

# Evaluating the Gene Expression of Mycobacteriophage XianYue

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## Abstract

Antibiotic resistance has become a prevalent issue in the 21<sup>st</sup> century. The over-prescription and frequent use of antibiotics have allowed host bacteria to escape the effects of antibiotic therapy. An alternative treatment for bacterial infection is bacteriophage (phage) therapy. Phage are viruses that infect and hijack the genetic machinery of its bacterial host which results in host cell death. Mycobacteriophage XianYue was isolated from a soil sample on the campus of the University of North Georgia. Using its bacterial host *Mycobacterium smegmatis*, a non-infectious mycobacterium, XianYue's gene expression was analyzed using quantitative polymerase chain reaction (qPCR) at different time points in its infection cycle. This data provides evidence for which genes are activated or repressed at different moments in its interaction with *Mycobacterium smegmatis*. Such genetic analysis allows for greater insight into the gene expression of similar mycobacteriophage within cluster A that are infectious to *Mycobacterium tuberculosis* (tuberculosis) or *Mycobacterium leprae* (leprosy). Understanding these activations and repressions will allow for genetic customization of phage treatment according to the case of the bacterially infected patient. Such customization of treatment will ultimately increase the survival outcomes of patients who are immune to antibiotic therapy.