Omics Technologies and Crop Improvement

EDITED BY **Noureddine Benkeblia**

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Preface

> "Generosity is not what comes from hand, but what comes from heart. Someone can never be better with his knowledge or his wealth, but could be with his value and attitude."

The question that was raised from the end of the twentieth century was how to feed a world population that will likely be ca. 8 billion by 2050, especially considering scientific studies reporting that some yields will probably drop. The main challenge is to address this issue by finding opportunities to improve yields of the main crops of cereals, roots and tubers, and grasses.

In the last three decades, the development of analytical techniques and new emerging technologies such as genomics, transcriptomics, proteomics, metabolomics, and other food-omics has provided promising possibilities for the analysis of crop productivity and possible ways of improving yield and productivity, limiting the land needed to produce this quantity of food, and finally improving the efficiency of resource use, insuring sustainable improvements in crop productivity. These improvements will doubtless lead to improvement in the nutritional, processing, and safety qualities of crops. In addition, these improvements will also have positive impacts on the environment by reducing pollution and the use of fertilizers, pesticides and other chemicals, and water. To achieve these goals, different approaches are suggested such as generating fully sequenced crop genomes or metabolic profiling of these crops.

This book provides additional information on how crops can be improved and how these improvements would be beneficial to humans, environmentally friendly, and socioeconomically sustainable.

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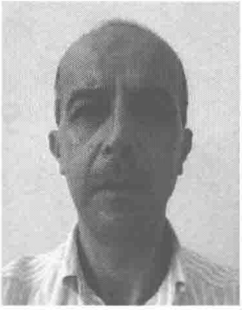
Editor



Noureddine Benkeblia is a professor of crop science involved in food science, focusing on food-plants biochemistry and physiology. His work is mainly devoted to pre- and postharvest metabolism in crops. A few years ago, he introduced a new concept in systems biology—metabolomics—to investigate the mechanisms of biosynthesis and accumulation of fructans in liliaceous plants. Professor Benkeblia received his BSc, MPhil, and Doctor in Food Sciences from the Institut National Agronomique (Algeria) and Doctor in Agriculture (PhD) from Kagoshima University (Japan). After a few years of teaching in Algeria, he joined the Institut National de la Recherche Agronomique, Avignon, France, as a postdoctoral scientist from 2000. From 2002 to 2007, he worked as a visiting professor at the University of Rakuno Gakuen, Ebetsu, Japan, and research associate at Hokaido University. Professor Benkeblia joined the Department of Life Sciences, the University of the West Indies, Jamaica, in 2008, continuing his work on the physiology, biochemistry, and metabolomics of fructan-containing plants in Jamaica. He also works on the postharvest physiology and biochemistry of local fruits. Professor Benkeblia has published over 150 papers, over 37 books and book chapters, and has been the recipient of many awards, including the University of the West Indies Award for the Most Outstanding Researcher in 2011 and 2013.

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Contents

CHAPTER 1

Omics Databases and Gene Expression Networks in Plant Sciences

Masaaki Kobayashi, Hajime Ohyanagi, and Kentaro Yano

CONTENTS

1.1 INTRODUCTION

Advances in next-generation sequencing (NGS) technology have opened up a new avenue for quantitative high-throughput sequencing studies. This approach encompasses complete genome sequencing (e.g., Huang et al. 2009; The Tomato Genome Consortium 2012; The Potato Genome Sequencing Consortium 2011), comprehensive analysis of DNA polymorphisms such as single nucleotide polymorphisms (SNPs) (e.g., Asamizu et al. 2012; Austin et al. 2011; Arai-Kichise et al. 2011; Yamamoto et al. 2010), and investigation of whole-genome gene expression profiles (e.g., Schmidt et al. 2011; Suzuki et al. 2013; Tsai et al. 2013). NGS platforms reveal further information on genomic DNA and cDNAs in various crops and other plants, including nonmodel plants.

Large-scale omics data, including sequence data, are very important for providing a better understanding of complex systems in organisms. In particular, the sequence data and gene expression data generated by NGS and microarray platforms, which are rapidly being accumulated as part of the International Nucleotide Sequence Databases Collaboration (INSDC) (e.g., Barrett et al. 2013; Kodama et al. 2012), facilitate large-scale comparative analyses among many experimental samples (e.g., species, organs, developmental stages, and growing conditions) (e.g., Jia et al. 2013; Morris et al. 2013; Novák et al. 2013). As examples, genes specifically expressed in some species and under certain biological conditions, genes with similar expression profiles, gene expression controlled by microRNAs, gene families with a shared ancestry, and speciation in many plant taxa will be elucidated by comparative analysis of large-scale omics data (e.g., Aya et al. 2011; Heyndrickx and Vandepoele 2012; Koenig et al. 2013; de Meaux et al. 2008; Sakurai et al. 2011).

In this chapter, we introduce the current status of web databases for omics data and bioinformatics tools for plant research. In addition, new bioinformatics approaches are discussed. Along with the recent vast increase in experimental data, it is becoming hard to perform analysis efficiently and effectively by conventional analytical approaches. Large-scale analysis with current methods requires extensive computer resources, such as central processing units (CPUs), memory modules, and computational time, even when large-scale computer systems are available to researchers. Novel methods that can treat large sets of omics data using a general laboratory computer system must be developed and utilized to acquire new knowledge efficiently. The significance of the availability of some new approaches (Hamada et al. 2011; Manickavelu et al. 2012; Nishida et al. 2012) with large-scale omics data is also introduced in this chapter.

1.2 INFORMATION ON WEB RESOURCES FOR GENE EXPRESSION DATA

Microarray and NGS technologies have been widely used as the main platforms to survey genome-wide gene expression. Collection of gene expression data under particular biological conditions (such as developmental stages, organs, and biotic and abiotic stresses) allows spatiotemporal expression profiles to be viewed and genes expressed under these conditions to be identified. Lists of specifically expressed genes facilitate further functional analysis of genomes, genes, and gene products.

Microarray platforms can simultaneously quantitate genome-wide gene expression levels. The current microarray platforms generally contain more than 40,000 DNA probes. Custom and commercial microarray chips have been designed for many plants, such as *Arabidopsis*, rice, cotton, maize, wheat, and soybean. The wealth of experimental platforms in various plant species has triggered the accumulation of expression data based on microarray technology. To promote practical usage of microarray data stored in public databases, it is required to deposit information on experimental and statistical methods into those databases according to the minimum information about a microarray experiment (MIAME) guidelines (Brazma et al. 2001).

1.2.1 Databases for Microarray Gene Expression Profiling

Microarray data have been provided from public databases, such as the NCBI Gene Expression Omnibus (GEO) (Barrett et al. 2013). At the time of writing (August 2013), data from more than 10,000 platforms and approximately 1,000,000 samples have been stored in the GEO (http://www.ncbi.nlm.nih.gov/geo/). Entire data sets can be searched for platform, gene expression data, and experiments. The expression profiles of each retrieved gene set are shown graphically on the web page.