IGB NEWS

Upcoming Events

Monthly Profiles

Happenings at IGB

Image Of The Month

IP @ IGB

Department Announcements

Volume 10 Number 3

UPCOMING EVENTS

IGB Distinguished Public Lecture

Genetic Analysis of Inherited Breast and Ovarian Cancer: From Gene Discovery to Precision Medicine and Public Health

April 17, 2017, 4:00 p.m.

Alice Campbell Alumni Center

601 S. Lincoln Avenue

Mary-Claire King, PhD

University of Washington School of Medicine

Medical Genetics and Genome Sciences

Lunch with the Core

ZEISS Celldiscoverer 7: Your Automated Platform for Live Cell Imaging

April 19, 2017, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Joe Huff

Product Marketing Manager

Zeiss Microscopy

IGB Seminar (MME)

Identifying the Micro from the Peta: Tales of Big Data in the Micro World

April 25, 2017, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Nikos Kyrpides, PhD

Prokaryotic Super Program

DOE Joint Genome Institute

IGB Fellows Symposium

May 4, 2017, 8:30 a.m.

612 Carl R. Woese Institute for Genomic Biology

Sua Myong, Johns Hopkins University

Scott Edwards, Harvard University

Register at **http://fellows.igb.illinois.edu/**

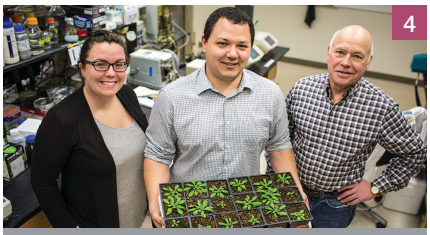
FEATURED NEWS

2

Geneticist Mary-Claire King to give Public Lecture

3

A New Tool for Engineering the Oldest Branch of Life



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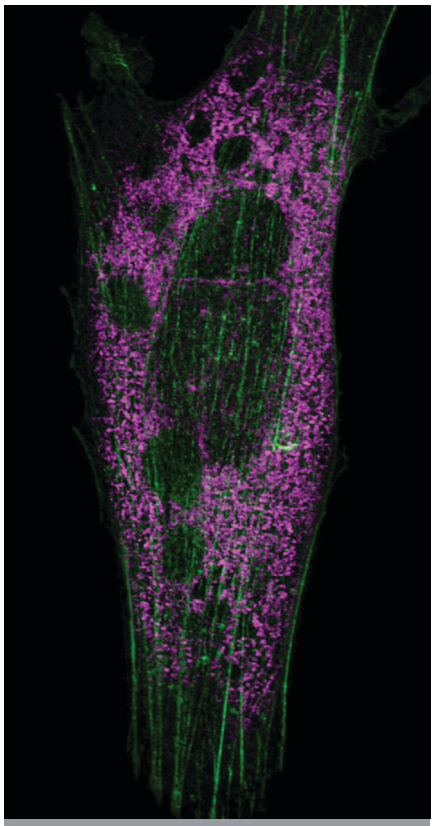
Protein has potential to save US farmers millions annually

5

On the Grid: Happenings at IGB

IMAGE OF THE MONTH



This month's image is of osteosarcoma cells subjected to sudden hyperosmotic stress, which develop circular indentations on the ventral side that push into the ER (magenta, sec61b). Image courtesy of Shahar Sukenik of the Martin Gruebele Lab.

IGB News

Share your news with the IGB. Send ideas on stories, articles, and features to *nvasi@illinois.edu*.

