
Preface

“Treasure your exceptions! When there are none, the work gets so dull that no one cares to carry it further. Keep them always uncovered and in sight. Exceptions are like the rough brickwork of a growing building which tells that there is more to come and shows where the next construction is to be.” Geneticist William Bateson offered this advice in 1908, around the dawn of modern genetics following the rediscovery of Gregor Mendel’s pea plant experiments, and it remains sound today.

Modern molecular biologists have access to the complete genome sequences of many species of interest, including many species of crops and other plants. To fully understand the natural history of an organism and its potential for change under natural selection requires understanding of how these genomes are regulated during growth, differentiation, and reproduction. It is now appreciated that these processes are affected in key ways by the epigenome which orchestrates genomic organization, expression and repair, and interacts with networks of gene, protein and metabolite regulation during eukaryote development. Many of the fundamental discoveries concerning the mechanisms of epigenetic regulation have arisen from studies performed in plants, often due to the investigation of phenomena which had initially been regarded merely as curiosities, the general relevance of which only later became clear. Discoveries made in this way range from transposons and nucleolar dominance to paramutation, and the inducible gene silencing which led to the discovery of RNAi.

This volume of “Methods in Molecular Biology” gathers together comprehensive descriptions of the techniques currently being used to define the details of the plant epigenetic landscape. Such a work is timely, as the number of sequenced plant genomes is rapidly increasing. The activity of these genomes is controlled by covalent modification, packaging with histones and chromatin-remodelling proteins, and the activity of small RNAs which together define the epigenome. We have concentrated especially upon the application of recently developed techniques to analyze plant phenomena with known epigenetic components, such as flowering time, imprinting, and dosage effects. We have drawn upon the expertise of colleagues applying contemporary high-throughput screens, microscopy, and bioinformatic techniques to laboratory models, notably *Arabidopsis thaliana*, although the techniques presented are applicable for studies in crops and non-model species of evolutionary or ecological significance.

It is our hope that these reviews of contemporary methods will advance the study of plant epigenetic phenomena, and allow the biological community to fully integrate our understanding of epigenetic mechanisms into models of plant function during development and evolution.

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