transitional fossils ... this makes our study organism, the gray short-tailed opossum, a fantastic living model to aid in the understanding of development of long extinct taxa," Urban said. "By using this modern analogue, we can learn so much more about these earlier species and the origins of mammals."

The team also explored changes in gene activity and individual cells that occurred during the cartilage breakdown process that allows mammalian ear bones to migrate to their final positions. They identified a set of genes whose increased activity was correlated with the self-destruction of the cells that connect the future jaw to the future ear. Among these genes, the researchers focused on a gene called *TGF-β* for further investigation.

When Urban and his colleagues treated developing opossums with a drug that blocks the signaling of the TGF-β protein, the death of cartilage cells was prevented and the ear bones remained a part of the jaw, their arrangement appearing to have slid backward through evolutionary time. This suggests that a chance mutation in a key gene could produce the same effect, providing a possible pathway by which the mammalian ear might have evolved.

> "By using this modern analogue, we can learn so much more about these earlier species and the origins of mammals."

New tool RODEO captures breadth of microbial biosynthetic potential



Lasso peptide structural features and common residues mined from RODEO analysis

IN AN AGE OF BOOMING BIOtechnology, we still rely on the bounty of the natural world. Microbes, rather than always making us sick, give us some of our best cures in the form of naturally occurring products such as penicillin and tetracycline.

Recently, "big data" genome technology has begun to help us discover nature's inventions. A team of researchers led by Associate Professor of Chemistry Douglas Mitchell (MMG) has created a tool that searches through microbial genomes, identifying clusters of genes that indicate an organism's ability to synthesize therapeutically promising molecules.

In a *Nature Chemical Biology* article, lead authors Jonathan Tietz and Christopher Schwalen and colleagues in Mitchell's laboratory described how their custom software learns to recognize predictive genomic features.

Mitchell's group is particularly interested in a class of molecules commonly referred to as RiPPs, a friendly acronym for a long name: ribosomally synthesized and post-translationally modified peptides. RiPPs, like proteins, are made of chains of linked amino acids, are encoded by genes, and undergo chemical modification (carried out by other proteins) after they are made.

RiPPs may seem unfamiliar, but they are already present in the average consumer's daily life. A bacterially-produced RiPP called nisin, for example, has been used as a pathogen-fighting additive in dairy products, meats, and beverages such as beer since the 1960s.

Traditionally, researchers found potentially useful natural products by screening microbes based on their biological activity. After decades of such efforts, which revealed a range of products including some RiPPs, the low-hanging fruit has been plucked; searches turn up the same common compounds over and over again.

Mitchell and colleagues use genome mining, essentially skimming through cells' recipe books to see what they might be able to produce, as a way to "climb higher" and find novel natural products, including RiPPs. To do this, the researchers needed to create software that could recognize the groups of genes whose products work together to synthesize a RiPP.

They decided to make it even tougher by focusing on a class of RiPPs called lasso peptides, named for their looping structure. The clusters of genes that produce lasso peptides are small and generic-looking, making them difficult to identify even in a manual search.

"If you want to show that you have a useful tool, you pick the hardest example," Mitchell said. "But also, as a chemist, lasso peptides are extremely interesting" because they are so chemically robust.

The informatics tool that Mitchell's laboratory designed, named RODEO (Rapid Open reading frame Description and Evaluation Online), was "trained" via machine learning on known examples of lasso-producing gene clusters, allowing the program to hone in on key features.

The resulting software robustly identified promising gene clusters in a broad array of microbial genomes, and could be easily customized to search for the gene clusters of other classes of RiPPs as well.

"We can now use genomic prioritization to find molecules that without any doubt are structurally novel," said Mitchell. "The challenge is, is that a useful molecule or not? So that's the next 10 years of discovery."

This work was supported by the NIH, the American Chemical Society, the David and Lucile Packard Foundation, and Robert C. and Carolyn J. Springborn Endowment for Student Support Program.

DOE funds major bioenergy research center

The DOE is doubling down on energy research at Illinois, funding a multi-million dollar Bioenergy Research Center to provide scientific breakthroughs for a new generation of sustainable, cost-effective biofuels and bioproducts.

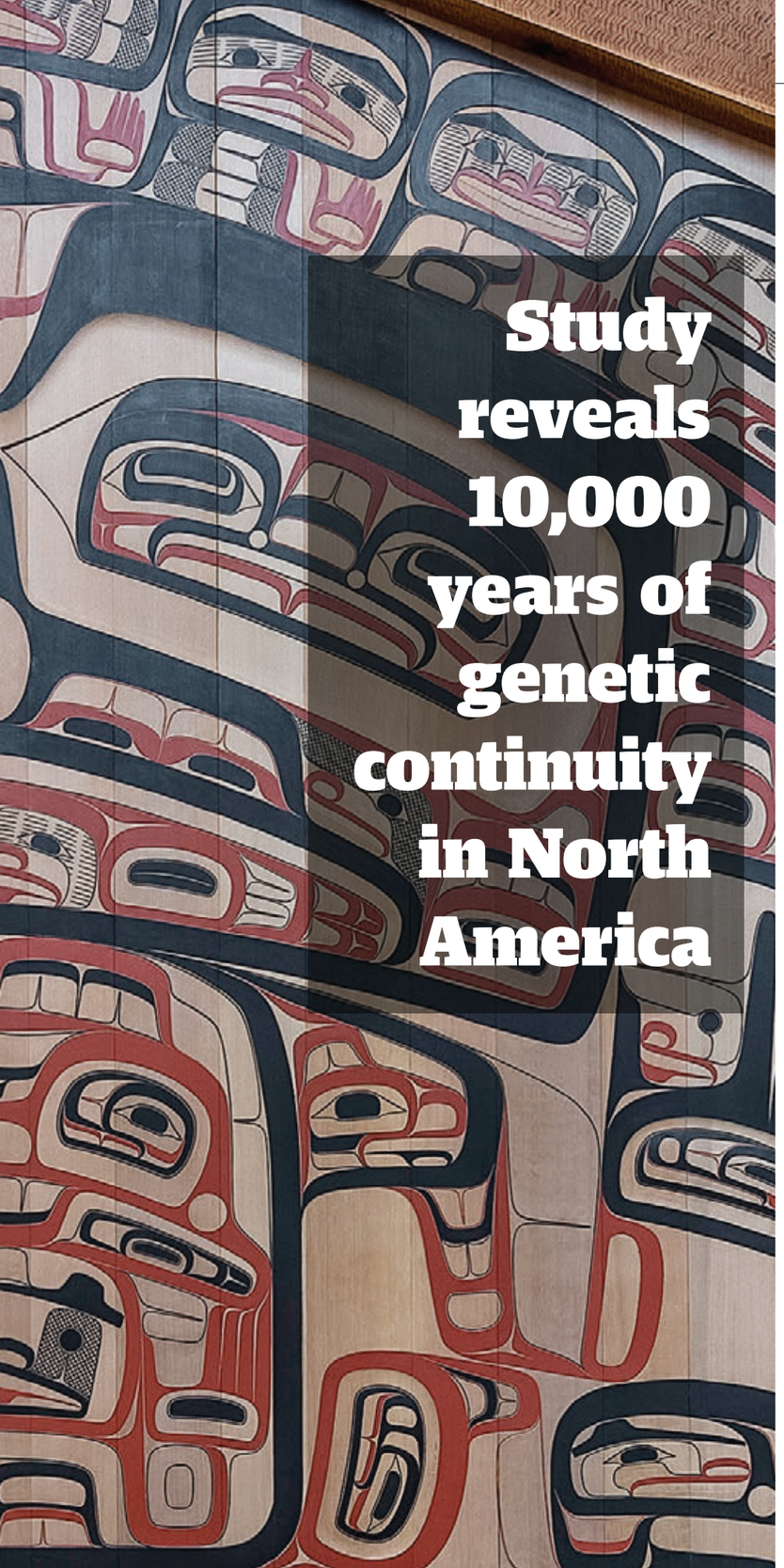
The DOE announced the $115 million Center for Advanced Bioenergy and Bioproducts Innovation (CABBI), pending Congressional appropriation, a collaboration between Illinois' Institute for Sustainability, Energy, and Environment (iSEE) and the IGB. CABBI includes 16 partner institutions. Evan H. DeLucia, G. William Arends Professor of Plant Biology and Baum Family Director of iSEE (EBI/GEGC), will serve as CABBI Director.

"This grant is a game-changer, and CABBI will be at the forefront as we press toward a new bio-based economy," DeLucia said. "Our Center's holistic approach will generate new products directly from biomass, reducing our nation's dependence on fossil fuels and making us more secure."

One of the major challenges the world faces is providing sustainable sources of energy that meet societal needs as the population continues to grow. DeLucia said Illinois is uniquely qualified to address the challenge with a world-class facility at IGB.

CABBI researchers will develop fuels and products by integrating three highly interconnected DOE priority areas: growing the right crops, turning plants into fuel, and determining the environmental and economic bottom line.

"We look forward to a day when we will have sustainable and economically sound production of fuels and chemicals from plants," DeLucia said. "A vibrant bioeconomy based on plant products will enhance the economic and ecological resilience of U.S. agriculture."



Study reveals 10,000 years of genetic continuity in North America

A STUDY OF THE DNA IN ancient skeletal remains adds to the evidence that indigenous groups living today in southern Alaska and the western coast of British Columbia are descendants of the first humans to make their home in northwest North America more than 10,000 years ago.

"Our analysis suggests that this is the same population living in this part of the world over time, so we have genetic continuity from 10,000 years ago to the present," said Associate Professor of Anthropology Ripan Malhi (CGRH/RBTE), who led the study with collaborators from multiple institutions around the world.

The findings, reported in the *Proceedings of the National Academy of Sciences,* also suggest that these early American peoples had a complex population history. The work was supported by the University of Illinois; the Canadian Museum of History in Gatineau, Quebec, Canada; and Pennsylvania State University.

The new work comes on the heels of earlier studies of ancient Americans that focused on mitochondrial DNA, which occurs outside the nucleus of cells and is passed only from mothers to their offspring.

"Mitochondrial DNA just traces the maternal line—your mother's mother's lineage—so, you're missing information about all of these other ancestors," said John Lindo, a postdoctoral researcher at the University of Chicago and first author on the paper. "We wanted to analyze the nuclear genome so we could get a better assessment of the population history of this region."

The team looked at genomic data from Shuká Káa (Tlingit for "Man Before Us"), an ancient individual whose remains date to about 10,300 years ago. They also analyzed the genomes of three more individuals from the nearby coast of British Columbia whose remains date to between 6,075 and 1,750 years ago.