FEATURE

Geneticist Mary-Claire King
to give IGB Distinguished Public Lecture

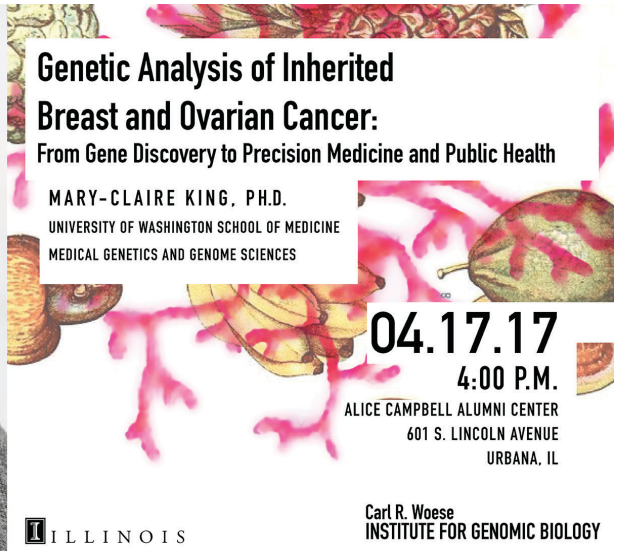
Mary-Claire King, Professor of Genome Sciences and of Medicine at the University of Washington School of Medicine, will speak as part of the IGB Distinguished Public Lecture series on 4:00 p.m. on April 17, 2017 at the Alice Campbell Alumni Center. King studies the genetics and interaction of genetics and environmental influences on human conditions such as HIV, lupus, inherited deafness, and also breast and ovarian cancer. Her talk is entitled "Genetic Analysis of Inherited Breast and Ovarian Cancer: From Gene Discovery to Precision Medicine and Public Health."

King is well-known for the discovery that a single gene on chromosome 17, later known as BRCA1, was responsible for many breast and ovarian cancers—as many as 5-10% of all cases of breast cancer may be hereditary. Her work revolutionized the study of numerous other common diseases, and King had successfully identified the gene before the Human Genome Project had been fully developed. 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.

The technique 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.

King has been working for several decades in collaboration with scientists around the world to identify genetic causes of hearing loss and deafness. They successfully cloned the first non-syndromic deafness-related gene in 1999. King continues to work with scientists to model international scientific cooperation in conjunction with conducting scientific research - hereditary deafness is common amongst some endogamous Arab communities. She has also contributed on the Human Genome Diversity Project, which seeks to delineate the distinctions among individuals in order to further understanding of human evolution and historical migrations. ■

King's 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.



A New Tool for Genetically Engineering
the Oldest Branch of Life

A new study by G. William Arends Professor of Microbiology Bill Metcalf and IGB Fellow Dipti Nayak has documented the use of CRISPR-Cas9 mediated genome editing in the third domain of life, Archaea, for the first time. Their groundbreaking work, reported in Proceedings of the *National Academy of Sciences* [DOI:10.1073/pnas.1618596114], has the potential to vastly accelerate future studies of these organisms, with implications for research including global climate change.

"Under most circumstances our model archaeon, *Methanosarcina acetivorans*, has a doubling time of eight to ten hours, as compared to *E. coli*, which can double in about 30 minutes. What that means is that doing genetics, getting a mutant, can take months—the same thing would take three days in E. coli," explains Nayak. "What CRISPR-Cas9 enables us to do, at a very basic level, is speed up the whole process. It removes a major bottleneck… in doing genetics research with this archaeon.

"Even more," continues Nayak, "with our previous techniques, mutations had to be introduced one step at a time. Using this new technology, we can introduce multiple mutations at the same time. We can scale up the process of mutant generation exponentially with CRISPR."

CRISPR, short for Clustered Regularly Interspaced Short Palindromic Repeats, began as an immune defense system in archaea and bacteria. By identifying and storing short fragments of foreign DNA, Cas (CRISPR-associated system) proteins are able to quickly identify that DNA in the future, so that it can then quickly be destroyed, 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. By pairing Cas9 with a specifically engineered RNA guide rather than a fragment of invasive DNA, the CRISPR system can be directed to cut a cell's genome in an arbitrary location such that existing genes can be removed or new ones added. This system has been prolifically useful in editing eukaryotic systems from yeast, to plant, to fish and even human cells, earning it the American Association for the Advancement of Science's 2015 Breakthrough of the Year award. However, its implementation in prokaryotic species has been met with hurdles, due in part to their different cellular processes.

