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13th Annual Symposium Coming to Manhattan

by Jennifer Rhodes

The 13th Annual Ecological Genomics Symposium is moving to Manhattan! The Hilton Garden Inn, in downtown Manhattan, will host the symposium November 6-8, 2015.

This year's symposium will feature a diverse array of established and emerging leaders in the field of ecological and evolutionary genomics. The symposium is scheduled to begin Friday evening, November 6, with talks and a poster session. Saturday will feature additional talks, a poster session and networking dinner. The symposium will conclude on Sunday, November 8. An optional tour of Konza Prairie is scheduled for Sunday afternoon upon the conclusion of the meeting.

The symposium's 6 featured speakers are:

- Scott Edward, Harvard University

- Michael Lynch, Indiana University
- Melissa Pespeni, University of Vermont
- Stacey Smith, University of Colorado, Boulder
- Joan Strassmann, Washington University, St. Louis
- Michi Tobler, Kansas State University

In addition to the six invited speakers, this year's symposium will feature an expanded number of speakers chosen from submitted abstracts.

The early registration fee is \$235 for faculty and \$135 for students. The early registration and poster abstract submission deadlines was Friday, September 25.

To discover more details, visit our website at ecogen.k-state.edu.



Summer Research Forum Held

Over 50 attended forum held on June 23, 2015 at Konza Prairie.

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Student News

Several students have recently won awards. Congratulations!

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New Faces

EGI welcomes several new people!

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EGI on Social Media

EGI has new Facebook and Twitter accounts.

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Ecological Genomics Summer Research Forum Held

The Ecological Genomics Research Forum was held at the Cortelyou Lecture Hall at the Konza Prairie Biological Station on Tuesday, June 23. Six graduate students and postdocs presented their research. New faculty members, Lydia Zeglin and Geoff Morris, provided interesting talks.



This event provided a great opportunity for the 18 undergraduate students from the Ecological Genomics REU and URM programs to present research in short data blitz talks.



Approximately 50 people attended the talks and participated in the evening barbeque. This event was funded with support from NSF REU, NSF URM in Ecological Genomics, and the KSU Division of Biology.

2015 Biology REU Program

Summer 2015 marked the 21st year of the Biology REU program. We selected 12 participants from over 165 applicants to our 10-week program. These participants conducted independent research projects with faculty mentors from Biology and Plant Pathology on many aspects of ecology and evolutionary biology. In addition, REUs attended seminars on grassland ecology and genomics, professional development seminars and networking events organized by the Graduate School's SUROP program, and several field trips to Konza Prairie Biological Station, Integrated Genomics Facility, and the KU Natural History Museum. REU participants presented their research mid-program at the EGI Research Forum and at a symposium at the end of the program.



URM Student Research Updates

Anastasia Weston

Genome size varies greatly across flowering plants (angiosperms), ranging approximately 2,400-fold. The objective of the current work is to generate a database of genome size estimates for all species of the wild sunflower genus *Helianthus*. This ongoing research will contribute to available resources and provide a framework for future studies investigating mechanisms of genome size evolution in this group of plants.

Matthew Ramos

I am researching the presence of yellow dwarf viruses in the Manhattan area. Yellow dwarf viruses (YDV) are a group of viruses in the family *Luteoviridae* that infect grasses in the family *Poaceae*, which includes crops such as wheat and corn, in which the viruses are known to reduce yield. The viruses are transmitted by aphids, a small insect that functions as the vector for them. Without the aphids/vectors, the viruses cannot get into their plant hosts. I am gathering data regarding which aphid vector species (of which there are several) are present, which are most common, and their plant preference. I also perform ELISA and PCR in aphid and plant tissue to find out which YDV viruses might be present.

Jasmine Sharp

Recent discovery reveals that *C.elegans* are known to inhabit rotting vegetal substrates. This information has lead us to locate and identify *C.elegans* relatives locally. We aim to broaden our understanding of the biogeography and diversity of the genus.

