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The word “evolution” traditionally evokes the study of fossils and the work of Charles Darwin, but evolution isn’t just yesterday’s news. It is an ongoing process that happens every day all around us. Now a new center, headquartered at [Michigan State University](http://msu.edu/) (MSU), studies evolution as it occurs in both natural and virtual settings.

BEACON — short for [Bio/computational Evolution in Action CONSortium](http://beacon-center.org/) — is a highly coveted science and technology center funded by the [National Science Foundation](http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503495) (NSF). [Erik Goodman](http://www.egr.msu.edu/people/profile/goodman), the director of BEACON, emphasizes the center’s multidisciplinary focus because it unites scientists who routinely study natural evolutionary processes — such as biologists, geneticists, ecologists and zoologists — with those who typically do not — such as computer scientists, engineers, horticulturists, philosophers and psychologists.

Projects range from gene interactions and the evolution of genomes to understanding how new species arise, and from evolving smarter electronic and robotic systems to studying the evolution of behavior and intelligence.

“In addition to making discoveries in basic science and finding real-world applications, BEACON is preparing a new generation of researchers,” said Goodman, an electrical engineering professor and one of the principal investigators instrumental in bringing BEACON to MSU. “They will have the insight that comes from firsthand experimentation with evolution in the lab and in the computer.”

[MSU AgBioResearch](#) evolutionary biologist [Richard Lenski](http://www.mmg.msu.edu/lenski.html), also one of the founding principal investigators, said the BEACON advancements are “tremendously exciting” and unique.

“They bring together students and faculty members with very diverse skills but a shared interest in understanding evolution and harnessing its power,” said the Hannah distinguished

professor of microbial ecology. “In one sense, we’re building on the agricultural practice of selective breeding but applying it in new ways and with new systems.”

Lenski is well-known within the evolutionary community for his longrunning experiment with *Escherichia coli* (*E. coli*), which spans more than 25 years and has produced in excess of 50,000 generations.

“To study evolution as it happens requires either a time machine, which we do not have, or organisms that replicate, mutate and evolve very fast, such as *E. coli*, so we can detect changes on a reasonable time scale,” explained Lenski, who has also worked with digital organisms in the Avida system, a scientific software platform that allows users to experiment with populations of actively evolving computer programs.

In addition to developing robust computing systems, the principles revealed can be used to gain insights into biological organisms and help solve industrial design problems as well.

The following projects, each involving MSU AgBioResearch scientists, provide a glimpse of the diversity of research generated through BEACON.

Optimizing choices through modeling

MSU AgBioResearch horticulturist [Erik Runkle](http://www.hrt.msu.edu/erik-runkle/) is utilizing his experience in applied greenhouse management on a collaborative project. In 2012, he participated in a conference on greenhouse models in Nanjing, China. Goodman also happened to be in attendance, but the two had never met. They bumped into each other, began discussing their work and realized a common thread: Goodman was also working on a greenhouse project, this one in collaboration with Chenwen Zhu, a professor at Tongji University in Shanghai, China. After returning to the States, Goodman asked Runkle to become part of BEACON and to collaborate on the project he had under way.

“It’s strange that it took a meeting in China to find someone in my own backyard working on a greenhouse project,” said Runkle, who is also an [MSU Extension](http://msue.anr.msu.edu/) specialist and associate professor in the Department of Horticulture.

The experiment involved testing and validating an evolutionary multi-objective optimization (EMOO) model in a greenhouse built in Shanghai. The model was developed to show how environmental inputs influence tomato yield and the amount of energy required to create that environment.

“I have done simplistic modeling on a wide range of flowering crops,” Runkle explained. “In

contrast, this is a complex, multi-objective model because it involves all the factors that influence fruit development of tomatoes and attempts to optimize yields and minimize energy inputs.” The approach uses computer algorithms based on evolutionary principles to hone in on desirable trade-offs. Solutions evolve to find the best answer, although sometimes there is more than one.

