

Bacterial pathogens in plants

Opinion

Plants are constantly attacked by a variety of pathogens including bacteria, fungi and viruses. Plants have evolved a machinery to combat these pathogen attacks. Unlike humans, plants lack a proper immune system. However, plants have developed a capable molecular and chemical system to detect invading microorganisms and prevent them before they can cause any extensive damage to plants.¹ A proper understanding of the plant defense mechanism is crucial for improving crop health and yield. Based on their lifestyles, plant pathogens can be divided into two major categories- Biotrophs and Necrotrophs. Most bacteria and viruses are considered as biotrophs, while fungi mostly adopt necrotrophic life style.² Compared to fungi and viruses, plant pathogenic bacteria cause relatively less damage and economic cost throughout the world.¹⁻⁴ Bacteria may live on plants with or without any signs of symptom development.¹ Bacteria that belong to either biotrophs or hemibiotrophs class of pathogens, interact with host plants through specialized genes and mechanisms to infect or colonize plants. Association of bacteria with plants may be detrimental or beneficial. Some bacterial species such as saprophytes do not cause diseases in plants, so they are considered as non-pathogens.² Mature bacteria colonize plants. Large population of pathogenic bacteria can be visualized as viscous suspension, as aggregates in liquid, or biofilm on plants. In the laboratory, they can be visualized as colonies on petri dishes or as an individual colony under a microscope. Normally, a higher population of bacteria, ~106 CFU (colony forming units/milliliter) is required to cause diseases in plants.¹

At molecular level, there is a need of identifying and characterize several virulence genes in bacteria and explore their locations and functioning in host plants.¹ These virulence genes can be the molecules secreted by bacteria upon infection in plants. For maximum understanding of bacterial genome, fully annotated sequences of bacteria are needed.⁵ Some powerful methods such as DNA microarray and proteomics studies^{6,7} have advanced our understanding of bacteria genome. Advancement in these techniques are enabling studies related to various aspects of bacterial pathogens such as identifying virulence factors, recognition of types of bacterial strains and their relationship with other known strains, studying pathogenicity caused by bacteria, and bacterial gene evolution, expression and regulation. All these studies of natural and mutant bacterial species are being used to improve plant health and disease management practices.¹

“How bacterial pathogens infect plants” has been a well-studied area of research in plant-bacterial interactions. Several mechanisms have been proposed to understand pathogenicity of bacterial pathogens in plants.^{8,9} These studies describe about several virulence and pathogenicity genes of bacteria. Bacteria usually use Type III secretion system to inject chemicals into plant cells. This system resembles with a syringe and plunger system that bacteria use to inject effector proteins to cause diseases and trigger defense responses in plants.¹⁰ Similar type of secretion system has been reported in animal and human bacterial pathogens.¹¹

Among all bacterial pathogens that infect plants, *Pseudomonas syringae* pathovars are the most common and well-studied ones.

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Pseudomonas syringae is a Gram-negative bacterium that causes various symptoms in plants such as blights, cankers, leaf spots and wilting.¹² Depending on the host, *P. syringae* is differentiated into >40 different pathogenic variants or pathovars. Most pathovars of *P. syringae* have been reported as economically important pathogens based on their impact on food production and environment. *P. syringae* has been used as a model pathogen system to understand the effector biology of the filamentous pathogens.¹³⁻¹⁵ As high-throughput sequencing technologies are applied to study bacterial genome, new *P. syringae* genomes are being released every year.¹⁶ This *P. syringae* model pathogen has opened new avenues in molecular studies of plant defense and pathogenicity. Mechanism of *P. syringae* infection and genetics of *P. syringae*-*Arabidopsis* (a model plant) interaction have been studied for years. Now, we have an improved understanding of plant-bacteria interaction. However, we still lack a thorough understanding of bacterial disease epidemiology and how bacteria make transition from one life style to other during an infection process.¹⁶⁻¹⁹

Over the years, use of new analyses, instrumentations, and techniques have enhanced our knowledge about pathogens. Recent advances in bioinformatics methods and genome sequencing techniques have enabled the sequencing of more than hundred bacterial genomes including plant pathogenic bacteria.¹ Various evolutionary and comparative genomics methods have enhanced our understanding of bacterial genome. However, scientists are still facing big challenges such as proper annotation of bacterial genomes and functions of all genes.¹ Recent advances in genomics and proteomics technologies will help us better understand plant and bacterial interaction at molecular level.

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Conflict of interest

The author declares no conflict of interest.

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