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.

Guest Editors

Dr. Valérie Geffroy

Institute of Plant Sciences Paris Saclay (IPS2), INRAE, 91192 Gif sur Yvette CEDEX, France

Dr. Patricia Faivre-Rampant

EPGV, INRA, Université Paris-Saclay, Evry, France

Deadline for manuscript submissions

closed (24 January 2020)

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Editorial Office MDPI, Grosspeteranlage 5 4052 Basel, Switzerland Tel: +41 61 683 77 34 genes@mdpi.com

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the Genes team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider Genes for your next genetics paper?

Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan

Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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