Left: Tsimshian artist David A. Boxley created the carved and painted cedar house front in the foyer of the Walter Soboleff Building, Sealaska Heritage's headquarters in Juneau. Photo by Ken Graham

> "We supported DNA testing of Shuká Káa because we believed science ultimately would agree with what our oral traditions have always said—that we have lived in southeast Alaska since time immemorial ... Science is corroborating our oral histories."

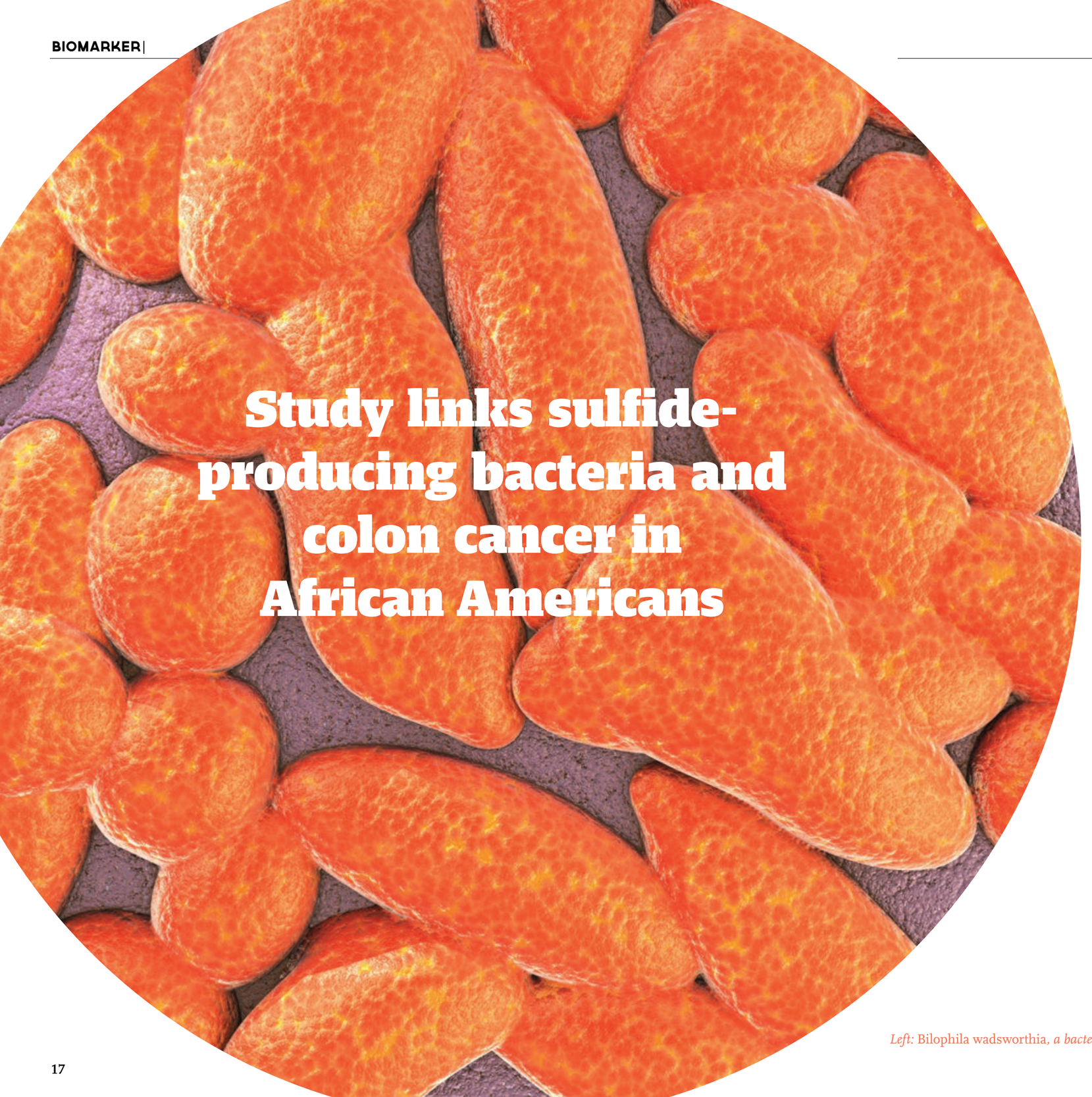
Above: Rosita Kaaháni Worl, PhD, president of Sealaska Heritage Photo by Scott Areman

"Interestingly, the mitochondrial type that Shuká Káa belonged to was also observed from another ancient skeleton dated to about 6,000 years ago," said Brian Kemp, a coauthor and associate professor of anthropology at the University of Oklahoma. "It seems to disappear after that. The nuclear DNA suggests that this is probably not about population replacement, but rather chance occurrence through time."

"The data suggest that there were multiple genetic lineages in the Americas from at least 10,300 years ago," Malhi said.

The descendants of some of those lineages are still living in the same region today, and a few are co-authors on the new study. Their participation is the result of a long-term collaboration between the scientists and several native groups who are embracing genomic studies as a way to learn from their ancestors, said coauthor Rosita Worl, who is president of the Sealaska Heritage Institute. Worl is Tlingit, Ch'áak' (Eagle) moiety of the Shangukeidí (Thunderbird) Clan from the Kawdliyaayi Hít (House Lowered From the Sun) in Klukwan, Alaska.

"We supported DNA testing of Shuká Káa because we believed science ultimately would agree with what our oral traditions have always said—that we have lived in southeast Alaska since time immemorial. The initial analysis showed the young man was native, and now further studies are showing that our ancestral lineage stems from the first initial peopling of the region," said Worl. "Science is corroborating our oral histories."



Study links sulfide-producing bacteria and colon cancer in African Americans

A NEW STUDY REVEALS THAT African-Americans have measurable differences in the number and type of bacteria that live in the colon—and those differences are related to their higher-than-average colon cancer risk.

The study, reported in the journal *Gut*, looked at colonic tissue biopsies from 197 African-Americans and 132 non-Hispanic whites collected over a two-year period ending in 2012. The researchers amplified microbial DNA from the samples, then looked at the abundance of various types of microbes.

The study found that African-Americans have more sulfide-producing bacteria in their colon than non-Hispanic whites in the U.S. do. Although these microbes are a normal part of the gut ecosystem, an overabundance of sulfide in the colon can lead to inflammation and can damage DNA, said animal sciences professor Rex Gaskins (RBTE), who led the new research with Nathan Ellis, the Faculty Director of the Genomics and DNA Sequencing Facilities in the Research Resources Center at the University of Illinois at Chicago at the time of the study.

"We found that African-Americans have an increased abundance of bacteria that make hydrogen sulfide, which we demonstrated more than a decade ago to be a potent genotoxin," Gaskins said.

The study also revealed that *Bilophila wadsworthia*, a bacterium that produces hydrogen sulfide from the amino acid taurine, was significantly more abundant in African-Americans with colon cancer than in their healthy counterparts.

"These bacteria are using nutrients associated with an animal-based diet," Gaskins said.

The relationship between *B. wadsworthia* abundance and colon cancer risk did not hold true for non-Hispanic whites, however.

Most cases of colorectal cancer—about 85 to 90 percent—are sporadic, rather than familial, Gaskins said. There may be a genetic element, but environmental factors like exposure to pollutants or dietary components also are required to spur the onset of cancer.

"You have to have a genotoxin to have colon cancer," Gaskins said. "And sulfide is a genotoxin."

African-Americans have significantly higher incidence of colon cancer than other Americans. In 2013, there were 33.5 colon cancer cases per 100,000 African-Americans, compared with 26.8 per 100,000 whites.

Explaining these disparities has not been easy. Native Africans have dramatically lower colon cancer rates than African-Americans, suggesting that environmental factors, including dietary habits, are a key to the problem, along with genetics.

A 2014 study on which Gaskins was a senior co-author found that when rural South African Zulus, who normally ate a low-fat, high-fiber diet, switched to a diet with a lot of meat and animal fat, sulfide-producing bacteria in their colon increased. This change took less than two weeks, the researchers found.

Scientists already knew that a diet high in red meat and animal fat was associated with an increased risk of developing colon cancer, Gaskins said.

"We are now beginning to connect the dots between these dietary factors and one's risk of developing colon cancer risk," he said. "Our research adds to the evidence that the microbes that inhabit the colon are part of the equation and should not be overlooked."

The NIH and the American Cancer Society supported this research.

"Our research adds to the evidence that the microbes that inhabit the colon are part of the equation and should not be overlooked."

Left: Bilophila wadsworthia, *a bacterium correlated with colon cancer in African-American patients*

Pictured: Ant from the genus Myrmoteras.
Photo by Steve Shattuck

Scientists discover spring-loaded mechanism in unusual species of trap-jaw ant

RESEARCHERS REVEALED HOW A group of trap-jaw ants can snap their jaws shut at speeds of up to 50 miles per hour—just fast enough to capture their elusive prey.

They reported their findings in the *Journal of Experimental Biology*.

The ants belong to the genus *Myrmoteras*, and are one of four groups of ants that have independently evolved the ability to quickly snap their powerful jaws shut to capture speedy prey. They feed primarily on springtails, tiny arthropods that fling themselves away from danger when they detect a threat. *Myrmoteras* ants hold their jaws open at a 280-degree angle until they encounter their prey and snap their jaws shut on their target in a fraction of a second.

"These ants are rarely seen in nature and almost impossible to keep alive in the lab," said Associate Professor of Animal Biology and Entomology Andrew Suarez (GNDP), who led the study with former graduate student Frederick Larabee, now a postdoctoral researcher at the Smithsonian Institution's National Museum of Natural History.

"Each group of trap-jaw ants has a different way to store and release energy. Working with this genus has been sort of a holy grail for us," Suarez said. "Studying these ants gives us insight into solutions for real-world issues related to energy storage and high-speed systems."

The jaws of *Myrmoteras* ants can snap shut in half a millisecond, much faster than the human eye can perceive. Such speed cannot be attained by muscle strength alone. Animals whose movements exceed this limitation, including trap-jaw ants, do so through anatomical adaptations—evolved body parts that act like springs or latches to enhance the motions produced by muscles.

To visualize the ants' jaws and understand what mechanism allows them to break the muscular speed limit, Larabee used a microscope and microcomputed tomography, which exposes tiny specimens to X-rays to discern their internal structures. His observations allowed him to determine how the jaws likely work.

Larabee detected a feature of the ant's mandible that allow it to lock its jaws open. Just before a strike, a lobe on the back of the ant's head compresses. A trigger muscle releases the jaws, executing the strike.

"What's interesting is that the arrangement of the muscles and how the jaws are locked open are completely different from other trap-jaw ants that have been studied," Larabee said. "It seems like it's a completely unique evolution of this system."

