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Secretion Systems: A Potent Weapon of Plant Pathogenic Bacteria

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ARTICLE ID: 49

Introduction:

For phytopathogenic bacteria to form surface structures for adhesion, aggregation, and bacterial motility as well as to secrete enzymes, proteases, toxins, and effectors that destroy and alter host cells, secretion systems are essential. In order for bacteria to allocate proteins to their proper sites for a coordinated and effective attack on the plant cell, a superabundance of generalised and specialised export and secretion systems are required. Moreover, secretion systems give bacteria a way to exchange nucleic acids, influence the evolution of pathogenicity, and compete against other microbes. The fundamentals of the type I–VII secretion systems and their functions in plant pathogenesis are the main topics of this article.

Secretion across the cytoplasmic membrane:

Proteins are secreted from the bacterial cytoplasm into other cell compartments, particularly into or across the cytoplasmic membrane. The two bacterial secretion pathways that are most frequently used to transport proteins across the cytoplasmic membrane are the general secretion (Sec) and twin arginine translocation (Tat) pathways (Natale*et al*., 2008). The Sec and Tat pathways, which have been discovered in all domains of life (bacteria, archaea, and eukarya), are the most highly conserved systems of protein secretion (Papanikou*et al*., 2007; Robinson and Bolhuis, 2004).Most proteins transported by the Sec and Tat pathways remain inside the cell, in either the periplasm or the inner membrane.In contrast, proteins transported by the Sec or Tat pathway to the cytoplasmic membrane or periplasm of gram-negative bacteria can either remain in those compartments or may be transferred outside of the cell with the aid of different secretion systems.

Secretion across the Outer Membrane:

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Gram-negative bacteria exclusively secrete over their outer membrane. In order to export proteins, gram-negative bacteria have developed a series of processes that fall into one of two categories:

1. Export the protein over the inner membrane using either the Sec or Tat pathways in a two-step process.
2. As a one-step procedure in which the protein is transported directly from the cytosol to the exterior of the cell.

Types of bacterial secretion systems:

Type I secretion system (T1SS):

Many Gram-negative bacteria, including pathogens of plants and animals, have been identified to have T1SSs, which transport their substrates in a single step through both the inner and outer bacterial membranes. T1SSs closely resemble a wide family of ATP-binding cassette (ABC) transporters, which export small compounds like antibiotics and toxins out of the cell (Symmons*et al*., 2009). Many T1SSs may be present in bacteria, each of which is responsible for transporting one or more unfolded substrates (Delepelaire, 2004). These substrates serve a variety of purposes, and they include adhesins, heme-binding proteins, and proteins containing repeats-in-toxins (RTX) motifs in addition to digestive enzymes like proteases and lipases. T1SSs have three essential structural components: (i) an ABC transporter protein in the inner membrane and (ii) a membrane fusion protein (MFP) that crosses the inner membrane and bridges it to the outer membrane, and (iii) the outer membrane factor (OMF) in the outer membrane (Thomas *et al*., 2014). The ABC transporter component connected to the T1SS performs a number of key activities, including interacting with the MFP and participating in substrate identification. It also catalyses ATP to give the energy needed to transport the substrate.

Type II secretion system (T2SS):

T2SSs transport folded proteins from the periplasm into the extracellular environment and are conserved in the majority of Gram-negative bacteria. Proteins secreted by the T2SS channel, which is only present in the outer membrane, must first be transported to the periplasm via the Sec or Tat secretion pathways, which move protein substrates across the inner membrane. Plant disease caused by members of the genera *Erwinia, Dickeya, Pectobacterium, Xanthomonas,* and *Ralstonia* requires the T2SS (Szczesny*et al*., 2010;

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Toth*et al*., 2003). The T2SS is used by soft-rot pathogens to breach the host barrier by secreting large quantities of various plant cell wall-degrading enzymes that result in loss of cell wall integrity and contribute to the symptoms of rotting disease. (Kazemi- Pour *et al*., 2004).

Type III secretion system (T3SS):

Many Gram negative bacterial pathogens possess T3SSs. Due to their structure, T3SSs have been compared to "injectisomes" and "needle and syringe"-like apparatuses. The base complex, also known as the basal body, the needle component, and the translocon are the three primary parts of the T3SS**.**They secrete a wide variety of proteinaceous substrates across both the inner and outer bacterial membranes. In addition, most T3SSs also transport substrates across a target eukaryotic cell membrane in the same step and, therefore, actually transport proteins across three membranes. The key function of the T3SS is to inject type III effectors (T3Es) directly into host cells. Translocation of T3SS effectors into host cells is essential for the virulence of many pathogens, including pathogenic species of *Yersinia, Salmonella, and Shigella*.

