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Volume 11 Number 4

UPCOMING EVENTS

IGB Pioneers Seminar (GEGC)

Plants, Oxygen and Water Extremes

May 18, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Julia Bailey-Serres, PhD

University of California, Riverside

Professor of Genetics and Director, Center for Plant Cell Biology

IGB Pioneers Seminar (GEGC)

TBD

August 28, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Dominique Bergmann, PhD

Stanford University, Department of Biology

IGB Seminar (CGRH)

TBD

September 4, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Olivier Gevaert, PhD

Stanford University, Department of Medicine

IGB Seminar (IGOH)

TBD

September 25, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

Kayla C. King, PhD

University of Oxford, Department of Zoology

IGB Seminar (RBTE)

TBD

October 16, 2018, 12:00 p.m.

612 Carl R. Woese Institute for Genomic Biology

George J. Christ, PhD

University of Virginia, Department of Biomedical Engineering and Orthopedic Surgery

FEATURED NEWS



2

Earth BioGenome Project aims to sequence 1.5M species



3

Respect Indigenous ancestors: community engagement urged



4

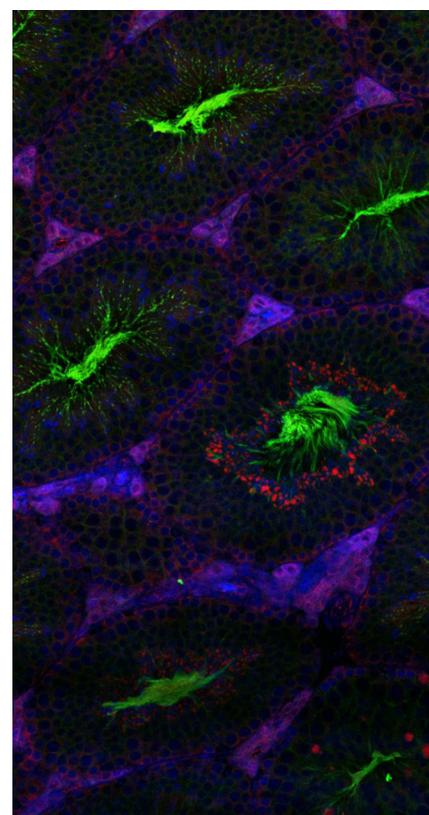
Monthly Profile: Katy Heath



5

On the Grid: Happenings at IGB

IMAGE OF THE MONTH



This month features a cross section of mouse testis showing germ cells and spermatogenesis. The green color is basigin expression, which is a cell membrane protein. The red color is claudin-4 expression, which is an epithelial tight junction protein. The blue color is DAPI staining of nuclei. This Image was taken using the Zeiss LSM 710, provided by Adam Kailiang Li of Dr. Romana Nowak's Lab, Department of Animal Sciences.

IGB News

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

FEATURE



Earth BioGenome Project aims to sequence genomes of 1.5M species

An international consortium of scientists is proposing a massive project to sequence, catalog and analyze the genomes of all known eukaryotic species on the planet, an undertaking the researchers say will take 10 years, cost \$4.7 billion and require more than 200 petabytes of digital storage capacity. Eukaryotes include all organisms except bacteria and archaea. There are an estimated 10-15 million eukaryotic species on Earth. Of those, the team proposes sequencing 1.5 million.

The proposed initiative, described in a paper in the *Proceedings of the National Academy of Sciences*, would require the cooperation of governments, scientists, citizen scientists and students from around the globe. The authors of the proposal compare it to the Human Genome Project, an international scientific research project from 1990 to 2006 that cost roughly \$4.8 billion in today's dollars and generated an estimated return-on-investment ratio of 141-to-1.

The Human Genome Project “involved a workforce of more than 47,000 people generating nearly \$1 trillion in economic activity,” the authors wrote.

They are calling their new proposal the [Earth BioGenome Project](#).

“For the first time in history, it is possible to efficiently sequence the genomes of all known species and to use genomics to help discover the remaining 80 to 90 percent of species that are currently hidden from science,” the authors wrote.

