



Mutational analysis of a predicted double β -propeller domain of the DspA/E effector of *Erwinia amylovora*

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Auteur	Siamer, Sabrina [1], Gaubert, Stéphane [2], Boureau, Tristan [3], Brisset, Marie-Noëlle [4], Barny, Marie-Anne [5]
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Mots-clés	AvrE [6], DspA/E [7], <i>Erwinia amylovora</i> [8], type 3 effector [9], β -propeller [10]
Résumé en anglais	<p>The bacterium <i>Erwinia amylovora</i> causes fire blight, an invasive disease that threatens apple trees, pear trees and other plants of the Rosaceae family. <i>Erwinia amylovora</i> pathogenicity relies on a type III secretion system and on a single effector DspA/E. This effector belongs to the widespread AvrE family of effectors whose biological function is unknown. In this manuscript, we performed a bioinformatic analysis of DspA/E- and AvrE-related effectors. Motif search identified nuclear localization signals, peroxisome targeting signals, endoplasmic reticulum membrane retention signals and leucine zipper motifs, but none of these motifs were present in all the AvrE-related effectors analysed. Protein threading analysis, however, predicted a conserved double β-propeller domain in the N-terminal part of all the analysed effector sequences. We then performed a random pentapeptide mutagenesis of DspA/E, which led to the characterization of 13 new altered proteins with a five amino acids insertion. Eight harboured the insertion inside the predicted β-propeller domain and six of these eight insertions impaired DspA/E stability or function. Conversely, the two remaining insertions generated proteins that were functional and abundantly secreted in the supernatant suggesting that these two insertions stabilized the protein.</p>
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