

From Recognition to Defense Responses in Rice Plant

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When plants are infected by plant pathogens, rapid cell responses are initiated for further inhibition from fast invasion of pathogens. Hypersensitive response (HR) of plant is well known defense response stopping pathogenesis process through rapid cell death. However, informations on the signaling pathway from reception of pathogen by host plants to appropriate resistant responses are very limited to date. Efficient perception of infection by pathogens and well-programmed signalling mechanism for appropriate responses are important for survival of plants. Plant have developed a sophisticated network(s) of defense/stress responses, among which one of the earliest signalling pathways after perception (of stimuli) is the evolutionary conserved Rop GTPase and mitogen-activated protein kinase (MAPK) cascade.

GTP-bound Rho proteins are hypothesized to interact with and activate downstream effectors, thus regulating local changes at cellular membrane. Plant possess a unique subfamily of the Rho family, termed Rop (Rho-related GTPase from Plant), and they have been characterized and some of them have been implicated as regulator of cell death leading to resistance responses. Rops are emerging as an important switch in plant signal transduction pathway.

Activation of MAPKs also has been observed in plants exposed to pathogens. Plant MAPKs are also up-regulated by fungal elicitor as well as well known plant signalling molecules such as salicylic, jasmonic acid and abscisic acid. It is considered that MAPKs are important signaling components in plant defense responses and the cascade of a MAPKKK-MAPKK-MAPK module is a general mechanism of defense signal transduction among eukaryotic organism. Recently, complete MAPK cascade was characterized in Arabidopsis from the receptor kinase (FLS2) through following MEKK1-MKK4/MKK5-MPK3/MPK6-WRKY22/WRKY29 pathway. Unfortunately, very few MAPKs have been identified and characterized in economically important monocot, rice. It is really important to understand the defense-related Rops and MAPK cascade through molecular characterization and functional analysis of MAPKs in rice. With the help of completed total genome sequencing of rice, unraveling the role of Rops and MAPK cascade in rice may help in establishing biological model in economically important rice as well as other major cereal crops.

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