Vaithish Velazhahan

Over 450 million years ago, land plants evolved from a group of green algae called Charophycean Green Algae. This transition from aquatic to terrestrial environments was aided by two groups of transcription factors, namely, class III and class IV homeodomain leucine zipper (HD-Zip) transcription factors that are highly conserved in all land plants. Our research is aimed at investigating the roles of these HD-Zip transcription factors and is expected to provide valuable insight into the genetic mechanisms underlying the evolution of land plants.

Mercedes Santiago

My research focuses on *Phlox pungens* a rare species endemic to Wyoming which exhibits morphological variation across its range. I am using microsatellites to look at the genetic diversity of sampled populations of the species, as well as samples of closely related species.

Halle Sparks

I am working in Dr. Brad Olson's lab studying multicellular evolution using Volvocine Algae. Many of the species we study are microscopic and range from unicellular to multicellular. I am particularly interested in looking at the genetic influences on cell adhesion in Volvocine algae, because cell adhesion is an important characteristic for multicellular organisms.

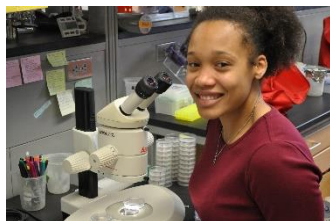
Congratulations, Garrett Hopper

Garrett Hopper successfully defended his Master's thesis investigating how darter morphology and trophic ecology vary along environmental gradients. Garrett's advisor was Dr. Michi Tobler.

Garrett is continuing his graduate career at KSU and will work towards his Ph.D. in Keith Gido's lab.



Congratulations, Dr. White



Corin White successfully defended her dissertation, entitled "Interaction between *Caenorhabditis elegans* and the Bacterial Pathogen *Stenotrophomonas maltophilia*." Corin's advisor is Dr. Michael Herman.

Corin has been accepted into the STRIDE (Scholars for Teaching, Research, Institutional Diversity and Excellence) program at the University of California, San Francisco. Her tentative start date is January 2016.

2 EGI undergraduates recognized for outstanding achievements

Two EGI undergraduates, Ella Popova and Mercedes Santiago recently were recognized as two of biology's most promising students. The Most Promising Student Award is intended to encourage students who are early in their careers and have demonstrated enthusiasm, creativity, and imagination in biologically-oriented courses and projects. Students are nominated by the faculty and award recipients are chosen by a committee within the Division of Biology. Selection is based on faculty letters of recommendation, quality and quantity of classroom work and extracurricular accomplishments, and an interview with the selection committee.

Both students presented their research at last year's symposium in Kansas City. Ella is a student in Dr. Herman's lab. Mercedes is a student in Dr. Ferguson's lab.

Lei and Culumber earn postdoctoral awards



Two EGI postdocs, Li Lei and Zach Culumber, recently earned K-INBRE mentored postdoctoral awards. Li Lei's project is titled, "Polyadenylation Site Usage Variation and Its Genetic Basis in *Arabidopsis*." Li is a postdoc in the lab of Chris Toomajian.

Zach will be investigating molecular pathways mediating responses to toxic hydrogen sulfide exposure. He is a postdoc in the lab of Michi Tobler.

Congratulations to both!!



New Faces

Samantha Sharpe



Originally from the San Francisco Bay Area, Samantha Sharpe majored in Biology at Carleton College, where she also swam, played water polo, and made friends with the plants in the Arboretum. Samantha has previously studied the effects of abiotic stress on *Arabidopsis* root growth and development. She is interested in plant conversation and using interdisciplinary approaches to answer ecological questions. Samantha is a new graduate student in the lab of Dr. Loretta Johnson.

