

Bacterial Pathogens Infecting Plants

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Introduction

Bacteria are the prokaryotic microorganisms infecting many economically important plants throughout the world resulting in death of the plants. They cause many different kinds of symptoms that include blight, canker, galls and overgrowths, wilts, leaf spots, specks, scab and soft rots etc. Bacteria vary in shape and sizes, cell wall structure, presence or absence of flagella, biochemical properties, as well as molecular basis. The taxonomy of plant pathogenic bacteria is in flux and the classification keeps on changing based on recent advancements in molecular techniques. In general, most of the phytopathogenic bacteria belong to family Xanthomonadaceae, Pseudomonadaceae, Rhizobiaceae and Enterobacteriaceae. The most virulent plant pathogenic bacteria in these families are *Pseudomonas*, *Ralstonia*, *Xanthomonas*, *Erwinia*, *Pectobacterium*, *Pantoea*, *Agrobacterium*, *Burkholderia*, *Acidovorax*, *Clavibacter*, *Streptomyces*, *Xylella*, *Spiroplasma*, and *Phytoplasma*.

Most of the plant pathogenic bacteria are aerobic and some of them are facultative anaerobes. They colonize all plant parts including xylem and phloem, inter and intracellular spaces. Disease symptoms can be visualized only after the bacterial cells has colonized and invaded at high levels in the infected tissue. Bacterial penetration is indirect process as they are unable to form mycelium, germ tube, appressorium, penetration peg etc. as formed by fungi. The epiphytic bacteria often reach population densities of between 10^6 - 10^7 cells/cm² of leaves, roots, apoplast, rhizosphere and other plant surfaces. Several phytopathogenic bacterial infection processes are unique and different from that of fungi and viruses. Bacterial pathogenicity depends upon bacterial secretion systems (types I, II, III, IV), quorum sensing (QS), plant cell-wall-degrading enzymes, toxins, hormones, polysaccharides, proteinases, siderophores, and melanin. The phytopathogenic bacteria are known to persist in the cells and this lead to the reoccurrence of disease by recovering growth and recolonizing the host plant

after the end of unfavourable environment. Moreover bacteria also become resistant to antibiotics used for management. The existence of resistance makes the eradication of bacteria difficult, despite of the defense responses and antimicrobial compounds produced by plants in response. This might be an important reason for crop disease outbreaks and recurrence in many economically important plants. Recent advances in the field of plant bacteriology advocates the importance of detection and management of these bacterial pathogens. Thus, it is imperative to improve our knowledge on basic infection process, pathogenicity, virulence factors, persistence and molecular tools for identification of these pathogenic bacteria for sustainable management.

Top bacterial plant pathogens

Pseudomonas syringae pathovars

Pathogen *Pseudomonas syringae* causes severe losses in many host plants and the bacterium is one of the best known as a plant pathogen and also serves as a model pathogen to understand ecology, virulence, pathogenicity, epidemiology and other molecular mechanisms. Multiple host plants are affected by this organism including cereals, annual crops, vegetables and woody plants. Ice-nucleating properties of *P. syringae* are primarily associated with frost damage to many crops. This pathogen is also known to coexist with different microorganisms in plant microbiota and this phenomenon influence the disease progression, pathogenicity, virulence and the level of immune responses in plants. Recent data advocates more than 10 species of *Pseudomonas* and over 60 pathovars with different host ranges.

Ralstonia solanacearum

Second important bacterial pathogen *Ralstonia solanacearum* is a Gram-negative, rod shaped, soil borne bacterium and motile with a polar flagellar tuft. It infects wide range of host plants infecting 200 plant species in over 50 families such as potato, tomato, egg plant, banana, soybean, ginger, tobacco, sweet pepper, olive etc. Bacteria enters the roots through wounds, colonizes the xylem tissue, moves up into the stem and causes wilt after successful colonization and mass-production of extracellular polysaccharides. This leads to systemic infection and ultimately death of the plants.

