

SCIENTISTS AT UA, COLLABORATING INSTITUTIONS DECODE MAIZE GENOME

Research to aid development of higher-yielding disease-resistant and drought-tolerant cultivars

By Lori Stiles, University Communications

Scientists from the University of Arizona led by Arizona Genomics Institute director Rod A. Wing and from collaborating institutions have deciphered the complete genetic code of the maize plant for the first time.

The researchers, who have been collaborating for the past four years on the National Science Foundation-funded Maize Genome Sequencing Project, have provided the complete sequence and structures of maize genes and their locations, in linear order, on both the genetic and physical maps of maize.

The milestone achievement and companion papers, published in the Nov. 2009 issues of *Science*, *PLoS Genetics* and the *Proceedings of the National Academy of Sciences*, provide a “gold standard” reference for scientists working to understand the biology and evolution of maize.

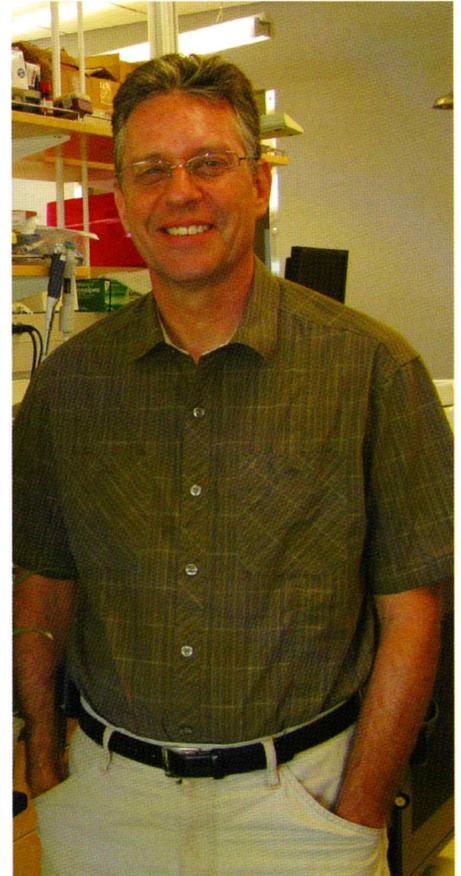
Fusheng Wei and Jianwei Zhang of Wing’s group at the Arizona Genomics Institute, or AGI, in the UA School of Plant Sciences, report their research in the paper, “The Physical and Genetic Framework of the Maize B73 Genome,” in *PLoS Genetics*.

Yeisoo Yu of AGI and Carol Soderlund, director of the Arizona Genomics Computational Laboratory, independently led the UA’s effort to generate a set of full-length cDNAs [complementary DNA], sequences that represent about 27,000 of the maize genome complement. They are co-authors on the Science paper, “The B73 Maize Genome: Complexity, Diversity and Dynamics.”

“The Arizona team’s work will have a great impact on basic research and provide a comprehensive foundation to systematically study maize biology with the goal of breeding higher yielding, disease-resistant and drought-tolerant cultivars,” said Wing.

The team’s pivotal research served as the foundation for other analyses and companion papers presented in the journals, Wing said.

Maize, which was domesticated over the past 10,000 years from a grass called “teosinte” native to Central America, is one of the world’s most important food crops. Last year in the United States alone, 12 billion bushels of maize grown on 86 million acres of land was valued at \$47 billion.



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Arizona Genomics Institute director Rod A. Wing, who led UA’s effort in sequencing the rice genome in 2005, led UA scientists in sequencing the corn (maize) genome.

“Contemporary society is now faced with growing demands for food and fuel in the face of global climate change and the potential for increased disease pressure,” Wei and Zhang wrote in a summary of their paper.

They said they undertook the maize genome sequencing project “to provide a comprehensive foundation to systematically understand maize biology with the goal of breeding higher yielding,

disease-resistant and drought-tolerant cultivars.”

Improved crops are needed because agriculturists are challenged to grow more crops on less land, with less water, and on poorer soil, Wing said.

Maize is a model organism for fundamental plant science, and so important to research that can be used to genetically improve its grass relatives such as sorghum, wheat and rice, the UA scientists said.

Such efforts are urgent: The United Nations predicts that world food output must grow by 70 percent over the next four decades to feed a projected extra 2.3 billion people by 2050.

“If current population projections are correct, we will have to double world food production in the next 30 to 40 years,” said Colin Kaltenbach, vice dean of UA’s College of Agriculture and Life Sciences. “Accomplishments such as this, achieved by Dr. Wing and his colleagues and collaborators, are the only way we will ever achieve this goal.”

Wing’s group led the construction of an integrated genetic and physical map of maize in a previous NSF-funded project that began in 1998. Genetic maps show the location of genes along a single DNA molecule; physical maps also show the order and spacing of the genes. The maps served as the blueprint, or roadmap, to sequence the genome.

Making the maps that were the template used to analyze the maize

genome sequence “was a major contribution by our lab and was extremely time consuming and painstaking because the maize genome is highly repetitive,” Wing said.

The maize genome contains 2.3 billion nucleotide sequences, about 85 percent of which are repetitive. Their function – if the repetitive sequences do have a function – is unknown.

In the Nov. 20 paper, Wei, Zhang and co-authors present a detailed account of how they sequenced the maize genome from a selected set of 17,000 artificially made segments of nucleic acid called “BAC” clones, or “bacterial artificial chromosomes,” a tool that biologists use to find gene sequences that encode proteins of interest.

They led the team in merging all 17,000 individual sequences into 10 sequences that represent the 10 chromosomes of maize.

“We promised to do the job, and we got it done,” Wei said. “This achievement took great team work. We really appreciated the support from the department, from the college and from the university during this project.”

The Arizona team collaborated with scientists from Washington University-St. Louis, Cold Harbor Laboratory and Iowa State University on the project.

The more than 27,000 sequences that Yu, Soderlund and their colleagues independently sequenced “represent the expressed

genes from various tissues and common environmental stress conditions,” Yu said.

“These maize sequences have an immense value for accurate identification of genes by determining the gene structures in maize genome sequences and for understanding their functions.”

Among the 27,000 maize sequences, Yu, Soderlund and their co-workers discovered about 1,600 unique maize genes – genes not found in other plant databases.

These unique maize genes are priority targets for studies that will provide information to better understand the biology and production of maize and cereal crops, Yu said. ☼

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