To use CRISPR in a cellular system, researchers have to develop a protocol that takes into account a cell's preferred mechanism of DNA repair: after CRISPR's "molecular scissors" cut the chromosome, the cell's repair system steps in to mend the damage through a mechanism that can be harnessed to remove or add additional genetic material. In eukaryotic cells, this takes the form of Non-Homologous End Joining (NHEJ). Though this pathway has been used for CRISPR-mediated editing, it has the tendency to introduce genetic errors during its repair process: nucleotides, the rungs of the DNA ladder, are often added or deleted at the cut site.

NHEJ is very uncommon in prokaryotes, including Archaea; instead, their DNA is more often repaired through a process known as homology-directed repair. By comparing the damage to a DNA template, homology-directed repair creates what Nayak calls a "deterministic template"—the end result can be predicted in advance and tailored to the exact needs of the researcher.

In many ways, homology-directed repair is actually preferable for genome editing: "As much as we want CRISPR-Cas9 to make directed edits in eukaryotic systems, we often end up with things that we don't want, because of NHEJ," explains Nayak. "In this regard, it was a good thing that most archaeal strains don't have a non-homologous end joining repair system, so the only way DNA can be repaired is through this deterministic homologous repair route."

Though it may seem counter-intuitive, one of Nayak and Metcalf's first uses of CRISPR-Cas9 was to introduce an NHEJ mechanism in *Methanosarcina acetivorans*. Though generally not preferable for genome editing, says Nayak, NHEJ has one use for which it's superior to homologous repair: "If you just want to delete a gene, if you don't care how … non-homologous end joining is actually more efficient."

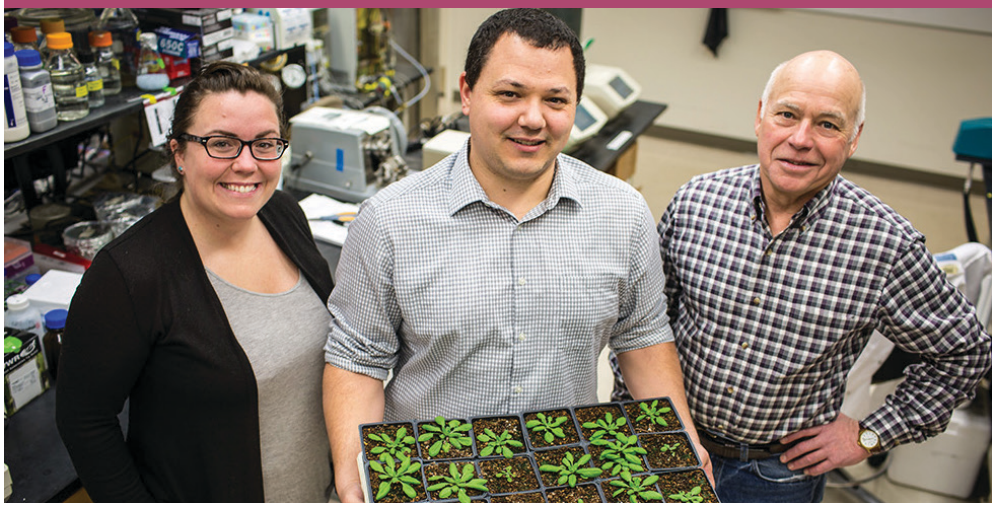
By using the introduced NHEJ repair system to perform what are known as "knock-out" studies, wherein a single gene is removed or silenced to see what changes are produced and what processes that gene might affect, Nayak says that future research will be able to assemble a genetic atlas of *M. acetivorans* and other archaeal species. Such an atlas would be incredibly useful for a variety of fields of research involving Archaea, including an area of particular interest to the Metcalf lab, climate change.

