A draft sequence of the rice genome (Oryza sativa L. ssp. japonica)  
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Abstract  
The genome of the japonica subspecies of rice, an important cereal and model monocot, was sequenced and assembled by whole-genome shotgun sequencing. The assembled sequence covers 93% of the 420-megabase genome. Gene predictions on the assembled sequence suggest that the genome contains 32,000 to 50,000 genes. Homologs of 98% of the known maize, wheat, and barley proteins are found in rice. Synteny and gene homology between rice and the other cereal genomes are extensive, whereas synteny with Arabidopsis is limited. Assignment of candidate rice orthologs to Arabidopsis genes is possible in many cases. The rice genome sequence provides a foundation for the improvement of cereals, our most important crops.