A similar initiative, the Earth Microbiome Project,

has enlisted the support of more than 500 scientists to sequence bacterial and archaeal genomes across the globe.

The reasons for undertaking such an ambitious project are many, said Gene Robinson, a leader of

To sequence, catalog and analyze the genomes of all known eukaryotic species on the planet would take 10 years, cost \$4.7 billion and require more than 200 petabytes of digital storage capacity.

the proposed effort, a professor of entomology and the director of the IGB.

“Genomics has helped scientists develop new medicines and new sources of renewable energy, feed a growing population, protect the environment and support human survival and well-being,” Robinson said. “The Earth BioGenome Project will give us insight into the history and diversity of life and help us better understand how to conserve it.”

Scientists have so far sequenced fewer than 15,000 species, most of them microbes, the team reports. However, the cost of genome sequencing has fallen to about \$1,000 for an average-sized vertebrate genome and is expected to continue to go down. New

technologies, including terrestrial and underwater robots, and an increase in citizen-scientist initiatives and consortiums of scientists focusing on specific groups of organisms are speeding the process of data collection and analysis.

“The Earth BioGenome Project will make use of existing resources and institutions whose mission is to procure and preserve the world's biodiversity,” Robinson said. “For example, the world's botanical garden collections hold more than a third of all plant species.”

The EBP project will support and promote international protocols for data storage and sharing. A coordinating council with members from Africa, Australia, Brazil, Canada, China, the European Union and the United States will head a global network of collaborators. The council also will include representatives of several current large-scale genomics projects including the Global Genome Biodiversity Network, the Global Invertebrate Genomics Alliance, the i5K Initiative to Sequence 5,000 Arthropod Genomes and the Genome 10K Project.

“The greatest legacy of the EBP will be a complete digital library of life that will guide future discoveries for generations,” Robinson said.

Robinson co-chairs the EBP Working Group with professor Harris A. Lewin, of the University of California, Davis; and W. John Kress, of the Smithsonian Institution. ■

*Written by Diana Yates.
Graphic by Mirhee Lee.*



Respect Indigenous ancestors: Scholars urge community engagement

A [new article](#) in the journal *Science* provides guidance for those intending to study ancient human remains in the Americas. The paper, written by Indigenous scholars and scientists and those who collaborate with Indigenous communities on studies of ancient DNA, offers a clear directive to others contemplating such research: First, do no harm.

Scientists studying ancestral remains have similar obligations to those that bind researchers working with living human subjects, the authors wrote. The descendants or people affiliated with those who lived hundreds or thousands of years ago deserve to be consulted before their ancestors are disturbed. Even in cases where the remains were collected long ago and moved far from their original burial place, and even when the surviving lineages are in doubt, scientists ought to consult Indigenous groups living on the land or claiming ancestral ties to the region where the ancestors were found, the authors said.

“Right now, there are inconsistent or no regulations for working with ancient ancestors,” said University of Illinois anthropology professor Ripan Malhi, a co-author of the report and member of the IGB’s Computing Genomes for Reproductive Health and Regenerative Biology & Tissue Engineering research themes. “And there are no requirements for working with descendant or affiliated communities, even though new scientific findings relating to their ancestors can have serious implications for them.”

Malhi partners with Indigenous communities to study ancient DNA from individuals found on lands their descendants still live on. Malhi, along with Indigenous scientists, scholars and other scientists who work with Native American and First Nations communities, worked to create the Summer intern-

ship for Indigenous Peoples in Genomics, which trains Indigenous scientists in genomics techniques and explores ethical concerns. Not consulting Indigenous communities before analyzing ancient DNA potentially harms those groups, said Alyssa

“There are no requirements for working with descendant or affiliated communities, even though new scientific findings relating to their ancestors can have serious implications for them.”

Bader, a co-author and graduate student at the University of Illinois.

“Genetic analyses can reveal information not just about the ancestors, but also their descendants. If genetic variants associated with specific diseases are identified in ancestors, for example, this can influence how we think about disease susceptibility in the descendant community – and that community could be stigmatized,” she said.

