Identification of genetic differences between *Herbaspirillum seropedicae* and *Herbaspirillum rubrisulbalbicans* using suppressive subtractive hybridization libraries

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Several species of the *Herbaspirillum genus* are nitrogen fixers capable of endophytic association with important agricultural crops, such as maize, rice, wheat, sorghum and sugar-cane. Among the those species, we have a particular interest in two closely related species, *Herbaspirillum seropedicae* and *Herbaspirillum rubrisubalbicans,* due to their contrasting pattern of colonization of the sugar-cane cultivar B4362. *H. seropedicae* is a diazotroph that promotes plant development and increases productivity whereas *H. rubrisubalbicans* causes the mottled stripe disease in this susceptible sugar-cane cultivar and also the red stripe disease in sorghum cultivars. To understand this contrasting phenotype and identify the factors that participate in the plant-bacterial interaction suppressive subtractive hybridization (SSH) libraries were obtained and the DNA inserts.The genomic library of DNA fragments exclusive of *H. seropedicae* SmR1 was sequenced revealing genes without counterpart in the *H. rubrisubalbicans* strain M1. Ninety six exclusive genes, out of the 296 DNA fragments sequenced, were identified. The majority of the genes found exclusively in *H. seropedicae* coded for hypothetical, conserved hypothetical proteins or phage related proteins. However, genes coding for sugar transport system, surface molecule biosynthesis such as exopolysaccharides, adhesion related protein, and poly-alkanoate biosynthesis were also found. These results can partially explain the contrasting phenotypes concerning sugar utilization, plant interaction and polyalkanoate biosynthesis observed in these two *Herbaspirillum* species.

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