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Response to fungal exudates of the rhizosphere isolate *Pseudomonas* sp. UMAF110 involves a GGDEF/EAL domain-containing protein.

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Pseudomonas sp. UMAF110, isolated from rhizosphere soil in Spain, display *in vitro* antagonism towards the pythopathogenic fungus *Rosellinia necatrix* and is able grow in fungal exudates (BM-RE medium). A transposon mutant library of this strain was constructed and several mutants were selected by their reduced competitiveness in BM-RE medium. *Pseudomonas* sp. UMAF110-G3, which contains the transposon into a gene encoding a putative REC/PAS/GGDEF/EAL protein, was selected for further characterization. Blastn searches using the sequence of the gene interrupted by the transposon in UMAF110-G3, here called *cmpA* (*c-di-GMP Metabolizing Protein*), yielded a single positive hit (98% cover, 78% identity) with a gene from a terpene-degrading *Pseudomonas* sp. strain isolated from soil. Context analysis of the *cmpA* gene in *Pseudomonas* sp. UMAF110 showed that this gene is located downstream from several genes involved in flagellar motility/chemotaxis. RT-PCR experiments further confirmed that *cmpA* form a transcriptional unit with the *che* gene cluster. Expression analysis of *cmpA* by qRT-PCR clearly showed upregulation of this gene after transfer of *Pseudomonas sp.* UMAF110 cells to BM-RE medium, suggesting a role for this operon in response to fungal exudates. Deletion of *cmpA* in *Pseudomonas* sp. UMAF110 did not affect the ability of the strain to form biofilms under the conditions tested. However, overexpression of wild type CmpA in *Pseudomonas putida* KT2440 negatively regulated biofilm formation in this strain. Together, these results suggest that CmpA could be involved in signal transduction pathways regulating flagellar motility/chemotaxis in response to fungal exudates.