
Preface

Plants are amazing organisms to study; many are stunningly beautiful, others are critical staple foods, some are important sources for pharmaceuticals, and others can help to elucidate molecular mechanisms required for a plant's development and its interactions with the biotic or abiotic environment. Plant research in the post-genomic era can strongly build on high-quality genome sequences of a large number of plant species, many of which being non-model plants including valuable crop species, plants important for their phylogenetic position, secondary metabolites, or other well-studied research questions. However, analysis of gene functions or even complex molecular mechanisms are still characterized in only a handful of plant model organisms such as *Arabidopsis thaliana* (thale cress), *Oryza sativa* (rice), or several tobacco species.

Meanwhile, functional genomics is vastly lagging behind the speed of genome sequencing as high-throughput gene function assays are difficult to design, specifically for non-model plants. Bioinformatics tools are useful for gene identification and annotation but are of limited value for predictions concerning gene functions as gene functions are uncovered best by experimental approaches. However, mutant collections and protocols for stable genetic transformation are costly and extremely time consuming. Virus-induced-gene-silencing (VIGS) is an easy-to-use, fast, and reliable method to achieve down regulation of target gene expression. Based on modified viral genomes, the method has been applied to diverse species across the angiosperm phylogeny and has yielded already important experiment-derived information on gene functions.

This book provides detailed protocols for VIGS experiments in several plant species including model and non-model plants. A series of methods is described to tackle the sometimes transient and variable phenotypes for researchers working in diverse fields interested in developmental biology, plant-pathogen or herbivore interactions, and plant secondary metabolites. Recently developed protocols for VIGS-derived microRNA production in the plant or protein overexpression are also included in this book, and some chapters are devoted to shortly summarize the molecular mechanisms of VIGS action and the vector systems developed so far and on how to change a plant virus into a VIGS vector.

I hope that this book will provide a valuable resource for researchers from diverse fields of plant biology interested in experimental approaches to analyze gene functions. I am grateful to the authors who have contributed their practical expertise, to John Walker, the series editor for his advice and encouragement, and to Tina Stickan for bringing in her organizational talent. All helped to make this book possible.

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Methods and Protocols

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