

### WHEAT GENOME

## Chinese Spring fervour

*Science* **361**, eaar7191 (2018).



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Bread wheat, *Triticum aestivum*, is one of the major sources of food for the world, and as such could have been expected to be an early target of genome sequencing. However, unlike other significant crop plants such as rice and maize whose genomes were decoded by 2002 and 2009, respectively, the size and complexity of the wheat genome has made it an almost intractable challenge. At last this has been rectified with the publication in *Science* of a fully annotated reference genome of a wheat variety called Chinese Spring, by the International Wheat Genome Sequencing Consortium consisting of researchers from well over 50 institutions.

Much of the difficulty for the sequencers stemmed from the fact that *T. aestivum* is hexaploid, having arisen from the hybridization of domesticated emmer or durum wheat (themselves tetraploid varieties) with another grass species, *Aegilops tauschii*, well over 3,000 years ago. The result is a genome with 21 pairs of chromosomes containing six copies of most genes. At around 16 billion base pairs in length, it is a little more than 5 times the length of the human genome, and was assembled from Illumina short-read sequences. The researchers achieved 94%

coverage, which is impressive given that 85% of the genome was found to consist of repetitive DNA within which nearly 4 million copies of transposable elements from 505 families have been annotated. The consortium also identified with high confidence 107,891 separate genes. Possibly the key feature of this genome sequence, and a mark of its quality, is that 90% of the genome has been placed into large, continuous stretches of greater than 4.1 Mb in length (superscaffolds), the largest of which, at 166 Mb, is longer than the entire genome of *Arabidopsis thaliana*.

Although this project is the result of some 18 years of work, its usefulness is only just beginning. With this sequence in hand it is possible to precisely locate all the currently known genetic markers for agronomically important traits, greatly speeding up the pace of conventional breeding. The sequence will also accelerate gene discovery, and facilitate genome engineering and editing.

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Published online: 27 August 2018  
<https://doi.org/10.1038/s41477-018-0262-2>