

Ralstonia solanacearum: An Arsenal of Virulence Strategies and Prospects for Resistance

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Abstract

Among Phytopathogenic bacteria, *Ralstonia solanacearum* is usually referred as an cosmopolitan set of phylogenetically related strains which is pathogenic to a wide range of plants, often mentioned in the literature as the *Ralstonia solanacearum* species complex (RSSC), due to their ability to infect multiple plant families. The infection occurs through the plant root and the bacteria have a strong tropism to reach the xylem vascular tissue where they multiply abundantly, causing an alteration of the water transport associated with the appearance of typical wilting symptoms.

Keywords: *Ralstonia solanacearum*, Virulence, Type III effector

Introduction

The multitude of reverse genetics studies performed to decode the molecular basis of pathogenesis. Thus, it was clear that the *R. solanacearum* virulence mechanism is multifactorial and the type III secretion system (T3SS) are essential for pathogenicity. The diversity of strains in the RSSC, variety of virulence factors and T3E (type III effectors) repertoires, as well as the long persistence of *R. solanacearum* in the environment, contribute to the difficulties in developing effective control strategies. Using chemical methods, physical treatments and cultural practices have been less extensively studied this past decade. Hence, biological control is frequently adapted, developed and studied. The search for plant resistance genes against bacterial wilt was initiated with classical genetic linkage mapping, highlighting quantitative sources of resistance in several crops, mainly in solanaceous plants (Demirjian *et al.*, 2022).

Regulation of virulence is dependent on the Phc quorum-sensing system

The pathogen, *R. solanacearum* GMI1000 uses host plant metabolites to enhance the biosynthesis of virulence factors. The L-glutamic acid from host plants is the key active component associated with increased extracellular polysaccharide production, cellulase activity, swimming motility, and biofilm formation in *R. solanacearum* GMI1000. Furthermore, genetic screening and biochemical analysis suggested that the RS01577, a hybrid sensor histidine kinase/response regulator was involved in L-glutamic acid signaling in *R. solanacearum*. Mutations in RS01577 and exogenous addition of L-glutamic acid to the GMI1000 wild-type strain had overlapping effects on both the transcriptome and biological functions of *R. solanacearum* (Shen *et al.*, 2020).

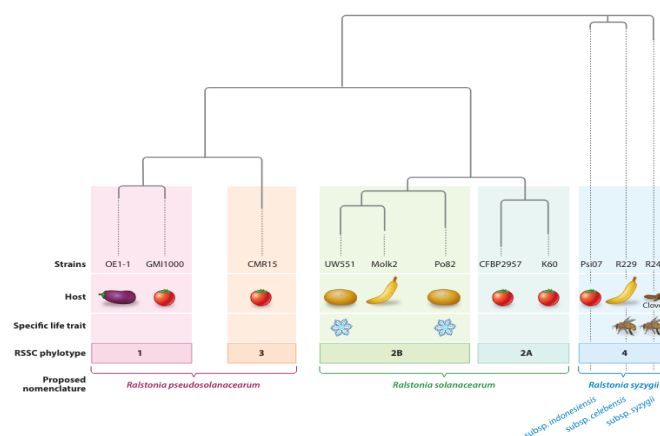


Fig. 1 The *Ralstonia solanacearum* species complex (RSSC)

Phylogenetic tree of the RSSC showing some representative reference strains, the hosts from which they have been isolated (host here refers to the original host the strain was isolated from, not necessarily the host range of the strain), and some specific traits (adaptation to cool temperatures and transmission by insect vectors).

Biofilm formation and resistance to stress in planta

Once inside the plant, the virus encounters harsh environmental circumstances, causing the plant to mount a defense. When the bacterial population is still small in the early stages of infection, this must be extremely important. However, bacteria possess a vast array of enzymes that can efficiently weaken these protective mechanisms.

Therefore, the generation of many ROS-scavenging molecules offsets exposure to reactive oxygen species (ROS), which build up in the apoplast as part of the basic plant defense response. *R. solanacearum* can promote the early phases of infection by breaking down plant defense phenolic components including hydroxycinnamic acid.

Selection of Adaptive Mutations In Planta

R. solanacearum was used in an evolution experiment where a clone of a single ancestor was propagated on eight distinct plant species, including susceptible and resistant host species, for about 350 generations. The pathogen was injected into the plant vascular system as part of the selection strategy used in this experiment, and the populations retrieved from xylem sap were then propagated outside the infection zone. In investigations of planta competition between developed clones and Their progenitor demonstrated that the virus can become more fit on both sensitive and resistant hosts, however the degree of the adaptive process varies according to the host. As a result, genes exhibiting adaptive gain-producing mutations have been identified. One such gene is the global regulator *efpR*.

Type III Secretion-Dependent Pathogenesis

From the multitude of reverse genetics studies performed to decipher the molecular basis of pathogenesis, it is clear that *R. solanacearum* virulence is multifactorial and that the type III secretion system (T3SS) is essential for pathogenicity, as the mutants defective for type III secretion are completely unable to cause disease on any host. The general protein secretion pathway (type II) is also important for infection but has been less characterized. Depending on the strain, 50–75 type III effector (T3E) proteins transit the T3SS and are translocated into plant cells. The fine orchestration allowing the translocation of

such a large number of effectors in *R. solanacearum* is still poorly understood but several chaperones (or secretion helper proteins) with a key role in this process have been characterized, allowing differentiation between early and late secretion T3E.

Genome-Wide Comparisons and Genes Under Selection

In vitro infection system to screen natural variability associated with the root growth inhibition phenotype caused by *R. solanacearum* in Arabidopsis during the first hours of infection. To analyze the genetic determinants of this trait, genome-wide association study was performed to identify allelic variation at several loci related to cytokinin metabolism, including genes responsible for metabolism of cytokinin. Further, the data clearly demonstrates that the cytokinin signaling was induced during the early infection process and cytokinin contributes to immunity against *R. solanacearum*. This study highlights a new role of cytokinin in root immunity (Alonso-Díaz *et al.*, 2021).

Conclusion

The diversity of the RSSC elucidated the presence of specific T3Es in specific strains which also polygenic factors and are responsible to cause virulence other than T3Es. In depth understanding of the disease cycle and host plant targets have been powerful levers to propose the new resistance strategies. Conclusively, to overcome the limitations of each method, an integrated, multifaceted disease control strategy has to be implemented for effective management of the disease. (Planas-Marques *et al.*, 2020).

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