Preface

Anthropogenic pressures are implicated in the degradation of invaluable natural resources. Assessing the impacts of global soil salinization on plant growth and productivity and identifying approaches for mitigation salinization are subjects of global importance. It is reported that about 7% of the total land on Earth and 20% of the total arable area are affected by a high salt content. Plant productivity is also affected by the elevated levels of salt content in the soil. The reason for the low production is that various metabolic processes that work independently or in coordination with one another are affected by the deleterious effects of salt.

Poly-omics – namely, proteomics, genomics, micromics, transcriptomics, metablomics, inomics, metallomics, etc. – have emerged as a powerful tool for understanding the mechanism of plant response toward salinity stress. The exploitation of different genes and proteins involved in the regulation of various environmental stresses will be very useful in generating crops with enhanced food production under salinity stress. With the help of metabolomics, we will recognize different metabolic pathways the plant is rearranging during stress. Plants perceive both external and internal signals and use them to regulate various responses for their development.

During salinity stress, plants respond in various ways and can withstand the stress. Salinity stress is responsible for osmotic, ionic, and oxidative stresses, which lead to reduced growth and development of the plant. Plants can tolerate these stresses by the accumulation of osmolytes and osmoprotectants. Another machinery is the expression of different types of enzymatic and non-enzymatic antioxidants. Understanding the full mechanism of salt tolerance through different means is an enigmatic subject for scientists in general and plant biologists in particular.

The outline of this volume, "*Salt Stress in Plants: Omics, Signaling and Adaptations*," encompasses the following: Chapter 1 deals with advances of metabolomics to reveal plant response during salt stress. Chapter 2 narrates the role of microRNAs (micromics) in response to salt stress in plants. Chapter 3 sheds light on the role of proteomics in salt-stressed plants. Chapter 4 discusses improving salinity tolerance in plants through genetic approaches. Chapter 5 describes the role of LEA proteins in salinity tolerance in plants. Chapter 6 highlights the effect the salt stress on crop production and the role of omics in salinity tolerance. Chapters 7, 8 and 9 deal with the role of different kinds of signaling molecules in plants under salt stress. Chapters 10 and 11 examine the approaches to improve salt tolerance in rice and maize. Chapter 12 highlights the role of phytochromes in stress tolerance. Chapter 13 discusses alleviating salinity stress through arbuscular mycorrhiza. Chapter 14 deals with breeding approaches in stress tolerance in citrus. Chapter 15 highlights the effect of salt stress in photosynthesis under ambient and elevated atmospheric CO_2 concentrations. Chapter 16 deals with nitrogen-use-efficiency in plants under salt stress. Chapter 17 sheds light on the response of salt-affected plants to cadmium, and Chap. 18 highlights the role of plant tissue culture in screening the salt tolerance in plants.

This volume will provide valuable information about the omic approaches, signaling, and responses of plants under salt stress. We would like to thank all the authors of this volume for their contributions. We are also thankful to my colleagues who helped us directly or indirectly in completing this volume. We are also grateful to Hanna Smith (Associate Editor, Springer) and Margaret Burns (Developmental Editor, Springer) for their help, suggestions, and timely publication of the volume.

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