



Gene expression profile of the plant pathogen *Fusarium graminearum* under the antagonistic effect of *Pantoea agglomerans*

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Genet. Mol. Res. 9 (3): 1298-1311 (2010)

Received March 18, 2010

Accepted May 15, 2010

Published July 16, 2010

DOI 10.4238/vol9-3gmr828

ABSTRACT. The pathogenic fungus *Fusarium graminearum* is an ongoing threat to agriculture, causing losses in grain yield and quality in diverse crops. Substantial progress has been made in the identification of genes involved in the suppression of phytopathogens by antagonistic microorganisms; however, limited information regarding responses of plant pathogens to these biocontrol agents is available. Gene expression analysis was used to identify differentially expressed transcripts of the fungal plant pathogen *F. graminearum* under antagonistic effect of the bacterium *Pantoea agglomerans*. A macroarray was constructed,

using 1014 transcripts from an *F. graminearum* cDNA library. Probes consisted of the cDNA of *F. graminearum* grown in the presence and in the absence of *P. agglomerans*. Twenty-nine genes were either up (19) or down (10) regulated during interaction with the antagonist bacterium. Genes encoding proteins associated with fungal defense and/or virulence or with nutritional and oxidative stress responses were induced. The repressed genes coded for a zinc finger protein associated with cell division, proteins containing cellular signaling domains, respiratory chain proteins, and chaperone-type proteins. These data give molecular and biochemical evidence of response of *F. graminearum* to an antagonist and could help develop effective biocontrol procedures for pathogenic plant fungi.

Key words: Phytopathogen; Microorganism interaction; Macroarray; Gene expression