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TRANSCRIPCIONAL, FUNCTIONAL AND VIRULENCE ANALYSIS OF A *PSEUDOMONAS SAVASTANOI* PV. SAVASTANOI GENOMIC REGION SHARED WITH OTHER PATHOGENS OF WOODY HOSTS

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The genome of the olive tree pathogen Pseudomonas savastanoi pv. savastanoi (Psv) NCPPB3335 (58.1% G+C) encodes a region of about 15 kb, named VR8 (60.4% G+C), which is absent in all sequenced Pseudomonas syringae strains infecting herbaceous plants, but shared with P. syringae pathovars infecting woody hosts. RT-PCR analysis of the VR8 genes revealed the existence of 4 possible operons, of which the antABC and catBCA operons are involved in the degradation of anthranilate and catechol, respectively. The antABC cluster is homologous to the anthranilate degradation genes found on plasmid pCAR1 of Pseudomonas resinovorans. The other two operons, here called AER-1901/2/3 and AER-1904/5, also show homology to genes related with the degradation of aromatic compounds. RT-qPCR and ß-galactosidase assays of a LacZ fusions showed that both anthranilate and 6-chloro-antrhanilate induce the antABC operon. In addition, anthranilate also induces the catB gene. To analyse the role in virulence of the VR8, we constructed several knockout mutants of this region. The volume of the knots induced in non lignified olive plants by Psv mutants affected in the antABC or catBCA operons resulted to be similar to those induced by the wild-type strain. However, the severity of the symptoms generated by the antABC mutant in lignified olive plants was significantly lower than that induced by the wildtype strain, suggesting a possible role of this operon in the degradation of lignin-derived compounds. At present, we are analysing the role in virulence of the other three operons and of the AER-1900 gene (a putative aerotaxis receptor).