

Molecular Basis of the Hrp Pathogenicity of the fire Blight Pathogen *Erwinia amylovora*

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Fire blight, caused by *Erwinia amylovora*, is one of the most destructive diseases of apples, pears, raspberries, and other rosaceous plants (1). The disease poses tremendous problems in international trading of fruits, and it remains as one of the major pathogens for which plant quarantine measures are in place. American strains of *E. amylovora* have spread to many countries in Europe and the Middle East since the early 20th century, and, in recent years, outbreaks of fire-blight-like diseases have occurred in Japan, Korea and Australia. *E. amylovora*, the first bacterium proven to cause disease in plants, is the type species of its genus and belongs to the family *Enterobacteriaceae*. *E. amylovora*, with well-studied *Escherichia coli* and non-plant pathogen *Pantoea agglomerans* (*Erwinia herbicola*) as closely related organisms, provides a good example for studying the evolution of plant pathogenicity.

To successfully infect its hosts, the pathogen requires a set of clustered genes termed *hrp* (2). *hrp* genes are also responsible for eliciting the defensive hypersensitive response in nonhost plants. Studies on the *hrp* system of *E. amylovora* have indicated that it consists of three functional classes of genes (3). Regulation genes including *hrpL*, *hrpS*, and *hrpXY* produce proteins that control the expression of other genes in the cluster (4,5). Secretion genes, many of which named *hrc*, encode proteins that may form a transmembrane complex, which is devoted to Hrp (type III) protein secretion (6,7). The type III system is evolutionarily related to the flagellar biogenesis system. Finally, several genes encode the proteins that are delivered by the protein secretion apparatus. They include harpins (*HrpN* and *HrpW*; 8,9), DspE (10), and other potential effector proteins that may contribute to parasitism inside the hosts. Harpins are glycine-rich heat-stable elicitors of the hypersensitive response in plants, and often are involved in virulence (8,9). They also induce systemic acquired resistance against a variety of pathogens (11), induces repellency against insects, and promotes the growth of tobacco and several other plants. The pathogenicity protein DspE is homologous and functionally similar to an avirulence protein of *Pseudomonas syringae* (12). In an effort to understand the functional mechanisms of these proteins, experiments to identify the plant receptors are in progress.

The region encompassing the *hrp/dsp* gene cluster of *E. amylovora* shows features characteristic of a genomic island: a cryptic recombinase/integrase gene and a tRNA^{Phe} gene are present at one end and genes corresponding to those of the *Escherichia coli* K-12 chromosome are found beyond the region (Kim and Beer, unpublished results). This island, designated the Hrp pathogenicity island, is more than 60 kilobases in size and carries as many as 60 genes. It apparently is composed of two large segments: one that is involved in pathogenesis and the other enriched with bacteriophage-related genes. Among the newly identified genes in the island include those that are probably regulated by *HrpL* and encode putative enzymes such as acetyltransferase, two carboxylase/ligase, and amidino-transferase. This raises a possibility that *E. amylovora* produces a modified tripeptide similar in structure to phaseolotoxin. If this turns out to be the case, it will be the first example of a phytotoxin synthesis system physically

linked to and controlled by *hrp* genes.

References

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