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Reviving rice

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Rice feeds over half the world population and the rice species *Oryza sativa* has become a model for understanding the genetics of cereal grasses. Draft sequences of the genomes of two main subspecies, japonica and indica, were generated by whole-genome shotgun sequencing and were published earlier this year. In the November 21 Nature two papers report complete sequences of rice chromosomes generated in a clone-by-clone approach by the International Rice Genome Sequencing Project. Kmita *et al.* report the sequence of rice chromosome 1, the longest chromosome (*Nature* 2002, **420:**312-316). They found 6,756 coding genes within the 43.3 megabases of sequence. Almost half of these matched homologs in *Arabidopsis* and around a third could be functionally categorized. The most abundant gene family was the serine/threonine receptor kinases. In an accompanying paper, Feng *et al.* (*Nature* 2002, **420:**316-320) report the sequence of rice chromosome 4, including the longest known sequence of a plant centromere (over 1.1 Mb). The finished sequence is 34.6 Mb long and contains 4,658 predicted coding genes. These two reports make a convincing case for the importance of high-quality finished sequences for accurate genome analysis.

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