Agrobacterium tumefaciens

Agrobacterium tumefaciens causes crown gall in many economically important host plants. This bacterium is best known for its interkingdom gene transfer and is used as biotechnological tool. Susceptible plants contain phenolic compounds that are perceived by the bacterial cells living free in the soil. The virulent bacteria possess several virulence genes located on an extrachromosomal element called tumour inducing plasmid (pTi) encoding genes for the synthesis of auxins and cytokinins, production of opines and their utilization. The interkingdom transfer of T-DNA into the chromosome of susceptible plant species results in formation of tumours on roots. Still, many molecular mechanisms underlying plant transformation by this bacterium are unclear and are of specific concern for bacteriologists.

Xanthomonas spp

Bacteria belonging to the genus *Xanthomonas* are responsible for diseases on more than 400 different economically important host plants. *Xanthomonas*, a large bacterial genus under the gamma subdivision of the Proteobacteria, consists of a range of pathogenic and non-pathogenic species. *Xanthomonas oryzae* pv. *oryzae* (Xoo) causes the most devastating disease called bacterial blight of rice in most of the rice growing countries all over the world. Xoo occurs at different stages during growth and results in leaf blight or “Kresek” symptoms. This Kresek phase causes acute wilting of young plants and ultimately leads to the death of plants. *Xanthomonas campestris* and pathovars cause diseases of many important agricultural crops throughout the world. *Xanthomonas campestris* pv. *campestris* (Xcc) causes black rot of crucifers, *X. euvesicatoria*, causes bacterial spot of pepper and tomato, *X. campestris* pv. *malvacearum* which causes angular leaf spot of cotton, *Xanthomonas campestris* pv. *vitians* causes black leaf spot of lettuce and *Xanthomonas campestris* pv. *pelargonii* causal agent of bacterial blight on plants in the genera *Pelargonium* and *Geranium*. These bacteria produce yellow pigments called xanthomonadin and the exopolysaccharide xanthan, responsible for the colour of colony and viscous cultures. Recent studies shows that lytic transglycosylases of *Xanthomonas campestris* pv. *campestris* are important for daughter cell separation and translocation of type III secretion system effectors. Besides, *Xanthomonas axonopodis* pv. *manihotis* (Xam) is the causal agent of bacterial blight of cassava, *Xanthomonas axonopodis* pv. *citri* causes citrus canker, *Xanthomonas axonopodis* pv. *eucalyptorum* causes bacterial blight of *Eucalyptus*, *Xanthomonas axonopodis* pv. *allii* causes blight of onion, *Xanthomonas axonopodis* pv. *punicae* causes bacterial blight in pomegranate.

Erwinia amylovora

Erwinia amylovora is the first identified bacterial pathogen. The bacterium is Gram negative; rod shaped belonging to family Enterobacteriaceae, and is the causative agent of the disease known as fire blight. Fire blight is considered as one of the most devastating diseases of apple and pear. Initial symptoms involve water soaking spots, followed by wilting and rapid necrosis of infected tissues. Infection of flowers, growing shoots and rootstocks and further movement of bacterial cells into vascular system makes it difficult to manage before time. This is important to note that the genome of *E. amylovora* is amongst the smallest of the plant pathogenic bacteria that has been sequenced so far, at only 3.89 Mb. In contrast to this it can adopt a biotrophic or necrotrophic lifestyle and could easily overwinter in dead apple leaves. The bacteria can manipulate host defence mechanisms to cause disease and the effector proteins such as AvrRpt2EA are transferred into hosts by type III secretion system (T3SS) to cause fire blight in susceptible *Malus* genotypes.