“Instead of picking one solution, you can look at predicted yields and know what the trade-offs are in energy consumption,” Runkle said. “It’s been intellectually stimulating. The group wanted someone who had real-world experiences with growing plants in greenhouses, and I wouldn’t have that without the MSU Extension component of my work.”

Ability to analyze massive data sets yields results in microbial evolution

Studying the genetics of food-borne bacteria and how they work is a primary research area of MSU AgBioResearch microbiologist and veterinarian [Linda Mansfield](http://www.mmg.msu.edu/mansfield.html) (<http://www.mmg.msu.edu/mansfield.html>). For one specific project, however, she realized she needed additional expertise. Mansfield turned to BEACON for guidance.

“There are researchers affiliated with BEACON who understand how to do massive computations and analyze large data sets for evolutionary projects,” said Mansfield, a professor in the MSU College of Veterinary Medicine with a joint appointment in the Department of Microbiology and Molecular Genetics. She is also one of the principal investigators for the MSU Enteric Research Investigational Network (ERIN).

She teamed up with [C. Titus Brown](http://www.egr.msu.edu/people/profile/ctb) (<http://www.egr.msu.edu/people/profile/ctb>), an assistant professor in the Department of Computer Science and Engineering, and **Jeffrey E. Barrick**, then an MSU postdoctoral researcher working with Lenski and now an assistant professor at the University of Texas, Austin. Brown has extensive knowledge in developing data analysis tools, and Barrick is an expert on the evolution of bacterial genomes. The three researchers, along with other collaborators, completed a BEACON project on the adaptation and evolution of *Campylobacter jejuni* in real time.

“*Campylobacter jejuni* is one of the most prevalent bacteria that cause gastrointestinal disease in the United States. It colonizes and may cause disease in a variety of animals, including birds, dogs, ferrets, mice and humans, but how this pathogen is able to infect such a diversity of hosts is not well understood,” explained Mansfield, who developed a mouse model to study the genetics of *Campylobacter jejuni* prior to the BEACON project.

Mansfield noticed that one of the strains of *Campylobacter jejuni* would adapt in mice and cause

more severe disease, so she wondered if the bacteria were actually evolving in real time in the host. The researchers conducted genome sequences of the original and evolved strains of the bacteria using Illumina, an automated sequencing method.

“Illumina sequencing is wonderful because it gives tremendous coverage of the entire genome. We got an accurate genome sequence that told us that the bug is evolving in the host in real time. It exists as a ‘quasi-species’ with many forms, unlike *E. coli*, which tends to have clones,” Mansfield said. She also believes that it’s highly likely that this bacterium is also evolving in humans and may account for some chronic diseases currently of unknown origin, such as Guillain-Barré syndrome, an autoimmune disease affecting the peripheral nervous system.

“The results of the study tell us that it will be difficult to develop a vaccine to protect against a bug like *Campylobacter jejuni*, so traditional vaccine strategies are probably not useful,” she explained. “This could explain why so many vaccines that have been tried against this bacterium in humans and animals have never worked.”

Mansfield credits BEACON’s impressive computational capabilities and the high-performance computers of iCER (MSU’s Institute for Cyber-Enabled Research) for analyzing the huge amounts of data necessary for projects like hers.

“By being able to access computers with large storage capacities and researchers with the skills to analyze and manage the data, we are starting to understand the types of neurological diseases that are produced by this bacterium,” she said. “Our long-term goal is to develop new interventions and treatments for food and waterborne pathogens.”

Using philosophy to help multidisciplinary teams communicate

MSU AgBioResearch philosopher [Michael O’Rourke](#) ([/news/researcher_profile_helping_research_collaborators_communicate_more_effectiv](#)) is conducting research through BEACON on how scientists can better communicate and collaborate in multidisciplinary teams.

