

Big Ideas from a Small Plant

Caroline Dean

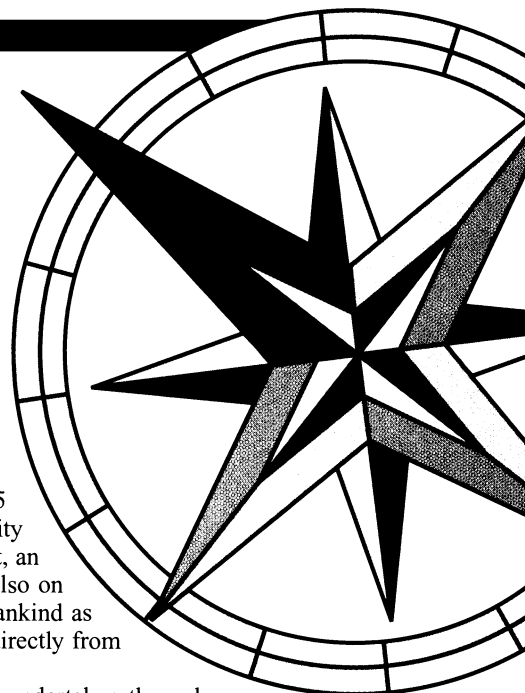
This week sees the publication (in the journal *Nature*) of the analysis of the whole genome sequence of the flowering plant *Arabidopsis thaliana*. The availability of the *Arabidopsis* genome sequence has catalyzed and facilitated the dissection of many plant processes, as evidenced by the huge increase in publications on *Arabidopsis* over the past 5 years and by a number of papers in this issue. It also opens up the possibility of obtaining a complete understanding of the mechanics of a flowering plant, an understanding that will have a huge impact not only on plant biology but also on all future plant breeding. This new knowledge will be as important to humankind as the human genome sequence, because all, including the very poor, benefit directly from improvements in food supplies.

The *Arabidopsis* project, including all the initial physical mapping, was undertaken through a multinational collaboration involving scientists and funding from eight countries. In 1996, the *Arabidopsis* Genome Initiative was established, and this group continues to manage the program. A key component at all stages of the effort has been the deposition of sequence information in public databases. This has been extremely important to the *Arabidopsis* and wider plant biology community, greatly facilitating positional cloning, mapping, and comparative analyses. The exemplary nature of this project provides a model for future work tackling large-scale problems—not only for future plant biology but for the biological sciences as a whole. We are at the beginning of an era of discovery, and progress will be slowed unless the development of resources for gene function analysis is also undertaken within a multinational framework and with the same openness and availability of materials. This requires the commitment of scientists and public funding bodies to think on an international level. It is also critical that an effective interface be created between the many companies working with the *Arabidopsis* genome information and publicly funded research, so that both parties can benefit.

The *Arabidopsis* sequence has the potential to serve as the platform from which to analyze all plant processes. Our goal must be to understand the circuitry required for a plant to develop throughout its entire life cycle and respond to biotic and abiotic challenges. Even with the sequence in hand, this is a massive task. It will not only require knowledge of the function of all the genes but an understanding of the integration of all the different pathways at different developmental stages and in different environments. The beauty of a concentrated effort in one species is that, in many cases, the interactions of pathways and processes will emerge from the analysis unintentionally. The detailed knowledge of the workings of a plant will open up many doors. We will be able to accurately predict the effect of adding or removing a new gene, clearly an important issue in these days of anxiety about genetically modified organisms. More important, complex processes in crop plants will be understood much faster by first analyzing these processes in *Arabidopsis* and then applying the knowledge comparatively. A better understanding of key traits in various crops will enable plant breeding to be undertaken in a more precise and rational fashion.

For *Arabidopsis* to be of most use as a reference organism for other plant species, we need to continue intensive research on *Arabidopsis* and not diversify effort too quickly into other plants. As the completion of the *Arabidopsis* sequence approached, one could hear the cry “*Arabidopsis* is done—now it’s time to work on my favorite plant.” Efforts to sequence the rice genome and to provide extensive expressed sequence tag coverage for many other plant species are quite advanced. Nevertheless, there must be an informed debate on the balance of future funding between increasing our understanding of how *Arabidopsis* works and determining genome sequences from a range of plant species. Those in the field must also consider how much work needs to be undertaken on crops themselves, as compared to the dissection of key traits in the most appropriate model organisms. If we play our cards right, we should be able to exploit the *Arabidopsis* sequence to provide biological information that may very quickly reveal the inner workings of many different plants and how they have evolved.

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