By many criteria, plant life dominates Earth. More than 250,000 species of flowering plants decorate the world — and the entire biosphere depends on plants for food and oxygen. The sequencing and analysis of the first genome from the plant kingdom is therefore a scientific event of some importance. Add in the fact that plants and animals have independently solved the problems of multicellular existence, and the sequence can be rightly seen as a landmark. The last common ancestor of plants and animals existed over one-and-a-half billion years ago, so comparisons between the genomes of plants and other eukaryotes will provide fundamental insights into how life works.

The genome in question is that of *Arabidopsis thaliana*, a modest little flowering brassica, related to broccoli and cauliflower. *A. thaliana* is the “model” plant for research. Its small size, short life cycle and prodigious seed production make it an easy and inexpensive organism to propagate in the laboratory, and with a (relatively) small genome, of about 120 Mb, it is an ideal choice for sequencing. For comparison, the genomes of maize and wheat are 2,500 Mb and 16,000 Mb, respectively. *A. thaliana* lacks much of the repetitious DNA that riddles the genomes of higher plants, but it does contain a complete set of genes for controlling developmental patterns, metabolism, responses to environmental cues and disease resistance. Thus its genomic sequence provides a means for analysing gene function relevant to a range of plant species, including commercially important crops.

Although papers on *A. thaliana* appear weekly, fewer than 10% of the nearly 26,000 genes have been studied in experiments on gene function. The completion of the genome sequence will broaden and accelerate research. The *Arabidopsis* research community embraced a collegial spirit from its inception, openly sharing information and resources around the world. So it is fitting that the community celebrates the completion of the *A. thaliana* genome — four years ahead of schedule and well within budget — with today’s publication of the sequences of the plant’s remaining three chromosomes (the first two were published in the 16 December 1999 issue of *Nature*) and a comprehensive overview of the annotation and analysis of the genome sequence.

In an accompanying News and Views article, Virginia Walbot discusses how the genome sequence enhances the understanding of plant evolution and reveals both the striking conservation of genetic mechanisms underpinning cellular processes and the intriguing differences between plants and other eukaryotes. A News Feature covers other plant genome initiatives underway. The package is completed by a poster illustrating the impact of *A. thaliana* genomics on plant biology and beyond, and the whole of the plant’s genome is captured on a CD-ROM, available on request from *Nature*.

As with all genomics research published in *Nature*, the papers published today on *A. thaliana* (plus the two previously published papers) can be freely accessed on *Nature’s* Genome Gateway (http://www.nature.com/genomics), which provides a portal to the latest in genome research.

In 1777 the British botanist and apothecary William Curtis described *A. thaliana* in his *Flora Londinensis* as a plant of “no particular virtues or uses”. With today’s publication of its genome it can justifiably claim to have risen to among the most significant plants in the kingdom.

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