However, the jaws of the *Myrmoteras* ants are only as fast as they need to be, Larabee said. While the peak velocity achieved by their jaws is comparable to that of other trap-jaw ants, their acceleration is considerably slower. The researcher hypothesized that the resulting lag may not make much difference in the ants' ability to capture prey: the springtails they eat take 10-50 milliseconds to effect an escape once they detect an attack, which leaves *Myrmoteras* enough time to snatch the soft springtail bodies in their knife-like jaws.

"They just need to be faster than the critters they're trying to eat, and their jaws are plenty fast for capturing springtails," he said.

The NSF, the Smithsonian Institution and the National Geographic Society supported this research.

" Studying these ants gives us insight into solutions for real-world issues related to energy storage and high-speed systems. "

Below: Andy Suarez, Associate Professor of Animal Biology and Entomology

Pictured: Field corn, used to make ethanol

New research could make ethanol production more efficient and economic

NEW RESEARCH AT THE Integrated Bioprocessing Research Laboratory (IBRL) could significantly change ethanol production by lowering operating costs and simplifying the dry grind process.

"There are currently more than 200 dry grind plants that are processing corn to produce ethanol," said Vijay Singh, director of IBRL and a professor of agricultural and biological engineering (GEGC). "The dry grind process requires two different enzymes to convert corn starch to glucose, which is further fermented to ethanol by yeast."

Singh says that process has been simplified by combined use and optimization of three new technologies.

Amylase corn, which is a new corn developed by transgenic technology, produces one of these enzymes in the grain itself. A newly engineered "superior yeast" provides the second enzyme and ferments the glucose, according to Singh.

"There is a high expression level of the first enzyme, α-amylase, in the new corn, so only a small amount [15 percent was tested in these studies] of this corn is required to be mixed with conventional dent corn," Singh said. "The superior yeast provides the second enzyme, glucoamylase, and also provides an alternate metabolic pathway to reduce byproduct formation during fermentation. Combined use of this corn and superior yeast can reduce the total enzyme addition by more than 80 percent."

Another approach to improve the dry grind process is to use high solids in the plant. However, according to Singh, high solid concentrations lead to high ethanol build-up in the tank.

"High ethanol affects the yeast viability and inhibits its fermentation performance, so we have added a third technology to the process. We remove the ethanol as it is being produced, using a vacuum flashing process that is patented technology from the University of Illinois," Singh said. "Only a couple of vacuum cycles of 1 to 1.5 hours can bring the ethanol concentration below the inhibitory levels without affecting yeast health and allow complete fermentation of corn solids up to 40 percent."

Deepak Kumar, a postdoctoral research associate in agricultural and biological engineering, says because the dry grind process uses a significant amount of water, using more solid material in the slurry—40 percent as opposed to 30-35 percent—means less water going into the process.

"When ethanol is produced, it is in a very dilute solution. You have a small amount of ethanol and a large amount of water," Kumar said. "We cut down the water use by pushing high solids. When we reduce the amount of water, we also reduce the amount of energy required to remove the water."

Singh believes this new research has the potential to improve the economics and process efficiencies and simplify the dry grind process.

"By developing highly optimized technologies, we will benefit the entire dry grind industry," he said.

Singh and Kumar received the 2016 Bioenergy Society of Singapore (BESS) Achievement Award for their research, which was funded by the USDA. Their paper was published in the journal *Biotechnology for Biofuels.*

New 3D model predicts best planting practices for farmers

The University of Illinois and the Partner Institute for Computational Biology in Shanghai collaborated to develop a computer model that can predict the yield of different crop cultivars in a multitude of planting conditions.

The model, published in *BioEnergy Research*, depicts the growth of 3D plants, incorporating models of the biochemical and biophysical processes that underlie productivity.

Teaming up with the University of São Paulo in Brazil, researchers used the model to address a question for sugarcane producers: How much yield might be sacrificed to take advantage of a possible conservation planting technique?

According to author Stephen Long (BSD/GEGC), Gutsgell Endowed Professor of Plant Biology and Crop Sciences, current sugarcane harvesters cut a single row at a time, which takes time and could lead to damage of crop stands.

But their model found that this problem could be solved if the crop was planted in double rows with gaps in between. This costs about 10 percent of productivity compared to traditional row spacing.

"This model could be applied to other crops to predict optimal planting designs for specific environments," said Yu Wang, a postdoctoral researcher who led the study. "It could also be used in reverse to predict the potential outcome for a field."

The authors predict this model will be especially useful when robotic planting, which allows for more planting permutations, becomes more commonplace.

This research was supported by the IGB, the Bill & Melinda Gates Foundation via the Realizing Increased Photosynthetic Efficiency (RIPE) project, the EBI, and the Chinese Academy of Sciences.

New handheld spectral analyzer uses smartphone to detect disease

RESEARCHERS HAVE DEVELOPED a technology that enables a smartphone to perform lab-grade medical diagnostic tests.

Costing only $550, the spectral transmission-reflectance-intensity (TRI) Analyzer from the lab of Professor of Electrical and Computer Engineering, Brian Cunningham (ONC-PM Theme Leader/MMG), attaches to a smartphone and analyzes patient blood, urine, or saliva samples as reliably as clinic-based instruments that cost thousands of dollars and require large, expensive instruments.

"Our TRI Analyzer is like the Swiss Army knife of biosensing," said Cunningham, also the Donald Biggar Willett Professor of Engineering and director of the Micro and Nanotechnology Lab at Illinois. "It's capable of performing the three most common types of tests in medical diagnostics, so in practice, thousands of already-developed tests could be adapted to it."

Their paper, published in *Lab on a Chip*, describes how their team used the TRI Analyzer to perform two commercially available tests—one that detects a biomarker associated with pre-term birth in pregnant women, and the PKU test for newborns that detects an enzyme essential for normal growth and development. Their test results were comparable to those acquired with clinic-grade spectrometer instrumentation.

Among the many diagnostic tests that can be adapted to their point-of-care smartphone format is an enzyme-linked immunosorbent assay (ELISA), which detects and measures a variety of proteins and antibodies in blood and is commonly used for a wide range of health diagnostics tests. The system is capable of detecting the output of any test that uses a liquid that changes color, or a liquid that generates light output (such as from fluorescent dyes).

"The TRI Analyzer is more of a portable laboratory than a specialized device," said Kenny Long, an MD/PhD student and lead author of the research, which was supported by funds from the NSF and the NIH.

> "Our TRI Analyzer is like the Swiss Army knife of biosensing. It's capable of performing the three most common types of tests in medical diagnostics, so in practice, thousands of already developed tests could be adapted to it."

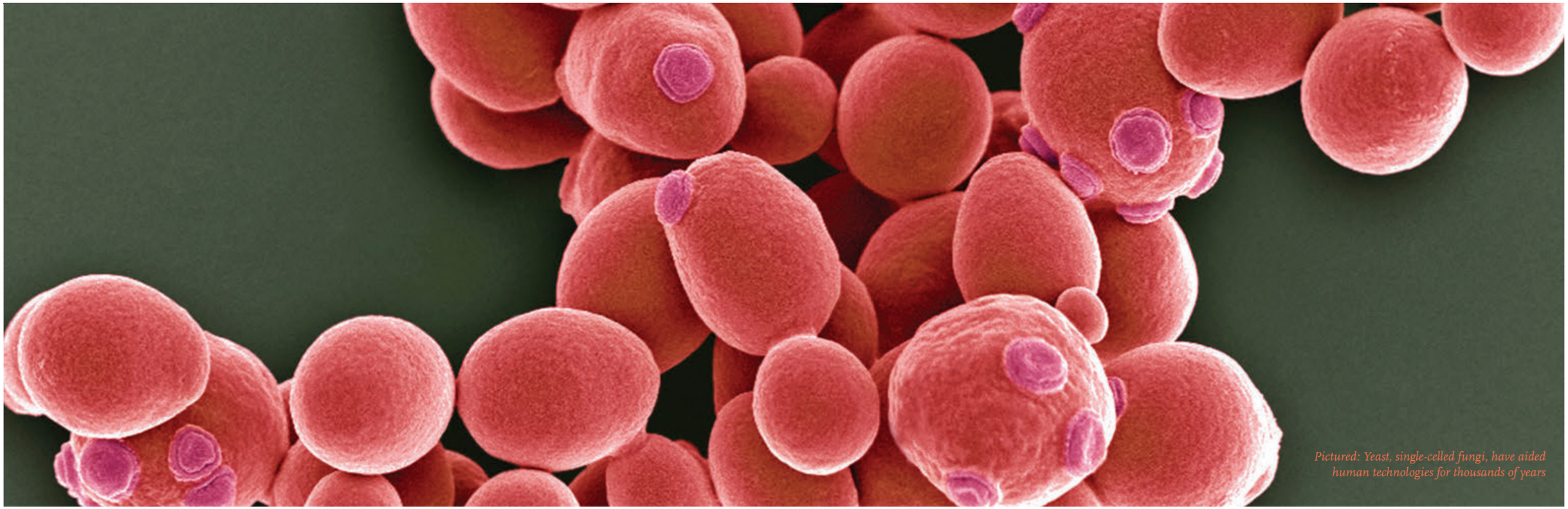
The TRI Analyzer operates by converting the smartphone camera into a high-performance spectrometer. The Analyzer illuminates a sample fluid with the phone's internal white LED flash or with an inexpensive external green laser diode. The light from the sample is collected in an optical fiber and guided through a diffraction grating into the phone's rear-facing internal camera. These optical components are all arranged within a 3D-printed plastic cradle.

This technology can simultaneously measure multiple samples by using a microfluidic cartridge that slides through an opening in the back of the cradle. This ability to analyze multiple samples quickly and reliably makes the Analyzer suitable for patients who lack convenient access to a clinic or hospital with diagnostic test facilities or for patients with urgent health situations requiring rapid results.

"Our Analyzer can scan many tests in a sequence by swiping the cartridge past the readout head, in a similar manner to the way magnetic strip credit cards are swiped," Long said.

In addition to its applications in health diagnostics, Cunningham said the TRI Analyzer can be used in applications for animal health, environmental monitoring, drug testing, manufacturing quality control and food safety. The patented technology is available for license.

Above: Brian Cunningham, Professor of Electrical and Computer Engineering



Pictured: Yeast, single-celled fungi, have aided human technologies for thousands of years

New capabilities for genome-wide engineering of yeast

ONE OF HUMANKIND'S OLDEST INDUSTRIAL partners is yeast, a familiar microbe that enabled early societies to brew beer and leaven bread and empowers modern ones to synthesize biofuels and conduct key biomedical research. Despite this utility, our ability to explore and influence its genomic activity has lagged.

