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Contribution of the metabolism of phenolic compounds to the virulence of *Pseudomonas savastanoi* in woody hosts

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Most strains of the *Pseudomonas syringae* complex isolated from the trunks of woody plants and belonging to phylogroups (PGs) 1 and 3 share a genomic region, named WHOP (from woody host and *Pseudomonas*), which is partially conserved in some PG2 strains. Annotation of the 14 ORFs encoded within this region, which is absent in the genomes of *P. syringae* strains infecting herbaceous hosts, yielded functions possibly involved in the metabolism of phenolic compounds. The genetic organization of this region was analyzed by RT-PCR in *Pseudomonas savastanoi* pv. *savastanoi* (Psv), the causative agent of olive knot disease. The WHOP region is organized in four operons (*antABC*, *catBCA*, *ipoABC* and *dhoAB*) and three genes transcribed independently (*antR*, *benR* and PSA3335_3206). HPLC analyses confirmed that the *antABC* and *catBCA* operons mediate the catabolism of anthranilate and catechol, respectively, through the β -keto adipate pathway. In addition, oxygenase activity on aromatic compounds, tested as the conversion of indole into indigo, was assigned to the *ipoABC* operon. Pathogenicity tests revealed that deletion of *antABC*, *catBCA* or *ipoABC* in Psv caused reduced symptoms in woody olive plants, while such phenotype was not observed in young micropropagated (non-woody) plants. Similarly, the *catBCA* and *dhoAB* operons and the PSA3335_3206 gene (encoding a putative aerotaxis receptor) are also required for full bacterial fitness exclusively in woody olive plants. At present, we are addressing the role in virulence of the orphan *benR* gene encoded in the WHOP region.