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The Characterization of two diverse magnetotactic bacteria: LEMS and MMS-1

Ulysses C. Pickard  
*Fort Valley State University*

Paul A. Howse  
*University of Nevada Las Vegas*

Dennis A. Bazylinski  
*University of Nevada Las Vegas, School of Life Sciences, Mentor*

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Magnetotactic bacteria (MTB) are a diverse group of prokaryotes that biomineralize membrane-bound magnetic crystals known as magnetosomes. The magnetosomes are aligned within the cell and consist of either magnetite (Fe$_3$O$_4$) or greigite (Fe$_3$S$_4$). The biomineralization of magnetosomes consists of several processes including: invagination of the cytoplasmic membrane, iron uptake into the cell and then into the magnetosome membrane vesicle, and crystallization of the mineral phase inside the vesicle. Mam genes control magnetosome biomineralization with most of the genes present in an island called a magnetosome island. Many of the mam genes are conserved between different species of MTB. The genes that are in the island have suggested that they play a significant role in the organization of the magnetosomes and how they align within the cell. The focus of this investigation is to determine if certain conserved mam genes are found in two isolated and metabolically diverse magnetotactic spirillums: LEMS and MMS-1.
The Characterization of Two Diverse Magnetotactic Bacteria: LEMS and MMS-1

Ulysses C. Pickard¹, Paul A. Howse², and Dr. Dennis A. Bazylinski²
¹ Fort Valley State University, 2 University Of Nevada, Las Vegas Nevada

Abstract

Magnetotactic bacteria (MTB) are a diverse group of prokaryotes that biomineralize membranes-bound magnetic crystals known as magnetosomes. The magnetosomes are aligned within the cell and consist of either magnetite (Fe₃O₄) or greigite (Fe₃S₄). The biomineralization of magnetosomes takes place through biologically driven processes; sequestration of the cytoplasmic membrane, iron uptake into the cell and then into the magnetosome membrane vesicle and crystallization of the mineral phase inside the vesicle. Some genes control magnetosome biomineralization with most of the genes present in an island called a magnetosome island. Many of the main genes are conserved between different species of MTB. The genes that are in the island have suggested that they play a significant role in the organization of the magnetosomes and how they align within the cell. The focus of this investigation is to determine if certain conserved main genes are found in two isolated and metabolically diverse magnetotactic species: LEMS and MMS-1. The information gained from the successful sequencing of these genes for MMS-1 and LEMS will provide a piece of the complex and difficult task of organizing and completing a genomic library.

Methods

1. In order to characterize magnetotactic bacteria, the first thing that must be done is to compare the genes of our magnetotactic spindles with other magnetotactic bacteria, which has been predicted to have the same gene by running a protein sequence alignment.

2. Total RNA was isolated from our MAGT-2 strain using QIAamp kit and reverse transcribed using the Superscript kit.

3. The PCR reaction was then performed using OneTaq kit and 10X PCR buffer.

4. The PCR product is then purified and sequenced using the BigDye Terminator cycle sequencing kit.

5. The PCR product is then sequenced and the sequence alignment is performed using CLUSTAL W software.

6. The gene product is then compared with other known magnetotactic bacteria using the BLAST program.

Conclusion/Future Research

In conclusion, the research was beneficial not only because manM and mmsK are known to be present in these strains of LEMS and MMS-1, but because the proteins encoded by these genes are novel. Further characterization of these genes will provide a better understanding of the magnetotactic bacteria. In the future, the primers developed for these genes may be used to identify the other magnetotactic bacteria via the alignment with the known genes and to identify the single or double stranded DNA. The genes that are in the island have suggested that they play a significant role in the organization of the magnetosomes and how they align within the cell. The focus of this investigation is to determine if certain conserved main genes are found in two isolated and metabolically diverse magnetotactic species: LEMS and MMS-1. The information gained from the successful sequencing of these genes for MMS-1 and LEMS will provide a piece of the complex and difficult task of organizing and completing a genomic library.

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