Título: GENOME OF THE MAGNETOTACTIC BACTERIUM *MAGNETOFABA AUSTRALIS* STRAIN IT-1

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Resumo:

The ability of a group of motile aquatic bacteria to sense magnetic fields and migrate along magnetic field lines is called magnetotaxis. Magnetotactic bacteria comprise a polyphyletic group of microorganisms characterized by the ability to synthesize cytoplasmic organelles called magnetosomes. Magnetosomes consist of a nano-sized magnetic crystal, composed of magnetite (Fe_3O_4) or greigite (Fe_3S_4), enveloped by a lipid membrane. Magnetosomes are organized in chains imparting to the cell body a magnetic moment, resulting in passive cell orientation to magnetic field lines while actively swimming propelled by flagella. Magnetosome synthesis is influenced by cell metabolism and regulated by specific genes involved in production of organelle structure and crystal precipitation. Thus, genomic studies on magnetotactic bacteria are important for characterization of metabolic pathways of new species and to understand magnetosome biomineralization and magnetotaxis evolution. Here, our objective is to acquire and analyze the whole genome of newly isolated and described magnetotactic bacterium species *Magnetofaba australis* strain IT-1. The genome of *M. australis* strain IT-1 was sequenced through pyrosequencing. Genome analysis was done using SABIA platform and sequence assembly generated 21 contigs. Preliminary analysis showed that the size of *M. australis* strain IT-1 incomplete genome is 4.98Mb approximately and GC content is 57.95%. Total coding genome corresponds to 84.91% of the sequences, comprising 45 tRNAs and 4,170 coding sequences. Comparative genome analysis showed that 51.1% of coding sequences in *M. australis* IT- 1 is similar to sequences found in the magnetotactic bacterium *Magnetococcus marinus* strain MC-1. Both strains are capable of nitrogen fixation, sulfur oxidation and carbon fixation through rTCA cycle. Noticeably, the high number of genes encoding transporters (262), signal transducers (270), and chemotaxis (64) found in *M. australis* strain IT-1 may reflect adaptation to a dynamic aquatic environment. Detailed analysis of common sequences in both strains is in progress. To obtain the complete genome, genomic DNA was extracted and used as template in PCR containing combinations of primers developed for this work based on contig sequences using Primer3Plus web platform. Purified amplifications will be sequenced by Sanger method to complete *M. australis* strain IT-1 genome.

Palavras-chaves: Genome, Magnetotaxis, Magnetosome, Magnetotactic Bacteria

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