

**Effect of ammonium ions on the differential  
expression of proteins in *Herbaspirillum seropedicae***

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*Herbaspirillum seropedicae* is an endophytic diazotroph found in economically important graminaceous species such as rice, sugarcane, wheat sorghum and maize. It reduces  $N_2$  to  $NH_3$  in a reaction catalyzed by the nitrogenase complex. The *Herbaspirillum seropedicae* genome was sequenced and genes involved in the nitrogen metabolism were assigned by similarity to published microbial genomes. To identify genes regulated by the availability of ammonium the protein expression profiles of *Herbaspirillum seropedicae* in response to different physiological conditions were examined using two-dimensional gel electrophoresis. The wild type strain SMR1 was grown either under ammonium limitation or ammonium excess conditions. Whole cell soluble proteins were separated by isoelectric focalization over a pH 3–10 or pH 4–7 range in the first dimension, followed by SDS-PAGE (12.5%) in the second dimension. Twenty-five protein spots were clearly induced in the SMR1 strain grown under ammonium-limiting condition when compared with the same strain grown in ammonium rich medium. The pI and MW of these 25 spots were determined and several proteins were identified by peptide mass fingerprint, such as the MoFe protein, a structural component of nitrogenase, and ABC-type amino acid transporters. Other proteins involved in the nitrogen metabolism and in the onset of nitrogen fixation in *H. seropedicae* will be presented.

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