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DECIPHERING MOLECULAR MECHANISMS UNDERLAYING BIOLOGICAL CONTROL OF THE FUNGAL PATHOGEN *ROSELLINIA NECATRIX* BY *PSEUDOMONAS PSEUDOALCALIGENES* AVO110

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Pseudomonas pseudoalcaligenes AVO110 was selected as an efficient avocado root tip colonizer, displaying antagonism towards *Rosellinia necatrix*, the causal agent of avocado white root rot. The most likely biocontrol mechanisms used by this strain is competition for niches and nutrients. In fact, AVO110 is able to colonise competitively the surface of fungal hyphae, using fungal exudates. In a previous study, we used signature-tagged mutagenesis (STM) to screen a library of AVO110 transposon mutants for their ability to grow in *Rosellinia* exudates (BM-RE medium). A pool of 26 growth-attenuated mutants (GAM) was identified.

In this work, we used the recently obtained draft genome sequence of AVO110 to analyse the genetic context of the genes affected by the transposon in seven GAM mutants. Among the traits affected, we have identified homologs of an exodeoxyribonuclease, a GGDEF/EAL/PAS protein, a transcriptional regulator, a histidine kinase, a putative enterotoxin, a peptidase and a putative small RNA. Phenotypic characteristics such as biofilm formation, persistence and colonisation of avocado roots and colonisation of fungal hyphae were studied. Mutants affected in the transcriptional regulator and the GGDEF/EAL/PAS proteins were altered in all features analysed when compared to the wild type strain. The remaining mutants presented variations in persistence and colonisation of fungal and root surfaces, except for that affected in a putative enterotoxin, which was only altered in fungal colonisation.

Finally, quantitative RT-PCR experiments were performed in BM-RE to evaluate the expression dynamics of these genes in the presence of the fungal metabolites along the time. Results showed no evident correlation between gene expression and phenotypic behaviour.