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Cellular L-arginine pools modulate c-di-GMP turnover and biofilm formation in Pseudomonas putida

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The intracellular second messenger cyclic diguanylate (c-di-GMP) is broadly conserved in bacteria, where it influences processes such as virulence, stress resistance and biofilm development. In the plant-beneficial bacterium *Pseudomonas putida* KT2440, the response regulator with diguanylate cyclase activity CfcR is the main contributor to c-di-GMP levels in the stationary phase of growth. When overexpressed, CfcR increases c-di-GMP levels and gives rise to a pleiotropic phenotype that includes enhanced biofilm formation and crinkly colony morphology. Our group has previously reported that insertion mutants in *argG* and *argH*, the genes that encode the last two enzymes in the arginine biosynthesis pathway, do not display the crinkly colony morphology phenotype and show decreased c-di-GMP levels even in the presence of *cfcR* in multicopy (Ramos-González, M.I. *et al.* 2016. Front. Microbiol. 7, 1093). Here we present results indicating that L-arginine acts both as an environmental and as a metabolic signal that influences the lifestyles of *P. putida* through the modulation of c-di-GMP levels and changes in the expression of structural elements of biofilms. Exogenous L-arginine partially restores c-di-GMP levels in arginine biosynthesis mutants, a response that is transduced through CfcR and possibly (an)other diguanylate cyclase(s). At least three periplasmic binding proteins, each forming part of an amino acid transport system, contribute in different ways to the response to external L-arginine. We propose that the turnover of the second messenger c-di-GMP is modulated by the state of global arginine pools in the cell resulting both from anabolism and from uptake.

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