Proteomics of Herbaspirillum seropedicae associated with wheat roots cv. CD 104 under nitrogen stress reveals high alcohol dehydrogenase abundance.

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The application of plant growth-promoting bacteria (PGPB) appears as an option to diminished cost agricultural production, due to their characteristics related to nitrogen fixation and plant growth promotion. Through bioinformatics tools, this work aimed to investigate proteins of H. seropedicae present in wheat roots (*Triticum aestivum* var lini) cv. CD 104, seeking to understand the responses of the bacteria in its association with the plant. Proteins were obtained by cultivating wheat in vitro in liquid MS medium without sucrose and nitrogen source, inoculated with *H. seropedicae* SmR1, in a culture room at 25 °C and 14 h photoperiod of light for 20 days, and identified by LC-MS/MS mass spectrometry, LTQ Orbitrap XL ETD and PattenLab V software. Protein data were processed in Blast2GO software, and proteins corresponding to enzymes present in the Kyoto Encyclopedia of Genes and Genomes (KEGG) catalog and the metabolic pathways in which they were possibly found were identified. Among the proteins identified from H. seropedicae, the enzyme ec: 1.1.1.1 - alcohol dehydrogenase had the highest percentage of expression, responsible for converting ethanol to acetaldehyde. This acetaldehyde is followed by a sequence of reactions until forming acetyl-CoA, a precursor of the citric acid cycle. The enzymes acetaldehyde dehydrogenase and acetyl-CoA synthetase were also identified in the proteome, which, associated with the high abundance of the alcohol dehydrogenase enzyme, may indicate that ethanol is present in the exudates of wheat roots, a metabolite generated when the plant is subjected to hypoxia or even anoxia, which leads to fermentation, causing the production and accumulation of ethanol. Furthermore, additional enzymes involved in the citric acid cycle have been identified, indicating an enhancement of the pathway that originates from acetyl-CoA produced through ethanol oxidation. Other diazotrophic bacteria are capable of metabolizing or co-metabolizing ethanol as a carbon source because of the limited availability of dicarboxylates in the rhizosphere. This compels these microorganisms to utilize alternative carbon sources, which also helps to mitigate the toxicity of ethanol in plant roots.

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