"*Methanosarcina acetivorans* is the one of the most genetically tractable archaeal strains," says Nayak. "[Methanogens are] a class of archaea that produce gigatons of this potent greenhouse gas every year, play a keystone role in the global carbon cycle, and therefore contribute significantly to global climate change." By studying the genetics of this 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.

In all, this research represents an exciting new direction in studying and manipulating archaea. "We began this research to determine if the use of CRISPR-Cas9 genome editing in archaea was even possible," concludes Nayak. "What we've discovered is that it's not only possible, but it works remarkably well, even as compared to eukaryotic systems."

This work was supported by the Division of Chemical Sciences, Geosciences, and Biosciences, Office of Basic Energy Sciences of the US Department of Energy. Dipti Nayak is a Simons Foundation Postdoctoral Fellow of the Life Sciences. ■

Written by Kathryne Metcalf. Photos by L. Brian Stauffer and Kathryn Faith.



Newly characterized protein has potential
to save US farmers millions annually

Instead of turning carbon into food, many plants accidentally make a plant-toxic compound during photosynthesis that is recycled through a process called photorespiration. University of Illinois and USDA/ARS researchers report in Plant Cell the discovery of a key protein in this process, which they hope to manipulate to increase plant productivity.

"Photorespiration is essential for C3 plants, such as rice and soybeans, but operates at the massive expense of fixed carbon and energy," said project lead Don Ort, USDA/ARS scientist and the Robert Emerson Professor of Plant Biology at Illinois. Ort leads the Genomic Ecology of Global Change theme at the IGB. "We have identified photorespiration as a primary target to improve photosynthetic efficiency as a strategy to improve crop yield. Successfully re-engineering photorespiration requires deep knowledge of the process, for which understanding of transport steps is most lacking."

Related to a family of transport proteins that move bile around in animals, the newly discovered role of the plant protein Bile Acid Sodium Symporter 6 (BASS6) is to transport the toxic product glycolate out of the chloroplast where it is recycled into a useful sugar molecule (glycerate) through a series of chemical reactions, which release carbon dioxide and harmful ammonia while sacrificing energy.

Since the 1960s, researchers have known that plant chloroplasts export two molecules of glycolate to recover one molecule of glycerate. However, the chemical equation did not add up until now with the discovery of the function of BASS6, the second glycolate transport protein to be described since the glycolate/glycerate exchange transporter "PLGG1" was described in 2013.

During photosynthesis in C3 crops, such as wheat and rice, the enzyme Rubisco will react with oxygen (instead of carbon dioxide) creating a plant-toxic compound that must be recycled, wasting energy. University of Illinois researchers—including USDA/ARS scientist Paul South (above, center), Robert Emerson Professor of Plant Biology and USDA/ARS scientist Don Ort (right), and Amanda Cavanagh (left)—report in Plant Cell *the discovery of a key protein in this process, which they hope to manipulate to increase plant productivity.*

"Now we're going to try to make a shortcut to avoid all the wasteful steps in photorespiration," said Paul South, a USDA/ARS postdoctoral researcher who led this work at the IGB. "We're building a shortcut to quickly process glycolate into glycerate instead of letting BASS6 and PLGG1 take the country roads. One of the benefits of the shortcut is that the plants don't produce ammonia, so they don't have to spend a lot of energy re-fixing the ammonia."

"We could feed around 200 million people with the calories lost to photorespiration each year just in the Midwestern United States," said co-author author Berkley Walker, an Alexander von Humboldt Postdoctoral Fellow at the University of Düsseldorf, citing his recently published simulations. "While we can't get all that yield back, even saving 5% of the energy in lost in photorespiration would be worth millions of dollars annually."

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The paper "Bile acid sodium symporter BASS6 can transport glycolate and is involved in photorespiratory metabolism in Arabidopsis thaliana" is published by Plant Cell (DOI: 10.1105/tpc.16.00775). Co-authors include Amanda Cavanagh at Illinois and Vivien Rolland and Murray Badger at the Australian National University.

