DONALD DANFORTH
PLANT SCIENCE CENTER

Researchers look to Relatives for Clues in Quest to Develop Sources of Bioenergy

ST. LOUIS, MO, May 14, 2012—Arranging DNA fragments into a genome sequence that scientists can interpret is a challenge often compared to assembling a puzzle except you don't have the box and have no idea what the picture is supposed to be. Sometimes clues from other publicly-available DNA sequences of related organisms can be used to guide the assembly process, but its usefulness depends on how closely related any two sequences are to one another. For example, a reference genome might be so distantly related from the one being assembled, it would be akin to comparing a Model-T to a contemporary hybrid car.

For researchers interested in switchgrass, a perennial grass that the U.S. Department of Energy (DOE) is investigating as a prospective biofuels feedstock, assembling the plant genome poses an even more complicated puzzle than usual because it has multiple copies of its chromosomes. The genome of a close switchgrass relative, foxtail millet (*Setaria italica*), is described in the May 13, 2012 edition of *Nature Biotechnology* "Reference genome sequence of the model plant Setaria".

For Dr. Tom Brutnell, a co-author on the study and director of the Enterprise Institute for Renewable Fuels at the Donald Danforth Plant Center, the *Setaria* genome is the starting point for his own research interests. "Now that we have the genome sequence, we can kick start the development of genetic tools for Setaria." His proposal under the DOE JGI's 2012 Community Sequencing Program builds off the availability of two *Setaria* genomes, that of foxtail millet and its wild ancestor green foxtail (*S. viridis*), which is also described in the paper. "What we really want is an *Arabidopsis* for the Panicoid grasses," he said, referring to the ubiquitous model plant used by many researchers. "Green foxtail is smaller than foxtail millet—we can get it to flower when it's just six inches tall and you go from seed to seed in six to eight weeks. In contrast, foxtail millet is a proper crop so it's taller, has a longer generation time of four months and no one has really developed efficient transformation methods for it. Our project with the DOE JGI allows us to tap the *Setaria* genomes to fast track *S. viridis* as a model genetic system."

One of the challenges in studying grasses for bioenergy applications is that they typically have long lifecycles and complex genomes. Jeremy Schmutz, head of the DOE JGI Plant Program at the HudsonAlpha Institute of Biotechnology, pointed out that foxtail millet (*Setaria italica*) has several advantages as a model. It's a compact genome and large quantities of it can be grown in small spaces in just a few months.

"We're not thinking of *Setaria* as a biofuel crop per se but as a very informative model since its genome is so structurally close to switchgrass," said Jeff Bennetzen, a BESC researcher, the study's co-first author and a professor at the University of Georgia. He originally proposed that the DOE JGI sequence the foxtail millet genome under the 2008 Community Sequencing Program. Schmutz said that roughly 80 percent of the foxtail millet genome has been assembled using the tried-and-true Sanger sequencing platform, along with more than 95 percent of the gene space—the functional regions of the genome. "The *Setaria* genome is a high quality reference genome," he said. "If you want to conduct functional studies that require knowing all the genes and how they are localized relative to one another, then use this genome."

One such area of study is adaptation. Since it is found all over the world, *Setaria* is considered a good model for learning how grasses can adapt and thrive under various environmental conditions. Additionally it appears to have independently evolved a pathway for photosynthesis that is separate from that used by maize and sorghum. "With the sequencing of the *Setaria* genome," the team noted in their paper, "evolutionary geneticists now have an annual, temperate, C4, drought- and cold-tolerant grass that they can comprehensively compare to other plants that have or have not yet evolved these adaptions." C4 plants are distinguished by their ability to conduct photosynthesis faster than C3 plants under high light intensity and high temperatures.

The DOE JGI Plant Program focuses on genomes that have been selected for their relevance to DOE missions in energy and environment, and leads the world in sequencing plants in this area. Aside from foxtail millet and switchgrass, other DOE Plant Flagship genomes sequenced include, among others, poplar and soybean. Several of these Flagship genomes are also part of the Gene Atlas project, currently in its pilot phase. Designed to be a reference by which researchers can look up the gene information gathered under several standard experimental conditions, the Gene Atlas is projected to offer researchers a method of interpreting their data by comparing them against “normal” results for these plants. New public releases of these Flagship genomes and of other plant projects occur periodically, and the sequence and analysis is made public at www.phytozome.net.

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Founded in 1998, the Donald Danforth Plant Science Center is a not-for-profit research institute with a mission to improve the human condition through plant science. Research at the Danforth Center will feed the hungry and improve human health, preserve and renew the environment, and enhance the St. Louis region and Missouri as a world center for plant science. The Center’s work is funded through competitive grants and contract revenue from many sources, including the National Institutes of Health, U.S. Department of Energy, National Science Foundation, U.S. Department of Agriculture, U.S. Agency for International Development, the Bill & Melinda Gates Foundation and Howard G. Buffett Foundation.

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