

Bioinformatics and transcriptomics analyses of the HrpL regulon in *Pseudomonas savastanoi* pathovars of woody host.

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The species *Pseudomonas savastanoi*, a member of the *Pseudomonas syringae* complex, includes four pathovars causing knots or excrescences in woody hosts: *P. savastanoi* pv. *savastanoi* (Psv), pv. *fraxini* (Psf), pv. *nerii* (Psn) and pv. *retacarpa* (Psr), comprising isolates from olive, ash, oleander and broom plants, respectively. One of the better characterized pathogenicity factor in this bacterial complex is the type III secretion system (T3SS) and its effector (T3E) repertoire. Transcription of the T3SS structural genes and most of its T3E genes is positively regulated HrpL. We have constructed $\Delta hrpL$ mutants in a model strain belonging to each of this four pathovars and analyzed the role of this gene in the pathogenicity of *P. savastanoi*. As previously reported for Psv and Psn, the *hrpL* gene is also necessary in Psf and Psr for both symptoms production during a compatible interaction and the induction of the hypersensitive response in a resistant host. To characterize the HrpL regulon, we are currently following two strategies (i) the bioinformatics identification of HrpL-dependent promoters in the genomes of several *P. savastanoi* pathovars and, (ii) a comparative RNAseq analysis of a wild-type Psv strain and its $\Delta hrpL$ mutant. The results obtained will be compared with those published for other *P. syringae* strains isolated from herbaceous hosts, in order to identify specific HrpL-dependent proteins involved in the interaction with woody hosts.