Christine Carson



CC Carson was raised in Columbia, Missouri and received her bachelor's degree from University of Missouri in soil science in the spring of 2015. During her term as an undergraduate, she became fascinated with soil microbes and their functions in grasslands. While her undergraduate research mainly focused on characterizing soil fungal communities in Central Missouri restored grasslands, Carson is interested in broadening her horizons as a soil ecologist. She is now beginning her MS work in biology with Lydia Zeglin at Kansas State University where she is excited to have the opportunity to examine the functions and community structure of bacteria that effect nitrogen availability at Konza Prairie Biological Station.

Fan Qiu



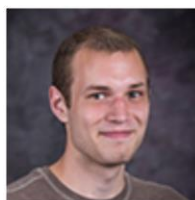
Fan got his PhD in Biology at the University of Florida in Spring 2015. His PhD work focused on population genetics, phylogenetics, and molecular evolution. He is now a postdoc in the lab of Dr. Mark Ungerer. His current research uses the transcriptomic approach to better understand the evolution of drought tolerance in wild grass species.

Nathan Morse



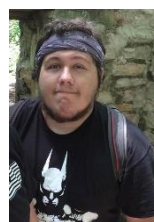
Nathan received his Bachelor of Science in biology from Northeastern State University with an emphasis in fisheries and wildlife management. His current research focuses on speciation processes and intercontinental exchange in a community of shrews and their parasites in Beringia. His other research interests are the evolutionary dynamics of facultative asexual reproduction in vertebrates, the maintenance of sex and, and freshwater and marine ecology. He is a graduate student in the lab of Dr. Andrew Hope.

Stephen Walterhouse



Stephen is a first year PhD student in the lab of Dr. Brad Olson, interested in the origin of life and evolutionary transitions (ex. evolution of multicellularity and development of chloroplast). He received his B.S. in biology at the University of South Carolina, where he also conducted research on eye size sexual dimorphism and interspecies variation in *Daphnia*, as well as opsin expression in *Daphnia*.

Nick Barts



Nick Barts received his bachelor's degree in Integrative Biology in 2015 from the University of Illinois at Urbana-Campaign. He is interested in understanding how ecological and evolutionary processes drive physiological and biochemical adaptations in vertebrates, particularly those adapted to "extreme" environments, and will begin working in the lab of Dr. Michi Tobler.

More than two decades of undergraduate research in ecology and evolutionary biology continues with NSF grant renewal

by Communications and Marketing

One of the longest running national undergraduate research programs at Kansas State University is receiving funding for three more years. Bruce Snyder, instructor of biology, and Ted Morgan, associate professor of biology, received more than \$312,000 from the National Science Foundation for K-State's Biology Research Experience for Undergraduates, or REU, program. The program supports independent summer undergraduate research at K-State.

With this renewal, nine undergraduate students from around the U.S. will be supported to train and conduct summer research at K-state annually for the next three years.

"Through our REU program, students are learning from and training alongside K-State experts in the fields of ecology and evolutionary biology, and climate

change," said Snyder, who coordinates K-State's REU program. "They discover what it is like to do independent research and decide if research is something they want to continue beyond their bachelor's degree." K-State's Biology REU program is one of the longest running REU-Site Programs in the nation, and has been continuously funded for 21 years. The current award is the eighth renewal and will fund the program into its 23rd year.

During the prior 21 years, more than 200 undergraduates have participated in the program and these independent research projects have produced data that have contributed to more than 80 publications in peer-reviewed scientific journals.

"Our REU program has been highly successful in terms of the quality of students we attract and produce,"

Morgan said. "Nearly all of the REU students go on to earn graduate degrees, several return to K-State for graduate school, and some are now in tenure track positions at universities. The program has a two decade legacy of excellence in undergraduate research training at K-State, and many of our former participants have become emerging leaders in our field."

The K-State Biology REU program is supported by the National Science Foundation, the Division of Biology, the Konza Prairie Biological Station and the Ecological Genomics Institute. In addition to the Biology REU program, there are five other REU-Site programs currently funding independent summer undergraduate research at K-State.

