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Current status of *Ralstonia solanacearum* as a threat

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Abstract

Ralstonia solanacearum is a highly destructive soil-borne bacterium that causes bacterial wilt in more than 450 plant species across 54 families severely affecting solanaceous crops such as potato, tomato and eggplant. Recognized as the world's second most damaging bacterial plant pathogen. It poses a major threat to global food security due to its rapid spread, genetic adaptability and persistence in diverse environments. The *Ralstonia solanacearum* species complex (RSSC) exhibits extensive genetic diversity, classified into phylotypes based on geography and survives through latent infections. Bacterial wilt is characterized by vascular browning, bacterial ooze and wilting, making it one of the most destructive plant diseases. Its management relies on a diverse set of strategies: cultural practices such as crop rotation, susceptible genotype, use of proper fertilizer and grafting; physical methods like soil solarisation, biofumigation and heat treatment, biological control using beneficial bacteria, fungi and bacteriophages. Additional approaches include organic amendments to enhance soil health, breeding resistant cultivars, innovative nanotechnology applications and targeted chemical measures. For long-term success an integrated approach that combines these methods is essential to sustainably suppress bacterial wilt and protect crop productivity.

Keywords: *Ralstonia solanacearum*, Solanaceous, phylotypes, Bacterial wilt

Introduction

Crop production is continually challenged by diverse pathogens that reduced both yield and quality. In which soil borne diseases are especially destructive due to their persistence in agricultural environments. Soil borne pathogens are a major contributor to crop losses across many economically important plants (Elphinstone *et al.*, 2005) ^[21]. Among them *Ralstonia solanacearum* the bacterium responsible for bacterial wilt is ranked as the world's second most destructive phytopathogen (Mansfield *et al.*, 2012) ^[59]. Bacterial wilt caused by *R. solanacearum* is the most devastating plant disease affecting more than 450 plant species across 54 botanical families with solanaceous crops being particularly highly susceptible. This pathogen exhibits considerable survival capacity in soil environments enabling persistence under diverse conditions (Paret *et al.*, 2010) ^[65]. Globally, it is regarded as one of the most destructive plant pathogens severely reducing both yield and quality in crops such as eggplant, tomato, pepper, potato and ginger (Cai *et al.*, 2021) ^[13]. Due to the destructive impact of bacterial wilt yield losses ranging from approximately 20 to 100 per cent have been reported worldwide. In India losses of 75 to 81 per cent have been documented varying with crop growth stage and prevailing environmental conditions (Wang *et al.*, 2023; Bamaniya *et al.*, 2025) ^[8, 91].

R. solanacearum spreads through multiple pathways such as contaminated water, infected planting materials, irrigation systems and runoff and farm equipment carrying infested soil (Heikrujam *et al.*, 2020) ^[34] also its behaviour varies with soil conditions and making their management complex. Modern plant disease management strategies face challenges related to climate change, pesticide resistance, residues and biodiversity loss (Senthilraja *et al.*, 2024) ^[80]. Hence effective management strategies is crucial to combat this devastating disease. This review highlights how pathogen survival, its race, pathogen distribution, damaging properties and its management strategies.

The pathogen: *Ralstonia solanacearum*

Ralstonia solanacearum is a cosmopolitan group of phylogenetically related strains that infect a wide range of plants. This diverse set of pathogens is collectively referred to as the *Ralstonia solanacearum* species complex (RSSC). RSSC complex (Gillings and Fahy, 1994) ^[27] causing bacterial wilt is considered one of the most obliterative plant pathogenic bacteria.

It is previously known as *Pseudomonas solanacearum* (Yabuuchi *et al.*, 1995) ^[93] which are Gram-negative, oxidase and exhibit positive reactions for both oxidase and catalase tests also it is aerobic bacilli that thrive in soil and water. This soil-borne bacterium is motile, equipped with a polar flagellum and exhibits a rod-shaped morphology measuring 0.5-1.5 µm (Hayward, 1991; Genin and Boucher, 2002) ^[26, 33]. *R. solanacearum* multiply in vascular elements of plants that are responsible for wilting symptoms on the infected plants (Holt *et al.*, 1994) ^[35]. It is classified within the β-proteobacteria group. The persistence of these bacteria are present in soils as well as aquatic environments (such as ponds and rivers) makes them extremely difficult to eliminate. Furthermore, international trade has accelerated their dissemination largely due to the latency period before disease symptoms become visible (Lampropoulos *et al.*, 2021) ^[51].