New findings also may interfere with ongoing treaty negotiations, she said.

“For Indigenous communities involved in negotiating land claims or repatriation, new genetic findings could either bolster or complicate those claims,” she said.

Studying ancient DNA without consulting descen-

dant communities is also a missed opportunity, said Concordia University professor Jessica Bardill, the lead author of the article.

“The engagements we highlight show that collaboration with communities not only strengthens the analysis but also can allow for better questions to be asked in the research, informed by community narratives about the ancestors, their lands and their relationships,” she said.

For these and other ethical and practical reasons, Malhi said, it’s in a scientist’s interest to identify and locate potentially affected groups, consult with them about the research and invite them to join the effort, thereby improving the scientist’s understanding of the context in which the ancient peoples lived. It also allows Indigenous communities to guide the science and ask research questions that are of interest to them.

“Engaging communities at the outset is critical for understanding their concerns or questions about research involving ancient relatives. Without feedback from the community, scientific interpretations remain one-sided and inherently biased,” said Nanibaa’ Garrison, a bioethics professor at Seattle Children’s Research Institute and the University of Washington School of Medicine, and a co-author of the article.

The National Institutes of Health and National Science Foundation support this work. ■

*Written by Diana Yates.
Photo by L. Brian Stauffer.*



Assistant Professor of Plant Biology Katy Heath focuses on the evolution of mutualisms, which are most generally defined as species interactions that increase the fitness of both (or all) partners using methods from the fields of quantitative genetics, population and molecular genetics, and ecology.

Katy Heath: Uncovering how species interact and evolve together

Early on in her research, Katy Heath became intrigued by interactions between species that are mutually beneficial. She began to wonder why these relationships survived as the species evolved.

“You have two species, they’re interacting, and they have to spend their energy and resources to make a benefit that they then hand over to a different species, which doesn’t fit well with our understanding of how natural selection works,” Heath said. “Natural selection favors genotypes that have high fitness—not those necessarily that give away a portion of their resources to others.”

Heath wondered how these opposing ideas could be rectified, and these questions led her to study interactions between plants and microbes. Today, she is an Associate Professor in the Department of Plant Biology at the University of Illinois and a faculty member in the IGOH theme.

Most of [her laboratory’s](#) research involves studying legume plants, such as peas and soybeans. These protein-rich plants are full of nitrogen, an element that surrounds us in the air, but organisms like plants and humans can’t directly incorporate nitrogen into their bodies.

“We need an organism to fix it for us, so to speak,” Heath said. “That process is something that bacteria can do. What I study is the interaction between legumes and the nitrogen-fixing bacteria that live in their roots.”

The bacteria, called rhizobia, are responsible for the nitrogen fixed in this interaction, which is important for agricultural systems as well as natural ecosystems.

“Legumes are one of the core groups of plants that are in natural ecosystems, one of the most diverse families of plants, so they’re everywhere,” Heath said. “But then from the evolution side, it’s super interesting to try to understand why rhizobia spend all their energy fixing nitrogen, which they just give over to their plants.”

Over time, Heath’s research has changed to include analyzing how bacteria evolve in nature. Genome sequencing has become more incorporated into her work.

“Now that we have genomics, we have sequencing data,” she said. “We can use these backwards-looking methods to try to infer something about how evolution has occurred.”

By looking at signatures in the genome, they can understand how organisms have changed over time. Heath has become more interested in bacterial population biology—studying how bacteria evolve and how classical evolution models can be applied to bacterial populations.

“That’s where I connect really well with the IGOH theme,” Heath said. “Our theme is focused on how microbial populations and microbial evolution unites all of the ecosystems on the planet.”

The underlying focus on infection, within the IGOH theme, has many implications for human systems—for example, the issue of antibiotic resistance has both health and economic implications.

Heath is currently working with Assistant Professor of Plant Biology Amy Marshall-Colon (GEGC) on a project to understand species interactions at the molecular and biochemical level. They want to learn more about what happens at the molecular level that creates benefits for both species.

