



Transcriptional profile of *Herbaspirillum rubrisubalbicans* in response of sugarcane apoplastic fluid

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To access the influence of sugarcane apoplastic fluid on the whole transcriptome profile of HCC103 strain of *Herbaspirillum rubrisubalbicans*, this bacterium was grown in JNFb medium in the presence or absence of RB867515 sugarcane apoplastic fluid and then analyzed for differentially gene expression with a next-generation sequencing (NGS)-based RNA-Seq analysis. RNA-seq reads were analyzed using the software edgePRO and the differential gene expression analysis was then performed using DESeq and edgeR package in BioConductor. A gene was considered to be differentially expressed when results from the above tests were all significant at a level of p value ≤ 0.05 and with the genes with fold change higher than 1.5 were considered induced and that one with fold change lower than 1.5 were considered repressed. Differentially expressed genes were further annotated with Gene Ontology (GO) terms using the Blast2Go platform. From the transcriptome sequencing, a total of 105 differentially expressed genes. Fifty-five were downregulated and fifty were upregulated by sugarcane apoplastic fluid. Data analysis revealed that genes related to bacterial flagella biosynthesis and chemotaxis were repressed by sugarcane apoplastic fluid. Moreover, genes involved in nitrogen metabolism, carbohydrates transport and multidrug transport efflux were activated. To validate the reliability of the RNA-seq results we will perform qRT-PCR analysis. It is expected that this study allow the identification of key genes of *H. rubrisubalbicans* HCC103 strain involved in the interaction with the sugarcane plant, stimulated or suppressed by the constituents of the apoplast liquid.

Keywords: *Diazotrophic bacteria; plant-bacteria interaction; RNA-Seq*