RSSC Phylotype diversity

RSSC complex are significant genetic and phenotypic diversity rather than a single homogeneous entity. This

complex contains many strains with different traits, such as different metabolic needs, different origins, different host ranges and specific conditions for optimal infection (García *et al.*, 2019) ^[25]. In that way RSSC strains are classified into four major phylotypes based on their geographical origins, viz Phylotype I (Asia), Phylotype II (the Americas), Phylotype III (Africa and the surrounding islands) and Phylotype IV (Indonesia, Japan and Australia). These phylotypes are reclassification based on genome analysis and average nucleotide identity where strains sharing at least 99 per cent similarity in their *egl* gene sequences are grouped (Safni *et al.*, 2014) ^[72]. Later this classification system was modified by Remenant *et al.* (2010) ^[70] suggesting that RSSC is composed of three species. This was formalised using DNA-DNA hybridisation analyses leading to the classification of RSSC into *R. solanacearum* (Phylotype II), *R. pseudosolanacearum* (Phylotypes I and III) and *R. syzygii* (Phylotype IV and the Blood Disease Bacterium strains) (Table.1; Fig. 1).

Table 1: Host, distribution and phylotype overview by race

Race	Host range	Distribution	Biovar	Phylotype Proposal
1	Tobacco, tomato, eggplant, groundnut, potato, pepper, ginger, olive, strawberry, geranium, eucalyptus and many weeds (Wide host range)	Asia, Australia, America	3, 4, 1	<i>R. pseudosolanacearum</i> Phylotype I, III
2	Banana and other <i>Musa</i> spp.	Caribbean, Brazil, Philippines Indonesia	1	<i>R. solanacearum</i> Phylotype II
3	Potato, tomato, some other Solanaceae	Worldwide	2	<i>R. syzygii</i> Phylotype IV
4	Ginger, cardamom, clove	Asia	3, 4	
5	Mulberry	China	5	

