Arabidopsis Functional Genomics

From our perspective, the field of plant biology has come a long way in a short time. Fifteen years ago, plant biologists worked on a wide spectrum of species with no consensus as to which should be treated as “models.” The acceptance of Arabidopsis as the major plant model system did not come easily. Tireless promotion by a small number of champions played an important part. A rapidly increasing number of genetic and genomic resources has also been a big draw. Of critical importance has been the enlightened leadership shown by federal agencies, particularly the National Science Foundation, first in its funding of the Arabidopsis Genome Initiative and more recently the Plant Genomics and Arabidopsis 2010 program.

For Plant Physiology, a journal devoted to covering a wide range of plant biology, our goal is to attract the very best in all subdisciplines. One way of doing this is to highlight particular questions or species as they emerge as fruitful lines of inquiry. In this special issue, we feature a remarkable diversity of biological questions addressed in Arabidopsis. We note with particular pride that among the authors of the articles are some of the most respected names in our field.

We also point to the increasing number of articles that are using genomics approaches to address fundamental questions in plant biology. In this issue are articles on research projects that use expression profiling, proteomics techniques, genomics approaches to map-based cloning, systematic analysis of gene families, and comparative genomics analyses. In addition, we have asked the recipients of recent Arabidopsis-related genomics grants to describe the progress of their projects.

It has become a mantra that the real power of genomics will be unlocked by the ability to compare genomes of different species. To date this has only been realized for bacterial genomes. However, with the recent publication of the rice genome, the day is rapidly approaching when we will have a multitude of plant genomes to compare. We will need to start developing the methods and the resources to take full advantage of this treasure trove of information. It is only fitting that comparative genomics will enlarge our scope to include once again a wide diversity of plant species. What has been learned in Arabidopsis, both from its genomic sequence and studies of gene function, will be used to begin to understand how evolutionary forces work on genomes to produce adaptive traits.

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