In an article in *Nature Communications*, Steven L. Miller Chair of Chemical and Biomolecular Engineering Huimin Zhao (BSD Theme Leader/MMG) and his coauthors described how their successful integration of several cutting-edge technologies—creation of standardized genetic components, implementation of customizable genome editing tools, and large-scale automation of molecular biology laboratory tasks—will enhance our ability to work with yeast. The results of their new method demonstrate its potential to produce valuable novel strains of yeast for industrial use.

"The goal of the work was really to develop a genome-scale engineering tool for yeast ... traditional metabolic engineering focused on just a few genes and the few existing genome-scale engineering tools are only applicable to bacteria, not eukaryotic organisms like yeast," said Zhao, who led the study. "A second innovation is the use of synthetic biology concepts, the modularization of the parts, and integration with a robotic system, so we can do it in high-throughput."

The team focused on yeast in part because of its important modern-day applications; yeasts are used to convert the sugars of biomass feedstocks into biofuels such as ethanol and industrial chemicals such as lactic acid, or to break down organic pollutants.

The group took the first step toward their goal of a novel engineering strategy for yeast by creating what is known as a cDNA library: a collection of over 90 percent of the genes from the genome of baker's yeast (*Saccharomyces cerevisiae*), arranged within a custom segment of DNA so that each gene will be, in one version, overactive within a yeast cell, and in a second version, reduced in activity.

Zhao and colleagues examined the ability of the CRISPR-Cas system, a set of molecules borrowed from a form of immune system in bacteria (CRISPR stands for Clustered Regularly Interspaced Short Palindromic Repeats, describing a feature of this system in bacterial genomes). This system allowed Zhao to make precise cuts in the yeast genome, into which the standardized genetic parts from their library could insert themselves.

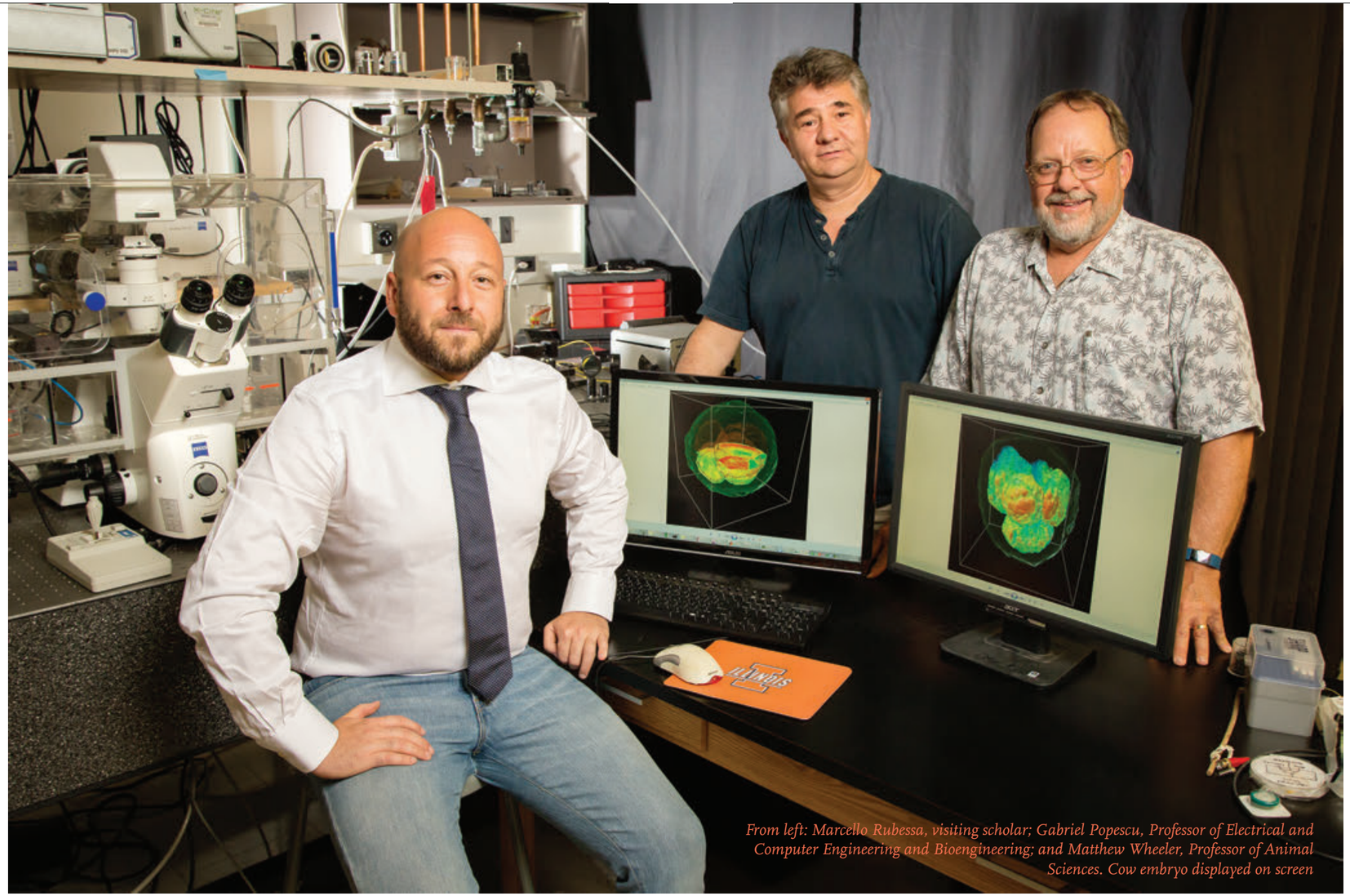
"The first time we did this, in 2013, there was no CRISPR ... the best we could get was one percent of the cells modified in one run," said Tong Si, an IGB Fellow. "We struggled a little on that, and when CRISPR came out, that worked. We got it to 70 percent [cells modified], so that was very important."

With gene activity-modulating parts integrating into the genome with such high efficiency, the researchers were able to randomly generate many different strains of yeast, each with its own unique set of modifications. These strains were subjected to artificial selection processes to identify those that had desirable traits, such as the ability to survive exposure to reagents used in the biofuel production process.

The work, which was funded by the Roy J. Carver Charitable Trust, IGB, Defense Advanced Research Program Agency, and National Academies Keck Futures Initiative on Synthetic Biology, paves the way for similar approaches to broad-scale, automated genome engineering of other eukaryotic species.

"The goal of the work was really to develop a genome-scale engineering tool for yeast."

New microscope technique reveals internal structure of live embryos



From left: Marcello Rubessa, visiting scholar; Gabriel Popescu, Professor of Electrical and Computer Engineering and Bioengineering; and Matthew Wheeler, Professor of Animal Sciences. Cow embryo displayed on screen

RESEARCHERS HAVE DEVELOPED a way to produce 3D images of live cattle embryos that could help determine embryo viability before *in vitro* fertilization in humans.

Infertility can be devastating for those who want children. Many seek treatment, and the cost of a single *in vitro* fertilization cycle can be $20,000, making it desirable to succeed in as few attempts as possible. Advanced knowledge regarding the health of embryos could help physicians select those that are most likely to lead to successful pregnancies.

The study, published in the journal *Nature Communications*, brought together electrical and computer engineering professor Gabriel Popescu and animal sciences professor Matthew Wheeler (RBTE) in a collaborative project through the Beckman Institute for Advanced Science and Technology at the University of Illinois.

Their method, called gradient light interference microscopy, or GLIM, solves a challenge that other methods have struggled with—imaging thick, multicellular samples.

"When looking at thick samples with other methods, your image becomes washed out due to the light bouncing off of all surfaces in the sample," said graduate student Mikhail Kandel, the co-lead author of the study. "It is like looking into a cloud."

GLIM can probe deep into thick samples by controlling the path length over which light travels through the specimen. The technique allows the researchers to produce images from multiple depths that are then composited into a single 3D image.

To demonstrate the new method, Popescu's group joined forces with Wheeler and his team to examine cow embryos.

"One of the holy grails of embryology is finding a way to determine which embryos are most viable," Wheeler said. "Having a noninvasive way to correlate to embryo viability is key; before GLIM, we were taking more of an educated guess."

Those educated guesses are made by examining factors like the color of fluids inside the embryonic cells and the timing of development, among others, but there is no universal marker for determining embryo health, Wheeler said.

"This method lets us see the whole picture, like a three-dimensional model of the entire embryo at one time," said Tan Nguyen, the other co-lead author of the study.

Choosing the healthiest embryo is not the end of the story, though. "The ultimate test will be to prove that we have picked a healthy embryo and that it has gone on to develop a live calf," said Marcello Rubessa, a postdoctoral researcher and co-author of the study.

"Illinois has been performing *in vitro* studies with cows since the 1950s," Wheeler said. "Having the resources made available through (Popescu's) research and the other resources at Beckman Institute have worked out to be a perfect-storm scenario."

The team hopes to apply GLIM technology to human fertility research and treatment, as well as a range of different types of tissue research. Popescu plans to continue collaborating with other biomedical researchers and has already had success looking at thick samples of brain tissue in marine life for neuroscience studies.

This research was supported by the NSF and the University of Illinois.

"One of the holy grails of embryology is finding a way to determine which embryos are most viable. Having a noninvasive way to correlate to embryo viability is key; before GLIM, we were taking more of an educated guess."

Combating antiviral drug resistance with dynamic therapeutics

ANTIVIRAL DRUG RESISTANCE has long been a problem in modern society. As viruses evolve, they develop resistance to drugs used to treat infections, making treatments that rely on them less effective against diseases such as influenza.

Now, a group of researchers is approaching this problem with a new idea: what if antiviral drugs could evolve along with viruses to stop this resistance?

Christopher Brooke, Assistant Professor of Microbiology (IGOH), is part of a DARPA-funded program called INTERfering and Co-Evolving Prevention that hopes to achieve this.

The program's goal is to develop a new class of biological therapeutics that can coevolve with viruses. That way, as the virus develops resistance to the therapeutic, the therapeutic would evolve and develop anti-resistance.

"It would be as dynamic as the pathogen, and so that would, ideally, eliminate or at least blunt the problem of evolved resistance," Brooke said.

His team of five researchers will work on developing a therapeutic specifically for influenza.

They hope to do this by creating therapeutics with a design based on viruses themselves. This idea is based on a natural phenomenon known as defective interference.

Under certain conditions, many viruses spontaneously produce virus mutants that are missing parts of their genome. These mutants, called defective interfering particles, compete with the virus and inhibit its ability to replicate.