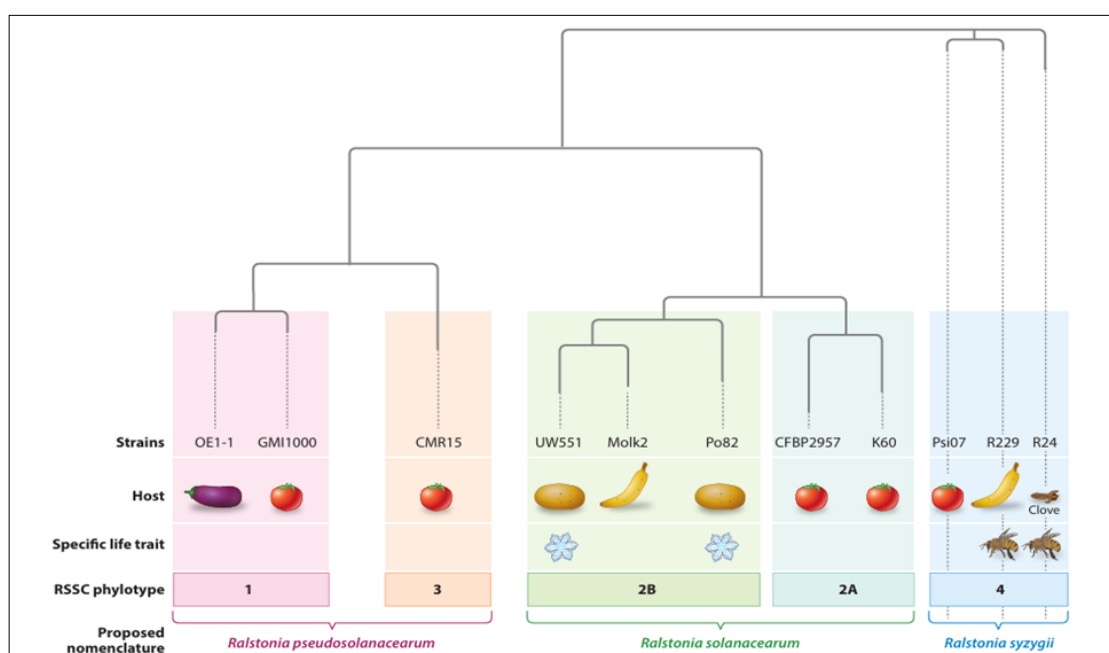


Fig 1: Phylogenetic tree of the *Ralstonia solanacearum* species complex (RSSC), showing representative strains, their original hosts and key traits such as cool-temperature adaptation and insect transmission. The former four-phylotype division and updated species nomenclature are indicated, with host symbols for eggplant, tomato, potato, banana and clove. (Referred from Vailleau and Genin, 2023) ^[26, 87]

Origin and distribution across world

Ralstonia solanacearum (RSSC Phylotype II) is believed to have originated in Central and South America regions noted for its extensive genetic diversity (Fegan and Prior, 2005) ^[23]. The pathogen was first associated with bacterial wilt in tobacco plants in 1920 (Parseval, 1922) ^[66]. In India Race 1, Biovar 3 strains of *R. solanacearum* are widely distributed

across coastal, hilly and foothill regions including Goa, Karnataka, Kerala, Maharashtra, Odisha, Jharkhand, West Bengal, the northeastern hill states, Himachal Pradesh, Jammu and Kashmir and Uttarakhand (Devi and Menon, 1980) ^[19]. Expanding this knowledge, Sagar and co-workers (2014) ^[73] reported the first occurrence of Phylotype IV, sequevar 8 (bv2T) causing potato bacterial wilt in the

mid-hill regions of Meghalaya. Complementary studies by Ramesh and colleagues (2014) ^[68] revealed significant genetic variability in solanaceous vegetables including the identification of new sequevars and underscoring the heterogeneous nature of *R. solanacearum* populations in India. More recently partial sequencing of the *egl* gene from 27 strains collected across four districts identified six distinct sequevars I-44, I-46, I-47, I-57, I-70 and I-71 with all except I-47 being reported for the first time in India highlighting the novel genetic diversity within the pathogen population (Saini *et al.*, 2025) ^[75].

Infection cycle of *R. solanacearum*

The life cycle of the *Ralstonia solanacearum* species complex (RSSC) has two main phases. In one, the bacterium infects host plants by producing virulence factors, evading defenses and multiplying within tissues. In the other, it persists in soil or water awaiting transmission to new hosts. This alternation between plant tissues and the external environment demands distinct survival strategies (Hayward, 1991) ^[33].

The pathogen overwinters in diseased plants, crop residues and vegetative organs such as potato tubers, ginger rhizomes, banana suckers or seeds of crops like tomato and capsicum. It also survives in the rhizosphere of weed hosts including *Solanum dulcamara*, *S. carolinense* and *S.*

cinereum (Van Elsas *et al.*, 2000) ^[88]. Such persistence often leads to latent infections when these hosts are further cultivated (Denny and Hayward, 2001) ^[17, 33]. Beyond soil RSSC endures in aquatic habitats. Contaminated irrigation water, municipal wastewater and facilities processing diseased plant material have all been identified as sources of inoculum (Elphinstone *et al.*, 1996; Janse *et al.*, 1998) ^[22, 37]. The pathogen usually enters plants through natural wounds, such as those formed during flower shedding or the growth of lateral roots, as well as through injuries caused by farming practices, nematodes or xylem feeding insects (Kelman and Sequeira, 1965) ^[44, 81]. The bacteria reach these entry points using flagella-driven swimming and chemotaxis which draws them toward root exudates (Fig. 2). Unlike many plant pathogens *R. solanacearum* can establish a systemic infection from a single entry site leading to bacterial wilt (Denny, 2006) ^[18]. Once inside the xylem provides a nutrient rich continuously flowing environment that supports bacterial growth. Here, RSSC forms biofilm clusters that block water vessels causing wilting and eventually plant death (Lowe-Power, 2018) ^[56]. Pathogenicity is regulated by quorum sensing when bacterial density reaches about 10^9 CFU/ml signaling molecules activate the PhcA regulator and virulence genes (Mansfield *et al.*, 2012) ^[59].

