

Transformation of soil Fe and Mn by phenazine-producing bacteria in the rhizosphere of dryland wheat

MELISSA K. LETOURNEAU¹, LINDA S. THOMASHOW²,
DAVID M. WELLER² AND JAMES B. HARSH*¹

¹Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164
(melissa.letourneau@wsu.edu,
*correspondence: harsh@wsu.edu)

²Root Disease and Biological Control Unit, USDA-ARS, Pullman, WA 99164 (thomashow@wsu.edu, wellerd@wsu.edu)

INTRODUCTION

Large populations of fluorescent pseudomonads producing high concentrations of the redox-active antibiotic phenazine-1-carboxylic acid have been discovered in dryland wheat fields throughout the low precipitation zone of the Columbia Plateau [1]. In culture, phenazines have been shown to reductively dissolve iron and manganese oxides [2] and to promote biofilm development via solubilization of Fe [3], but these effects have not been investigated in soil or in agroecosystems. Using wild-type and mutant pseudomonads, we have developed growth chamber experiments to test the hypothesis that phenazine-producing rhizobacteria enhance bio-availability of Fe and Mn under dryland conditions.

RESULTS

Phenazine-producing rhizobacteria and isogenic mutants impaired in phenazine synthesis both significantly influenced soil Mn chemistry *relative to* soil Fe chemistry under dryland conditions. Both strains also significantly increased wheat above-ground biomass. These results suggest that soil Mn chemistry is more readily influenced by rhizobacteria than soil Fe chemistry, that soil Mn and Fe chemistries are tightly coupled, and that phenazine-producing rhizobacteria may employ multiple mechanisms to enhance bio-availability of micronutrients under dryland conditions. Additional growth chamber, culture, and microscopy experiments for comparison of the impact of phenazine-producing rhizobacteria upon Fe and Mn bio-availability under irrigated and dryland conditions are underway.

[1] Mavrodi *et al* (2012) *Appl Environ Microb* **78**, 804-812.

[2] Hernandez *et al* (2004) *Appl Environ Microb* **70**, 921-928.

[3] Wang *et al* (2011) *J Bacteriol* **192**, 365-369.