

**CONSTRUCTION AND SEQUENCING OF A cDNA LIBRARY OF
Oryza sativa ROOTS INOCULATED WITH *Herbaspirillum
seropedicae***

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Rice (*Oryza sativa*) is the staple food for half of the world's population, whose continuing growth imposes a need for a substantial increase in its production. Improvement of rice productivity can be achieved through inoculation with plant growth-promoting rhizobacteria (PGPR). *Herbaspirillum seropedicae* is an important endophytic diazotroph that can increase the nitrogen content of rice plants by 31-54% under axenic conditions. In order to better understand the rice-*H.seropedicae* interaction, cDNA libraries were constructed from roots inoculated with this bacterium. The 5' ends ESTs were sequenced, assembled and compared with public databases. The great majority of sequences (92%) were *singlets*. Sequence analysis showed that 46% of the sequences are not similar (e-value > 1e⁻⁰⁶) to any database entry and may be considered novel rice genes. Further sequencing and analysis may allow their identification and functional classification. Among the annotated rice ESTs from roots inoculated with *H. seropedicae* the most abundant were those involved in cellular and metabolic processes. A high number (10%) of the sequences were similar to genes involved in environmental interaction, which includes several biotic and abiotic stimuli, e.g. light and pathogens. These ESTs will be further investigated and can contribute to the understanding of plant-bacterial interaction.