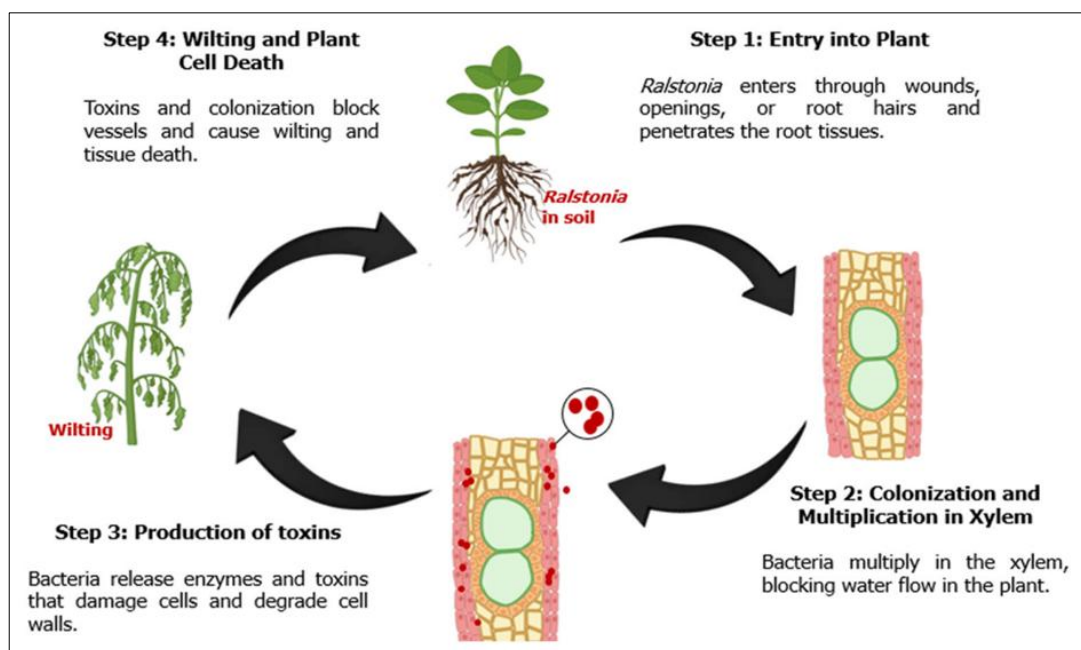


Fig 2: Life cycle of *Ralstonia solanacearum* species complex referred from Sabu *et al.* 2025 ^[71]

Plant disease symptoms

Infected plants show clear symptoms such as vascular browning, bacterial ooze, drooping leaves and wilting (Buddenhagen and Kelman, 1964) ^[12, 44]. The first visible sign is usually wilting of leaves at branch tips eventually the plant fails to recover and dies (Dey and Sen, 2023) ^[20].

In bananas, moko disease causes rapid wilting in young plants, breaking of petioles at sharp angles and plant death. Older plants show inner leaf discoloration and drooping followed by outer leaves until the whole plant collapses (Sequeira and Kelman, 1965) ^[44, 81]. During fruiting, peduncles display scars from fallen male flowers, the terminal bud blackens and fruits show stunted growth, premature ripening, splitting, internal discoloration and rot