This work is supported by Realizing Increased Photosynthetic Efficiency (RIPE), a research project engineering plants to more efficiently turn the sun's energy into food to sustainably increase worldwide food productivity. This international collaboration is funded by a $25 million grant from the Bill & Melinda Gates Foundation.

A photo gallery with pictures related to this work is available online at http://bit.ly/2mGgIp5. ■

Story and photograph by Claire Benjamin

ON THE GRID
HAPPENINGS AT THE IGB

IGB AT THE FIELD

THE WORLD OF GENOMICS AT THE FIELD MUSEUM

Explore The World of Genomics May 18-20 at The Field Museum during a special event presented by the IGB. Meet with IGB scientists in Stanley Field Hall and take part in hands-on activities to discover the fascinating world of genomic science and its impact on our lives.

Learn about how genes affect behavior and health by examining bee brains in 3D, witness the drug discovery pipeline in action, see how scientists are learning to grow enough food for tomorrow by identifying better crops yourself and observe how life begins and adapts in our ever-changing world by interacting with samples of the earliest life on Earth. Visit https://www.fieldmuseum.org/at-the-field/programs/world-genomics for more info.

ONLINE COURSE

coursera

IGB MOOC

The IGB's Massive Open Online Course (MOOC) "Genomics: Decoding the Universal Language of Life" is open for enrollment. This beginner level course contains 6 weeks of study and encompasses topics drawn from the IGB's expansive research portfolio such as 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. There are several enrollment options available through Coursera, and more information can be found at https://www.coursera.org/learn/genomics-research.

AWARDS

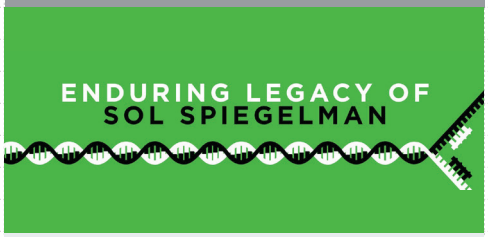
JOHN GERLT

John Gerlt, Gutgsell Professor of Biochemistry (MMG) was awarded the 2017 Gordon Hammes Lectureship, sponsored jointly by Biochemistry and the ACS Division of Biological Chemistry, which recognizes and honors an individual whose scientific contributions have had a major impact on research at the interface of chemistry and biology.

RUBY MENDENHALL

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, to engage scholars, artists, writers, and public historians to better formulate new historical narratives of Chicago's past.

SYMPOSIUM



THE ENDURING LEGACY OF SOL SPIEGELMAN

In honor of University of Illinois microbiologist Sol Spiegelman and his work with recombinant DNA technology, the IGB is hosting the symposium "The Enduring Legacy of Sol Spiegelman." We are featuring a public lecture and a series of plenary talks from October 20-22, 2017.

Our national panel of speakers, including two Nobel Laureates, encompasses diverse disciplines such as microbiology, biochemistry, cellular and development biology, neuroscience, and biomolecular engineering, and will be presenting on current and future work in their respective fields. Register now at http://spiegelman2017.igb.illinois.edu/.

FELLOWS

IGB FELLOWS SYMPOSIUM

IGB FELLOWS SYMPOSIUM

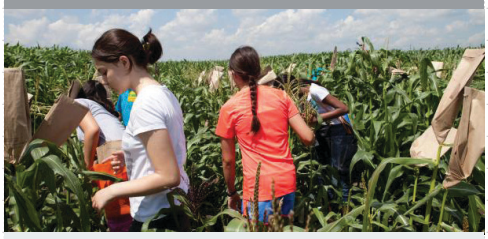
Current IGB research and issues in the life sciences will be presented during a day-long series of lectures by faculty, students, and Fellows from across campus at the IGB's annual Fellows Symposium.

