Special Issue

NLR Gene Evolution in Plants

Message from the Guest Editors

Disease resistance (*R*) genes are of major importance in crop breeding. The major class of *R* genes encodes nucleotide-binding and leucine-rich repeat immune receptors (NLRs) and corresponds to one of the largest and most diversified gene families in plant genomes. NLR act inside plant cells by recognizing directly or indirectly enemy molecules in order to activate defense response. In turn, pathogens actively attempt to evade and interfere with plant response pathways, leading to a coevolutionary armrace. Consequently, plants need to maintain diversity at NLR genes to cope with an ever changing array of pathogens. NLR genes are often localized in complex clusters, structural organization that may favour their dynamic evolution and diversification. This Special Issue focuses on the evolution of NLR genes in plants, and welcomes original research articles as well as review articles that summarize recent progress and discuss future needs/opportunities in a wide range of areas including, but not limited to, molecular breeding, comparative genomics, functional genomics, genetic/genomic diversity, genome-editing, NLR-engineering, and molecular evolution of NLR in plants.

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