The draft genome of *Methylobacterium mesophilicum* strain SR1.6/6 and transcriptional profiles revealing insights into the bacteria-plant interaction

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Bacteria-plant interaction is highly mediated by exuded plant root molecules which act as signals influencing the ability of each strain to colonize the roots and survive in the rhizosphere. Hence, bacteria ability to metabolize differential carbon source rises as a key feature conferring advantage on its adaptive processes. Methylotrophic bacteria are known to present the methanol dehydrogenase enzyme, which confers the ability to oxidize methanol, a common compound released by plant tissues during metabolic process. Here, we have sequenced by 454-pyrosequencing technology the draft genome of *Methylobacterium mesophilicum* strain SR1.6/6, and developed an *in vitro* system to study this bacteria transcriptional profiles by RNA-Seq approach in two different treatments in interaction with soybean seedlings plants; *i)* biofilm cells – root adhered bacterial cells were removed by sonication, and *ii)* planktonic cells – bacteria cells in suspension (*i.e.* interacting only with root exudates). Genomic data have had an average depth of 37-fold coverage of the genome and yielded 242 contigs. Among these, 187 large contigs represented 96% of the genome sequence (estimate size of 6.8 Mb) with a GC content of 69.5%. The application of RNA-Seq technology resulted in a broad gene expression profile mapped into the drafted genome, resulting in a total of 1,930 gene clusters. After that, these clusters were filtered according to their abundance and differential occurrence in each treatment resulting in 280 differential expressed genes. Functions related to methanol/etanol metabolism, cell division, oxidative stress response, siderophore production, peptidoglycan and hopanoid biosynthesis were induced in bacterial cells adhered to plant roots, while genes related to essential cell metabolism were mostly observed in planktonic and control treatment. Our results provide deep insights into the mechanisms modulating bacteria-plant interaction, significantly distinguishing biofilm to planktonic treatment, showing that the physical contact is a crucial step on bacteria-plant association. In addition, these results pinpoint specific bacteria gene expression patters in response to molecular signals secreted by plant and highlight metabolic process that support this associated bacteria-plant lifestyle and behaviour.