Scott Edwards, Professor of Organismic and Evolutionary Biology from Harvard University joins Sua Myong, IGB Fellow alumna and Associate Professor of Biophysics at Johns Hopkins University as the featured keynote speakers.

Register today at http://fellows.igb.illinois.edu/.

ON THE GRID
HAPPENINGS AT THE IGB

SUMMER CAMP

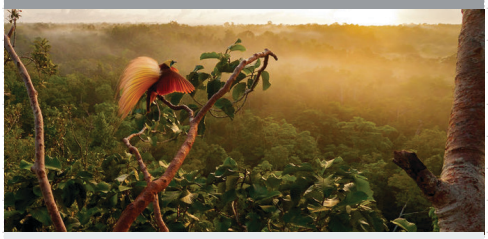


POLLEN POWER!

Join us for Pollen Power!, our summer camp that provides an opportunity for girls to study plant responses to climate change. Small research groups led by female graduate students will use million-dollar microscopes to image pollen, giving the campers first-hand experience in a research environment with female mentors. The camp is designed for girls who are entering 6th, 7th or 8th grade in the Fall 2017, and who have an interest in plants and the environment.

Visit http://pollensummercamp.illinois.edu/ for more info and to register.

GENOMICS



BIOLOGISTS PROPOSE TO SEQUENCE THE DNA OF ALL LIFE ON EARTH

A small group of researchers announced its intent to, eventually, sequence "all life on Earth" through an initiative called the Earth BioGenome Project. These lower-resolution genomes could be improved as needed by comparing them with the family references or by doing more sequencing, says EBP co-organizer Gene Robinson, IGB director.

Read the full story at http://www.sciencemag.org/news/2017/02/biologists-propose-sequence-dna-all-life-earth.

PARTNERSHIP

IGB ANNOUNCES NEW PARTNERSHIP WITH ZEISS LABS@LOCATION PROGRAM

A new agreement between the IGB and ZEISS has named the Core Facilities at IGB as 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 the Core and be available to all users during that time.

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

"ZEISS training is really valuable," said Core Facilities Director Glenn Fried, "but until now, you've had to send your people to the ZEISS Microscopy Customer Center in New York twice a year to see that benefit. Now all of my staff, as well as graduate students, postdocs, and faculty, can come to those classes at the IGB."

Fried 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. Though the IGB has equipment for that purpose, Fried says that the ZEISS Celldiscoverer 7 offers improved clarity and visibility, allowing for sharper and more accurate images. Read more at http://www.igb.illinois.edu/news/igb-announces-new-partnership-zeiss-labslocation-program.

ANNIVERSARY

GOVERNOR RAUNER RECOGNIZES IGB FOR 10 YEARS OF SCIENTIFIC CONTRIBUTION TO ILLINOIS

Governor Bruce Rauner officially recognized the IGB for celebrating ten years of genomic research addressing major societal issues in the areas of agriculture, environmental conservation, health, and technology. The IGB houses a broad portfolio of interdisciplinary life sciences research on the University of Illinois at Urbana-Champaign campus.

"We are proud to recognize the Carl R. Woese Institute for Genomic Biology for ten years of cutting-edge scientific research," said Governor Rauner. "Carl Woese changed human understanding of biology, and this institute is using the new science of genomics to push the boundaries of our understanding of critical issues facing society."

The IGB was dedicated on March 29, 2007 with special funding from the Illinois Legislature, and operates under the mission of advancing life sciences research and stimulating bioeconomic development in the state of Illinois. Members of the IGB work collaboratively, utilizing a team-based framework that leverages expertise from many distinct disciplines in science and engineering and unites fundamental and applied research approaches to tackle grand scientific challenges.

A proclamation issued by the Governor officially records March 29, 2017 as the 10th anniversary of the Institute and recognizes its societal, scientific, and scholarly contributions made to research within the state of Illinois. Read the full text of the announcement and proclamation at http://www.igb.illinois.edu/news/governor-recognizes-igb-10-years-scientific-contribution-illinois.