(Fig. 3 (b)). Cutting open infected pseudostems reveals yellowish brown or black vascular bundles (Buddenhagen, 1960) ^[11]. In ginger, bacterial wilt causes rolling, curling, yellowing and necrosis of leaves, leading to stunting, decline and plant death with rhizomes becoming rotten and discolored and vascular bundles showing browning (Trujillo, 1964) ^[86]. In potato, a typical sign is bacterial slime exuding from the eyes or stem-end of infected tubers, which distinguishes it from other rots; cutting the tuber reveals browning and necrosis of the vascular ring and in severe cases, yellowish disintegrated tissue and slime are squeezed out, while foliar symptoms may occur even when some tubers remain healthy (Archana *et al.*, 2024) ^[5]. A common diagnostic feature across hosts is vascular

browning, where cutting the stem base and placing it in clean water releases white bacterial ooze (Kumar *et al.*, 2017) ^[50] (Fig. 3 (a)). Disease development is favoured by

high temperatures (30-35 °C) and heavy soils with high moisture content (Mondal, 2011) ^[62].



Fig 3: Damage symptoms of (a) Browning and necrosis of potato tuber and (b) Gummy excudes in banana (Sarkar *et al.*, 2025) ^[77]

Yield losses in indian states

Ralstonia solanacearum has caused significant yield losses in India particularly in solanaceous crops such as tomato, potato and brinjal. Wang and his co-workers reported bacterial wilt leading to 20-100% yield losses worldwide, with Indian outbreaks typically ranging between 10-90% depending on crop and region. The pathogen was especially destructive in humid and subtropical zones such as Kerala, Karnataka and Northeast India, where localized epidemics in tomato and brinjal fields often exceeded 50% losses. In Sikkim, 10-90% crop damage reported in tomato and brinjal across East Sikkim villages such as Assam Linzay, Phadamchen, Sajong and Singtam (Bamaniya *et al.*, 2025) ^[8]. Similarly, in Himachal Pradesh severe outbreaks in potato and tomato were reported (Sharma *et al.*, 2025) ^[83]. Across Kerala, Karnataka and the northeastern states solanaceous crops and banana plantations suffered 30-70% losses. The pathogen's persistence was high in soil and water due to its wide host range and adaptability to tropical climates make it a major threat to smallholder farmers particularly in organic farming systems where chemical control is limited.

Detection methods

Detection of *R. solanacearum* is critical for early management of bacterial wilt and several traditional and modern techniques are available. Classical methods include bacteriophage recognition, phospholipid fatty acid analysis, serodiagnosis, PCR, LAMP (Loop-mediated isothermal amplification) and FISH (Fluorescence in situ hybridization), which allow identification of races and biovars (Singh, 2017) ^[84]. Multiplex-PCR has been used to simultaneously detect *R. solanacearum* and *Clavibacter michiganensis* in potato peels (Sebastien *et al.*, 2014) ^[79]. Recent advances include real-time PCR assays targeting specific genes such as *egl* and *fliC*, which provide rapid and highly sensitive detection within hours (Bhatt *et al.*, 2024) ^[10]. Loop-mediated isothermal amplification (q-LAMP) has been optimized for potato tubers, enabling field-level diagnosis with minimal equipment (Zhang *et al.*, 2026) ^[95]. Immuno-based assays such as ELISA and lateral flow devices now offer portable, farmer-friendly detection with high specificity (Agarwal, 2024) ^[2]. Additionally, nanoparticle-based biosensors are emerging as innovative tools capable of detecting low pathogen loads directly in soil and plant tissues (Jiang *et al.*, 2025) ^[40]. Together, these methods from classical microbiological assays to

cutting-edge molecular and nanotechnological tools provide a comprehensive toolkit for rapid and reliable detection of *Ralstonia solanacearum*, enabling timely prophylactic measures to reduce yield losses.

Management practices

Cultural practices

Cultural practices improve crop yield and reduce pathogen impact (Ajilogba and Babalola, 2013) ^[3]. Crop rotation is a cost-effective method where different crops are grown on the same land in successive seasons. Continuous cropping of hosts like tomato encourages pathogen buildup, while rotation with non-host crops reduces disease (Janvier *et al.*, 2007) ^[38]. Recent studies confirm this effect for example, tobacco rotated with maize showed higher yields and reduced bacterial wilt compared to continuous potato cropping (Ma *et al.*, 2024) ^[57].