Discover EGI on social media

The Ecological Genomics Institute's social media presence recently grew with the creation of both Facebook and Twitter accounts. Like us on Facebook and follow us on Twitter to find out the latest EGI news and events.



facebook.com/kstateecogen

[@ecogenksu](https://twitter.com/ecogenksu)



Research shows that genomics can match plant variety to climate stress

by Greg Tammen

A new study led by a Kansas State University geneticist has shown that genomic signatures of adaptation in crop plants can help predict how crop varieties respond to stress from their environments.

It is the first study to document that these genomic signatures of adaptation can help identify plants that will do well under certain stresses, such drought or toxic soils, said Geoff Morris, assistant professor of agronomy at Kansas State University and a researcher affiliated with the university's Feed the Future Innovation Lab for Collaborative Research on Sorghum and Millet.

Researchers conducted the study with sorghum, one of the oldest and most widely grown cereal grain crops in the world. Sorghum is grown in Africa and Asia as well as in some of the world's harshest crop-growing regions. More than 43,000 sorghum varieties around the world have been collected and stored in crop gene banks, which are centers that serve as repositories for crop diversity.

"While sorghum is grown in some of the toughest climates in the world, we need to continue to increase the amount of grain it produces and its resilience to harsh environments because nearly half a billion people depend on sorghum as a staple food source," Morris said. "We want this important crop plant to produce more food and have less loss."

Sampling from the crop gene banks, Morris and colleagues at Cornell University and the International Crops Research Institute for Semi-Arid Tropics, or ICRISAT, took "snapshots" of genetic information in the genomes of about 2,000 sorghum varieties. Because each sorghum variety was from a particular known location in an African or Indian village, the researchers were able to tie the genetic differences of each variety to its survival in a particular environment.

With this data, Morris and colleague Jesse Lasky from Columbia University's Earth Institute were able to map each plant variety's "genomic signature" of environmental adaptation. This signature reflects how different plant varieties from around the world have adapted to stressors in their environment, such as drought and toxic metals in the soil.

The team then applied a drought stress to plants in the field to test whether genomic analysis could help predict what varieties would continue to thrive under drought. The team tested drought response in hundreds of different sorghum varieties at ICRISAT in India and at the University of Texas at Austin. Data showed that the genomic signatures identified what varieties were likely to do well under stress.



Researchers cataloged the findings in a database that aims to help sorghum breeders with limited resources in developing countries have better predictions of what sorghum varieties will thrive in the environment and in a growing season's forecasted weather.

"Genomic analysis will never replace testing in the field, but it can help us identify useful varieties and genes for increasing stress tolerance," Morris said. "We hope that this approach will help us develop new climate-smart varieties for farmers in the world's toughest crop-growing regions."

The study, "Genome-environment associations in sorghum landraces predict adaptive traits," is freely available through *Science Advances*, the American Association for the Advancement of Science's new open-access journal.

The study is part of a project funded by the National Science Foundation and the Bill and Melinda Gates Foundation to build new technologies for crop improvement in developing nations.

Evolution study finds recent agricultural pest stems from one fly generation's big genetic shift

by Greg Tammen

A new study involving a Kansas State University entomologist reveals that the genes of a fruit fly that has plagued American apple producers for more than 150 years is the result of an extremely rapid evolutionary change.

Greg Ragland, assistant professor of entomology, is co-lead author on a study involving biologists at Rice University, the University of Notre Dame and several other universities. The study looked at the processes that cause a new species to emerge, which may threaten existing, economically important crops. Scientists think that strong environmental changes, such as a drastic change in seasonal weather, can rapidly "push" different sections of an organism's genome — its genetic blueprint — into changing.

For the study, researchers focused on the U.S. fruit fly species *Rhagoletis pomonella*, or the apple maggot fly. Traditionally, the fly lays its eggs in the fruit of the Hawthorn tree, which is native to North America but not considered economically important because of the fruit's overripe taste. In the 1850s, a small group of these flies began laying their eggs in apples.

