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EVALUATION OF ALTERNATIVE IAA BIOSYNTHETIC PATHWAYS IN THE BACTERIA FROM THE PSEUDOMONAS SYRINGAE COMPLEX

Backgrounds

Indole-3-acetic acid (IAA) is a phytohormone belonging to the auxin group which production is widely distributed among plant-associated bacteria. In phytopathogenic bacteria, several IAA biosynthetic pathways have been described. The best characterized is the indole-3-acetamide (IAM) pathway, where tryptophan is initially converted into IAM by a monooxygenase (*iaaM* gene), and later transformed to IAA in a reaction catalysed by a hydrolase (*iaaH* gene). *Pseudomonas savastanoi* pv. *savastanoi* NCPPB 3335 (Psv), which synthesizes IAA through IAM, encodes two paralogs of these two genes organized in two operons (*iaaMH-1* and *iaaMH-2*). Previously, we have demonstrated that a Psv mutant in the *iaaMH-1* operon produces an amount of IAA significantly lower than that synthesized by the wild type strain. This strain, shows a reduced virulence in olive plants. In contrast, a mutant in the *iaaMH-2* operon (which encodes a *iaaM-2* pseudogene), produces IAA levels similar to those of the wild type strain and is not affected in virulence. Unexpectedly, the *iaaMH-1* mutant and the double mutant *iaaMH-1/iaaMH-2* synthesize a residual amount of IAA, suggesting the existence of an alternative route for the production of this compound in Psv.

Objectives

Identification of the alternative IAA biosynthetic pathway active in the Psv mutant devoid of the IAM pathway.

Determination of the IAA biosynthetic pathway encoded by other strains of the *P. syringae* complex with different host spectrum.

Methods

Candidate genes search, directed mutagenesis and functional analysis.

Conclusions

Besides the IAM pathway, bacteria from the *P. syringae* complex encode other pathways for the biosynthesis of IAA.

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