“I use philosophical concepts and methods to structure dialog among collaborators that allows them to learn about one another’s research,” said O’Rourke, a professor in the Department of Philosophy. “The goal is to enhance their understanding about how others operate as research scientists and then enhance their communicative capacity so they can interact more efficiently and effectively with one another.”

He became involved with BEACON while working at the University of Idaho on the Toolbox Project, a seven-year project funded in part by NSF that revolves around structured sets of philosophical prompts to facilitate communication. The work caught the attention of **James Foster**, a professor at the University of Idaho and a leader of BEACON's efforts there. O'Rourke's communication work was part of the proposal that eventually received NSF approval.

"Toolbox workshops enable crossdisciplinary collaborators to engage in a structured dialogue about their research assumptions," O'Rourke said. "This yields both self-awareness and mutual understanding, supplying the collaborators with a robust foundation for effective collaborative research."

Since coming to MSU in 2012, O'Rourke has worked with **[Robert Pennock](http://lymanbriggs.msu.edu/faculty/bios/user.cfm?UserID=27)** (<http://lymanbriggs.msu.edu/faculty/bios/user.cfm?UserID=27>), a professor in the MSU Lyman Briggs College, to develop a curriculum on the responsible conduct of research (RCR) specifically for BEACON. NSF requires RCR training for all BEACON student participants. In addition, one of BEACON's goals is to practice and promote ethical and responsible research by implementing cross-disciplinary and multi-institutional ethics programs that inform and guide all BEACON participants. Some of the concepts for the curriculum were presented in July during the 2013 Beacon Congress.

"Collaborative science is an increasingly important part of finding solutions to complex problems," O'Rourke said. "This is a new approach to RCR training based on intrinsic scientific virtues such as curiosity, objectivity, skepticism and integrity, as an alternative to the traditional legalistic approach based on conveying a list of dos and don'ts for people to follow."

Looking to nature for examples of cloning

MSU AgBioResearch horticulturist **[Ning Jiang](http://www.hrt.msu.edu/ning-jiang)** (<http://www.hrt.msu.edu/ning-jiang>) is a natural fit with BEACON because her work focuses on plant evolutionary mechanisms. She studies transposable elements (TEs), also called jumping genes, proving that genes and genomes frequently modify themselves.

"A genome sequence is in a certain order. Normal genes do not move. They stay in the same place in the genome. If the order of the genetic material changes, a gene's function can change," said Jiang, an associate professor in the Department of Horticulture. "Transposable elements are special genes because they jump around in the genome. During this process, the copy numbers increase, potentially disrupting or changing normal gene function."

Jiang studies a specific class of transposable elements called MULEs, short for mutator-like

elements. MULEs carrying fragments of genes are called Pack-MULEs and have the potential to create new genes in a genome and affect plant evolution.

“This is so important to evolution because this type of element is changing the gene structure in a genome-wide way,” she said. “You cannot do this by transformation, the genetic alteration or addition of a single gene. It is a systemic change of the gene structure.”

Jiang became interested in Pack-MULEs when she was a postdoc at the University of Georgia. It was after MSU AgBioResearch molecular geneticist [Michael Thomashow](http://www.prl.msu.edu/faculty/thomashow_michael) discovered that increasing a plant’s expression of certain regulatory genes helps it withstand freezing temperatures, drought and high salt concentration.

“I wondered why a supposedly insignificant transposable element carried such an important gene,” Jiang explained. That led to a research project that showed that there are at least 3,000 Pack-MULEs in the rice genome. “Pack-MULEs are important for evolution because they recycle gene fragments.”

Jiang considers Pack-MULEs examples of the cloning work that has always existed in nature.

“Pack-MULEs grab one fragment from this gene, another from another gene. They fuse together to make a new open reading frame,” Jiang said. “People say genetic modification is not natural, but nature does these things all the time. If you don’t have a mechanism for variations, the organism will not evolve. We would not be who we are today without evolution and genes modifying themselves, as well as other genes.”

To read more about BEACON visit: beacon-center.org (<http://beacon-center.org/>)