

## **Adaptive Strategies of *Bacillus thuringiensis* Isolated from Acid Mine Drainage Site in Sabah, Malaysia**

### **ABSTRACT**

The adaptive process in bacteria is driven by specific genetic elements which regulate phenotypic characteristics such as tolerance to high metal ion concentrations and the secretion of protective biofilms. Extreme environments such as those associated with heavy metal pollution and extremes of acidity offer opportunities to study the adaptive mechanisms of microorganisms. This study focused on the genome analysis of *Bacillus thuringiensis* (Bt MCMY1), a gram positive rod shaped bacterium isolated from an acid mine drainage site in Sabah, Malaysia by using a combination of Single Molecule Real Time DNA Sequencing, Scanning Electron Microscopy (SEM) and Fourier Transform Infrared Spectroscopy (FTIR). The genome size of Bt MCMY1 was determined to be 5,458,152 bases which was encoded on a single chromosome. Analysis of the genome revealed genes associated with resistance to Copper, Mercury, Arsenic, Cobalt, Zinc, Cadmium and Aluminum. Evidence from SEM and FTIR indicated that the bacterial colonies form distinct films which bear the signature of polyhydroxyalkanoates (PHA) and this finding was supported by the genome data indicating the presence of a genetic pathway associated with the biosynthesis of PHAs. This is the first report of a *Bacillus* sp. isolated from an acid mine drainage site in Sabah, Malaysia and the genome sequence will provide insights into the manner in which *B. thuringiensis* adapts to acid mine drainage.