
Preface

One of the central questions of biology is how the genome of an organism encodes all the information necessary for its operation. Finding comprehensive answers to this is a monumental task. While efforts to answer this question are still in their infancy and it is not yet clear how to best approach this, there is no doubt that the problem of decoding the genome requires knowledge of the genome sequences (information), phenotypes (the final output), and the molecular processes linking the two. The term genomics is being used to classify a broad spectrum of methods and approaches currently in use to answer these questions. It is also frequently used to distinguish studies that involve multiple genes from those that are focused on a single gene.

The last few years have seen tremendous advances in multiple technical areas that have enabled unprecedented progress in genomics. There are three areas that I consider outstanding. The most obvious one is the development of the so-called next-generation sequencing. This has enabled the sequencing of whole genomes at reasonable cost and has not only allowed for sequencing the genomes of many plant species but has also allowed for the accurate determination of genotypes of large mutant collections and natural strains across multiple plants species. Moreover, these sequencing methods are being very successfully used for the sequencing-based elucidation of chromatin features and transcriptomes at a genome-wide scale as well as for a diverse set of large-scale molecular assays whose outputs are DNA sequences. The second outstanding area is related to the efficient assessment of phenotypes at a very large scale. This has been driven by an increase in throughput and accuracy in quantifying molecular phenotypes such as transcriptomes, proteins, metabolites, as well as phenotypes that relate to growth and morphology. The latter was possible through advances in high-throughput image acquisition and computer-vision-based image processing. Importantly, combined with the ever-increasing numbers of genomes available, these advances in the quantification of phenotypes have enabled the genome-wide mapping of phenotypes onto the genome, such as through genome-wide association mapping. The third area that I'd like to mention relates to methods of molecular biology. Enabled by lab automation and robotics, new highly efficient methods for molecular cloning, and the availability of cheap next-generation sequencing, genome-scale datasets of molecular interactions can now be produced. This area also includes the rapid evolution of genome-editing methods with TALENs or CRISPR/Cas9. With these tools, it has now become possible to test genetic hypotheses beyond just a few genes and even at the genome scale. In the same vein, recent progress in microscopy has allowed for the investigation of highly resolved molecular interactions in vivo, thereby significantly extending our view beyond the single gene/protein to a network based one. Overall, it is an exhilarating time to be studying biology; for the first time, we truly have the means to generate and test hypotheses at a genome-wide scale.

In this book, I have assembled protocols that revolve around these three pillars of progress, spanning genotypes, phenotypes, and the molecular processes in between. Importantly, they are not restricted to the predominant model species *Arabidopsis thaliana*, and I hope

that this will encourage and facilitate other researchers to expand their research to other species. These protocols were written by leading scientists in their fields and are very much at the forefront of what is currently state of the art in plant genomics. I hope that this book will serve as an inspiration for further studies in plant genomics and will enable a widespread use of these methods.

Vienna, Austria

Wolfgang Busch

Plant Genomics

Methods and Protocols

Busch, W. (Ed.)

2017, XI, 317 p. 74 illus., 60 illus. in color., Hardcover

ISBN: 978-1-4939-7001-8

A product of Humana Press