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Research cracks corn genome code, promising higher yields

By Agri-Pulse Staff

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In a major step toward potentially higher grain yields, greater drought and disease resistance, and more efficient nitrogen use, a research consortium has completed high-quality sequencing of the corn (maize) genome.

Science magazine announced the milestone in a Nov. 20 cover story which details ways in which the achievement could benefit corn, wheat, barley and other grain crops. The successful research consortium was led by the Genome Sequencing Center (GSC) at Washington University in St. Louis, MO and included the University of Arizona, Iowa State University and Cold Spring Harbor Laboratory in New York. This sequencing project was part of a joint Department of Agriculture (USDA)/Department of Energy/National Science Foundation (NSF) effort that was funded by NSF under the auspices of the National Plant Genome Initiative (NPGI).

The NPGI, which began in 1998, is an ongoing effort to understand the structure and function of all plant genes at levels from the molecular and organismal to interactions within ecosystems. The NPGI focuses on plants of economic importance and plant processes of potential economic value.

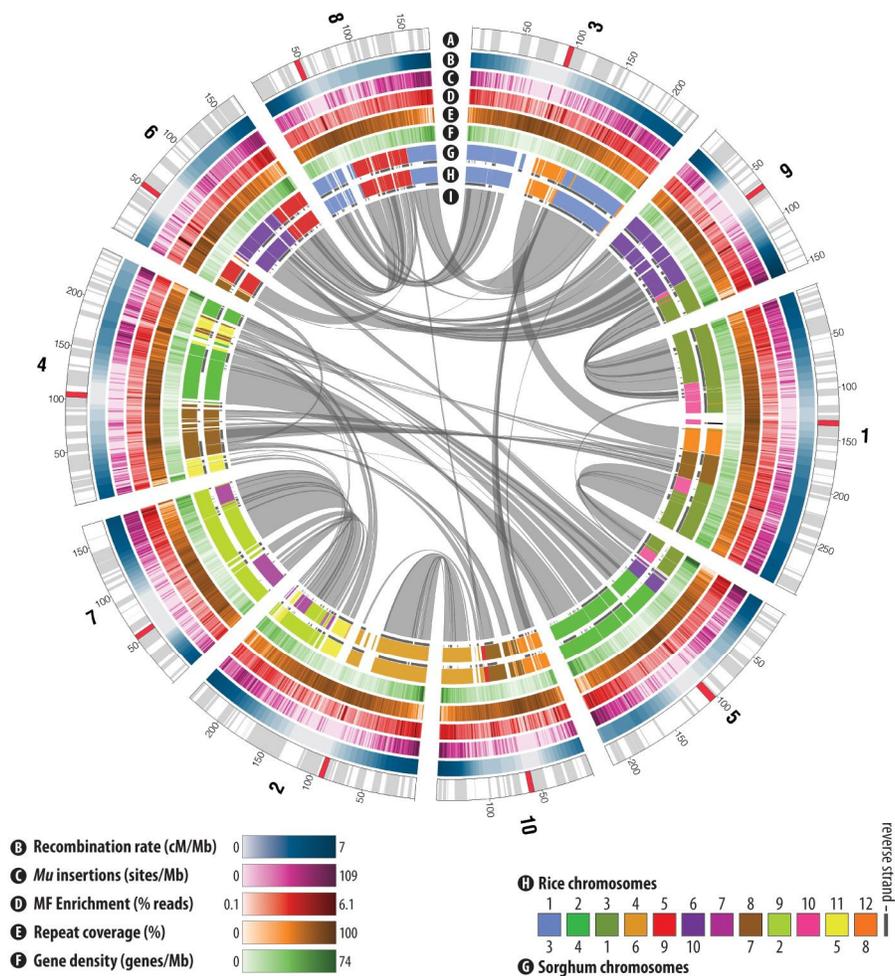
“Production of a high quality maize genome sequence was a high priority for the NPGI from the beginning,” said Jane Silverthorne of NSF. “This accomplishment builds on technological advances and basic research into maize biology that were essential to the design of the most cost-effective strategy to assemble and anchor the genes onto the genetic and physical maps.”

Real-world applications

The same *Science* Nov. 20 issue also announces the results of two other NPGI-funded studies that were enabled by the new maize sequence. One of these studies produced a so-called HapMap of the maize genome, which describes the genetic differences between various strains of maize that are currently bred around the world. This resource will help researchers identify the genes that control various maize traits. The HapMap was produced by a team led by Edward S. Buckler of USDA and Cornell University and Doreen H. Ware of USDA and Cold Spring Harbor Laboratory.

The other NPGI-funded study that also appears in the November 20, 2009 issue of *Science* builds on the new maize genome sequence by identifying a surprisingly widespread biological process that determines the level of expression of certain genes present in hybrid strains of maize. This study was produced by a team led by Patrick S. Schnable of Iowa State University.

“Sequencing the corn genome provides scientists with new information and tools to access the vast array of genes available to improve corn,” said Kay Simmons of USDA’s Agricultural Research Service. “This new sequence information can be exploited to translate basic discoveries to the field for the benefit of corn growers, the corn industry, and consumers.”



New sequence of maize genome. The ten chromosomes of the maize genome are shown here, with concentric circles reflecting various characteristics of the genome. Thin ribbons connect duplicate regions in the maize genome, thereby revealing large related segments and reflecting the maize genome’s complicated structure. Credit: *Image courtesy of Science/AAAS.*

Rick Wilson, lead investigator and director of the GSC, adds: “The new maize sequence will pave the way for the development of maize breeding programs that will improve the quality and quantity of maize crops, and thereby benefit people living throughout the world.”

Science also reports on the sequencing by a Mexican consortium led by Luis Herrera-Estrella of CINVESTAV, Irapuato, Mexico of the popcorn variety Palomero toluqueño,

which is bred in central Mexico. Comparisons between Palomero toluqueño and the NSF-funded genome sequence, which is from a maize strain that is inbred in mid-western regions of the U.S., reveals important clues about how maize has been domesticated over the last 10,000 years and highlights the importance of biodiversity.

Significance of sequence for research

This new maize sequence provides significant refinements over the draft sequence that was announced in February 2008. These refinements include the elimination of redundancy and improvements in the ordering and orientation of chromosomal segments.

Because maize has served as a model plant for basic genetics research for the last 100 years, the completion of its genome sequence has important implications for basic research, as already evidenced by the immediate publication of the two companion papers in *Science*. In addition, the November 20, 2009 issue of *PLoS Genetics* features an editorial on the new maize sequence and ten more companion studies, each of which either provides background information on the development of the maize sequence or uses the new maize sequence to produce additional insights into maize genetics. In addition to advancing research on maize, the maize genome sequence is also expected to advance other cereal genome sequencing projects, such as those for wheat and barley.

A daunting task

The maize sequencing project, which was initiated in 2005, is a notable achievement because it was completed quickly and because the maize genome is among the most challenging genomes sequenced to date. The complexity of the maize genome is partly due to its size: with 2.5 billion base pairs covering ten chromosomes, the maize genome is almost as big as the human genome. “The maize genome is the largest plant genome sequenced to date,” says Wilson.