

Scientists complete chromosome-based draft of the wheat genome

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Wheat is grown on more than 531 million acres around the world and produces nearly 700 million tons of food and feed each year. Scientists are working to create a full genetic map of the plant in order to improve its resistance to diseases and drought as well as improve its food yield. Credit: Kansas State University

Several Kansas State University researchers were essential in helping scientists assemble a draft of a genetic blueprint of bread wheat, also known as common wheat. The food plant is grown on more than 531

million acres around the world and produces nearly 700 million tons of food each year.

The International Wheat Genome Sequencing Consortium, which also includes faculty at Kansas State University, recently published a chromosome-based draft sequence of wheat's genetic code, which is called a genome. "A chromosome-based draft sequence of the hexaploid bread wheat genome" is one of four papers about the wheat genome that appear in the journal *Science*.

The genetic blueprint is an invaluable resource to plant science researchers and breeders, said Eduard Akhunov, associate professor of plant pathology and a collaborator with the International Wheat Genome Sequencing Consortium.

"For the first time, they have at their disposal a set of tools enabling them to rapidly locate specific genes on individual wheat chromosomes throughout the genome," Akhunov said. "This resource is invaluable for identifying those genes that control complex traits, such as yield, grain quality, disease, pest resistance and abiotic stress tolerance. They will be able to produce a new generation of [wheat varieties](#) with higher yields and improved sustainability to meet the demands of a growing world population in a changing environment."

Although a draft, the sequence provides new insight into the plant's structure, organization, evolution and genetic complexity.

"This is a very significant advancement for [wheat genetics](#) and breeding community," Akhunov said. "The wheat genome sequence provides a foundation for studying genetic variation and understanding how changes in the genetic code can impact important agronomic traits. In our lab we use this sequence to create a catalog of single base changes in DNA sequence of a worldwide sample of wheat lines to get insights into the

evolution and origin of wheat genetic diversity."

Akhunov, Shichen Wang, a programmer and bioinformatics scientist in plant pathology, and Jesse Poland, assistant professor of plant pathology, collaborated with the International Wheat Genome Sequencing Consortium to order genes along the wheat chromosomes.

Other Kansas State University researchers in the department of [plant pathology](#) involved include Bikram Gill, university distinguished professor and director of the Wheat Genetics Resource Center, and Bernd Friebe, research professor, who developed genetic material that was essential for obtaining the chromosome-based sequence of the wheat genome.

A second paper in *Science* details the first reference sequence of chromosome 3B, the largest chromosome in common wheat.

"The wheat genome only has 21 chromosomes, but each chromosome is very big and therefore quite complicated," Akhunov said. "The largest chromosome, 3B, has nearly 800 million letters in its [genetic code](#). This is nearly three times more information than is in the entire rice genome. So trying to sequence this chromosome—and this genome—end-to-end is an extremely complicated task."

In order to analyze the vast amount of genetic information, researchers used a technique called shotgun sequencing. This divided the wheat genome into chromosomes and then split each chromosome into smaller segments. Chromosomal segments were analyzed by short gene sequences and overlapping sequences were stitched together with computer software.

The chromosome-based draft sequence the critical step before the full [wheat genome](#) is sequenced, Akhunov said. The sequencing approach

developed for the 3B chromosome can now be applied for sequencing the remaining chromosomes in wheat. The consortium estimates the full genome sequence will be available in three years.

The research is funded by the U.S. Department of Agriculture's National Institute of Food and Agriculture.

"Wheat is a staple source of food for the majority of the world. As the global population continues to rapidly increase, we will need all the tools available to continue producing enough food for all people in light of a changing climate, diminishing land and water resources and changing diets and health expectations," said Sonny Ramaswamy, director of USDA's National Institute of Food and Agriculture and a former Kansas State University faculty member. "This work will give a boost to researchers looking to identify ways to increase wheat yields."

More information: "A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome," by K.F.X. Mayer et al. www.sciencemag.org/lookup/doi/.../1126/science.1251788

"Structural and functional partitioning of bread wheat chromosome 3B," by F. Choulet et al. www.sciencemag.org/lookup/doi/.../1126/science.1249721

"Ancient hybridizations among the ancestral genomes of bread wheat," by T. Marcussen et al. www.sciencemag.org/lookup/doi/.../1126/science.1250092

"Genome interplay in the grain transcriptome of hexaploid bread wheat," by M. Pfeifer et al. www.sciencemag.org/lookup/doi/.../1126/science.1250091

Provided by Kansas State University

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