

Type III secretion system effectors and host specificity in *Pseudomonas savastanoi* pathovars of woody hosts

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The species *Pseudomonas savastanoi*, a member of the *Pseudomonas syringae* complex, includes five pathovars causing knots or excrescences in woody hosts: *P. savastanoi* pv. *savastanoi*, pv. *fraxini*, pv. *nerii*, pv. *retacarpa* (Psr) and pv. *mandevillae*, comprising isolates from olive, ash, oleander, broom and dipladenia plants, respectively. Comparative genomic analysis of all available *P. savastanoi* genomes included in these five pathovars defined a total of 45 type III secretion system effector (T3E) genes, including 24 core genes, four genes exclusive of Psr and several genes encoding pathovar-specific truncations. Noticeably, hierarchical clustering based on the presence, absence and truncations of T3E genes, correlated with the core genome phylogeny of these strains, indicating that the five pathovars contain characteristic sets of T3Es, which are thus likely contributing to define their pathogenicity profile. To unravel the role of T3Es in the host specificity of *P. savastanoi* pathovars we followed two different approaches: i) construction of knock out mutants affected in T3E genes exclusively encoded by specific pathovars and, ii) heterologous expression of T3E genes in strains belonging to pathovars lacking these T3Es or encoding specific truncations. Virulence assays of these strains in their natural hosts and in hosts infected by other *P. savastanoi* pathovars, allowed us to identify several T3Es with a role in the host specificity of this bacterial pathogen of woody hosts.