“It’s not always that a good interaction for the plant is good for the bacteria,” Heath said.

They will analyze 200 strains of bacteria to see how beneficial they are for plant hosts and to better understand the genomic and biochemical basis of these interactions.

“(We will use) mapping approaches to understand what genomic regions generate the variation we see in the trait we care about (the benefits to plant hosts),” Heath said.

Overall, she is interested in understanding the underlying molecular variations that are shaped by coevolution, the process by which two species influence each other’s evolution.

As Heath’s research has progressed, her work has incorporated several fields and techniques, such as

ecology, evolutionary genetics, sequencing, genome manipulation and engineering.

“The challenge, which is both fun but also really hard for any individual scientist to keep on top of, is the diversity of techniques and fields,” Heath said. “Trying to master all those fields is really hard.”

But Heath said this is what is beneficial about being a part of the IGB.

“You have all these complementary types coming together,” she said.

Another challenge comes with working across disciplines and knowing the next step to take.

“(You’re) always trying to learn new things while trying to maintain movement forward,” Heath said. “It’s hard to know where to move next. But you don’t get bored — that’s one thing I can say; I’m never bored.”

She has often found that answering one question in her research means opening up even more questions.

“That means it’s always interesting,” she said. “My thinking has really moved and morphed on how mutualisms remain in existence over millions of years.”

Many theories describe mutual relationships in nature as being static, but Heath has pushed the idea that these interactions are actually dynamic and involve several mechanisms.

“That’s why I’ve become so interested in doing molecular biology,” she said. “Fundamentally, the traits aren’t measurable unless you’re doing molecular biology, because they’re all happening at a scale we can’t look at.”

Heath hopes her research can integrate scientific fields that often don’t work together. She believes collaborations between those who study evolution, ecology, and molecular biology would be beneficial.

“That fits very well within the (IGOH) theme and the mission of the IGB,” she said. “The ability to connect with people who are interested in those questions in different systems is pretty exciting.” ■

Written by Emily Scott. Photo by L. Brian Stauffer.

ON THE GRID HAPPENINGS AT THE IGB

AWARDS



JEFFREY MOORE

Jeffrey Moore, Murchison-Mallory Professor of Chemistry and Professor of Materials Science and Engineering (BSD), received the 2018 Stephanie L. Kwolek Award from the Royal Society of Chemistry, for the conception, testing, and validation of the mechanophore hypothesis and for research leading to self-healing polymers.



STEPHEN MOOSE

Stephen Moose, Professor of Crop Sciences (BSD/GEGC) was awarded the Karl E. Gardner Outstanding Undergraduate Adviser Award from the College of Agricultural, Consumer and Environmental Sciences.

DEAN NAMED



RUBY MENDENHALL

Ruby Mendenhall (CGRH/GNDP) has been named the Assistant Dean for Diversity and Democratization of Health Innovation at the Carle Illinois College of Medicine. Mendenhall is an associate professor of sociology, African American studies, urban and regional planning, gender and women's studies and social work.

CAMPS



2018 SCHOLAR ATHLETE SUMMER CAMPS

The IGB is working with the Division of Intercollegiate Athletics (DIA) to offer summer sports camps for scholar athletes with hands-on learning experiences. Designed specifically for middle and high school athletes, campers will learn about the latest scientific discoveries in genomics and will be provided with the biological knowledge required to reach optimal performance levels in their sport. Camps are currently being offered in Gymnastics, Tennis and Golf. Visit the IGB's [Scholar Athlete Summer Camp](#) page for more information.

GENOMICS FOR™

GENOMICS FOR TEACHERS



GENOMICS FOR TEACHERS SUMMER COURSE

The IGB will be offering our newest Genomics For™ course in partnership with Illinois Extension and the Illinois-Indiana Sea Grant on Tuesday, June 19th from 8:00am to 3:30pm. Teachers will receive 6 CPDUs and a stipend for attending, and topics covered will include invasive species, fish, and water quality.

Please contact Erin Louer at emckern2@illinois.edu with questions or to request more information.

