

***Ralstonia solanacearum*: an emerging threat as a mysterious plant pathogen**

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Ralstonia solanacearum is a Gram-negative bacterium. Due to extensive genetic diversity amongst strains, it is also known as the *R. solanacearum* species complex. It causes lethal wilt disease in more than 450 plant species across the globe and its host range is expanding each year. *R. solanacearum* exhibits puzzling infection behaviour and high aggressivity on plants. Due to its unpredictable nature, pathogenicity studies in the case of *R. solanacearum* are still a big challenge. This note discusses about the *R. solanacearum* pathogen in the context of bacterial wilt disease which is considered as an emerging threat for crops and decorative plants.

Ralstonia solanacearum is a soil-borne, Gram-negative bacterial phytopathogen¹. It causes a lethal wilt disease in a wide range of plant species around the globe. Till date, more than 450 of its host plant species are known, and the range is expanding each year²⁻⁵. It includes many important crops and ornamental plants such as tomato, potato, brinjal, chilli, peanut, pepper, rose and eucalyptus^{6,7}. In the post-genomic era, *R. solanacearum* bacterial wilt is also being considered as one of the most devastating systemic wilt diseases of crop plants^{8,9}. It is also known as the Granville wilt in tobacco, brown rot in potato and Moko disease in banana. In the case of *R. solanacearum*, due to extensive diversity amongst the different bacterial strains, it is now known as the '*Ralstonia solanacearum* species complex (RSSC)'¹⁰. Recent studies on *R. solanacearum* genetics have revealed that strains of this species complex evolved in widely distinct geographical regions and conditions, which have acquired differential adaptation capabilities towards native flora and newly introduced hosts¹¹. In early attempts of classification amongst different strains of *R. solanacearum* isolated from various hosts and different geographical locations, there were five races and six biovars based on their ability to cause disease in different hosts, their biochemical properties such as various types of sugars as well as carbohydrates utilization¹. However, with the increase in the knowledge on pathogen diversity, this early system of classification is inconvenient¹². Further this bacterium is classified in under four different phylotype I-IV (phylotype I – Asia, phylotype II – America, phylotype III – Africa and the Indian Ocean, and phylotype IV – Australia, Japan and Indonesia) based on genetic composition variation known as

'phylotype-sequevar system classification', which are given more preference over the race and biovar systems¹³. Further, each phylotype had been classified into different sequevars based on the *egl* endoglucanase structural gene sequence similarity. In case of *R. solanacearum*, phylogenetic analyses propound that this lethal wilt pathogen is a highly diverse bacterial species and all four major phylotypes are deeply separated with evolutionary lineages from phylotypes I to IV (ref. 14). Molecular-level variation analyses on RSSC distinctly showed that geographic isolation and spatial distance are the two significant determinants of genetic variation amongst the phylotypes¹⁵. In the recent past, based on the study of genomic and proteomic methods, the taxonomy of RSSC was further revised to consist of three species: *R. pseudosolanacearum*, *R. solanacearum* and *R. syzygii*^{16,17}. This newly proposed classification system of species division is congruent with the previously reported phylotype classification based on ITS region sequence analysis and DNA sequence of the endoglucanase gene (*egl*)¹⁸, so that the *R. solanacearum* strains belong to phylotype II, *R. syzygii* to phylotype IV and *R. pseudo solanacearum* to phylotypes I and III.

