

**Title: TRANSCRIPTOME PROFILING OF *HERBASPIRILLUM RUBRISUBALBICANS* M1
UNCOVER MECHANISMS FOR EFFICIENT DIAZOTROPHIC COLONIZATION OF GRASSES**

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Abstract:

Herbaspirillum rubrisubalbicans was first described as a bacterium capable of causing the mottled stripe disease in sugar cane and red stripe disease in sorghum. In both cases the disease is mild, causing loss of the infected leaves and minor loss in productivity. Although this bacterium has been isolated as a phytopathogen, its host range as a pathogen seems restrict. Indeed, *H. rubrisubalbicans* has been isolated in most cases from non-symptomatic plants and it has been tested with success as plant growth promoter. In this work, we determined the transcript profile by RNA-seq of *H. rubrisubalbicans* M1 growing epiphytically on roots of the susceptible cultivar *Sorghum bicolor* cv. A07, and found traits potentially involved in both beneficial and pathogenic interaction of this microorganism with graminaceous plants. At an early colonization stage, these bacteria were able to use diverse available carbon sources, possibly derived from plant root exudate. After imported through ABC-type transporters, such substrates were catabolized via pentose phosphate pathway, glyoxylate cycle, tricarboxylic acid cycle and electron transfer chain. Carbon and energy obtained were used for lipids and aminoacids synthesis and dynamically stored as polyhydroxybutyrate granules. Moreover, nitrogen fixation seemed very active judging by *nif* genes expression level. Extensive cell wall modification was apparent by up-regulation of peptidoglycan and lipopolysaccharide biosynthesis, porins, secretion systems and other membrane proteins. While exopolysaccharide biosynthesis and T6SS-1 genes were expressed but not differentially regulated in epiphytic cells, T6SS-2, flagellin and pilin coding genes were induced. This remodeling of cell wall could be required for bacterial attachment onto root surface, and also to move on it. Root epiphytic *H. rubrisubalbicans* up-regulated genes for two MAMPs, flagellin and peptidoglycan. Although the products of these genes could be initial factors that ultimately determined the observed red stripe disease in older inoculated plants, most of the changes in gene expression observed suggest that *H. rubrisubalbicans* is well adapted to colonize the plant rhizosphere, showing several traits important for survival in such competitive environment. Perhaps the ability of over-colonizing plants together with a few pathogenicity factors may shift the interaction from benign or neutral to pathogenic in the susceptible cultivars.

Key words: *Herbaspirillum rubrisubalbicans*, rhizosphere, RNA-seq.

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