CONSERVATION



CONSERVATIONISTS HIGHLIGHT RHINO AND ELEPHANT SPECIES FOR PROTECTION

Professor of Animal Sciences Alfred Roca (CGRH/GNDP) is leading conservation efforts concerning segments of the rhinoceros and forest elephant population.

The little-known and smallest member of the rhinoceros family, the Sumatran rhinoceros, is critically endangered. Today between 30 and 100 are isolated on the islands of Sumatra and Borneo in Southeast Asia. Researchers urge conservationists to translocate the two island groups—

representing two subspecies of the Sumatran rhino—and to create a cell bank to preserve the genetic diversity uncovered by this work. In the future, preserved cell lines could be used to create artificial gametes, to reverse the effects of inbreeding and harmful mutations.

Across Central Africa, the dwindling forest elephant populations are genetically quite similar to one another—conserving this critically endangered species across its range is crucial to preserving local plant diversity in Central and West African Afrotropical forests. Through protection of this species, many additional species could be saved.

“Forest elephants are the heart of these ecosystems—without them, the system falls apart, and many other species are jeopardized,” said Roca.

Read the full articles on the [Sumatran rhinoceros](#) and the [forest elephants](#) on the IGB website.

ON THE GRID HAPPENINGS AT THE IGB

COMMUNITY



SCIENCE AT THE MARKET

In partnership with the Department of Physics, the IGB will be at the Urbana Farmer's Market at Lincoln Square mall on June 9th for "Science at the Market." IGB members will be present to answer questions about genomics and the research at our institute, and will guide visitors through hands-on activities such as the Strawberry DNA Lab which will show how to extract DNA from strawberries, and Yummy DNA for building DNA structures out of edible components.

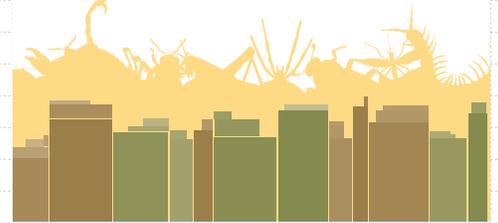
SING



SUMMER INTERNSHIP FOR INDIGENOUS PEOPLES IN GENOMICS

The [Summer internship for Indigenous peoples in Genomics](#) (SING) Workshop is a one-week workshop aimed at discussing the uses, misuses and limitations of genomics as a tool for indigenous peoples' communities. The workshop will also assist in training indigenous peoples in the concepts and methods currently used in genomics. The 2018 SING Workshop will be held July 22-28 at the University of Washington, Seattle.

SYMPOSIUM



11TH ANNUAL ARTHROPOD GENOMICS SYMPOSIUM

The University of Illinois at Urbana-Champaign is pleased to host the Arthropod Genomics Symposium, Thursday to Saturday, June 7-9, 2018. It has been 18 years since the sequencing of the genome of *Drosophila melanogaster*, and over three hundred arthropod genomes have been sequenced since then. The Arthropod Genomics Symposium is an opportunity to reflect on recent progress and explore future directions.

For more information and to view the agenda, please visit <http://arthropod.igb.illinois.edu/>.

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.

Tabatabaie, S., Emad, A., Zhao, S. D., & Sinha, S. (2018). A closer look at cross-validation for assessing the accuracy of gene regulatory networks and models. *Scientific Reports*, 8(1), [6620]. DOI: 10.1038/s41598-018-24937-4

Abidi, S. N. F., & Smith-Bolton, R. K. (2018). Cell fate changes induced by a Distal-less enhancer-trap transgene in the *Drosophila* antennal imaginal disc. *Scientific Reports*, 8(1), [4950]. DOI: 10.1038/s41598-018-23093-z

Tapsin, S., Sun, M., Shen, Y., Zhang, H., Lim, X. N., Susanto, T. T., ... Wan, Y. (2018). Genome-wide identification of natural RNA aptamers in prokaryotes and eukaryotes. *Nature Communications*, 9(1), [1289]. DOI: 10.1038/s41467-018-03675-1