Influenza produces these defective interfering particles regularly, and it has been hypothesized that they are detrimental to the virus.

"We're not totally convinced that's the case," Brooke said.

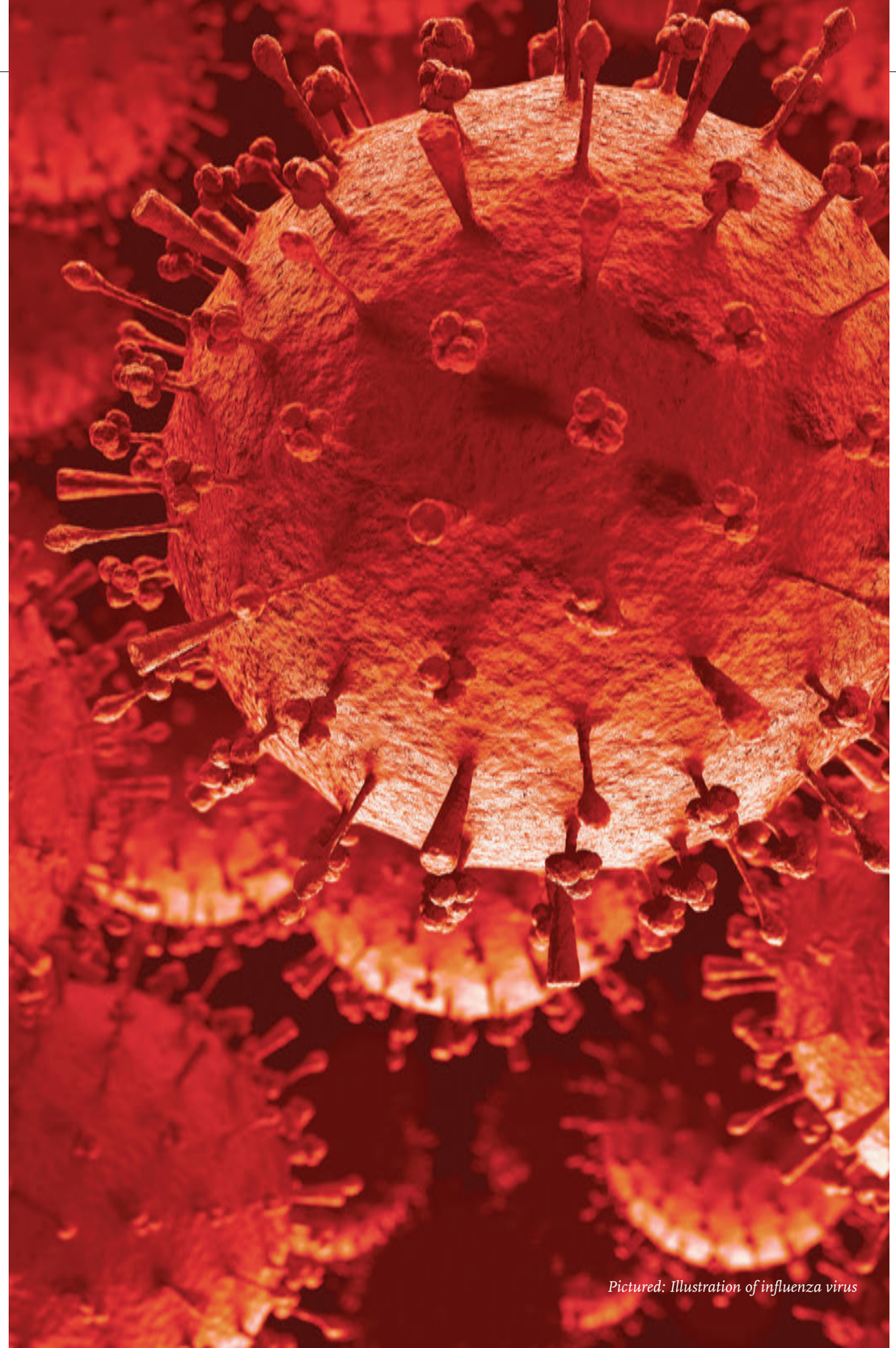
He and his colleagues will instead make changes to the particles and see if they have a detrimental effect on the viral population.

"This program is basically trying to see if we can take that idea ... and engineer versions of these that can act as therapeutics," Brooke said.

Using the advantages of mathematical modeling, which involves using mathematical concepts to describe real world situations, the team will decide which particles they want to test in the lab.

They will work on identifying and characterizing every possible defective interfering particle that can be generated by influenza virus, and then analyze how these particles affect viral replication and transmission, how they affect the host cell, and other characteristics.

Their end goal is to identify a particle known as a therapeutic interfering particle that could be introduced to an individual infected with influenza to decrease disease severity and limit forward transmission without promoting the evolution of resistance.



Pictured: Illustration of influenza virus

"The program's goal is to develop a new class of biological therapeutics that can coevolve with viruses."

Regardless of whether this research will contribute to the ultimate goal of eradicating the influenza virus, the researchers expect to gain valuable information on how virus populations evolve, which is an area Brooke's lab has already been exploring.

There are many large-scale questions that Brooke and his lab hope to answer: Why is influenza so good at outrunning host immunity? Why are other viruses not? How does influenza's genome affect how it evolves?

Through this research, these questions could be addressed.

"We're going to learn a huge amount about how influenza virus populations behave and evolve," Brooke said.

For Brooke, this research is a chance to continue studying viruses, which fascinate him.

"They're super weird and they're really interesting," he said. "They're always surprising us in terms of what we find them doing and how they work."

Above: Timothy Fan, Professor of Veterinary Medicine, with his dog, Ember

Cancer research aims to serve both pets and people

TEAMWORK BETWEEN VETERINARY MEDICINE AND ENGINEERING IS ENABLING researchers to test a bone cancer drug delivery system in animals bigger than the standard animal model, the mouse. They are using the experimental therapy to treat dogs—mammals closer in size and biology to humans—with naturally occurring bone cancers, which also are a lot like human bone tumors.

In clinical trials, dogs tolerated all tested doses of cancer-drug-laden nanoparticles with no signs of toxicity. As in mice, the particles homed in on tumor sites, thanks to a coating of the drug pamidronate, which preferentially binds to degraded sites in bone. The nanoparticles also showed anti-cancer activity in mice and dogs.

The researchers report their results in the *Proceedings of the National Academy of Sciences*; the research was supported by the Morris Animal Foundation, the NIH and the NSF.

The dogs were companion animals with bone cancer that were submitted for the research trials by their owners, said veterinary clinical medicine professor Timothy Fan (ACPP/ONC-PM), who led the study with materials science and engineering professor Jianjun Cheng (RBTE).

"We wanted to see if we could evaluate these drug-delivery strategies, not only in a mouse model, but also at a scale that would mimic what a person would get," Fan said. "The amount of nanoparticle that we ended up giving to these dogs was a thousand-fold greater in quantity than what we would typically give a mouse."

"Human bone tumors are much bigger than those of mice," Cheng explained. "Nanoparticles must penetrate more deeply into larger tumors to be effective. That is why we must find animal models that are closer in scale to those of humans."

Mice used in cancer research have other limitations. Researchers usually inject human or other tumor cells into their bodies to mimic human cancers, Fan said. They also are bred to have compromised immune systems, to prevent them from rejecting the tumors.

"That is one of the very clear drawbacks of using a mouse model," Fan said. "It doesn't recapitulate the normal immune system that we deal with every day in the person or in a dog."

There also are limitations to working with dogs, he said. Dogs diagnosed with bone cancer often arrive at the clinic at a very advanced stage of the disease, whereas in humans, bone cancer is usually detected early because people complain about the pain and have it investigated.

"On the flip side of that, I would say that if you are able to demonstrate anti-cancer activity in a dog with very advanced disease, then it would be likely that you would have equivalent or better activity in people with a less advanced stage of the disease," Fan said.

Fan is involved in several promising efforts to produce new cancer therapies while simultaneously elevating the care of pet animals. A drug developed in collaboration with chemistry professor Paul Hergenrother (ACPP Theme Leader) and used to successfully treat pet dogs with glioblastoma and other cancers, PAC-1, is now in clinical trials for use in human patients. Fan is partnering with the Morris Animal Foundation to run an innovative program that aims to test five new drugs in five years for less than $5 million.

"...if you are able to demonstrate anti-cancer activity in a dog with very advanced disease, then it would be likely that you would have equivalent or better activity in people with a less advanced stage of the disease."

Above: postdoc Johannes Kromdijk, plant biology professor Stephen Long, and postdoc Katarzyna Glowacka in RIPE program greenhouse

RIPE research project fuels scientific breakthroughs

SWEAT SNEAKS BENEATH KATARZYNA Glowacka's sunglasses as she tiptoes around the carefully organized research plots. The tiny plants reach up to grasp the sun, creating a mosaic of greens and yellows as they grow and mature, a tapestry of hope for the researchers who have cared and cultivated them.

Scientists have spent most of their summer in this one-acre field at the University of Illinois South Farms. More than three years of sweat, tears, and countless hours of work and research have been poured into the little sprouts.

These plants are part of Realizing Increased Photosynthetic Efficiency (RIPE), an international research project with the aim of ensuring food security for millions of people, especially those in Sub-Saharan Africa and Southeast Asia. The project is funded by the Bill and Melinda Gates Foundation, the Foundation for Food and Agriculture Research, and the U.K. Department for International Development.

The goal of this multi-million research project is to help increase the yields of crops—like rice and cassava—that these families already like and know how to grow. More farmers will produce more food to feed their families and sell for disposable income, increasing their access to medicine, education, and opportunities for the future.

RIPE has engineered these plants to photosynthesize more efficiently, enabling them to recover more quickly in fluctuating light conditions.

Glowacka and postdoctoral researcher Johannes Kromdijk worked together for three years preparing their tobacco plants for this field trial. The plants represent years of photosynthesis research, including critical work by principal investigators Stephen Long, Gutgsell Endowed Professor of Plant Biology and Crop Sciences (BSD/GEGC), and University of California, Berkeley researcher Krishna Niyogi—an expert on the molecular processes underlying photoprotection.

> "RIPE (is) an international research project with the goal of ensuring food security for millions of people."

In 2016, Glowacka, Kromdijk and Long reported in the journal *Science* that they can increase plant productivity by boosting levels of three proteins involved in photosynthesis. Their work confirmed that photosynthesis can be made more efficient to increase plant yield, a hypothesis some in the scientific community once doubted was possible.

"The United Nations predicts that by 2050 we're going to need to produce about 70 percent more food on the land we're currently using," Long said. "My attitude is that it is very important to have these new technologies on the shelf now because it can take 20 years before such inventions can reach farmer's fields. If we don't do it now, we won't have this solution when we need it."

