Scientists unveil draft sequence of corn genome

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A team of scientists led by Washington University in St. Louis has begun to unlock the genetic secrets of corn, a crop vital to U.S. agriculture. The researchers have completed a working draft of the corn genome, an accomplishment that should accelerate efforts to develop better crop varieties to meet society's growing demands for food, livestock feed and fuel.

Corn, also known as maize, underlies myriads of products, from breakfast cereal, meat and milk to toothpaste, shoe polish and ethanol.

The genetic blueprint will be announced on Thursday, Feb. 28, by the project's leader, Richard K. Wilson, Ph.D., director of Washington University's Genome Sequencing Center, at the 50th Annual Maize Genetics Conference in Washington, D.C.

"This first draft of the genome sequence is exciting because it's the first comprehensive glimpse at the blueprint for the corn plant," Wilson says. "Scientists now will be able to accurately and efficiently probe the corn genome to find ways to improve breeding and subsequently increase crop yields and resistance to drought and disease."

The $29.5 million project was initiated in 2005 and is funded by the National Science Foundation (NSF), the U.S. Department of Agriculture and the U.S. Department of Energy. "Corn is one of the most economically important crops for our nation," says NSF director Arden L. Bement Jr. "Completing this draft sequence of the corn genome

constitutes a significant scientific advance and will foster growth of the agricultural community and the economy as a whole."

The team working on the endeavor, including scientists at the University of Arizona in Tucson, Cold Spring Harbor Laboratory in New York and Iowa State University, has already made the sequencing information accessible to scientists worldwide by depositing it in GenBank, an online public DNA database. The genetic data is also available at maizesequence.org.

The draft covers about 95 percent of the corn genome, and scientists will spend the remaining year of the grant refining and finalizing the sequence. "Although it's still missing a few bits, the draft genome sequence is empowering," Wilson explains. "Virtually all the information is there, and while we may make some small modifications to the genetic sequence, we don't expect major changes."

The group sequenced a variety of corn known as B73, developed at Iowa State decades ago. It is noted for its high grain yields and has been used extensively in both commercial corn breeding and in research laboratories.

The genome will be a key tool for researchers working to improve varieties of corn and other cereal crops, including rice, wheat and barley. "There's a lot of great research on the horizon," says plant biologist Ralph S. Quatrano, Ph.D., the Spencer T. Olin Professor and chair of Washington University's Department of Biology. "The genome will help unravel the basic biology of corn. That information can be used to look for genes that make corn more nutritious or more efficient for ethanol production, for example."

Corn is only the second crop after rice to have its genome sequenced, and scientists will now be able to look for genetic similarities and

differences between the crops, Quatrano adds.

"The maize genome sequence will be of great interest to maize geneticists and biologists around the world, but also will be an important resource for plant breeding and biotechnology companies," says project collaborator Rob Martienssen, Ph.D., of Cold Spring Harbor Laboratory. "The maize sequence will be an invaluable reference for research, especially in renewable energy and biofuels, similar in significance to the human genome sequence for biomedical research".

The genetic code of corn consists of 2 billion bases of DNA, the chemical units that are represented by the letters T, C, G and A, making it similar in size to the human genome, which is 2.9 billion letters long. By comparison, the rice genome is far smaller, containing about 430 million bases.

The challenge for Wilson and his colleagues was to string together the order of the letters, an immense and daunting task both because of the corn genome's size and its complex genetic arrangements. About 80 percent of the DNA segments are repeated, and corn also has 50,000 to 60,000 genes, roughly double the number of human genes. Mobile genes, or transposons, make up a significant portion of the genome, further complicating sequencing efforts.

"Sequencing the corn genome was like putting together a 1,000 piece jigsaw puzzle with lots of blue sky and blue water, with only a few small sailboats on the horizon," Wilson explains. "There were not a lot of landmarks to help us fit the pieces of the genome together."

Source: Washington University in St. Louis