

Researchers complete draft genome sequence for cassava

November 9 2009

A team of academic, government and industry researchers has completed a first draft of the cassava (*Manihot esculenta*) genome. The project is an important first step in accelerating the pace of research on this subsistence crop and addressing some of the many limitations that face cassava farmers around the world.

Cassava is a root crop that serves as the primary food source for more than 750 million people each day. Although it has many properties that make it an important food across much of [Africa](#) and Asia, it also has many limitations. Cassava has poor nutritional content and is susceptible to many pathogens, particularly in Africa, where one third of the continental harvest is lost each year to viral diseases. One of these, Cassava Brown Streak Disease, or CBSD, is currently the major threat to food security in some parts of Eastern Africa.

In response to the urgency of this threat, and building upon the newly available cassava [genome](#) sequence, the Bill & Melinda Gates Foundation has awarded a \$1.3 million grant to University of Arizona researchers who will lead an international consortium to develop a genome variation database that will provide breeding tools to aid [farmers](#) in improving cassava, with a special focus on increased resistance to the CBSD virus.

Steve Rounsley, associate professor in the School of Plant Sciences at the UA and a member of the BIO5 Institute, will coordinate the project that includes partners at the Institute for Genome Sciences, University of

Maryland, Baltimore, the U.S. Department of Energy Joint Genome Institute (DOE JGI), and 454 Life Sciences, a Roche Company.

The impetus for the genome sequence began in 2003 with the formation of The Global Cassava Partnership (GCP-21), co-chaired by Dr. Claude Fauquet, director of the International Laboratory for Tropical Agriculture Biology (ILTAB) at the Donald Danforth Plant Science Center (DDPSC) in St. Louis, and Dr. Joe Tohme of the International Center for Tropical Agriculture (CIAT) in Cali, Colombia. This, in turn, led to a 2006 proposal by Fauquet, Tohme and 12 other international scientists to DOE JGI's Community Sequencing Program, which was selected for a pilot project.

The full genome project gathered momentum in early 2009 when 454 Life Sciences and DOE JGI each pledged the resources to use 454's Genome Sequencer FLX platform with long-read GS FLX Titanium chemistry to rapidly generate the DNA sequence data needed for the project. "This is a perfect example of how quickly things can happen when everyone is aligned behind an important cause. Most of the data for the genome were generated within 8 weeks of getting DOE JGI and 454 Life Sciences on board," said the UA's Rounsley, who led the collaboration.

More than 61 million sequencing reads were generated and assembled into a draft genome that contains an estimated 95 percent of cassava genes. It is one of the first large genome projects to primarily use 454 Life Sciences' long-read sequencing platform, which enabled both improved quality of the draft, and its rapid generation.

"We are pleased to contribute our sequencing technology to this important global initiative," explained Michael Egholm, Chief Technology Officer and Vice President of Research and Development at 454 Life Sciences. "This project, along with other recently completed

complex plant genome projects, demonstrates that 454 Sequencing systems are rapidly becoming the standard for de novo sequencing and assembly."

The availability of the genome sequence enables the newly-funded project to study how cassava varieties differ from each other. "The contributions of 454 Life Sciences and DOE JGI in making the cassava genome a reality have opened a new chapter in cassava research worldwide. We're excited about the opportunity for cassava breeders to access new tools for improving a staple African crop," said Katherine Kahn, program officer with the Agricultural Development initiative at the Bill & Melinda Gates Foundation.

Researchers will use next-generation technologies to sample many varieties of cassava and develop a large database of markers that can be used to identify genes involved in many important traits. The team will collaborate with researchers in Kenya, Uganda and Tanzania in applying these genetic markers toward identifying resistance to Cassava Brown Streak Disease. All of the information and tools the project develops will be freely available worldwide.

Traditional cassava improvement is slow and difficult. The availability of large numbers of markers will help make breeding schemes more efficient. For instance, traits that may only show up in mature plants can be identified in seedlings with a cheap DNA test. Since cassava is used for industrial starch production, and has potential as a biofuel source, there are commercial applications of these breeding tools. However, the most important applications will be those that improve the lives of those who depend upon cassava for their daily calorie intake.

"With the first cassava genome in hand, we can cheaply and quickly sequence other varieties that will give us thousands of little signposts - mile markers if you like - that will help us identify key genes for

increasing the plant's resistance to the virus," Rounsley said.

"By 2050, 90 percent of humankind will live in developing countries where agriculture is the most important economic activity. Crops grown by small farmers are central to international food security, health, economic growth, energy needs, poverty reduction and social stability," Fauquet said. "The information contained in the cassava genome will provide tremendous opportunities to improve this important crop, bringing it into the mainstream of plant research thereby reducing the time and cost of delivering improved cultivars to farmers who need it most."

This grant is part of the foundation's Agricultural Development initiative, which is working with a wide range of partners to provide millions of small farmers in the developing world with tools and opportunities to boost their yields, increase their incomes and build better lives for themselves and their families. The foundation is working to strengthen the entire agricultural value chain - from seeds and soil to farm management and market access—so that progress against hunger and poverty is sustainable over the long term.

The annotated draft genome sequence is available at DOE JGI's Phytozome Web site, www.phytozome.net/cassava .

Source: University of Arizona ([news](#) : [web](#))

Citation: Researchers complete draft genome sequence for cassava (2009, November 9) retrieved 19 April 2024 from <https://phys.org/news/2009-11-genome-sequence-cassava.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is

provided for information purposes only.