Xylella fastidiosa

Xylella fastidiosa is gram-negative, aerobic bacterium infecting plants and is transmitted exclusively by xylem fluid feeding sap insects. *X. fastidiosa* has been reported to cause bacterial leaf scorch, oleander leaf scorch, coffee leaf scorch, alfalfa dwarf, phony peach disease, the economically important Pierce's disease of grapes, citrus variegated chlorosis, olive quick decline syndrome. This was the first phytopathogen to have its genome completely sequenced. Bacteria can move upstream and downstream along plant xylem by type IV pili. The bacteria actively multiply in xylem and block the translocation processes by forming a biofilm. Moreover, the detection and identification of *X. fastidiosa* is also not easy. Several researchers have developed different protocols by utilizing specific primers capable of recognizing target sequences on genomic DNA and are rapidly becoming the most widely accepted methods for the detection and identification of *X. fastidiosa* strains. Further, more research should be focused on management of this notorious plant pathogenic bacterium that represents a threat to global food crops worldwide.

Dickeya spp* and *Pectobacterium spp

The pectinolytic bacteria belonging to genus *Dickeya* and *Pectobacterium* are causative agents of maceration or rotting. *Dickeya* is a gram negative that belongs to the family *Pectobacteriaceae*. *Dickeya* genus is distinguished into different species such as

Dickeya dadantii, *Dickeya dieffenbachiae*, *Dickeya chrysanthemi*, *Dickeya paradisiaca*, *Dickeya zaeae*, *Dickeya dianthicola*, *D. dadantii* subsp. *dieffenbachiae*, *D. solani*, *Dickeya aquatica*, *Dickeya fangzhongdai*. *D. dadantii* infect the fleshy plant parts like tubers, rhizomes, stems and leaves and results in localized symptoms and is also capable of infecting the xylem, resulting in a systemic infection that causes wilting. The strains of *D. solani* are highly virulent on potato. Recent studies advocates that highly virulent *D. solani* produce higher number of metabolized compounds and are having faster metabolic rate, and can easily tolerate unfavorable pH and osmolarity.

Similarly *Pectobacterium carotovorum* and *Pectobacterium atrosepticum* were previously classified under *Erwinia carotovora* subspecies *carotovora* and subspecies *atroseptica* and were known as pathogenic bacteria causing soft rots. They are necrotrophic pathogens responsible for yield losses of important crops worldwide. Pathogenicity of these bacteria is dependent on the production and secretion of different extracellular plant cell wall-degrading enzymes also called exoenzymes i.e. pectate lyases (Pel), polygalacturonases (Peh), proteases (Prt), and cellulases (Cel), which results in extensive tissue maceration, rotting, and death of the whole plants. There are 12 recognized species that falls in the genus *Pectobacterium*- *P. carotovorum*, *P. atrosepticum*, *P. cacticidum*, *P. aroidearum*, *P. aquaticum*, *P. betavasculorum*, *P. wasabiae*, , *P. parmentieri*, *P. peruviense*, *P. polaris*, *P. punjabense*, and *P. zantedeschiae*.

Future outlook

Global environmental changes have greatly influenced the plant diseases as pathogens respond differently to the changing environmental factors. Many bacterial pathogens are becoming resistant to the antimicrobial compounds that are currently in use. Different virulence mechanisms such as the production of toxins and virulence proteins, pathogen colonization, reproduction, survival and spread are greatly influenced by climate. Instead of this plant resistance mechanisms such as pattern-triggered immunity and effector-triggered immunity, RNA interference, defence hormone networks and other molecular resistance mechanisms are all affected by environmental factors. Day by day new species, pathovars, strains and biotypes of bacteria are emerging with higher potential to cause severe damage to the crops. For this reason research efforts are now focusing on alternative methods to control bacterial pathogens. The discovery of different virulence factors associated with disease



development has led to escalated research towards discovering the possible biological control measures to target the specific genes responsible for extracellular polysaccharide secretion, type secretion effector proteins, quorum sensing regulation, toxin and hormonal production. Now days the molecular detection tools have also facilitated researchers to focus on specific genes of pathogens that are responsible for virulence. Understanding the pathogenicity and virulence in plant pathogenic bacteria could provide useful tools for management of bacterial plant diseases that are now a potential threat to global agriculture. Moreover, this is the need of the hour to amalgamate all the traditional and recent molecular knowledge to understand the multi dimensional plant-pathogen interactions and to focus on production of disease-resistant crop plants that are resilient to changing environment.

