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.

Ramanjulu Sunkar
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Contributors

EDIT Ábrahám • Institute of Plant Biology, Biological Research Center, Szeged, Hungary
Catalina Arenas-Huertero • Department Biologia Molecular de Plantas, Instituto de Biotecnologia, Universidad Nacional Autonoma de Mexico, Cuernavaca, Morelos, Mexico
Marianne Bordenave • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France
Viswanathan Chinnusamy • Department of Botany and Plant Sciences, University of California, Riverside, CA, USA
Françoise Cochet • Université Pierre et Marie Curie-Paris6, CNRS, PCMP, Paris, France
Timothy D. Colmer • School of Plant Biology, The University of Western Australia, Crawley, WA, Australia
John C. Cushman • Department of Biochemistry & Molecular Biology, University of Nevada, Reno, NV
Karl-Josef Dietz • Biochemistry and Physiology of Plants, Faculty of Biology, Bielefeld University, Bielefeld, Germany
Sathya Elavarthi • Department of Plant and Soil Sciences, Oklahoma State University, Stillwater, OK, USA
Takahiro Endo • Bioinformatics and Systems Engineering Division, RIKEN Yokohama Institute, Yokohama, Japan
László Erdei • Department of Plant Physiology, University of Szeged, Szeged, Hungary
Mohamed Ali Ghars • Borj Cedria, Adaptation des Plantes aux Stress Abiotiques, Hammam Lif, Tunisia
Cécile Hourton-Cabassa • UPMC-Univ Paris 06, PCMP, Paris, France
Junko Ishida • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan
Niranjani Jambunathan • Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK, USA
Xiaoyun Jia • Department of Plant and Soil Sciences and KTRDC, University of Kentucky, Lexington, KY, USA
Mary Prathiba Joseph • Institute of Plant Biology, Biological Research Center, Szeged, Hungary
Eli Kaminuma • Bioinformatics and Systems Engineering Division, RIKEN Yokohama Institute, Yokohama, Japan
Shuji Kawaguchi • Bioinformatics and Systems Engineering Division, RIKEN Yokohama Institute, Yokohama, Japan
Makiko Kawashima • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan
Jong-Myong Kim • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan
HANS-HUBERT KIRCH • Institute of Molecular Physiology and Biotechnology of Plants (IMBIO), University of Bonn, Bonn, Germany

PETER KLEIN • Biochemistry and Physiology of Plants, Faculty of Biology, Bielefeld University, Bielefeld, Germany

NORIO KOBAYASHI • Bioinformatics and Systems Engineering Division, RIKEN Yokohama Institute, Yokohama, Japan

KAREN L. KOSTER • Department of Biology, The University of South Dakota, Vermillion, SD, USA

YUKIO KURIHARA • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan

ANNE-SOPHIE LEPRINCE • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

JEFFREY LEUNG • Institut des Sciences du Vegetal, CNRS, Gif sur Yvette, France

RAMAMURTHY MAHALINGAM • Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK, USA

NIELS MANESS • Horticulture and Landscape Architecture Department, Oklahoma State University, Stillwater, OK, USA

BJORN MARTIN • Department of Plant and Soil Sciences, Oklahoma State University, Stillwater, OK, USA

AKIHIRO MATSUI • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan

VENUGOPAL MENDU • Department of Plant and Soil Sciences and KTRDC, University of Kentucky, Lexington, KY, USA

YOSHIKI MOCHIZUKI • Bioinformatics and Systems Engineering Division, RIKEN Yokohama Institute, Yokohama, Japan

TAEKO MOROSAWA • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan

RANA MUNNS • CSIRO Plant Industry, Canberra, ACT, Australia

ANANDA MUSTAFIZ • Plant Molecular Biology, International Centre for Genetic Engineering and Biotechnology, New Delhi, India

MEENAKUMARI MUTHURAMALINGAM • Biochemistry and Physiology of Plants, Faculty of Biology, Bielefeld University, Bielefeld, Germany

KIRANKUMAR S. MYSORE • Plant Biology Division, The Samuel Roberts Noble Foundation, Ardmore, OK, USA

