

Rice Genome Helps Put Other Cereals "On the Map"

KEITH WELLER (K7577-1)



The genome of rice is being used by ARS scientists to fill in the genetic map of maize and sorghum.

Think of how superior a map showing roads, terrain, rivers, and cities is to one showing just a featureless land mass. That's the thought behind the research of ARS computational biologist Doreen Ware and colleagues working with genome maps of rice, maize, and sorghum.

"Rice is the first crop whose genome has been almost completely sequenced," says Ware, who is with ARS's Ithaca, New York-based U.S. Plant, Soil, and Nutrition Laboratory. "But it'll be at least 3 to 4 years before comparably detailed, sequence-based maps are available for maize and sorghum,

two important cereal crops in the same family as rice. That's because of the cereal genomes' large size and complexity."

And that's why Ware, using genome maps and data already in the public domain, is probing rice's genome sequence to fill in as many details as possible about maize and sorghum. Genomes are complete sets of organisms' genetic material.

"We're enhancing known information so that points of similarity between the genomes of each crop are highlighted," she says. "We're focusing on the genomes' infrastructure."

Ware is based on Long Island, at the Cold Spring Harbor Laboratory, a private, nonprofit institution focusing on cancer, neurobiology, plant genetics, and bioinformatics that allows her access to cutting-edge genomics expertise and equipment.

"Young Investigators" Award Helps

Ware has received a \$1.3-million "Young Investigators" award from the National Science Foundation for this study. The foundation is an independent federal agency supporting fundamental research and education across all fields of science and engineering. Ware's grant runs through 2008.

"This work will add to our understanding of genome organization and the evolutionary relationship between three agronomically important crops," says Ware. "It will also develop methods for building and finishing comparative maps that can both be applied to future genome-scale projects and help identify genes involved in traits important to agriculture."

Ware says the public data she's using "will give information for locating specific genes. I'll be able to explore whether genes are in the same or different locations on the genomes of the three crops. The genes' position may yield clues toward understanding how

crop genomes have evolved."

Understanding evolutionary changes is important, Ware adds, because familiarity with ancestral genomes allows scientists to look at the genetic makeup of current crops and make best guesses as to which genes are likely to perform the same functions.

"Ultimately, this project will help scientists and growers identify genes responsible for traits that will lead to stronger, more nutritious crops," says Ware, who is being assisted by researchers at Texas A&M University, the University of Missouri, and Purdue University.

Ware plans to develop a pilot high school curriculum based on her work.—By **Luis Pons**, ARS.

This research is part of Plant, Microbial, and Insect Genetic Resources, Genomics, and Genetic Improvement, an ARS National Program (#301) described on the World Wide Web at www.nps.ars.usda.gov.

Doreen H. Ware is with the U.S. Plant, Soil, and Nutrition Research Center, Cold Spring Harbor Laboratory, 1 Bungtown Rd., Cold Spring Harbor, NY 11724; phone (516) 367-6979, fax (516) 367-8389, e-mail ware@cshl.edu. ★