R. solanacearum is generally present in the soil and water, and under suitable conditions, it enters into the host plant through the roots¹⁹. Thereafter, this bacterial pathogen rapidly colonizes and spreads through the plant. Inside the xylem, this vascular pathogen multiplies extensively and produces high amounts of EPS (exopolysaccharide)⁵. Due to extensive colonization and high EPS production, it creates a blockage in the water transport pathway of the plants resulting in a vascular dysfunction which ultimately leads to wilting symptom and plant death

(Figure 1)^{20,21}. It has also been observed that *R. solanacearum* is potent and colonizes its hosts plant asymptotically through latent infections. Such behaviour of this wilt pathogen is still poorly understood by the scientific community²². *R. solanacearum* also shows variable modes of adaptation. In soil and water it exists as a saprophyte until it invades the roots of suitable host plants, where it lives as a parasite. *R. solanacearum* is also considered as the second most devastating bacterial phytopathogen around the world²³. In addition to its genotypic variation and lethality, this bacterial pathogen has an extraordinary capacity to survive in the soil for many years and forms latent infections within indigenous weeds, resulting in a big challenge in the eradication of this bacterium^{2,24}. The presence of *R. solanacearum* was earlier reported only in tropical and subtropical regions², but later cold-tolerant strains were also characterized in Europe and North America^{25,26}. Due to the exceptionally wide host range, aggressiveness and adaptability, this bacterial wilt pathogen is emerging as a big threat causing huge damage to agriculturally important plant such as tomato, potato, eggplants, chilli and many other host crops in subtropical, tropical and warm temperature geographical regions^{27,28}. There is not a single potent approach available so far to deal with this pathogen and its associated disease²⁹.

In 1896, for the first time this bacterial pathogen was originally mentioned by Erwin F. Smith as the causative agent of lethal wilt disease of solanaceous plants. Initially, this disease was observed in potato, tomato as well as in eggplant. Subsequently, it was reported in tobacco plant³⁰. This bacterium was initially identified *Bacillus solanacearum* and later as *Pseudomonas solanacearum*.

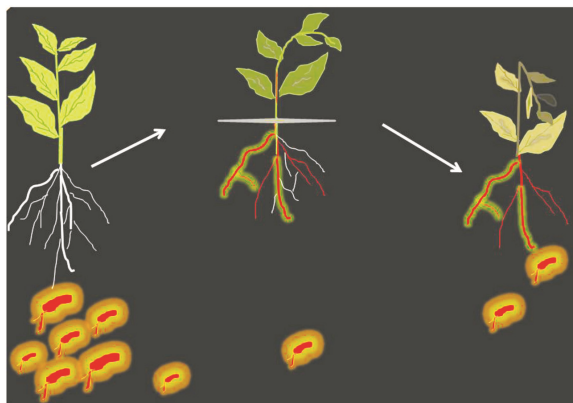


Figure 1. *Ralstonia solanacearum* and its infection cycle. *R. solanacearum* resides in soil, in favourable conditions it enters plant through root, colonizes and spreads there and ultimately kills the plant, and again comes back to soil and then searches for new host.

However, the most recent genus of *Ralstonia* was established in 1995 and is known as *R. solanacearum*³¹.

R. solanacearum bacterial wilt disease is endemic in geographical regions around the world such as subtropical, tropical and warm temperature³². The literature indicates that new host plants of *R. solanacearum* are being reported every year⁵. Even in India, *R. solanacearum* bacterial wilt disease is prevalent and presence of this bacterium has reported from most states across the country³³. In this context, *R. solanacearum* infection, disease progression and its adaptation to a wide range of plant species is still a mystery and the cryptic virulence behaviour of this wilt pathogen has been well reported by many concerned researchers²².

In spite of many studies on this bacterium across the world, several basic, important questions have remained unanswered related to *R. solanacearum* survival and its interaction with host plant during infection, disease progression and wilting. A few research questions that still remain unanswered are:

- (1) How does this bacterial wilt pathogen multiply and produce high amounts of sugar-rich EPS in a nutrients-limited environment inside the xylem tissue by tuning its own metabolism and altering the biochemistry of the xylem sap?
- (2) How can this wilt bacterium successfully colonize through the xylem vessel against high flow in big trees such as the eucalyptus?
- (3) *R. solanacearum* infection is still not well understood. Therefore, other crucial question is, why is this bacte-

rium present inside the host plant without manifesting any wilt related symptom or plant death?

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