KENTARO NAKAMINAMI • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan

MASANORI OKAMOTO • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan

MELVIN J. OLIVER • USDA-ARS Plant Genetics Research Unit, University of Missouri, Columbia, MO, USA

CSABA PAPDI • Institute of Plant Biology, Biological Research Center, Szeged, Hungary

ELODIE PARRE • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

LILA PEAL • Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK, USA

MICHAEL PUCKETTE • Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK, USA
Contributors

JENNY RENAUT • Department of Environment and Agrobiotechnologies (EVA), Proteomics Platform, Centre de Recherche Public – Gabriel Lippmann, Belvaux, Luxembourg

JOSE LUIS REYES • Department Biologia Molecular de Plantas, Instituto de Biotecnologias, Universidad Nacional Autonoma de Mexico, Cuernavaca, Morelos, Mexico

LUC RICHARD • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

HORST RÖHRIG • Institute of Molecular Physiology and Biotechnology of Plants (IMBIO), University of Bonn, Bonn, Germany

JOSE LUIS REYES • Department Biologia Molecular de Plantas, Instituto de Biotecnologias, Universidad Nacional Autonoma de Mexico, Cuernavaca, Morelos, Mexico

LUC RICHARD • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

HORST RÖHRIG • Institute of Molecular Physiology and Biotechnology of Plants (IMBIO), University of Bonn, Bonn, Germany

KHIROD K. SAHOO • Plant Molecular Biology, International Centre for Genetic Engineering and Biotechnology, New Delhi, India

IMMA PEREZ SALAMÓ • Institute of Plant Biology, Biological Research Center, Szeged, Hungary

ARNOLUDE SAVOURÉ • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

MOTOAKI SEKI • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan; Kihara Institute for Biological Research, Yokohama City University, Yokohama, Japan

MUTHAPPAM Senthil-Kumar • Department of Crop Physiology, University of Agricultural Sciences, GKV, Bangalore, Karnataka, India; Plant Biology Division, The Samuel Roberts Noble Foundation, Ardmore, OK, USA

KAZUO SHINOZAKI • Gene Discovery Research Team, Gene Discovery Research Group, RIKEN Plant Science Center, Tsukuba, Japan

SNEH L. SINGLA-PAREEK • Plant Molecular Biology, International Centre for Genetic Engineering and Biotechnology, New Delhi, India

SUDHIR K. SOPORY • Plant Molecular Biology, International Centre for Genetic Engineering and Biotechnology, New Delhi, India

NESE SREENIVASULU • Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

MARC STRICKERT • Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

ELKE STRÖHER • Biochemistry and Physiology of Plants, Faculty of Biology, Bielefeld University, Bielefeld, Germany

RAMANJULU SUNKAR • Department of Biochemistry and Molecular Biology, Oklahoma State University, Stillwater, OK, USA

LÁSZLÓ SZABADOS • Institute of Plant Biology, Biological Research Center, Szeged, Hungary

MAHO TANAKA • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan

GUILLIANG TANG • Department of Plant and Soil Sciences and KTRDC, University of Kentucky, Lexington, KY, USA

NATASHA L. TEAKLE • School of Plant Biology and Center for Ecohydrology, The University of Western Australia, Crawley, WA, Australia

TAIKO KIM TO • Plant Genomic Network Research Team, Plant Functional Genomics Research Group, RIKEN Plant Science Center, Yokohama, Japan

TETSURO TOYODA • Bioinformatics and Systems Engineering Division, RIKEN Yokohama Institute, Yokohama, Japan

MAKARLA UDAYAKUMAR • Department of Crop Physiology, University of Agricultural Sciences, GKV, Bangalore, Karnataka, India
PAUL E. VERSLUES • Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan

JACQUES DE VIRVILLE • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

DELPHINE LEFEVRE-DE VOS • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

PATRICIA A. WALLACE • CSIRO Plant Industry, Canberra, ACT, Australia

ULRICH WOBUS • Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

ALAIN ZACHOWSKI • Université Pierre et Marie Curie, PCMP, UR5 EAC7180 CNRS, Paris, France

JIAN-KANG ZHU • Department of Botany and Plant Sciences, University of California, Riverside, CA, USA