DEPARTMENT ANNOUNCEMENTS

BUSINESS

TEMPORARY SUSPENSION OF THE PREMIUM PROCESSING OPTION FOR H-1B VISAS

Martin McFarlane, Director of International Student and Scholar Services, has discussed the temporary suspension by USCIS of the Premium Processing option for H-1B applications. As a result of the temporary suspension of the Premium Processing option for H-1B visas, Martin is advising Departments to plan for an estimated 8 - 12 month time frame in order to obtain approval for an H-1B visa application. (Previously, the H-1B visa approval process had been taking from 4 to 6 months when the Premium Processing option was used.) We are bringing this to your attention so that you can plan accordingly when sponsoring international scholars on H-1B visas.

If you have any questions or concerns regarding H-1B visa applications for your current or pending IGB international employees, please feel free to contact Jacinda King who oversees the HR office at the IGB at *jking@illinois.edu* or 244-2276.

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On Friday, March 3rd, USCIS announced that they would be temporarily suspending Premium Processing for H-1B application effective April 3rd. While the exact length of the suspension is not known, USCIS are stating this may last six months, which would mean Premium Processing for H-1B applications would not be available again until October 2017.

EXPECTED TIMELINE
There are two significant timelines to be aware of- the time it takes to prepare a complete H-1B application that can be submitted to USCIS, and the time it takes for USCIS to process that application.

Prior to USCIS submission
ISSS needs to obtain both a Prevailing Wage (PW) and a Labor Condition Application (LCA) before an H-1B application can be submitted. An LCA usually takes 1-2 weeks, however a PW can take a few days to 3 months, depending on whether this can be calculated by ISSS or whether it needs to be requested from the Department of Labor. More information on this is below. This means from when you submit a request to ISSS for an H-1B, it can take 1-4 months before it is ready to be filed with USCIS.

After USCIS submission
If ISSS can submit an application prior to April 3rd, 2017, you have the option of requesting Premium Processing. This means action would be taken in 15 calendar days. However after April 3rd, this option will not be available for approximately six months. USCIS processing time on these applications is approximately 7-8 months.

Overall timeline
Without Premium Processing, the approval process for an H-1B will take an estimated 8-12 months. Departments should plan as best they can for this lengthy process.

Prevailing Wage
We expect many departments will be interested in asking ISSS to calculate a PW ourselves rather than request one from the Department of Labor to avoid the approximate 3 month wait for DOL to respond. However whether ISSS can do the PW without the Department of Labor relies both on the risk the department is willing to assume, and very importantly, the type of job requested.

ISSS can conduct an in-house prevailing wage determination for H-1B extensions, and for new postdoctoral, faculty, and university-specific positions if the required data is available. All other H-1B requests must have a prevailing wage determination conducted through the U.S. Department of Labor. There will not be an option to request ISSS process these 'in-house'.

By allowing ISSS to conduct an in-house prevailing wage determination for an H-1B request, the department/unit is foregoing the "safe harbor" option of a U.S. Department of Labor prevailing wage determination. If the in-house prevailing wage assessment were to be challenged at a future date, the department/unit would be liable to pay any differential back wages and/or fines. The department/unit must also acknowledge that if the subsequent Labor Condition Application or H-1B petition is denied due to prevailing wage issues, the H-1B employee may have to immediately depart the U.S.

PAYROLL ISSUES
H-1B Extensions
H-1B extensions can have their prevailing wage determined by ISSS, as stated above. Therefore it only takes approximately one month for ISSS to submit the extension request to USCIS. 2-3 weeks after this, we should receive a receipt notice verifying we have filed a request to extend the H-1B. Based on this receipt notice, the individual can continue to work for up to 240 days beyond the expiry of their current H-1B while waiting for approval. If approval is not received within these 240 days, the individual must stop work and stop being paid.

