

IDENTIFICATION OF *Herbaspirillum rubrisubalbicans* GENES INVOLVED IN PLANT-BACTERIA INTERACTION.

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Departamento de Bioquímica e Biologia Molecular - Universidade Federal do Paraná, Paraná, Brazil. Projeto de Sequenciamento Genômico de *Herbaspirillum rubrisulbalbicans*.

Herbaspirillum rubrisubalbicans is a plant endophytic bacterium that causes the red stripe disease in some varieties of sugar cane of non-commercial value in Brazil. It is physiologically and genetically closely related to *H. seropedicae*, a non-pathogenic species. To compare the gene content of these two bacterial species we have partially sequenced the genome of *H. rubrisubalbicans* strain M1. Two genomic libraries containing approximately 15,000 recombinant clones were constructed in the pUC19 vector. These genomic libraries were sequenced yielding a total of 16 Mbp corresponding to 2 million non-redundant bases or 30% of the estimated genome size. Bioinformatic analyses allowed the identification of genes potentially involved in plant-bacteria interaction. Among these, the Type Three Secretion System (TTSS) genes *hrcC*, *hrpE*, *hrcJ*, *hrpX*, *hrcU*, *hrpQ*, *hrcN*, *hrpO* and *hrcV* were found. Comparison with the TTSS gene cluster of *H. seropedicae* suggested the presence in *H. rubrisualbicans* of genes coding for secreted protein with potential pathogenic activity such as *hrpO*, absent from the genome of *H. seropedicae*. We have also identified the *rml* genes, which are involved in the biosynthesis of bacterial surface components and probably in the early stages of the colonization process.

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