

## **Characterization of RND-type multidrug efflux systems in the plant-pathogenic bacterium *Pseudomonas syringae***

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Plant-pathogenic bacteria are continually exposed to deleterious chemicals naturally occurring in their environment such as antimicrobial plant metabolites and toxins produced by other epiphytic microorganisms. Bacteria have developed various ways to resist the toxic effects of antimicrobial compounds. Extrusion of toxic agents from cells by multidrug efflux (MDE) is one of these mechanisms. This project aims to identify and characterize RND-type pumps of the plant pathogen *Pseudomonas syringae* and to gain knowledge about their natural functions.

*Pseudomonas syringae* pv. *tomato* DC3000 represents a model for studying the molecular basis of pathogenesis, as it infects different plant species, including tomato, several crucifers, and the model plant *Arabidopsis thaliana*. The availability of the complete sequence of *P. s.* pv. *tomato* DC3000 has allowed functional genomics approaches to identify candidate genes encoding for MDE transporters. At least 11 possible operons encoding RND-type transporter were identified in the *P. s.* pv. *tomato* DC3000 genome. Knockout mutants will be generated to study the role of RND-type transporters in multidrug resistance and virulence of *P. s.* pv. *tomato* DC3000. To learn more about the natural functions of these transporters and their role during pathogenesis, we will analyze the expression of these efflux pumps during infection of the host plant.