Another innovative research endeavor to come out of the RIPE project came from the laboratories of Long and Professor of Civil and Environmental Engineering Praveen Kumar.

Their paper in *Global Change Biology* showed that soybean crops with fewer leaves have an increased yield. They attribute this yield boost to increased photosynthesis, decreased respiration, and diversion that would have been invested in more leaves than seeds.

"We are trying to identify non-conventional techniques that can give us a quick boost in yield so that we can get closer to those predicted demands," said first author and postdoctoral researcher Venkatraman Srinivasan. "Soybeans are one of the four major staple crops and also the most important vegetable protein source in the world. If we can increase the yield of soybeans, we can solve the problems of protein demand and food production at the same time."

Through these discoveries and others that are likely to come, these scientists are on their way to making RIPE's goals a reality.

Workshop 'bridges' empirical, theoretical understandings of climate and crop yield

Researchers from the University of Illinois, the University of Birmingham, and other institutions around the world gathered at the IGB to discuss how to improve the capacity to predict the impact of climate change on future crop yield.

"Our objective is to improve the ability of computer models to simulate the way crops are going to respond to rising carbon dioxide concentrations," said co-organizer and Associate Professor of Plant Biology Andrew Leakey (GEGC). "That's an important exercise because the models are used to make projections about how future climate will impact food and fuel availability."

The workshop was supported by a seed grant from the Birmingham-Illinois Partnership for Discovery, Engagement and Education (BRIDGE).

Leakey and his colleagues decided the best way to improve crop models was to bring together model developers with experimentalists.

Modeling experts are particularly focused on representing and predicting the impact of rising carbon dioxide levels on crop yield. However, interactions between plants and their environment are incredibly complex.

Gathering data on how crops are responding to a changing climate is also a significant experimental challenge. The University of Illinois and the University of Birmingham are among a handful of institutions with established experimental systems that can perform such Free-Air Carbon Dioxide Enrichment (FACE) experiments.

The workshop's organizers recognized the mutual need for better communication between modelers and experimentalists, and several collaborative relationships were launched. These are expected to lead to significant scientific and practical advances in our ability to understand crop responses to climate change.

Pictured: Heart Spring, Yellowstone National Park. Photo by Tom Murphy

Outreach

New book celebrates a union of Art and Science at Yellowstone

Mammoth Hot Springs in Yellowstone National Park represents a confluence of two seemingly contrasting views of the world. Its dramatic rock formations, diverse wildlife, and the flow of water for which it is named offer countless examples of natural beauty; yet scientists are drawn to these same features because of the unique opportunities they represent to better understand geological and biological processes.

A recently published volume created by Professor of Geology and Microbiology and Roy J. Carver Biotechnology Center Director Bruce Fouke (BCXT) and internationally known nature photographer Tom Murphy, *The Art of Yellowstone Science: Mammoth Hot Springs as a Window on the Universe*, uses a meticulously crafted collection of photographs to show these two views both stem from a common origin of curiosity and awe.

"In the pages of this book, Mammoth Hot Springs photographic art is melded with the natural sciences to search for common laws of nature through the power of observation and willingness to embrace the unexpected," Fouke and Murphy wrote in a description on the book's website, artofyellowstonescience.igb.illinois.edu. "This new appreciation of nature at Mammoth is then applied to challenges faced by society, now and in the future."

Geneticist Mary-Claire King gives IGB distinguished public lecture

Mary-Claire King, Professor of Genome Sciences and of Medicine at the University of Washington School of Medicine, spoke as part of the Spring IGB Distinguished Public Lecture series at the Alice Campbell Alumni Center. King studies the genetics and interaction of genetics and environmental influences on human conditions such as HIV, lupus, inherited deafness, and also breast and ovarian cancer.

King is well known for the discovery, made before the Human Genome Project had been fully developed, that a single gene on chromosome 17, later known as *BRCA1*, is responsible for many breast and ovarian cancers—as many as 5-10 percent of all cases of breast cancer may be hereditary. Her research has contributed to a greater understanding of how genetic information can aid cancer patients in making informed decisions about their present and future wellness.

King's talk was titled "Genetic Analysis of Inherited Breast and Ovarian Cancer: From Gene Discovery to Precision Medicine and Public Health." It explored the path her research took to lead to her seminal discovery, and how it has continued to expand since. The approach King developed to identify *BRCA1* has since proven valuable in the study of many other illnesses, and King has built on that research by identifying *BRCA2* and extending her technique to other diseases and conditions.

IGB introduces Coursera community to genomic research

What is a genome? This question is the starting place for the IGB's Massive Open Online Course (MOOC), "Genomics: Decoding the Universal Language of Life." The course, available in both scheduled and self-paced formats on Coursera, contains six weeks of content and encompasses topics drawn from the IGB's expansive research portfolio.

Students learn how genes work, why microbes play such an important role chemically, how DNA sequencing can be used to predict risk to health and wellness, and what differences exist in genetically modified plants. An honors track offers the opportunity to complete detailed writing projects that explore scientific and social topics in greater depth.

IGB Director and Swanlund Professor of Entomology Gene Robinson is the main instructor for the course. In addition, each module features several IGB researchers as guest instructors. These guest instructors cover both basic biological concepts and their connections to genomic research applications.

Gene Robinson and May Berenbaum featured on Reddit's Ask Me Anything

IGB Director and Swanlund Chair in Entomology Gene Robinson, with Swanlund Chair and Head of Entomology May Berenbaum (GEGC/IGOH), were featured on Reddit's Ask Me Anything (AMA). The popular series has included celebrities, scientists, authors, artists, U.S. presidents and more, and allows individuals to post questions online to be answered by the host.

An excerpt from their introduction to the online event read:

"We are two scientists who are fascinated by honey bees: their complex social lives, their collective ability to adapt to environmental challenges, their sophisticated cognitive abilities, and the vital role they play in agriculture and food production. We also share a common experimental approach: exploring the behaviors, life history, evolution, and health of honey bees and other insects by studying their genomes."

Questions from participants ranged from the risks and benefits of pesticide use and threats to the health of pollinator populations, to the future possibilities of robot bees and details of bee social life and cognitive abilities. Berenbaum even responded to a request to brainstorm titles for a hypothetical sitcom featuring bees as characters: "'Bee-witched' doesn't quite work ... How about 'Bee's Company'? 'The Honey Mooners'? Hey, wait—I know! 'The Golden Girls'!!"

Although questions can no longer be submitted, the AMA remains available online for anyone to view.

Outreach

iGEM team claims bronze at annual Giant Jamboree in Boston

The University of Illinois International Genetically Engineered Machine (iGEM) team received a bronze medal at the annual iGEM Giant Jamboree last September for its development of a unique genetic component. Their designed promoter, a region of DNA that helps control the activity of a nearby gene, allows for greater predictability and control of that activity.

The iGEM Foundation is a non-profit organization devoted to promoting synthetic biology through education and competition within a collaborative community. High school and undergraduate teams design and construct genetically engineered machines—known as "BioBricks"—using standard biological parts. The submitted BioBricks are then added to iGEM's Registry of Standard Biological Parts, which is available to researchers worldwide.

The 2016 team was the ninth from the University of Illinois to compete at the iGEM Giant Jamboree. The team of six undergraduate students—Caroline Blassick, Jonathan Chang, Viraat Goel, Augustine Koh, Mariam Saadah, and Hiba Shahid—received guidance from two faculty advisors: Assistant Professor of Biochemistry Auinash Kalsotra (GNDP/ONC-PM) and Assistant Professor of Bioengineering Ting Lu (BCXT/BSD/MME).

Funding for the 2016 team was provided in part by the IGB, the University of Illinois, Integrated DNA Technologies, New England Biolabs, and MathWorks.

Pictured: iGEM Jamboree.
Photo by iGEM Foundation and Justin Knight

Outreach Events

The IGB strives to be a place "Where Science Meets Society." Several annually recurring events comprise the cornerstone of our community engagement efforts. Throughout the academic year, they continued to stand out as moments of celebration and recognition of all that we gain through a shared appreciation of the science of genomes.

Genome Day

GENOME DAY, held each year in mid-fall, is an open-house style event at the Orpheum Children's Science Museum where community members learn about DNA, genes, genomes, and evolution through a series of hands-on activities for all ages. In recent years, we have added multilingual support to the event, thanks to the members of the Illinois chapter of SACNAS (Society Devoted to Advancing Hispanics, Chicanos & Native Americans in Science) and the Chinese Students and Scholars Association.

Art of Science

Our ART OF SCIENCE exhibits feature images from IGB's research portfolio, enhanced to highlight the beauty and fascination encountered daily in scientific endeavors. The past year has continued to bring new developments to the program, from a new location for the opening of Art of Science 7.0 at Urbana's [co][lab], to a plethora of new locations around the state for traveling exhibits, to the inception of an Art of Science zine.

Pollen Power

This year also brought the fifth annual POLLEN POWER camp, a week-long day camp offered each July to middle school girls with a passion for science. Funded in part by the NSF and the IGB, the camp is co-organized by plant biologists Lisa Ainsworth (GEGC) and Andrew Leakey (GEGC), IGB Core Facilities, and IGB Outreach staff. Female graduate students act as counselors for the plant science-themed camp, which provides attendees with experience operating high-powered microscopes, printing 3D replicas of pollen grains, recording "news broadcasts" that discuss past and future climate, and, this year, experiencing virtual reality representations of scientific data.

Research

Slow motion waves of jumping genes in the human genome

Nature is full of parasites—organisms that flourish and proliferate at the expense of another species. Surprisingly, these same competing roles of parasite and host can be found in the microscopic molecular world of the cell. A new study by physicists Chi Xue and Nigel Goldenfeld (BCXT Theme Leader/ CGRH/GNDP) has demonstrated that dynamic elements within the human genome interact in a way that echoes populations of predators and prey.

The findings, published in *Physical Review Letters* and supported by NASA and the NSF, are an important step toward understanding the complex ways that genomes change over the lifetime of individual organisms, and how they evolve over generations. Goldenfeld and Xue embarked on this work because of their interest in transposons, small regions of DNA that can move from one part of the genome to another during the lifetime of a cell, a capability that has earned them the name "jumping genes."

Some transposons cannot jump on their own, and instead can only steal spots from others. Xue and Goldenfeld's results predicted that these competing populations of jumping genes are expected to oscillate. Too many "parasitic" elements, and their "hosts" start to suffer, and soon there are not enough to exploit. The parasites start to suffer, and their hosts make a comeback.

The model made the additional, surprising prediction that these oscillations occur over a timescale that is longer than the human lifespan—waves of transposons pushing and pulling at each other in slow motion across generations of the human genomes that carry them.