Type IV secretion system (T4SS):

Of all the secretion systems, the T4SS is the most versatile. Gram-negative, gram-positive, wall-less bacteria as well as Archaea all include the T4SS and homologs of its components (Bhatty*et al*., 2013). T4SSs can also target bacterial and eukaryotic cells, such as those found in fungi, plants, and animals. T4SSs can secrete a wide range of substrates, including single proteins, protein-protein complexes, and DNA-protein complexes. They are ancestrally related to bacterial DNA conjugation systems. Mostly found in Gram-negative bacteria, these macromolecular complexes carry substrates through both the inner and outer membranes**.**T4SSs can perform a variety of functions due to their capacity to transfer both DNA and proteins, including conjugative transfer of DNA, DNA uptake and release, and direct translocation of effector proteins or DNA/protein complexes into recipient cells. The T4SS of *Agrobacterium tumefaciens* is used to transfer oncogenic DNA into plant cells, and it has served as the model for research on T4SS assembly and function.

Type V secretion system (T5SS):

T5SS substrates are distinctive in that they secrete themselves, in contrast to other secreted substrates that do so with the aid of a specialised secretion apparatus or membrane

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channel. These proteins or groups of proteins carry their own β-barrel domain, which inserts into the outer membrane and forms a channel through which either the remainder of the protein or a separate protein is transported. T5SS can be divided into three main groups based on the number of proteins involved in the secretion process. These groups include chaperone-usher, two-partner, and autotransporter secretion. Serine proteases, lipases, cytotoxins, invasions, and adhesins are among the diverse roles of the T5SS passenger domains, which collectively have a broad impact on bacterial fitness, aggregation, biofilm formation, and virulence (Grijpstra*et al*., 2013). T5SS candidate proteins exceeding 3,000 amino acids in length have been reported in *Xanthomonasaxonopodis* and *Xylellafastidiosa* and characterized for secretion and roles in adhesion (Voegel*et al.,* 2010).

Type VI secretion system (T6SS):

There is still a lot to learn about the structure and function of T6SSs because they are relatively new discovered bacterial secretion systems. T6SSs translocate proteins into a variety of recipient cells, including targets that are eukaryotic cells and, more frequently, other bacteria. T6SSs are thought to be involved in bacterial communication and interactions in the environment because, in contrast to many other described Gram negative secretion systems, they may transport effector proteins from one bacterium to another in a contact-dependent way. Although other T6SS effector proteins have also been identified, it has been suggested that some structural elements of the T6SS apparatus may also function as effector proteins.This secretion apparatus may have a role in fostering interspecies bacterial competition because of the variety of forms and activities of these effectors, many of which are aimed against the bacterial cell wall and membrane. T6SS has been reported in many bacterial pathogens, including *Pseudomonas aeruginosa*, *Serratiamarcescens*etc (Russel *et al*., 2011).

Type VII secretion system (T7SS):

Only gram positive bacteria have been reported to have T7SS. Mycomembrane, a layer of the cell wall that is extensively lipidated is found in some species of gram-positive bacteria like *Corynebacteria* and *Mycobacteria*. On the outside of the bacterium, these lipids create a very thick, waxy, hydrophobic covering that acts as a solid defence against various environmental stresses and antimicrobial treatments. In order to transport proteins through their inner and mycomembranes, these bacteria use specialised systems known as T7SSs.

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T7SSs were originally identified in *Mycobacterium tuberculosis*, where they are called ESX systems. T7SSs have a number of functions in the pathogenesis and physiology of bacteria.

Conclusion:

Bacterial pathogens use a variety of strategies to enter hosts, damage tissue areas, and prevent the immune system from fighting back. The secretion of proteins across phospholipid membranes is a crucial weapon of these mechanisms for many bacterial pathogens. In addition to aiding eukaryotic cell attachment, secreted proteins can also scavenge resources in an environmental niche, directly intoxicate target cells, and otherwise interfere with their normal functioning. As was covered in this article, a variety of techniques, usually involving the utilisation of specific protein secretion systems, can be used to move these proteins out of the bacterial cytoplasm. Because of this, research on protein secretion systems has become a key area of interest in the study of bacterial pathogenesis.

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