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Mapping bread. Because of its unwieldy genome, wheat has stumped DNA sequencers--until now.

CREDIT: CATHERINE FEUILLET

and not just because it's 17 gigabases long. *Triticum aestivum* contains three sets of chromosomes rolled into one nucleus. This so-called hexaploid arrangement arose in two steps. First, two wild grasses combined genomes to make what was the ancestor to durum (pasta) wheat. Later, this hybrid hybridized with another wild wheat species. The resulting genome has three sets of DNA--known as the A, B, and D genomes--which are quite similar but not identical.

Another complication is the fact that, like corn and the human genome, the bread wheat genome is rife with repetitive sequences. Repetitive DNA and similar sequences are a sequencer's nightmare because the sequence is generated in pieces that must be matched up correctly to figure out the order of the bases along each chromosome. The wheat genome "was thought to be intractable," says Gill.

To overcome these obstacles, Feuillet and her colleagues are attacking the bread wheat genome chromosome by chromosome--an early strategy used for sequencing the yeast genome and, initially, the human genome. She picked the largest, 3B (chromosome 3 of the B genome), which by itself is double the size of the entire rice genome, containing about 6000 genes. Her group teamed up with Jaroslav Dolezel of the Institute of Experimental Botany in Olomouc, Czech Republic, whose team has developed a way to sort similar chromosomes by size so as to be able to sequence each chromosome independently. In all, the researchers were able to position more than 1000 markers on the chromosome that will help them and others hunt for useful genes. The map is reported in tomorrow's issue of [Science](#).

The divide-and-conquer tactic also puts financing--and sequencing--the entire wheat genome

A Giant Leap for Wheat Genome

By Elizabeth Pennisi
ScienceNOW Daily News
2 October 2008

"Divide and conquer" has been a winning military strategy since Roman times. Now an international team has applied this approach to tackle the wheat genome, which is five times the size of the human genome and much more complicated. Plant geneticist Catherine Feuillet of INRA-UBP in Clermont-Ferrand, France, and her colleagues have isolated one of wheat's 42 chromosomes and made a physical map of it, placing more than 1400 molecular landmarks along its 995 million bases.

"For wheat researchers languishing in genomic poverty, this is the beginning of genomic empowerment," says Bikram Gill, a plant geneticist at Kansas State University in Manhattan. The map will not only assist in sequencing but also help researchers more easily find genes important to increasing yields and dealing with drought and disease.

Like computer memory, genome sequencing capacity has been rising exponentially and decreasing in cost, making possible the deciphering of ever-larger genomes.

Nonetheless, the wheat genome has seemed too daunting,

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more in reach. "Chromosomes can be 'divided up' into manageable packages amongst the wheat groups in different countries," explains Graham Moore of the John Innes Centre in Norwich, U.K. For example, the French government is supporting Feuillet's completion of 3B, and the U.S. government is supporting Gill's mapping of several other chromosomes. Given that wheat feeds more than one-third of Earth's population, says Gill, "this is good news for world food security."

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A Physical Map of the 1-Gigabase Bread Wheat Chromosome 3B


Etienne Paux, Pierre Sourdille, Jérôme Salse, Cyrille Saintenac, Frédéric Choulet, Philippe Leroy, Abraham Korol, Monika Michalak, Shahryar Kianian, Wolfgang Spielmeier, Evans Lagudah, Daryl Somers, Andrzej Kilian, Michael Alaux, Sonia Vautrin, H el ene Berg es, Kellye Eversole, Rudi Appels, Jan Safar, Hana Simkova, Jaroslav Dolezel, Michel Bernard, and Catherine Feuillet (3 October 2008) *Science* **322** (5898), 101. [DOI: 10.1126/science.1161847]

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