Two cholesterol treatments at odds: statins counter benefits of exercise

For those who suffer from high cholesterol levels, a multi-pronged approach is often recommended to improve health: diet modifications, exercise, and medications can all play a role. Unfortunately, these interventions may not always interact in desirable ways. New research by Associate Professor of Kinesiology and Community Health Marni Boppart (RBTE) added to a growing body of evidence that statins interfere with the beneficial outcomes of exercise.

In the study, which was funded by the University of Illinois Center for Health, Aging, and Disability, mice genetically disposed to have high cholesterol levels were treated with injections of either a statin, simvastatin (sometimes marketed as Zocor), or a neutral saline solution. Some mice from each group were offered access to a running wheel for exercise, while others were not.

Boppart and her colleagues found that while the mice treated with simvastatin did have lower cholesterol levels after two weeks than those treated with saline, they also had decreased grip strength—whether they had exercised on the running wheel or not. Statin-treated mice with access to the running wheel had decreased muscle force and increased susceptibility to muscle fatigue compared with the saline-treated mice.

The mice that received simvastatin also gradually decreased their daily running distance over the two weeks of treatment. In a publication in *PLoS One*, the researchers suggested that these results could indicate that a history of exercise might not protect against these negative effects of statin treatment, which might become more extreme with more prolonged use.

Two undergrads improve plant carbon-cycle models

In the summer of 2012, two undergraduate students tackled a problem that plant ecology experts had overlooked for 30 years.

The students demonstrated that different plant species vary in how they take in carbon dioxide and emit water through stomata, the pores in leaves. The data boosted the accuracy of mathematical models of carbon and water fluxes through plant leaves by 30 to 60 percent.

In hindsight, the discovery might seem obvious, said plant biology professor Andrew Leakey (GEGC), who mentored the students and is a co-author of the study.

Plant physiologists know there is diversity in the way plant stomata behave. But for the last 30 years, the research community has failed to describe that diversity in mathematical models, Leakey said, mostly because few plant biologists know how to convert their insights into the mathematical equations that modelers need.

Therefore, modelers have assumed that the stomata of all species behave in the same way. This oversimplification likely led to errors in model predictions.

Kevin Wolz and Mark Abordo conducted the research when they were both undergraduate students. They collected leaves from 15 tree species and used gas exchange equipment to measure how the leaves responded to different light and atmospheric conditions.

Their study, published in *Nature Ecology and Evolution*, found a significant amount of variation in the way different tree species responded. Altering standard models with the new data dramatically improved the models' accuracy. The NSF and the EBI supported this research.

Slowing dangerous bacteria may be more effective than killing them

Researchers have discovered a mechanism that allows bacteria of the same species to communicate when their survival is threatened.

The study suggests it may be possible to slow dangerous infections by manipulating the messages these microbes send to each other, allowing the body to defeat an infection without causing the bacteria to develop resistance to the treatment.

The study, reported in the *Proceedings of the National Academy of Sciences*, builds on work conducted by other researchers at Illinois, including biochemist John Woodland Hastings, who died in 2014, and John Cronan (MMG), a professor and the head of the department of microbiology.

"Bacteria are intelligent little organisms," said biochemistry professor Satish Nair (MME/MMG), co-author of the study with postdoctoral researcher Shi-Hui Dong and other colleagues. "They can survive almost anywhere and quickly adapt to new conditions."

When bacteria compete with other microbes for scarce resources, the more successful group will produce a unique molecule—an antibiotic—to kill off the other species. Over time, however, bacteria have adapted to resist antibiotics.

Nair and Dong's NIH-funded study targeted the group signal that bacteria use to slow down growth, rather than the antibiotic signal to kill. Understanding how bacteria produce the signal paves the way for developing molecules that can disrupt the communication of specific bacteria, with little chance for drug resistance to develop.

A new tool for genetically engineering the oldest branch of life

A study by G. William Arends Professor of Microbiology Bill Metcalf (MMG Theme Leader) and IGB Fellow Dipti Nayak (BCXT) has demonstrated the first successful use of CRISPR-Cas9 mediated genome editing in the third domain of life, Archaea. Their groundbreaking work, funded by the DOE and the Simons Foundation and reported in *Proceedings of the National Academy of Sciences*, has the potential to vastly accelerate future studies of these organisms.

"Under most circumstances our model archaeon, *Methanosarcina acetivorans*, has a doubling time of eight to ten hours ... what that means is that doing genetics, getting a mutant, can take months," Nayak explained. "What CRISPR-Cas9 enables us to do, at a very basic level, is speed up the whole process."

CRISPR, short for Clustered Regularly Interspaced Short Palindromic Repeats, is an immune defense system in archaea and bacteria that acts by identifying and storing short fragments of foreign DNA so that similar sequences can be quickly destroyed in the future, protecting the organism from viral invasion. Since its discovery, a version of this immune system—CRISPR-Cas9—has been modified to edit genomes in the lab.

"[Methanogens are] a class of archaea that produce gigatons of this potent greenhouse gas [methane] every year, play a keystone role in the global carbon cycle, and therefore contribute significantly to global climate change," Nayak said. By studying the genetics of *Methanosarcina acetivorans* and similar organisms, Nayak and Metcalf hope to gain not only a deeper understanding of archaeal genetics, but of their role in broader environmental processes.

News

IGB announces new Infection Genomics for One Health research theme

The IGB announced its newest research theme, Infection Genomics for One Health (IGOH).

The theme will study how infection is transmitted, how new diseases emerge, and how antimicrobial resistance plays a role in the infection process through the lens of the interaction of genes, genomes and microbial organisms, within both human and agricultural ecosystems.

The theme will incorporate the concept of One Health, which recognizes that human health is fundamentally dependent on the wellbeing of the surrounding ecosystem, whether natural or industrial.

Microbes form hidden linkages that connect these ecosystems and shape their health and disease. Predictive models for the movement of genes, genomes, and microbes among these interconnected microbial ecosystems are desperately needed to develop strategies to address urgent and critical threats to human health.

IGOH's aim is to develop a broad and predictive framework for infection biology that will directly address these challenges.

Rachel Whitaker, Associate Professor of Microbiology, will serve as the theme's leader. The theme's faculty members include researchers from areas such as entomology, animal biology, microbiology, computer science and bioengineering, and more.

"We have seen increasing evidence recently of the risk of epidemic outbreaks, and of the impact of the environment on the health and wellbeing of its inhabitants," said IGB Director and Swanlund Professor of Entomology Gene Robinson. "To determine the changes that microbial communities undergo and the dynamics that result has immense potential to add important new insights to our understanding of critical human and environmental health challenges."

Research to investigate oil field biosouring with new technology

A new IGB research project seeks to solve a $90 billion global problem in the oil industry while making oil drilling less harmful to the environment.

Bruce Fouke (BCXT), Professor in the departments of Geology and Microbiology and director of the Roy J. Carver Biotechnology Center, was awarded a three-year grant from the Dow Chemical Company to study a process known as oil field biosouring.

Co-investigators include IGB affiliate Professor Charles Werth (BCXT) at the University of Texas at Austin, and Robert Sanford, Research Associate Professor in Geology at Illinois.

Biosouring results from seawater being pumped deep underground in order to maximize the amount of oil extracted. Seawater contains a chemical called sulfate. When bacteria in the ground ingest sulfate, they create sulfide, a highly corrosive chemical. This reduction, from sulfate to sulfide, is known as microbial biosouring.

Sulfide's corrosive nature creates the single largest maintenance expense for oil companies: replacement of underground oil field pipes and plumbing systems.

Fouke and his IGB research colleagues plan to better understand how biosouring happens and how to stop it by using a technology they developed called the GeoBioCell.

The GeoBioCell is an experimental microfluidics test bed that can be used to track the interactions between water, rock, microbes, oil and gas in a controlled environment.

By recreating biosouring conditions within the GeoBioCell, researchers will be able to test different scenarios to try and reduce or stop the process and understand how oil and gas is produced while better protecting the environment.

Woese undergraduate research scholar embraces challenges

Since his freshman year of college, Yuhao Min has been passionate about research.

He got a chance to pursue what he loves through IGB's Carl R. Woese Undergraduate Research Scholarship. The scholarship awards funding to undergraduate students so they can pursue interdisciplinary research at IGB over the summer.

As the 2017 recipient, Min pursued research with Huimin Zhao (BSD Theme Leader/MMG), Steven L. Miller Chair in Chemical Engineering, and Wilfred van der Donk (MMG), Richard E. Heckert Endowed Chair in Chemistry.

Min's collaborative research project is focused on engineering a peptidic anticancer compound, nisin, a peptide that has been used as a food preservative but also has a broad antimicrobial spectrum. It has been shown to be a potential therapeutic for treating cancers such as head and neck squamous cell carcinoma.

"We want to optimize this peptide, using the tools we developed before, to make it more potent, more stable, and more specific toward the cancer," Min said.

As a double major in chemistry and molecular and cellular biology, Min finds himself fascinated by the interdisciplinary approaches that his research has taken.

"I find when you look into a problem from another perspective, you can always find some other solution to the specific problems," he said.

IGB receives Grand Challenges Explorations grant

The IGB was awarded funding from Grand Challenges Explorations, an initiative funded by the Bill & Melinda Gates Foundation, which supports innovative thinkers worldwide to explore ideas that can break the mold in how we solve persistent global health and development challenges.

Patrick Degnan (CGRH/IGOH/MME), Assistant Professor of Microbiology, will pursue an innovative global health and development research project titled "CRISPR capture: surveillance of AMR in mobile microbiomes."

To receive funding, Degnan and other Grand Challenges Explorations winners demonstrated a bold idea in one of six critical global health and development topic areas.

Degnan, in collaboration with Professor of Anthropology Rebecca Stumpf (BCXT/CGRH) and Associate Professor of Microbiology Rachel Whitaker (IGOH Theme Leader/BCXT), will work to better understand how antimicrobial resistance (AMR) spreads in different environments by examining the flow of AMR genes in microorganisms between adjacent human and chimpanzee populations in eastern Africa. Their research will eventually allow for more targeted measures to slow the spread of AMR in human and agricultural pathogens.

"We can't just focus on human pathogens anymore. We can't just focus on animal pathogens or plant pathogens, but we have to think about infection biology as a whole," said Degnan. "To be able to understand how to stop transmission, we need to find out what transmission is, and our research is really geared towards that."

New center will apply computing to large-scale genomic problems

The University of Illinois is leading a new center that seeks to develop a new platform for generating, interpreting, and applying genomic data for a wide variety of applications.

