Aug 9th, 10:15 AM - 12:00 PM

Magnetosome genes in the Gammaproteobacterium strain BW-2

Lucero Rivera
Arizona Western College

Denis Trubitsyn
University of Nevada, Las Vegas, denis.trubitsyn@unlv.edu

Dennis A. Bazylinski
University of Nevada, Las Vegas, dennis.bazylinski@unlv.edu

Repository Citation
Rivera, Lucero; Trubitsyn, Denis; and Bazylinski, Dennis A., "Magnetosome genes in the Gammaproteobacterium strain BW-2" (2011). Undergraduate Research Opportunities Program (UROP). 9.

This Event is brought to you for free and open access by the Undergraduate Research at Digital Scholarship@UNLV. It has been accepted for inclusion in Undergraduate Research Opportunities Program (UROP) by an authorized administrator of Digital Scholarship@UNLV. For more information, please contact digitalscholarship@unlv.edu.
Magnetosome Genes in the Gammaproteobacterium
Strain BW-2

Lucero Rivera¹, Denis Trubitsyn² and Dennis A. Bazylinski²

¹Arizona Western College, Department of Science, Math, and Agriculture
²School of Life Sciences, University of Nevada at Las Vegas

Abstract

Magnetotactic bacteria (MTB) biomineralize intracellular nanometer-sized, magnetic crystals surrounded by a lipid bilayer membrane known as magnetosomes. These crystals, which consist of magnetite (Fe₃O₄) or greigite (Fe₃O₄·nH₂O), cause the cell to align along the geomagnetic field lines as they swim, a phenomenon known as magnetotaxis. Strain BW-2 is a magnetite-producing magnetotactic bacterium isolated from Badwater Basin, Death Valley National Park (California) and is one of only two species of MTB that are known to phylogenetically belong to the Proteobacteria class of the Prokaryota phylum. The biomineralization of magnetite in magnetotactic bacteria is mediated by a series of genes that include the mam, mms, and mnt genes that presumably control the production of and the size and shape of the magnetite crystal within the magnetosomes. Magnetosome genes have not yet been found in the genomes of newly discovered magnetotactic Gammaproteobacteria.

In this study, we use polymerase chain reaction with degenerate primers designed from mom genes found in other MTB, and DNA sequencing to search for and amplify possible mom genes in the genome of strain BW-2. In addition, with enough DNA sequence, we may be able to find evidence of the presence of a magnetosome gene island in this organism. Positive results from this study will be instrumental in determining evidence for lateral gene transfer of the magnetosome gene island to the Gammaproteobacteria and the evolution of magnetotaxis based on magnetite biomineralization in general.

Introduction

Magnetotactic bacteria (MTB) are Gram-negative prokaryotes that display a phenomenon known as magnetotaxis where these organisms align along geomagnetic field lines as they swim (Leifer et al. 2011). MTB experience a torque in a magnetic field that causes them to passively align along magnetic field lines: cells are not being pulled in any direction (as shown in Figure 1) and even dead cells align but don't swim. This phenomenon is caused by the ability of MTB to biomineralize intracellular magnetic crystals (Figure 2) that consist of either an iron oxide or iron sulfide surrounded by a lipid bilayer known as magnetosomes (Bazylinski and Frankel, 2004). Most of these organisms organize magnetosomes in one or more chains (Bazylinski and Frankel, 2004). The control of production and specific characteristics that these crystals display is mediated by a series of genes known as the mam, mms, and mnt genes. These genes are organized in the genomes of MTB of the Alpha- and Deltaproteobacteria within a genomic island known as the magnetosome island. Genomic islands are typically surrounded by transposable elements such as insertion sequences, transposases, and pseudogens (Bazylinski and Frankel, 2004). Because of this, magnetosome genes and the trait of magnetotaxis is thought to have been transmitted to many different bacteria through horizontal gene transfer.

The purpose of this study is to search for and amplify mam genes in the newly-isolated Gammaproteobacterium strain BW-2. If enough DNA sequence is obtained, it may be possible to show evidence for the existence of the magnetosome island in this organism thus also providing evidence for horizontal gene transfer of the magnetosome island to the Gammaproteobacteria.

Results

Figure 2. Transmission electron micrograph of a cell of strain BW-2 (A) and a magnetosome chain from the organism (B).

Table 1. Degenerate PCR primers used to amplify magnetosome genes in strain BW-2.

Future Directions

Studying magnetite biomineralization in magnetotactic bacteria is important because magnetite magnetosomes have been shown to have unique magnetic, physical and optical properties that can be exploited in a very large number of scientific, commercial, and medical applications (Lang and Schiller, 2006) including magnetic cell separation and the diagnosis and treatment of cancerous tumors.

Methods

The polymerase chain reaction (PCR) using degenerate primers (Table 1) for specific magnetosome genes was employed to amplify possible mam genes in strain BW-2. Primers were designed from mam genes found in magnetotactic Alpha- and Deltaproteobacteria. PCR products were sequenced (Functional Biosciences, Inc., Madison WI) while some PCR products were cloned into pGEM-T Easy Vector (Promega) prior to sequencing.

Discussion

Here we show strong evidence that the magnetosome genes, mamK, mamO, and mamM, are present in the genome of BW-2. Although, no evidence for the presence of a large number of other magnetosome genes was found in strain BW-2, the genes may still be present. This is most likely due to the fact that the degenerate primers we used were designed from gene sequences from magnetotactic Alpha- and Deltaproteobacteria. Our results suggest that some genes control Gammaproteobacterium may be highly divergent enough that most of the primers we used were not effective. We also expected to amplify a fragment approximately 4 kb long, based on data from magnetotactic Alpha- and Deltaproteobacteria, between the genes momK and momO with primers designed directly from strain BW-2. However, we did not, and it may be that the fragment could not be amplified for a number of reasons, one likely possibility being that the organization of the magnetosome genes is different in strain BW-2 compared to other MTB (Figure 3).

Acknowledgements

This project was funded by the U.S. National Science Foundation (NSF) grant DBI 1005223. REU Site: A Broad View of Environmental Microbiology. Research in the Bazylinski lab is supported by U.S. NSF grant EAR 0920718.

References