

RNA-seq transcriptional analysis of rice roots colonized by *Herbaspirillum seropedicae* SmR1

Tadra-Sfeir, M.Z.¹; Pankievicz, V.C.S.¹; Balsanelli, E.¹; Batista, M.B. ¹; Souza, E.M¹.;
Pedrosa, F.O.¹

¹Department of Biochemistry and Molecular Biology, Universidade Federal do Paraná, Curitiba, PR, Brazil;

Introduction: *Herbaspirillum seropedicae* is a Betaproteobacterium capable of colonizing epiphytically and endophytically important commercial grasses, promoting plant growth and increasing productivity. **Objectives:** In this study, we used high-throughput sequencing (RNA-Seq) to compare the transcriptional profiles of planktonic and rice root-attached *H. seropedicae* SmR1 recovered 3 days after inoculation. **Material and Methods:** Root-attached bacteria were recovered 3 days after inoculation and planktonic cells were collected at the same time. The total RNA was purified using Trizol and mRNA was enriched using the Ribozero kit (Epicentre™). mRNA enriched samples were used for library construction using the Ion Total RNA-Seq Kit v2 (Thermo Scientific™) following the manufacturer instructions. The RNA-Seq libraries were sequenced on the Ion Proton™ (Thermo Scientific™). **Results and Discussion:** Four hundred and eighty seven genes were found regulated, three hundred and fifty were upregulated and one hundred and thirty seven were downregulated. Data analysis revealed that genes related with nitrogen metabolism and polyhydroxybutyrate (PHB) synthesis were activated. Several genes associated with polysaccharide biosynthesis, peptidoglycan turnover and outer membrane protein biosynthesis were activated, suggesting reorganization of cell wall envelope components. Many ABC transporter genes were also regulated in the bacteria attached to the roots. **Conclusions:** The results revealed extense molecular adaptation of *H. seropedicae* SmR1 to the rice root rhizosphere.

Key words: RNA-seq, Rice, *Herbaspirillum seropedicae*

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