Growing susceptible tomato varieties after corn, okra, cowpea or resistant tomato delays wilt symptoms by 15-20 days and reduces disease severity by 30 to 40 per cent (Nion and Toyota, 2015) ^[63]. Similarly, rotating potatoes with millet, beans, sorghum or maize can double yields and cut disease severity by up to 80 per cent (Katafiire *et al.*, 2005) ^[42]. Intercropping of maize and beans helps in reduction of 55% disease incidence in potato cultivation (Chadfield *et al.*, 2022) ^[15].

Proper fertilizer management further reduces wilt occurrence. Calcium is especially effective higher Ca levels in tomato stems lower pathogen populations and disease severity (Nion and Toyota, 2015) ^[63]. Lime (CaCO_3 or $\text{CaMg}(\text{CO}_3)_2$) application in bacterial wilt infected field shows a significant reduction in wilt incidence (Cao *et al.*, 2022) ^[14]. Combined N + P + K fertilizers can reduce disease by 60 per cent and improve potato yield. Organic fertilizers and rock dust also help manage wilt by improving nutrient balance (Hacisalihoglu *et al.*, 2007) ^[30]. Silicon and chitosan applications strengthen plant resistance and reduce bacterial wilt frequency while silicon fertilizers enhance tomato yield and lower pathogen populations (Hartmann, 2002) ^[31]. Farmyard manure improves soil properties, boosting tomato growth and reducing wilt severity. Grafting is another effective technique, where a desired plant variety is joined to a disease resistant rootstock (King *et al.*, 2008; Louws *et al.*, 2010) ^[47, 55].

Physical approaches

Physical control methods such as soil disinfection, hot water treatment and soil solarization are effective against bacterial wilt (Nion and Toyota, 2015) ^[63]. Thirty days of soil solarization before planting reduces pathogen inoculum, lowers disease severity and improves yield and germination (Kumar and Hayward, 2005) ^[33, 49]. Solarization works by trapping sunlight under plastic sheets to raise soil temperature, killing pathogens, weed seeds and pests without toxic residues. In India, studies from RPCAU Bihar and CSKHP Himachal Pradesh (Arun *et al.*, 2025) ^[6] found that combining solarization with farmyard manure and biocontrol agents further reduced bacterial wilt in tomato and potato fields, while also improving soil health.

Heat based methods are also effective in reducing bacterial wilt. For example, microwaving ginger seeds at 42 °C or heating infected soil at 52 °C for three days lowered bacterial populations by 50 to 86 per cent. Another experiment showed that treating infected ginger seeds with hot air for 28 minutes produced healthy rhizomes without affecting plant growth. These approaches demonstrate that controlled heating can suppress pathogens and help farmers grow healthier crops (Kumar and Hayward, 2005) ^[33, 49].

Biofumigation also called biological soil disinfection (BSD) is a newer approach. It uses gases released from decomposing plant residues to suppress soil borne pathogens. These gases include organic acids and sometimes metal ions, which inhibit the growth of harmful bacteria (Momma, 2008) ^[61]. Organic amendments like molasses or wheat bran also release antimicrobial compounds that kill *R. solanacearum* (Nion and Toyota, 2015) ^[63]. Studies reported by Sharma *et al.*, 2025 ^[83] showed that biofumigation with *Brassica* residues and farmyard manure significantly reduced bacterial wilt in tomato and potato fields, while improving overall soil quality.

Biological methods

Biological control means using living organisms to fight harmful ones through interactions like mutualism, antagonism or parasitism (Sahu *et al.*, 2017) ^[74]. It offers long term disease suppression, lowers the cost of nonrenewable inputs and is self-sustaining (Whipps, 2001; Wang *et al.*, 2021) ^[90, 92]. Because effective agents are limited, biocontrol microbes are not widely used against bacterial wilt. Still, many studies show that bacteria, fungi and bacteriophages can suppress *R. solanacearum*.

