

PROTEOMIC ANALYSIS OF SmR1, GlnK and GlnB LINEAGE OF *Herbaspirillum seropedicae*

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Herbaspirillum seropedicae is a diazotrophic, endophytic bacterium associated with important plants such as corn, rice and sugarcane. This organism can increase the productivity of these plants by biological nitrogen fixation and phytohormone production. The present study aimed at determining the differential proteome of the wild type (SmR1) and the GlnK and GlnB mutants under conditions of limitation and excess of NH_4^+ . The microorganism was cultivated in NFbHP malate containing either 20mM or 2mM of ammonium. The proteins were separated by bidimensional electrophoresis. Isoelectricfocusing was performed using IPG strips pH 4-7 and SDS-PAGE was performed in a vertical system using 11% polyacrylamide gels. The gels were stained with Coomassie Blue and their images were analyzed using the Imagemaster Platinum software. Proteins were excised from gels and identified using a Maldi-ToF/MS mass spectrometer. The peptide mass fingerprint profile was compared with the *H. seropedicae* data base of the Genopar Consortium using the "Protein Prospector v3.2.1" software. Twelve protein spots differentially expressed were observed. The Elongation factor TS (EF-TS) protein was induced while the NADPH: quinone oxidoreductase and DNA-directed RNA polymerase (alpha chain) proteins were repressed under NH_4^+ limitation in the SmR1 strain. The identification of the other differentially expressed proteins will be presented.

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