
Preface

A number of abiotic factors such as drought, salinity, extreme temperatures (very low and very high), low or high light intensity, deficiency or toxic levels of nutrients have huge impacts on crop productivity. In the last few decades, we are witnessing tremendous efforts to understand the molecular, biochemical, and physiological basis of stress tolerance, but it is also critical that the available techniques be applied in an effective manner by the research community. This volume is not intended to cover every minor technique available for understanding plant stress tolerance, but it does cover the most important widely used techniques including the most recent ones. *Plant Stress Tolerance: Methods and Protocols* includes a wide range of protocols catering to the needs of plant physiologists, biochemists, and molecular biologists interested in probing plant stress tolerance.

This volume begins with chapters on dehydration tolerance (Mel Oliver, John Cushman and colleagues), salinity tolerance (Rana Munns), cold tolerance (Chinnusamy and Sunkar), and oxidative stress (Karl-Josef Dietz), which introduces the concepts, mechanisms, and current knowledge in these areas. Following these chapters are two overview chapters covering the microarray analysis of stress-associated transcriptomes (Sreenivasulu and colleagues) and the importance of glyoxalase (Sopory and colleagues) during plant response to abiotic stress.

At the molecular level, identification of stress-responsive genes is an initial step toward understanding plant stress tolerance. Protocols describing the identification of stress-regulated genes using diverse approaches such as genetic screens (Szabados and colleagues), tiling arrays (Seki and colleagues), subtractive suppression hybridization (Mahalingam and colleagues), and yeast one-hybrid and two-hybrid assays (Karl-Josef Dietz) are provided. Next is a chapter devoted to the functional characterization of stress-responsive genes by VIGS (Senthil-Kumar and colleagues). Identification of stress-regulated proteins at a global level is a complementary approach, and two chapters (proteome analysis using DIGE by Jenny Renaut and redox proteomics by Karl-Josef Dietz and colleagues) describe the relevant protocols. Small regulatory RNAs have emerged as new players in plant stress regulatory networks. Two chapters deal with the identification of stress-regulated microRNAs from plants exposed to stress by cloning (Sunkar and collaborators) and/or using microRNA arrays (Guiliang Tang and colleagues).

Oxidative stress is a commonly observed secondary stress as a consequence of diverse primary stresses (drought, salinity, low temperature, heavy metals, air pollution, biotic stress, etc.). The changes in reactive oxygen species (ROS), damage to the lipids, and membrane dysfunctions are well-characterized biochemical changes in response to stress. Niranjani Jambunathan provides commonly used protocols to determine the levels of ROS, lipid peroxidation, and ion leakage. Superoxide dismutases, catalase, peroxidase, etc., are protective enzymes during oxidative stress, and determination of their activity is an important assay to evaluate tolerance potential of the plant species. Sathya Elavarthi and Bjorn Martin contributed a detailed protocol on assaying those enzymes. Hans-Hubert Kirch provided a protocol to assay aldehyde dehydrogenases, which are an important part of oxidative stress regulatory networks.

Accumulation of compatible solutes (proline, sugars, glycine betaine, and some of the inorganic ions such as K^+) is often observed in plants subjected to drought and salt stress, and the phenomenon is referred to as osmotic adjustment. Chapters devoted to measuring the osmotic adjustment (Paul Verslues), proline levels (László Szabados), enzymes involved in proline metabolism (Arnould Savouré), and sugar (Niels Maness) are provided. Finally, a chapter on measuring Na^+ , K^+ , and Cl^- content critical for assessing salt tolerance is provided (Rana Munns).

I thank Prof. John Walker, chief editor, for providing me this opportunity and all contributors for making it possible to bring together this useful collection of methods for all of us who are working in this discipline. I also thank Dr. Gary Thompson, Head, department of Biochemistry and Microbiology, Oklahoma State University, for his encouragement to take up this task and Dr. B. Ravi Prasad Rao for his assistance in formatting these chapters.

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