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## Preface

Functional genomics is a young discipline whose origin can be traced back to the late 1980s and early 1990s, when molecular tools became available to determine the cellular functions of genes. Today, functional genomics is perceived as the analysis, often large-scale, that bridges the structure and organization of genomes and the assessment of gene function. The completion in 2000 of the genome sequence of *Arabidopsis thaliana* has created a number of new and exciting challenges in plant functional genomics. The immediate task for the plant biology community is to establish the functions of the approximately 25,000 genes present in this model plant.

One major issue that will remain even after this formidable task is completed is establishing to what degree our understanding of the genome of one model organism, such as the dicot *Arabidopsis*, provides insight into the organization and function of genes in other plants. The genome sequence of rice, completed in 2002 as a result of the synergistic interaction of the private and public sectors, promises to significantly enrich our knowledge of the general organization of plant genomes. However, the tools available to investigate gene function in rice are lagging behind those offered by other model plant systems. Approaches available to investigate gene function become even more limited for plants other than the model systems of *Arabidopsis*, rice, and maize.

The challenge to determine the function of the tens of thousands of plant genes, many of them showing no detectable homology to genes for which cellular roles have been identified in bacteria, yeast, or animals, has triggered an avalanche of novel methodologies. The aim of *Plant Functional Genomics: Methods and Protocols* is to provide in a single volume a detailed description and guide to some of the most commonly used approaches to investigating plant gene function. Rather than focusing solely on model organisms, this collection also covers recent efforts devised for investigating a wide variety of plants, plant pathogens, and even some algae.

*Plant Functional Genomics: Methods and Protocols* is organized into five parts, three of which represent the detailed sequence of steps in which a protocol for the discovery of genes and their functions is carried out. Chapters in the first part describe how to identify genes in complex systems that include large genomes, few cells, and mixed cell systems (such as plant and pathogens together). The second part describes powerful computational and statistical tools to help predict gene function on the basis of comparative genomics or from the

analysis of complex genome sequences. Descriptions in the third part focus on several methods that permit the discovery of gene function by loss-of-function mutant analyses, a classical approach that remains very useful. However, it is evident that the high level of genetic redundancy present in large genomes creates formidable obstacles to the successful identification of mutant phenotypes. Thus, gain-of-function approaches can often be a powerful complement to mutant analyses. Effective methods for gain-of-function studies are covered in the fourth part. Finally, because establishing gene function relies on the identification of phenotypes, chapters in the fifth part expand the concept of phenotypes, including the use of multiple outputs as the ultimate phenotypic result of changes in gene activity.

In its assessment of the quality of both new and established technologies, *Plant Functional Genomics: Methods and Protocols* is aimed at plant biologists with a wide range of interests. The combination of detailed computational, molecular, and genetic protocols focusing on both general and specific problems should allow scientists with little or no experience in the specific areas covered to investigate gene function associated with their particular system of interest, and to do so using the most recent methodologies.

To conclude, I would like to thank all those who helped with revising and compiling the material for this collection, especially Diane Furtney. Special thanks go to the authors of the individual chapters who responded with patience and enthusiasm to my numerous requests for additional information or format changes.

***Erich Grotewold***



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