
Preface

At present, *Arabidopsis thaliana* is acknowledged as the most important plant model system by the scientific community. Over the last years, the continuous efforts of plant scientists have led to the generation of a vast array of biological tools, and the development and optimization of research methodology that has altogether prompted the generation of a massive amount of highly valuable experimental data. Both scientific information and biological materials have been made accessible efficiently through shared public/private resources such as TAIR and the various biological stock centers, in a praiseworthy example of collaboration for the optimal use of scientific resources. These initiatives have fueled the investigation in essentially every aspect of plant biology.

Arabidopsis research has thus fundamentally influenced our understanding of the basic biology and ecology of plants. Also importantly, the knowledge gained from this model species is already being translated to other plants, particularly crops, at an always-faster pace. It is expected that this transfer will soon continue to satisfy the increasing demand for improved agricultural products, including food, fiber, and biofuel. Interestingly, moreover, *Arabidopsis* is becoming an important model system for researchers studying other multicellular organisms, recognizing the advantages of this experimental system for the elucidation of basic, universal biological questions.

We have prepared this third edition of *Arabidopsis* Protocols in an effort to compile some of the most recent methodology developed to exploit the *Arabidopsis* genome. To this, we have relied on the experience of a significant group of leading experts in the methodologies described. These methodologies cover from the guided access to public resources, to genetic, cell biological, biochemical, and physiological techniques, including both those that are widely used and those novel ones likely to open new avenues of knowledge in the near future. In addition, considering the recent unparalleled progress of the “omics” tools in *Arabidopsis*, we include sections on genome, transcriptome, proteome, metabolome, and other whole-system approaches.

As in previous editions, we have tried to present a collection of step-by-step protocols, described at a level of detail enough to be followed both by experienced researchers and beginners. We would finally like to thank all our contributing colleagues whose expertise and effort has been essential for attaining the highest scientific standard in this book.

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