

Structural Analysis of the BamA-B complex in *Acinetobacter baumannii*

Abigael N. Gichaba, Robert E. Stephenson, and Nicholas Noinaj
Department of Biological Sciences, Purdue University

ABSTRACT

There are 2 types of bacteria, gram-negative and gram-positive bacteria. Gram-negative bacteria have both a plasma membrane and an outer membrane, while gram-positive only have a plasma membrane. The outer membranes of gram-negative bacteria have outer membrane proteins which are essential for the bacteria's survival. Also located within the outer membrane is a multicomponent protein complex named the beta-barrel assembly machinery (BAM) complex. BAM is responsible for folding and inserting outer membrane proteins into the outer membrane. This protein complex serves an essential role but not much is understood about its function. In this study, two subunits of the BAM complex (BamA and BamB) in *Acinetobacter baumannii* were recombinantly expressed in *E. coli* and then purified, crystallized and analyzed using biophysical methods in order to gain a better understanding of the *A. baumannii* BAM complex structure. In efforts to prepare the BamAB complex, two milligrams of BamA and two milligrams of BamB were mixed in buffer. The sample was ran through a size-exclusion column (Superdex 200 Increase GL) and analyzed for complex formation. Results showed we were not able to obtain a properly assembled complex with the current protocol, however, we will be screening different detergents in hopes of finding one that will foster BamA-B complex formation. The information gained from solving this structure will further aid in understanding the mechanisms of this important protein.

KEYWORDS

BAM, AB Complex, *Acinetobacter Baumannii*, Purification