Chen, J., Cao, X., An, Q., Zhang, Y., Li, K., Yao, W., ... Yu, B. (2018). Inhibition of cancer stem cell like cells by a synthetic retinoid. *Nature Communications*, 9(1), [1406]. DOI: 10.1038/s41467-018-03877-7

Singh, R., Jones, T., Wai, C. M., Jifon, J., Nagai, C., Ming, R., & Yu, Q. (2018). Transcriptomic analysis of transgressive segregants revealed the central role of photosynthetic capacity and efficiency in biomass accumulation in sugarcane. *Scientific Reports*, 8(1), [4415]. DOI: 10.1038/s41598-018-22798-5

Neu, L., Bänziger, C., Proctor, C. R., Zhang, Y., Liu, W. T., & Hammes, F. (2018). Ugly ducklings - The dark side of plastic materials in contact with potable water. *npj Biofilms and Microbiomes*, 4(1), [7]. DOI: 10.1038/s41522-018-0050-9

Wang, Z., Dien, B. S., Rausch, K. D., Tumbleson, M. E., & Singh, V. (2018). Fermentation of undetoxified sugarcane bagasse hydrolyzates using a two stage hydrothermal and mechanical refining pretreatment. *Bioresour. Technol.*, 261, 313-321. DOI: 10.1016/j.biortech.2018.04.018

Yildiz, G., Ding, J., Gaur, S., Andrade, J., Engeseth, N. E., & Feng, H. (2018). Microencapsulation of docosahexaenoic acid (DHA) with four wall materials including pea protein-modified starch complex. *International Journal of Biological Macromolecules*, 114, 935-941. DOI: 10.1016/j.ijbiomac.2018.03.175

RECENT PUBLICATIONS

Chen, S., Li, W., Xie, X., Brechtel, J., Chen, B., Li, P., ... Liaw, P. K. (2018). Nanoscale serration and creep characteristics of Al_{0.5}CoCrCuFeNi high-entropy alloys. *Journal of Alloys and Compounds*, 752, 464-475. DOI: 10.1016/j.jallcom.2018.04.137

Liu, G., Zhang, Y., van der Mark, E., Magic-Knezev, A., Pinto, A., van den Bogert, B., ... Medema, G. (2018). Assessing the origin of bacteria in tap water and distribution system in an unchlorinated drinking water system by SourceTracker using microbial community fingerprints. *Water Research*, 138, 86-96. DOI: 10.1016/j.watres.2018.03.043

Liu, J., Chatham, L., Aryal, R., Yu, Q., & Ming, R. (2018). Differential methylation and expression of HUA1 ortholog in three sex types of papaya. *Plant Science*, 272, 99-106. DOI: 10.1016/j.plantsci.2018.04.001

Edwards, J. D., Pittelkow, C. M., Kent, A. D., & Yang, W. H. (2018). Dynamic biochar effects on soil nitrous oxide emissions and underlying microbial processes during the maize growing season. *Soil Biology and Biochemistry*, 122, 81-90. DOI: 10.1016/j.soilbio.2018.04.008

Vachaspati, P., & Warnow, T. (2018). SVDquest: Improving SVD-quartets species tree estimation using exact optimization within a constrained search space. *Molecular Phylogenetics and Evolution*, 124, 122-136. DOI: 10.1016/j.ympev.2018.03.006

Kim, H., Oh, E. J., Lane, S. T., Lee, W. H., Cate, J. H. D., & Jin, Y. S. (2018). Enhanced cellobiose fermentation by engineered *Saccharomyces cerevisiae* expressing a mutant cellobiohydrolase and cellobiose phosphorylase. *Journal of Biotechnology*, 275, 53-59. DOI: 10.1016/j.jbiotec.2018.04.008

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Berding, K., Holscher, H. D., Arthur, A. E., & Donovan, S. M. (2018). Fecal microbiome composition and stability in 4- to 8-year old children is associated with dietary patterns and nutrient intake. *Journal of Nutritional Biochemistry*, 56, 165-174. DOI: 10.1016/j.jnutbio.2018.01.002