Bacteria

Most biocontrol agents (BCAs) are bacteria (90%), while fungi make up about 10% (Wang, 2023) ^[91]. Common bacterial BCAs include *Pseudomonas*, *Bacillus*, *Streptomyces* and *Paenibacillus* (Nion and Toyota, 2015) ^[63]. Recent studies show that *Enterobacter cloacae* from potato plants reduced bacterial wilt by 26.5% (Malek *et al.*, 2023) ^[58] and *Paenibacillus polymyxa* in potato soil lowered disease by 80% (Soliman, 2020) ^[85]. In tomato, *Pseudomonas aeruginosa* and *P. syringae* controlled wilt through host resistance and antibiosis (Mohammed *et al.*, 2019). Agarwal and his co-workers isolated 40 endophytic bacteria from *Gnetum gnemon* and found that *Bacillus velezensis* and *Staphylococcus warneri* showed strong antibiosis activity. *Bacillus licheniformis* was especially effective, reducing wilt by 67% with soil drenching and seed priming and achieving 71% reduction in artificial inoculation tests. Field trials also showed that combining soil solarization with *B. licheniformis* reduced *R. pseudosolanacearum* in ginger fields. This bacterium is now marketed as a biocontrol product called “Bacillich” for managing ginger bacterial wilt (Bhai *et al.*, 2019) ^[9].

Fungi

Aside from bacteria some fungi also act as biocontrol agents against *Ralstonia solanacearum*. In greenhouse studies, treatment with *Glomus versiforme* reduced pathogen populations on tomato roots and xylem by 26.7%, 79.3% and 81.7%, while also increasing soluble and cell-wall-bound phenols that strengthen plant resistance (Zhu and Yao, 2004) ^[96]. Another fungus, *Pythium oligandrum*, suppressed bacterial wilt by regulating the plant's ethylene signaling pathway (Hase *et al.*, 2006) ^[32]. Other fungi such as *Parmotrema tinctorum* (Gomes *et al.*, 2003) ^[28], *Scutellospora* sp., *Glomus margarita* and *G. mosseae* have also been recognized as effective biocontrol fungi against wilt (Kim *et al.*, 2003) ^[46]. Overall, inoculation with *Glomus* species not only reduced pathogen levels but also boosted root phenols, thereby inducing host resistance.

Bacteriophages

Bacteriophages are viruses that infect and kill bacteria and they are now being explored as effective biocontrol agents in agriculture. Ramírez *et al.* (2020) ^[69] isolated eight lytic phages tested against 65 strains of *R. solanacearum*; two phages provided 100% protection against Moko disease when applied as a cocktail. Wafula ^[89] and colleagues identified phages SN1 and WT1, which showed strong lytic activity along with high heat and acid tolerance, making them suitable under varied field conditions. In banana soils, lytic phages were also effective in reducing *R. solanacearum* populations. Later, Alvàrez *et al.* (2019) reported waterborne phages (three from the Podoviridae family) that successfully managed bacterial wilt when applied through irrigation water the first demonstration of phage use via irrigation for this pathogen.

Organic matter

Organic soil amendments play an important role in improving crop productivity. They enhance the soil's physical, chemical and biological properties which helps plants grow better (Bailey and Lazarovits, 2003) ^[7]. These amendments stimulate disease-fighting microbes and may contain vitamins, growth regulators or toxins that affect soil bacteria. For example, compost treatment increased enzymes like ascorbate peroxidase and glutathione reductase, which strengthened plant resistance against bacterial wilt (Youssef and Tartoura, 2013) ^[94]. Organic matter comes from living organisms and is divided into plant residues (about 80%), animal waste (10%) and simple organic matter (10%). Biological additions also introduce beneficial microbes into soil, which influence microbial communities depending on the type and amount added (Larkin, 2008) ^[52]. A new approach is using organic hydroponic systems, where rhizosphere biofilms form only on organic roots. This method has shown promise in controlling bacterial wilt (Fujiwara *et al.*, 2012) ^[24].

