
Preface

Plant biology is at the crossroads, integrating the data from genomics into knowledge and understanding of important biological processes. With the generation of genome sequence data from model and other plants, databases are filled with sequence information of genes with no known biological function. While bioinformatics tools can help analyze genome sequences and predict gene structures, experimental approaches to discover gene functions need to be widely implemented. This book deals with plant functional genomics using reverse genetics methods, namely, from gene sequence to plant gene functions. The methods developed and described by leading researchers in the field are high-throughput and genome-wide in the models *Arabidopsis* and rice as well as other plants to provide comparative functional genomics information.

This book describes methods for the analysis of high-throughput genome sequence data, the identification of noncoding RNA from sequence information, the comprehensive analysis of gene expression by microarrays, and Metabolomic analysis, all of which are supported by scripts to aid their computational use. A series of mutational approaches to ascribe gene function are described using insertion sequences such as T-DNA and transposons as well as methods for the silencing and overexpression of genes. The cataloging of developmental mutant phenotypes as well as analysis of functions using specific phenotype screens described can be adapted to any lab conditions. The integration of the diverse comparative functional genomics information in a database, such as Gramene, provides the capabilities for an understanding of how plant genes work together in a systems biology view.

Blacksburg, VA

Andy Pereira

Plant Reverse Genetics

Methods and Protocols

Pereira, A. (Ed.)

2011, XI, 282 p. 63 illus., 2 illus. in color., Hardcover

ISBN: 978-1-60761-681-8

A product of Humana Press