

# Preface

Ever since agricultural cultivation came into existence, plant systems and their functions are manipulated rapidly both by humans and nature. Biotic and abiotic stresses adversely affect crop productivity. Plant breeding and genetic engineering have enabled maximizing crop productivity even under minimal stress conditions. However, such tools also have their limitations and so the reverse genetic and functional genomic approaches came into practice. With the availability of genome sequences in several plant species, the major focus has been on identification of the functional role of several signaling networks and components involved in regulating stress tolerance pathways. A signaling cascade begins with sensing the stimulus, and the basic outcome of any signaling machinery is to bring out the final response. But at the start and end of any phenomenon, there are certain characters that play their role to assist the process. There are various molecules inside the cellular machinery, which are involved in transducing the signals.

Calcium plays a pivotal role in regulating the physiological and developmental processes in plants. Till now, several calcium sensors have been discovered, which regulate the diverse signaling pathways involved in plant growth and development. One of the major calcium sensors CBL (calcineurin B-like) is decoding the calcium signal during various environmental stresses in plants. Calcium-mediated signal is transduced downstream by CBL-interacting protein kinases (CIPKs), which generally phosphorylate the target proteins such as transcription factors or transporters/channel leading to a response. Mutant-based approach has provided valuable information in the functional analysis of individual members of *CBL* and *CIPK* gene family in Arabidopsis. Both *CBL* and *CIPK* gene families have previously been identified and characterized in Arabidopsis and rice. Identification and characterization of *CBLs* and *CIPKs* in other plant species such as *Oryza sativa*, *Pisum sativum*, *Cicer arietinum*, *Zea mays*, *Populus euphratica*, *Vitis vinifera*, *Malus domestica*, *Gossypium hirsutum*, *Sorghum bicolor*, *Brassica napus*, *Vicia faba*, *Phaseolus vulgaris*, *Ammopiptanthus mongolicus* and *Triticum aestivum* are still at a juvenile stage.

An up-to-date research in the field of CBL–CIPK signaling transduction components, basic and advanced, in various genera has been reviewed here. Also,

current understanding and knowledge of genome-wide organization, evolution, structure, sub-cellular localization, and biochemical properties of CBLs and CIPKs in plants is discussed in various sections of this book. In the first few sections, there is a basic overview of the field of CBL–CIPK signaling, which is accompanied by genomic organization of CBL and CIPK component throughout the plant kingdom. CBL and CIPK proteins distributed in the plant cell and also in different tissues and organs might be involved in executing a particular function. The expression analysis of *CBLs* and *CIPKs* during different developmental stages as well as under different physiological conditions also hints toward their functional role during these particular conditions. So, not only the change in mRNA level but protein modification may also be a strategy to provide specificity for CBL–CIPK signaling. In the subsequent sections, phosphorylation, interaction, and biochemical properties of CBLs and CIPKs are discussed. Finally in a few sections, the targets of CBL–CIPKs and the functional role identified for several CBLs and CIPKs during different environmental stresses, nutrient deficiency, and developmental stages is discussed case-by-case in Arabidopsis and other higher plant species.

Overall, this comprehensive study is focused on the diverse role of the CBL–CIPK module in different stress signaling and also to identify a newly emerging role of this calcium-signaling module in plant growth and development across different plant species. In addition, besides Arabidopsis, it provides a backbone of knowledge to perform detailed molecular investigation in crop plant species and could possibly enable in designing strategies to tame abiotic stress tolerance and development in important agronomical crop plants. This book will act as a handy and informative source in this field for students as well as advanced researchers.

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