Working with colleagues at Mayo Clinic, researchers in the Center for Computational Biotechnology and Genomic Medicine (CCBGM) will advance pressing societal issues, such as enabling patient-specific treatment of cancer and other diseases and supporting humanity's growing need for food by improving the efficiency of agriculture.

The center is funded for five years through the National Science Foundation's Industry/University Cooperative Research Center program.

CCBGM will seek to address challenges in computational genomics by developing new computer platforms that can more efficiently scale to the rapidly growing volume, velocity, and variety of genomic data.

Researchers also will work to enhance the capability of computers to evaluate data and provide actionable intelligence for treatment. They will design new architectures that can optimize genomic analysis workflows, providing unprecedented speed and energy efficiency while preserving the accuracy of the analytics.

The center is part of CompGen, an initiative between the IGB and the Coordinated Science Laboratory. Through CompGen, researchers have built a new instrument that will serve as the computational engine of the center.

"We are very excited to work with some of the leading companies in computing technology, pharmaceuticals, and agricultural biotechnology to create the computational breakthroughs that are necessary to realize the fruits of the genomic revolution," said Gene Robinson, Swanlund Professor of Entomology and Director of the IGB.

IGB creates partnership with ZEISS labs@location program

An agreement between the IGB and ZEISS has named the Core Facilities at IGB an official ZEISS labs@location Partner.

The model facility will allow researchers from around the U.S. to test-drive new instruments in the IGB's Core Facilities microscopy suite. This partnership represents the first North American location of the ZEISS labs@location partner program, already in use across Europe.

The agreement will allow IGB and Illinois researchers access to select cutting-edge technologies immediately following—or in some cases before—their broad release. New instruments, on loan from ZEISS, will cycle through Core Facilities and be available to all users during that time.

In addition, the agreement provides for training taught by ZEISS personnel at the IGB that will better position Core Facilities staff and researchers to best utilize new equipment. ZEISS instrument specialists will provide valuable instruction and instrument demos to Illinois and visiting scientists, as well as assist in training the IGB Core Facilities staff to provide similar instruction themselves.

Glenn Fried, director of IGB Core Facilities, anticipates that one of the first new instruments under the agreement will be a ZEISS Celldiscoverer 7, a new automated microscopy platform for high throughput live cell imaging that allows for sharper, more accurate images.

"This is a really exciting thing for the Core and for everyone who uses our instruments," Fried said. "Researchers will have access to the newest technology—like ZEISS Celldiscoverer—long before they would if we had to write a grant or even just went out and bought it."

AWARDS

Andrew Alleyne, Professor of Mechanical Science & Engineering (BSD) was awarded the Society of Women Engineers (SWE) Advocating Women in Engineering Award.

Rashid Bashir, Bioengineering Professor (RBTE) received a Campus Award for Excellence in Faculty Leadership.

Girish Chowdhary, Assistant Professor of Agricultural and Biological Engineering (GEGC) was elected to the grade of Associate Fellow, Class of 2018 in the American Institute of Aeronautics and Astronautics (AIAA).

John Cronan, Professor and Head of Microbiology and Professor of Biochemistry (MMG) was elected to the National Academy of Sciences.

John Gerlt, Gutgsell Professor of Biochemistry (MMG) was awarded the 2017 Gordon Hammes Lectureship.

Paul Hergenrother, Professor of Chemistry (ACPP Theme Leader) received the Arthur C. Cope Scholar Award by the American Chemistry Society (ACS).

Princess Imoukhuede, Assistant Professor of Bioengineering (RBTE) received a National Science Foundation Faculty Early Career Development Program CAREER Award.

Thomas Kehl-Fie, Assistant Professor of Microbiology (MMG) was named a 2017 Vallee Scholar by the Vallee Foundation.

Hyunjoon Kong, Professor and Centennial Scholar in Chemical and Biomolecular Engineering (RBTE) was named an American Institute for Medical and Biological Engineering (AIMBE) Fellow.

Stephen Long, Gutgsell Endowed Professor of Crop Sciences and Plant Biology (GEGC), was appointed to the Newton Abraham Visiting Professorship in the Department of Plant Sciences at the University of Oxford, United Kingdom.

Zeynep Madak-Erdogan, Assistant Professor of Nutrition (ONC-PM) was awarded a 2017-18 NCSA Faculty Fellowship.

Ruby Mendenhall, Associate Professor in Sociology, African American Studies, Urban and Regional Planning, and Social Work (CGRH/GNDP) received the Black Metropolis Research Consortium Fellowship, sponsored by the Melon Foundation, and was awarded a 2017-18 NCSA Faculty Fellowship.

Jeffrey Moore, Murchison-Mallory Professor of Chemistry and Professor of Materials Science and Engineering (BSD) was elected to the National Academy of Sciences.

Donald Ort, Robert Emerson Professor of Plant Biology, USDA/ARS Photosynthesis Research Unit and Adjunct Professor of Crop Sciences (GEGC Theme Leader) was elected to the National Academy of Sciences.

Gene Robinson (Director) was invited to serve as a member of the Convergence Advisory Group of the National Academies of Sciences, Engineering, and Medicine.

Rebecca Stumpf, Associate Professor of Anthropology (BCXT/CGRH/IGOH) received a Campus Award for Excellence in Undergraduate Teaching.

Andrew Suarez, Professor of Animal Biology (GNDP) received a Campus Award for Excellence in Undergraduate Teaching.

Tandy Warnow, Founder Professor of Bioengineering and Computer Science (BCXT, CGRH/IGOH) was elected a 2017 Fellow of the International Society for Computational Biology (ISCB).

Huimin Zhao, Steven L. Miller Chair in Chemical and Biomolecular Engineering (BSD Theme Leader/MMG), was recognized by the Society for Biological Engineering (SBE) with the 2017 Biotechnology Progress Award for Excellence in Biological Engineering Publication.

GRANTS

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

Hyunjoon Kong
Marni Boppart
National Institutes of Health
"Development of a Liposomal Nanostimulator to Improve Stem Cell-Based Revascularization Therapy"

Hyunjoon Kong
University of Illinois at Chicago/ Department of Defense
"Histatin Peptides as a Treatment for Ocular Surface Injury and Prevention of Corneal Neo-Vascularization"

Deborah Leckband
Vivian Tang
University of Illinois at Chicago/ National Institutes of Health
"Restoration of Lung Vascular Barrier Integrity"

Ravi Iyer
Wen-Mei Hwu
Gene Robinson
Bryan White
Matthew Hudson
National Science Foundation
"Computing and Genomics—an Essential Partnership for Biology Breakthroughs"

Ravi Iyer
Victor Jongeneel
Mayo Clinic & Illinois Alliance (Mayo Clinic Fellowship)
"Mayo Clinic and Illinois Alliance Fellowships for Technology-based Healthcare Research"

Donald Ort
Friedrich-Alexander-University-GATES
"Metabolic Engineering of Carbon Pathways to Enhance Yield of Root and Tuber Crops"

Ripan Malhi
National Institutes of Health
"Expanding the Impact of the Summer Internship for Native Americans in Genomics (SING) Short Course"

Roderick Mackie
Isaac Cann
U.S. Department of Agriculture
"Congress on Gastrointestinal Function 2017: Microbiology and Nutrition"

Patrick Degnan
Rebecca Stumpf
Rachel Whitaker
Gates Foundation
"CRISPR Capture: Surveillance of AMR Amongst the Mobile Microbial Dark Matter"

Rachel Whitaker
Cystic Fibrosis Foundation
"Individualized Early Detection of High-risk *Pseudomonas aeruginosa* Infections in Cystic Fibrosis"

Huimin Zhao
Cargill, Incorporated
"Automated Pathway Optimization with iBioFAB"

Rebecca Stumpf
Rebecca Smith
Rachel Whitaker
Gates Foundation
"Microbial Forensics to Track Zoonotic, Epizoonotic, and Anthropogenic Routes of Antimicrobial Resistance in Western Uganda"

Wen-Tso Liu
British Petroleum - University of CA, Berkeley
"Evaluating Co-digestion as a Method of Waste Activated Sludge Minimization at Purified Terephthalic Acid Wastewater Treatment"

Tony Grift
Alan Hansen
British Petroleum - University of CA, Berkeley
"Soil Analysis in Sugar Cane"

Mayandi Sivaguru
Mead Johnson & Company LLC
"Imaging Based Characterization of Milk and Vegetable-based Samples"

Elizabeth Parkinson
William Metcalf
National Institutes of Health
"Discovery of Novel Natural Products via Characterization of LC/HRMS Associated Gene Cluster Families"

Monica Uddin
University of Washington/ National Institutes of Health
"Child Trauma and the Development of Neural Systems Underlying Emotion Regulation"

Bruce Fouke
Dow Chemical Company
"Controlling Hydrocarbon Formation Damage to Enhance Souring Control and Energy Production"

William Metcalf
Microbial Pharmaceuticals. Inc.
"A Metabologenomics Platform for Large-Scale, High-Throughput Natural Product Discovery"

Rachel Whitaker
Paul G. Allen Family Foundation
"Microbial Evolution through Viral Gene Flow in Natural Populations"

Monica Uddin
Derek Wildman
Peiyong Qu
National Institutes of Health
"Epigenomic Predictors of PTSD and Traumatic Stress in an African American Cohort"

Lisa Stubbs
National Institutes of Health
"A Mouse Model for AUTS2-linked Neurodevelopmental Disorders"

Brendan Harley
Rohit Bhargava
Iwona Jasiuk
Gregory Underhill
Matthew Wheeler
National Science Foundation
"MRI: Acquisition of a 3D Bioprinting System to Generate Composite Biomaterials for Regenerative Medicine"

John Gerlt
National Institutes of Health
"Novel Strategies for the Discovery of Microbial Metabolic Pathways"

Huimin Zhao
Christopher Rao
Department of Energy
"Genome-scale Design and Engineering of Non-model Yeast Organisms for Production of Biofuels and Bioproducts"

Stephen Long
Li-Qing Chen
Donald Ort
Vijay Singh
Department of Energy
"Building on Success in Systems Design of High Yielding Low-input Energycanes for Marginal Lands"

Pictured: iGEM members and sophomores in bioengineering, Rachel Walker and Maggie Barbero, work in IGB

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

Stay connected to news, events, and program information at the Carl R. Woese Institute for Genomic Biology. By joining our mailing list, you'll receive our e-newsletter, publications, and details about seminars, workshops, and symposia at the IGB.

Visit *www.igb.illinois.edu/subscribe*.

For more information:

Contact:
Alaina Kanfer
Director of External Relations and Strategic Partnerships
217.244.0876
akanfer@illinois.edu

www.igb.illinois.edu/GIVE