

Abstract N.
Session:
(to be completed by the Organizing Committee)

14th International Conference on Plant Pathogenic Bacteria (ICPPB)

ABSTRACT SUBMISSION FORM

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The *iaaL* gene in the *Pseudomonas syringae* complex: functional characterization and biological activity

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Phytopathogenic bacteria of the *Pseudomonas syringae* complex are causal agents of diseases in a wide variety of woody and herbaceous plants with agronomic and ornamental interest. Indole-3-acetic acid (IAA) is an auxin phytohormone whose production is widely distributed among plant-associated bacteria. Some *P. syringae* strains can further metabolize IAA to the amino acid conjugate 3-indole-acetyl- ϵ -L-lysine (IAA-Lys), a process involving the enzyme IAA-Lys synthase, encoded by the *iaaL* gene. IAA-Lys is less biologically active than IAA, so it has been speculated that the conjugation of IAA with L-Lysine could allow the bacteria to control the levels of free IAA accumulated in the bacterial cytoplasm and/or secreted to the plant tissues. The *iaaL* gene is widespread in the *P. syringae* complex, and three different alleles (*iaaLPsv*, *iaaLPsn* and *iaaLPto*) have been described [1]. Recently, we have identified a fourth allele (*iaaLPsf*) specifically encoded in the genome of strains isolated from *Fraxinus excelsior*. However, comparative analyses of the biochemical and biological activities of the different *iaaL* alleles have not been performed. In this work, the genomic context of these four alleles in a collection of *P. syringae* complex strains has been analyzed. In addition, we have constructed strains overexpressing each of these *iaaL* alleles and analysed their biological activities using an elongation assay of *Arabidopsis thaliana* roots. Finally, expression of these alleles in *E. coli* allowed the purification of these four IaaL proteins and the analysis of their specific activities using an *in vitro* enzymatic coupling assay.

Funded by Ministerio de Ciencia, Innovación y Universidades (Spain) grant PID2020-115177RB-C21 / AEI/10.13039/501100011033, co-financed by FEDER.

[1] Matas *et al.*, 2009. Appl. Environ. Microbol., 75, 1030-1035.