Tucker, E. K., & Nowak, R. A. (2018). Methylmercury alters proliferation, migration, and antioxidant capacity in human HTR8/SV-neo trophoblast cells. *Reproductive Toxicology*, 78, 60-68. DOI: 10.1016/j.reprotox.2018.03.008

Urban, M. A., Romero, I. C., Sivaguru, M., & Punyasena, S. W. (2018). Nested cell strainers: An alternative method of preparing palynomorphs and charcoal. *Review of Palaeobotany and Palynology*, 253, 101-109. DOI: 10.1016/j.revpalbo.2018.04.002

Ainsworth, E. A., & Lemonnier, P. (2018). Phloem function: a key to understanding and manipulating plant responses to rising atmospheric [CO₂]? *Current Opinion in Plant Biology*, 43, 50-56. DOI: 10.1016/j.pbi.2017.12.003

Soman, C., Keymer, D. P., & Kent, A. D. (2018). Edaphic correlates of feedstock-associated diazotroph communities. *GCB Bioenergy*, 10(5), 343-352. DOI: 10.1111/gcbb.12502

Kumar, D., Juneja, A., & Singh, V. (2018). Fermentation technology to improve productivity in dry grind corn process for bioethanol production. *Fuel Processing Technology*, 173, 66-74. DOI: 10.1016/j.fuproc.2018.01.014

Swaminathan, S., Abeysekera, N. S., Knight, J. M., Liu, M., Dong, J., Hudson, M. E., ... Cianzio, S. R. (2018). Mapping of new quantitative trait loci for sudden death syndrome and soybean cyst nematode resistance in two soybean populations. *Theoretical and Applied Genetics*, 131(5), 1047-1062. DOI: 10.1007/s00122-018-3057-y

Bardill, J., Bader, A. C., Garrison, N. A., Bolnick, D. A., Raff, J. A., Walker, A., & Malhi, R. S. (2018). Advancing the ethics of paleogenomics. *Science*, 360(6387), 384-385. DOI: 10.1126/science.aag1131

Hetrick, K. J., Walker, M. C., & Van Der Donk, W. A. (2018). Development and Application of Yeast and Phage Display of Diverse Lanthipeptides. *ACS Central Science*, 4(4), 458-467. DOI: 10.1021/acscentsci.7b00581

O'Dwyer, J. P. (2018). Whence Lotka-Volterra? Conservation laws and integrable systems in ecology. *Theoretical Ecology*, 1-12. DOI: 10.1007/s12080-018-0377-0

Parkinson, E. I., Tryon, J. H., Goering, A. W., Ju, K. S., McClure, R. A., Kemball, J. D., ... Metcalf, W. W. (2018). Discovery of the Tyrobetaïne Natural Products and Their Biosynthetic Gene Cluster via Metabologenomics. *ACS chemical biology*, 13(4), 1029-1037. DOI: 10.1021/acscchembio.7b01089

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Rendeiro, C., & Rhodes, J. S. (2018). A new perspective of the hippocampus in the origin of exercise-brain interactions. *Brain Structure and Function*, 1-19. DOI: 10.1007/s00429-018-1665-6

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Ren, Y., Reddy, J. S., Pottier, C., Sarangi, V., Tian, S., Sinnwell, J. P., ... Asmann, Y. W. (2018). Identification of missing variants by combining multiple analytic pipelines. *BMC bioinformatics*, 19(1), [139]. DOI: 10.1186/s12859-018-2151-0

Dau, H., Duursma, I., Kiah, H. M., & Milenkovic, O. (2018). Repairing Reed-Solomon Codes With Multiple Erasures. *IEEE Transactions on Information Theory*. DOI: 10.1109/TIT.2018.2827942

Lorente-Sorolla, J., Truchado-Garcia, M., Perry, K. J., Henry, J. Q., & Grande, C. (2018). Molecular, phylogenetic and developmental analyses of Sall proteins in bilaterians. *EvoDevo*, 9(1), [9]. DOI: 10.1186/s13227-018-0096-z

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