Breeding and genetic engineering approaches

The most efficient and eco-friendly way to manage bacterial wilt is by cultivating resistant cultivars (Nion and Toyota, 2015) ^[63]. Breeding programs in vegetables and field crops have produced resistant lines though success depends on genetic diversity, host-pathogen interactions and agronomic traits (Elphinstone *et al.*, 2005) ^[21]. Somatic hybrids of *Solanum melongena* and *S. aethiopicum* showed resistance, while potato genotype CF6 reduced wilt severity by 90-100%. Resistant tomato plants restricted pathogen movement in xylem was preventing wilt. However, resistance often correlates negatively with yield and quality, limiting farmer acceptance. Biotechnology offers promise such as tomato lines carrying the NPR1 gene from

Arabidopsis which induced systemic resistance and reduced wilt (Lin *et al.*, 2004) [53]. Despite progress crops like ginger still lack resistant cultivars due to limited genetic variation. Mutation breeding with gamma rays has produced resistant ginger mutants, currently under field evaluation (Prasath *et al.*, 2011) [67]. Overall, resistant cultivars remain a key strategy though future efforts must balance disease resistance with yield and consumer acceptance.

Nano technological approaches

Nanotechnology has rapidly advanced in the 21st century and offers new solutions for detecting and controlling soil pathogens like *Ralstonia solanacearum* (Khan *et al.*, 2021; Guo *et al.*, 2022) [29, 45]. Recent studies show that nanoparticles can act as biosensors and antibacterial agents. Metallic oxide nanoparticles such as ZnO, FeO and CuO have been tested against tomato bacterial wilt, with CuO NPs showing the strongest disease suppression and improving plant growth (Jiang *et al.*, 2021) [39]. Chitosan nanoparticles (ChNPs) also proved effective, reducing disease severity *in vivo* and causing bacterial cell wall damage, flagella loss and lysis (Kaari *et al.*, 2022) [41]. Additionally, AgNP-loaded ChNPs demonstrated strong antibacterial activity against *R. solanacearum* (Santiago *et al.*, 2019) [76].

Chemical approaches

Chemical approaches include the utilization of synthetic chemicals for the control of plant diseases. Over the years bacterial wilt has been managed using a variety of chemical techniques. It remains one of the most widely used strategies for managing bacterial wilt, with pesticides such as fumigants (methyl bromide, 1,3-dichloropropene, chloropicrin) and bactericides (streptomycin sulphate, triazolothiadiazine) showing strong suppression of *R. solanacearum* in crops like tomato and tobacco, reducing field incidence by up to 100% (Lin *et al.*, 2010; Schreinemachers and Tipraqsa, 2012) [54, 78]. Plant activators such as validamycin-A and acibenzolar-S-methyl (ASM) have been reported to induce systemic resistance, while combinations like ASM with thymol significantly decreased disease severity and improved tomato yield (Hong *et al.*, 2011) [36]. Other compounds, including bleaching powder (Sharma and Kumar, 2000) [82], silicon amendments (Dannon and Wydra, 2004; Wang *et al.*, 2023) [16, 91] and chitosan (Kirkegaard *et al.*, 1996) [48] have also reduced wilt by enhancing host resistance. Innovative chemical approaches include polymer-based soil treatments that trap or coagulate pathogen cells (Kawabata *et al.*, 2005) [43] and phosphoric acid solutions with bacteriostatic effects (Norman *et al.*, 2006) [64]. While chemical pesticides remain effective, their environmental risks and economic costs highlight the need for careful threshold-based application in high-value crops.

Conclusion

Ralstonia solanacearum remains one of the most destructive soil borne pathogens, threatening global food security through its wide host range, genetic diversity and persistence in soil and water. Effective management requires an integrated approach combining cultural practices, physical methods, biological control, organic amendments, resistant cultivars, nanotechnology and chemical strategies. While each method offers partial suppression, their combined application ensures sustainable disease management and improved crop productivity. Continued research into pathogen diversity, detection tools and eco friendly control measures is vital to safeguard their host crops and smallholder farming systems.

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