H-1B Amendments and Change of Status Applications
These applications do not benefit from the '240 day' rule that H-1B extensions receive. Individuals awaiting these benefits must remain in their previous status until the new H-1B is approved.

NEW H-1B APPLICATIONS
New H-1B applications will be subject to this lengthy process. New hires should be made aware of this. We recommend departments consult with HR regarding possible wording in offer letters to reflect the possibility that start dates may need to be changed, amended, or cancelled. ■

OPERATIONS AND FACILITIES

BLOOD DRIVE

The next IGB blood drive will be held on Monday, May 1, from 9:00am to 1:00pm in the IGB conference room near Array Cafe. Please call or email Darci Edmonson at 244-2200 or at *darci@illinois.edu* to schedule a convenient appointment time. Or, if you prefer to register online please visit www.bloodcenterimpact.org. ■

RECENT PUBLICATIONS

Please include your connection to the IGB in your author byline when submitting publications, as it will greatly help track potential newsworthy items and increase the possibility of coverage.

Uddin, M., Jansen, S., & Telzer, E. H. (2017). Adolescent depression linked to socioeconomic status? Molecular approaches for revealing premorbid risk factors. *BioEssays*, 39(3), [1600194]. DOI: 10.1002/bies.201600194

Hackett, L. P., Seo, S., Kim, S., Goddard, L. L., & Liu, G. L. (2017). Label-free cell-substrate adhesion imaging on plasmonic nanocup arrays. *Biomedical Optics Express*, 8(2), 1139-1151. DOI: 10.1364/BOE.8.001139

Yendrek, C. R., Tomaz, T., Montes, C. M., Cao, Y., Morse, A. M., Brown, P. J., ... Ainsworth, E. A. (2017). High-throughput phenotyping of maize leaf physiological and biochemical traits using hyperspectral reflectance. *Plant Physiology*, 173(1), 614-626. DOI: 10.1104/pp.16.01447

Shao, Y., Wolf, P. G., Guo, S., Guo, Y., Rex Gaskins, H., & Zhang, B. (2017). Zinc enhances intestinal epithelial barrier function through the PI3K/AKT/mTOR signaling pathway in Caco-2 cells. *Journal of Nutritional Biochemistry*, 43, 18-26. DOI: 10.1016/j.jnutbio.2017.01.013

Lan, Z. J., Krause, M. S., Redding, S. D., Li, X., Wu, G. Z., Zhou, H. X., ... Lei, Z. M. (2017). Selective deletion of Pten in theca-interstitial cells leads to androgen excess and ovarian dysfunction in mice. *Molecular and Cellular Endocrinology*, 444, 26-37. DOI: 10.1016/j.mce.2017.01.043

Lewis, C. J. T., Pan, T., & Kalsotra, A. (2017). RNA modifications and structures cooperate to guide RNA-protein interactions. *Nature Reviews Molecular Cell Biology*, 18(3), 202-210. DOI: 10.1038/nrm.2016.163

Yu, H., Le, H., Lumetta, S., Cunningham, B. T., Kaale, E., & Layloff, T. (2017). Smartphone-based thin layer chromatography for the discrimination of falsified medicines. In *IEEE Sensors, SENSORS 2016 - Proceedings [7808847] Institute of Electrical and Electronics Engineers Inc.*. DOI: 10.1109/ICSENS.2016.7808847

Thor, S., Peterson, J. R., & Luthey-Schulten, Z. (2017). Genome-Scale Metabolic Modeling of Archaea Lends Insight into Diversity of Metabolic Function. *Archaea*, 2017, [9763848]. DOI: 10.1155/2017/9763848

Kwon, L., Race, C., Foreman, M., & Cunningham, B. (2017). An automated microfluidic assay for the detection of cancer biomarkers in serum using photonic crystal enhanced fluorescence. In *IEEE Sensors, SENSORS 2016 - Proceedings [7808960] Institute of Electrical and Electronics Engineers Inc.*. DOI: 10.1109/ICSENS.2016.7808960

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