"At some point the flies jumped to apples, with the adult flies evolving the ability to lay eggs in the fruit and the maggots the ability to consume the fruit," Ragland said. "To do that, regions of the genome had to change from one generation to the next. The result of these flies infesting apples is now a huge issue for the apple production industry because it has introduced a new agricultural pest through an evolutionary event."

Apples mature earlier in the year than Hawthorn fruit. Because of this different maturation window, the group of flies had to begin their lifecycles earlier to match the growth cycle of apples, their new host fruit.

According to Ragland, these seasonal differences essentially equate to two different groups, or taxa, of the fly — one synchronized with Hawthorn fruit similar to its ancestors and one synchronized with apples. As the behavioral and physical differences in the two flies continue to build each generation, scientists think they may be seeing the formation of a new species.

Work starting as far back as the late 1800s began to reveal these observable differences. This new study builds on that work by showing that environmental differences can



change many regions of the genome on time scales even shorter than 150 years.

Researchers discovered this process of rapid adaptation through experiments that looked at the evolutionary differences in the genomes of both flies. They collected flies that laid eggs in Hawthorn fruit and raised one group under seasonal conditions typical of either native Hawthorn fruit or apple-infesting populations. Researchers found that they could replicate the shift from Hawthorn fruit to apples first seen in the 1850s even though all of the flies in the experiment initially laid their eggs in Hawthorn fruit.

"The rapid pace of evolution required to produce the apple-infesting group was initially a surprising result," said Scott Egan, assistant professor at Rice University and co-lead author. "Our results are even more surprising, though, showing that just a few generations of natural selection may have generated apple fly populations that physically and genetically resemble the ones that we see today."

Initially, the team sequenced the genomes of both Hawthorn and apple flies. Following the

experiment, they sequenced the flies reared under the short-term Hawthorn-like and apple-like conditions. They found pronounced differences between the short-term rearing conditions across the entire genome. When they compared these results, they found that the genetic changes from the short-term experiment lined up almost completely with the genetic changes between the Hawthorn and apple groups.

"This suggests that many regions of the genome may evolve in as little as a few generations," said Jeff Feder, professor at the University of Notre Dame and co-author. "The genome-wide changes we observe are very likely the result of environmental differences that are driving the formation of new species."

In addition to observing the evolutionary "jump" between host fruits by the two flies, the study sheds new light on how seasonality affects evolution. Better understanding these evolutionary shifts may help scientists better predict when these shifts could happen and what new agricultural pests may result.

"One of the big takeaways is that species are not static; they are fluid to the environment they live in," Ragland said. "From an evolutionary perspective, environmental change can lead to very pronounced genomic differences over very short time scales. They can potentially change all kinds of traits."

The study, "Experimental evidence of genome-wide impact of ecological selection during early stages of speciation-with-gene-flow," will appear in an upcoming issue of the scientific journal *Ecology Letters*.

The National Science Foundation, the U.S. Department of Agriculture and the Environmental Change Initiative at Notre Dame funded the study.

Recent Publications

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Oliver, A.K., Brown, S.P., Callaham, M.A., **Jumpponen, A.** 2015. Polymerase matters: non-proofreading enzymes inflate community richness estimates by up to 15%. *Fungal Ecology* **15**: 86-89. DOI: 10.1016/j.funeco.2015.03.003.

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Mendola, M., Baer, S.G., **Johnson, L.C.**, Maricle, B.R. Ecotypic variation in functional traits of a dominant grassland species: Implication for plant and ecosystem response to climate change. *Ecology*. **96**(9):2433-2445.

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Johnson, L., J. T. Olsen, H. Tetreault, R. K. Goad, M. M. Mendola, A. DeLaCruz, H. Bryant, **T. Morgan**, M. Knapp, **N. M. Bello**, S. Baer and B. Maricle. Intraspecific variation of a dominant grass and local adaptation in reciprocal garden communities along a US Great Plains' precipitation gradient: Implications for grassland restoration with climate change. *Evolutionary Applications*. Doi:10.1111/eva. 12281.