

Preface

In nature, plants are frequently exposed to various abiotic stresses such as drought, extreme temperatures, submergence, high salt levels, heavy metals, mineral deficiency, and toxicity. Plants are seldom exposed to a single abiotic stress, but are more frequently exposed to multiple stressors. For instance, high temperatures and drought are commonly encountered together, and the impact of these two stressors on plants can be aggravated by mineral toxicities. It has been projected that abiotic stressors may adversely affect yields in up to 70 % of staple food crops. Among the various abiotic stresses, drought is the most common and lethal for plants, particularly in critical growth stages, and may result in the complete failure of crops. Conventional breeding approaches, such as selection, hybridization, hybrid breeding, wide hybridization, and ideotype breeding, have been used in the past and have resulted in the development of abiotic stress-tolerant crop varieties. However, given the increasing demand of food due to an increasing world population, particularly in Asia, the pace of conventionally bred varieties is very slow. Drought is a complex trait and is governed by a number of genes with complex interactions and low heritability, and thus is hard to investigate. Additionally, the utilization of wild relatives for the development of drought-tolerant crop varieties has been slow due to cross incompatibility, the complex genetic nature of drought resistance, and cumbersome breeding and phenotypic procedures. Advances in molecular genetics have revealed complex cascades of events at the cellular level that control the adaptation of crop plants to drought, and that numerous genes are involved in the initiation of abiotic stress-related defenses. These genes can be divided into three major categories. The first group consists of genes concerned with direct protection of essential proteins and membranes, such as osmoprotectants, free radical scavengers, late embryogenesis abundant (LEA) proteins, heat shock proteins, and chaperones. The second group comprises membrane transporters and ion channels, involved in water and ion uptake. The third group consists of regulatory proteins, including kinases and transcription factors that are involved in transcriptional regulation of stress-related genes. These transcription factors are distributed in several families, such as the MYB, bHLH, bZIP, NAC, and AP2/EREBP families.

In the past few years, considerable effort has gone into deciphering the mechanisms underlying plant responses to water deficit with the aim to develop crop plants resilient to drought stress. In this book *Drought Tolerance in Plants, Vol 2: Molecular and Genetic Perspectives* we present a collection of 21 chapters written by experts in the field of drought tolerance in plants. It is a timely contribution to a topic that is of great importance for future food security. Chapter 1 describes our current understanding of plant drought responses from the gene to the whole plant. In this chapter, the authors review, in depth, morphological, physiological, biochemical, and molecular mechanisms associated with drought responses and adaptations of crop plants. Chapter 2 describes the genetic basis of cellular and developmental mechanisms and traits conferring drought stress tolerance. Chapter 3 aims to uncover the process of drought signal perception, amplification, and transduction, and to help readers understand the convergent signaling networks in plants exposed to multiple stressors. Chapter 4 deals with the molecular adaptation strategies of plants under drought stress. The authors discuss signaling molecules, transcription factors, drought-responsive genes, and the regulation of gene expression associated with the modulation of drought stress tolerance. Chapter 5 unravels the recent advances in decoding the ABA signaling pathways in plant cells that are involved in drought tolerance. Chapter 6 provides a comprehensive overview of plant responses to drought at the genetic level. The authors critically discuss plant transcriptomic studies investigating drought responses in model plants and how transcriptomic data can be used to evaluate drought tolerance in plants. Chapter 7 provides an in-depth overview of metabolomic studies related to drought responses, discussing preparation techniques for metabolomics, analytical advances, metabolic responses to drought stress, and metabolic engineering of compatible solutes for drought tolerance in plants, as well as the future of metabolomics as a tool to study drought tolerance. Chapter 8 summarizes the importance of microRNAs, including drought-responsive miRNAs and their targets, and the strategies to use miRNAs to enhance plant drought tolerance. Chapter 9 deals with the chloroplastic proteomics of plants in response to drought, salinity, heat, light, and ozone stress. The authors critically discuss the importance of alteration of protein structure under various abiotic stresses. Chapter 10 is concerned with the metabolic responses of plants under drought and other abiotic stress conditions and concentrates on the importance of stress duration and intensity, as well as the importance of developmental stage. Chapter 11 provides an overview of the various definitions of drought, basic principles of plant water relations, and the similarities and differences of drought responses and tolerance in wheat and barley genotypes at different developmental stages, at physiological, biochemical, and molecular levels. In this chapter, the authors provide a brief account of breeding strategies and the potential of molecular approaches to enhance drought tolerance in wheat and barley. Chapter 12 discusses common stress-responsive transcription factors, their interaction networks and epigenetic control, bioinformatics studies, and the molecular modification of transcription factors involved in abiotic stress tolerance. Chapter 13 addresses the historical development of mutation breeding, mutation breeding strategies for various plant species, including tilling and eco-tilling, the

application of mutation breeding for the improvement of quantitative traits, breeding strategies for developing drought-tolerant crop plants, and future perspectives for mutation breeding. Chapter 14 describes various methods to identify candidate genes for drought responses and tolerance, and provides a list of candidate genes from model to cultivated crop plants, which might be used for the improvement of drought tolerance by genetic engineering. Chapter 15 deals with the principles of microarray, gene expression profiling, and gene ontology enrichment analysis under drought stress and the future applications of these techniques. Chapter 16 deals with system biology approaches for drought stress tolerance, which include transcriptome reprogramming under drought, proteomic insights, the crucial roles of metabolomics and transcriptomics, and the quest for systems biology approaches that can be used to understand plant adaptation to drought. Chapter 17 represents a comprehensive overview of oxidative stress and reactive oxygen species (ROS), ROS signal transduction pathways, the effects of ROS on plant growth and metabolism, transgenic plants with higher enzymatic and nonenzymatic defense systems, and their tolerance to drought stress and future perspectives. Chapter 18 investigates the potential for engineering glycine betaine (GB) metabolism for drought tolerance. In this chapter, the authors summarize the biosynthesis of GB, genetically engineered biosynthesis of GB for drought tolerance, the roles of GB in drought tolerance, and GB-induced expression of genes associated with drought tolerance. Chapters 19 and 20 overviews the transgenic approach to produce drought-tolerant plants, including past achievements, challenges, and perspectives. In these chapters, the authors discuss the examples of genetically engineered crops for drought tolerance, including the environmental and food safety assessment of genetically modified crops. Chapter 21 discusses chromatin and drought tolerance. In this chapter, the authors present a comprehensive discussion of chromatin, transcriptional control of drought stress via chromatin modifying genes, and future strategies for chromatin control of sustainable drought tolerance in crop plants.

We hope that this volume will be helpful in building approaches to combat drought stress in plants. This volume will, it is hoped, serve as a key source of information and knowledge to graduate and postgraduate students, teachers, and abiotic stress researchers around the globe. We also believe that it will be of interest to a wide range of plant scientists, including plant breeders, biotechnologists, molecular biologists, agronomists, and physiologists who are interested in drought responses and tolerance of crop plants. This book would not have been possible without the contributions of the experts who were eager to share their knowledge in molecular and genetic perspectives in drought stress, and our heartiest gratitude to all of them. We would like to extend thanks to Dr. Kenneth Teng, the editorial staff of Springer, New York in enabling this book project. Finally, our special thanks to all of the staff members of Springer, Switzerland who are directly or indirectly

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