

TITLE: GENOMIC INSIGHTS ON THE NITROGEN METABOLISM IN *TELMATOBACTER* SP. AB60, *ACIDOBACTERIA*

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ABSTRACT:

Acidobacteria physiology and their role in the biogeochemical cycles remain relatively unknown compared to another widespread phylum such as *Proteobacteria*. The use of polysaccharides as carbon source has improved the cultivability of *Acidobacteria*, specially from the Class *Acidobacteriia*, former subgroup 1. In fact, the carbon usage by *Acidobacteriia* has received a lot of attention due to the large number of glycosyl hydrolases genes in their genomes. However, other aspects of their metabolism were neglected as their use of nitrogen or phosphorous. We have obtained a few isolates of *Acidobacteriia* from the Cerrado, which soils are acidic and poor in phosphorous and nitrate. The objective of this work was to investigate the nitrogen metabolism pathways present in the genome of the isolate *Telmatobacter* sp. AB60, an *Acidobacteria* from the Class *Acidobacteriia*. The genome of *T. sp. AB60* was previously sequenced using the Illumina MiSeq platform. The presence of genes involved in the nitrogen metabolism was investigated using the KEGG pathways database and the tools available in the Integrated Microbial Genomics & Microbiomes (IMG-ER) in the Joint Genome Institute (JGI) platform. The presence of both glutamine and glutamate synthetases genes are in accordance with *T. sp. AB60* physiology, since $(\text{NH}_4)_2\text{HPO}_4$ is the sole source of nitrogen in the chemically defined medium VL-55 used to grow of *T. sp. AB60*. On the other hand, the genomic analysis revealed the presence of genes for assimilatory nitrate (*nasAB*) and nitrate (*nirA*) reduction. These genes have been previously reported in *Acidobacteria* genomes but the genic clusters of other *Acidobacteria* contain both *nirA* and *nasAB*, whereas in *T. sp. AB60* these genes are located in different regions of the genome. Nitrate or nitrite reduction was observed only in few *Acidobacteria* in culture, but differently of *T. sp. AB60*, they require small amounts of yeast extract for growth. Comparison of the deduced amino acid sequences of NasA and NirA revealed that the *Acidobacteria* genes more closely related to each other than to any other phylum. Assimilatory nitrate reduction is an important biological process responsible for more than 10^4 megatons of inorganic transformations of nitrogen per year. The next step of this work is to test for nitrate and nitrite reduction in cultures, and then broaden our knowledge of the *Acidobacteriia*'s role in the nitrogen cycle of the Cerrado.

Keywords: *Acidobacteria*, Nitrogen cycle, assimilatory nitrogen reduction

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