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GTPases
Versatile Regulators of Signal Transduction in Plants

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Preface

In the signaling pathways, the activation or inactivation of the proteins is determined by several regulatory components. One of the major regulatory controls is phosphorylation–dephosphorylation cascade mediated by kinases and phosphatases; besides this, G proteins including heterotrimeric and small GTPases also act as essential regulatory switch in the modulation of these signaling pathways. Rho family of GTP-binding proteins (GTPases) acts as binary molecular switches that mediate large number of intracellular signals in eukaryotes. They acquire an activated conformation when bound to GTP (guanosine triphosphate) and are inactivated by hydrolysis of GTP to GDP (guanosine diphosphate). In recent years, a wealth of information has been generated for understanding Rho protein functions in plants. Accordingly, GTPases are instrumental in relaying signals ranging from actin and microtubule arrangement, cell cycle progression, vesicle trafficking, cell morphology, and root hair elongation in plants.

Chapter 1 provides an overview of small GTPases in eukaryotes. The small GTPase superfamily has evolved enormously in metazoan lineage and was classified into five subfamilies (Ras, Rab, Rho, Ran, and Arf) based on their distinct functions in the cell. Three different regulatory proteins (GEFs, GAPs, and GDIs) control the nucleotide state of Rho proteins. GEFs (guanine nucleotide exchange factors) are the activation factors that catalyze the exchange of GDP for GTP. On the other hand, GAPs (GTPase activating proteins) cause Rho proteins inactivation by inducing their intrinsic GTP hydrolysis activity. Finally, GDIs (guanine nucleotide dissociation inhibitors) show specific affinity for inactivated GTPases and prevent them from further activation. Chapter 2 conveys an overview of Rho GTPases in plants and also discusses their known functional role and cross talk in myriad of signaling pathways.

Among the six Ras superfamily GTPases classified in animals, five have been identified in plants, whereas Ras subfamily of GTPases is altogether absent in plants. Additionally, Cdc42 and Rho subfamilies are absent in plants, but instead they possess a novel group of Rac-like signaling molecules, also known as ROP GTPases. More than 90 ROP proteins have been identified in *Arabidopsis*, and with

an extensive database search, we could identify 85 ROPs in *Oryza sativa*. Chapter 3 covers the identification and classification of ROP GTPases in plants.

The evolution of functionally distinct Rac-like GTPases in plants, and, furthermore, due to several gene duplication events, bifurcations of these into distinct subfamilies in both monocots and dicots have generated interest towards their phylogenic evolution. The detailed comparative phyletic and correlative analyses between plants and animals as well as their domain organization have been included in Chapter 4.

During the past several years, remarkable progress has been made towards elucidation of functions that are mediated by Rho proteins in plants. It is not surprising that the immense cellular functions of ROP proteins in plants encompass developmental and stress responses as well. Chapter 5 consists of the expression analysis of identified Rho GTPases in *Arabidopsis* and rice under stress, development, and phytohormone treatment that would be beneficial for gleaning out their specialized and overlapping functional role. Since then several studies have recognized numerous signaling pathways that are controlled by Rho proteins. Chapter 6 lists some of the extensively studied and essential roles of ROPs in plants.

A requisite for the suitable subcellular localization of Rho family GTPases is their posttranslational lipid modification by hydrophobic side groups. The prenylation and palmitoylation of the C-terminal CAAX motif is needed as a lipid anchor to facilitate their plasma membrane association. Chapter 7 deciphers the mechanism of posttranslational lipid modification and membrane association of ROP GTPases in plants. The regulatory mechanism of Rho GTPases and their regulator and effector molecules are discussed in Chapter 8.

Meanwhile, researchers have put a concerted effort to develop new methods and techniques to study GTPases and their roles in plants. It was speculated that, since GTPases exist as a multigenic family, they might be functionally redundant and are possibly involved in signaling cross talk. The level of functional intricacy displayed by GTPases creates complications in their structural study. Several new genetic and biochemical approaches have been devised to study their biological functions. Chapter 9 reviews some of the promising prevailing techniques to study GTPases in living cells. Finally, the future prospects including importance of elucidation of regulatory mechanism of ROP proteins to get an insight into their core principles and actions have been discussed in Chapter 10.

Rho GTPases signaling pathways are a model for cell biologists to elucidate signal transduction pathways. We hope this book will prove beneficial to both students and researchers in this field and will enable them to understand the mechanisms and importance of these versatile signaling molecules in plants.

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