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

Repository Citation  
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 (Fe₃O₄). The biomineralization of magnetosomes takes place through distinct cellular processes: shunting 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. Fe(II) ions 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 suggest 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 spirochaetes: 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 spirochaetes with other magnetotactic bacteria who have been studied to have the same gene by sequencing a portion of the DNA.
2. PCR was the primary tool used to determine the similarity of DNA of other MTB using Man primers to amplify with 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.

Introduction

Magnetotactic Bacteria are a highly diverse group of prokaryotes that biomineralize membrane-bound magnetic crystals known as magnetosomes. Magnetosomes are intracellular structures, forming magnetic iron mineral crystals enveloped by a phospholipid bilayer membrane known as the magnetosome membrane (Boryt et al., 1985; Komor et al., 2006; Bazylinski et al., 2007). The RM contains proteins that are unique to the RM and that it is likely that these proteins play the key roles in magnetic biomineralization in magnetosomes. The proteins and the genes that encode for these are called the RM (magnetosome membrane) or RM (magnetic particle membrane specific) proteins (or main or minor genes (Bazylinski et al., 2007)). The magnetosomes in every magnetotactic bacteria genome examined showed they are in these proximity. The genomic region that contained the magnetosome genes in EM. globuliformis also contained 42 mobile elements of transpose of the insertion sequence type and integrases Gifford et al., 2005. These mobile elements are common and important features in genome islands (Maillon and Chandler, 1996; Maillon et al., 1999). The similarity organization of the magnetosome operons in different magnetotactic bacterial strains presumably that the magnetosome gene island might have been transferred horizontally to generate the different types of bacteria. This would explain the great diversity of the group. The MIs undergo frequent rearrangements, which allows it to retain many of the genes, but still, diverse magnetotactic bacteria not every single gene of the island is present in every species. The goal of this study is to determine what many genes are present in those that are predicted, and the results are found in similar species of magnetotactic bacteria.

Conclusion/Future Research

In conclusion, the research was beneficial not only because mainM and mainF genes were to be present in these strains of LEMS magnetotactic spirochaetes, but also because the more detailed analysis can be made in the interest of trying to completely characterize these spirochaetes in a genomic library for magnetotactic bacteria. In the future, the primers developed for these genes may be more specific to prevent the multiple products that degenerate primers offer. Further characterization of genes predicted to lie within the conserved region of the Magnetotactic island are expected to continue with less time constraint to provide much more detailed results.

Acknowledgements

I would like to thank my mentor. Dr. Dennis A. Bazylinski, Dr. Paul House for helping me understand the techniques for dealing with microorganisms, PCR technology, and helping prepare fresh samples of DNA. Dr. Christopher LeFevre (post-doc) for helping me obtain vital information concerning the magnetosome island. Ms. Marion Smith for helping me improve my writing techniques. Mr. Jerry Povey for troubleshooting, and Mr. Fredrica Arden for providing invaluable advice when I was unsure about how to follow non-standard protocols. This project was funded by NSF Grant #