PO-3. Biosynthesis and regulation of the antifungal herbicolin A in a *Pantoea agglomerans* rhizobacterium active against a broad spectrum of plant-pathogenic fungi

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The plant microbiome plays a crucial role in plant growth and protection against phytopathogens through multiple mechanisms, for example, improving nutrient acquisition and disease resistance. The bacterium *Pantoea agglomerans* 9Rz4 was isolated from the rhizosphere of oilseed rape due to its ability to antagonise the growth of different fungal pathogens of agronomic relevance [1]. However, the mechanisms behind these antifungal properties are unknown. By screening a library of random transposon mutants, we have isolated mutants of 9Rz4 deficient in their antifungal properties. The combination of *de novo* genome sequencing and chemical analysis allowed us to determine that the strain 9Rz4 produces the non-ribosomal peptide antifungal herbicolin A, as well as to identify and characterise the corresponding biosynthetic cluster. The expression of the herbicolin A gene cluster is maximal in stationary phase of growth. A quorum sensing mutant of 9Rz4, defective in the biosynthesis of acyl-homoserine lactones, shows reduced production of herbicolin A and, as a consequence, a lower antifungal activity. *In planta* assays revealed that 9Rz4 does not negatively impact on plant growth, but also that herbicolin A does not affect rhizosphere colonisation by the 9Rz4. Assessing bacterial potential as biopesticides is fundamental for transitioning to green alternatives to agrochemicals. *Pantoea agglomerans* 9Rz4 is active against a broad range of fungal phytopathogens and our results lay the foundation for the possible future use of this bacterium as a biocontrol agent in agriculture.

[1] Berg G., *et al*. (2002) *Appl Environ Microbiol* 68: 3328–3338.

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