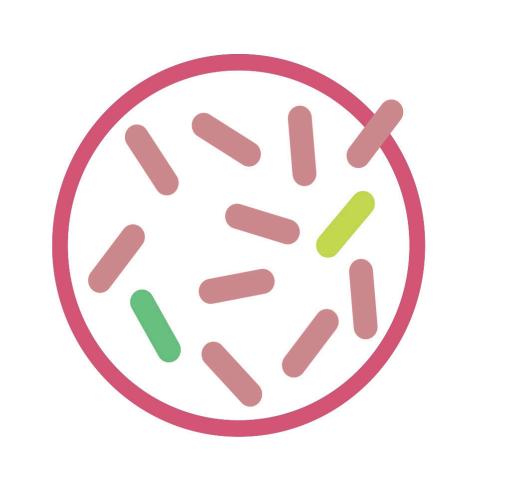
Abstract:

Bacteriophages, viruses that infect bacteria, possess the potential to be utilized for therapeutic purposes. Despite being the most abundant biological entity, the biological function of many phage genes has not been established. Our lab is analyzing each gene of the phage Phayonce, which infects Mycobacterium smegmatis. First, individual genes are inserted into an inducible expression vector. Then, these plasmids were used to transform *M. smegmatis* and determine if individual genes have toxic effects on host cells. Because functions of gene number 50 and 52 of Phayonce cannot be inferred by sequence comparison, they were selected for analysis. These genes were cloned into the pExTra inducible expression vector and used to transform M. smegmatis. We assessed cytotoxicity of these gene products by assaying host cell growth rates on media that induces expression of the phage genes. Our results will establish a biological role of these bacteriophage proteins that could be developed into therapeutic strategies to combat bacterial diseases.



Bacteriophages account for a large majority of all organisms in the biosphere. A phage will only infect one, or a few, specific species of bacteria. The number of individual phages that are isolated are substantial and have increased in recent years, but the functions of individual genes remain unknown.

The SEA-GENES project aims to analyze phage genomes in order to identify cytotoxic genes

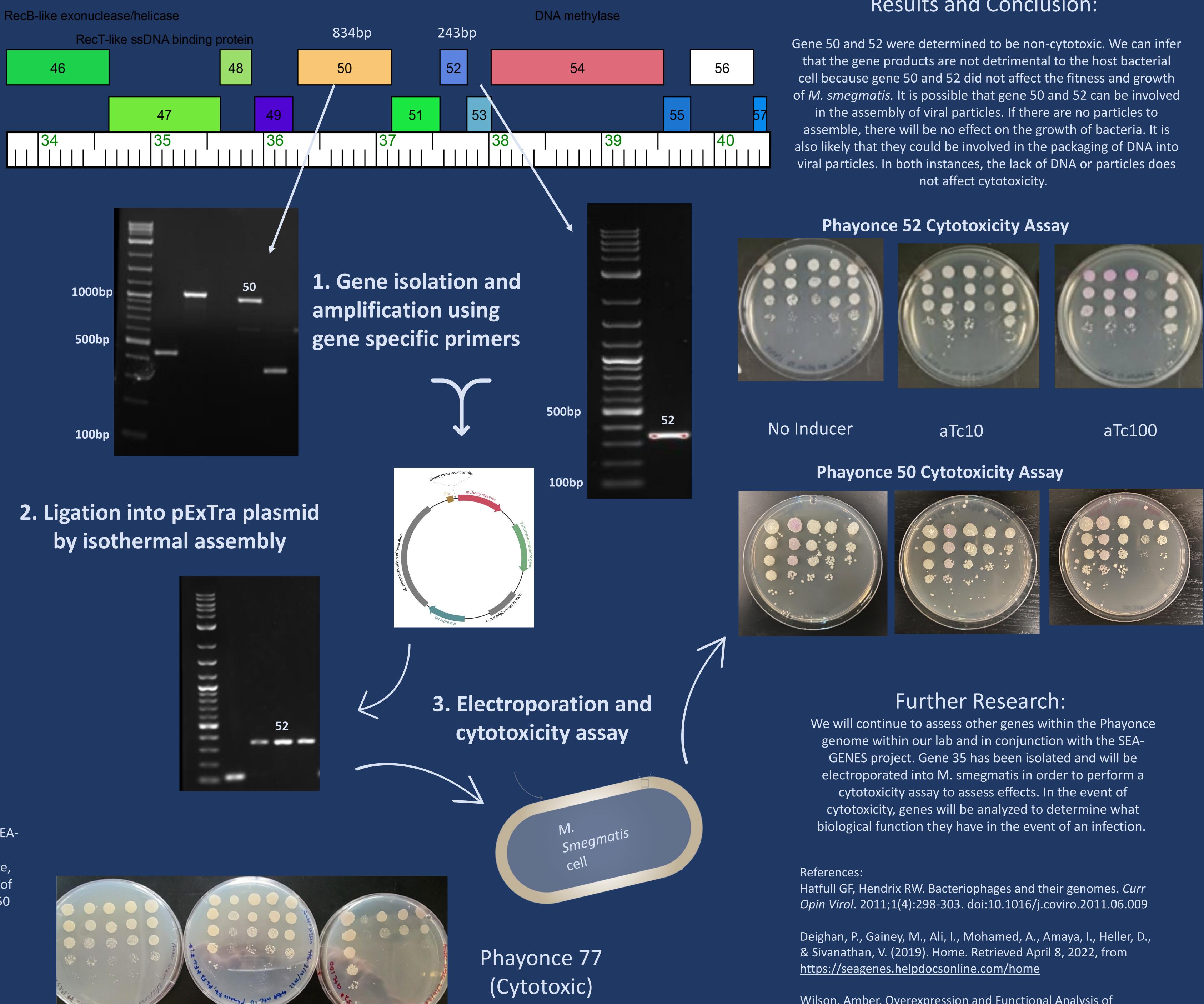


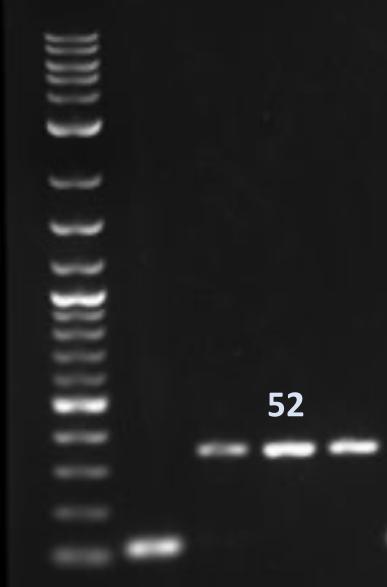


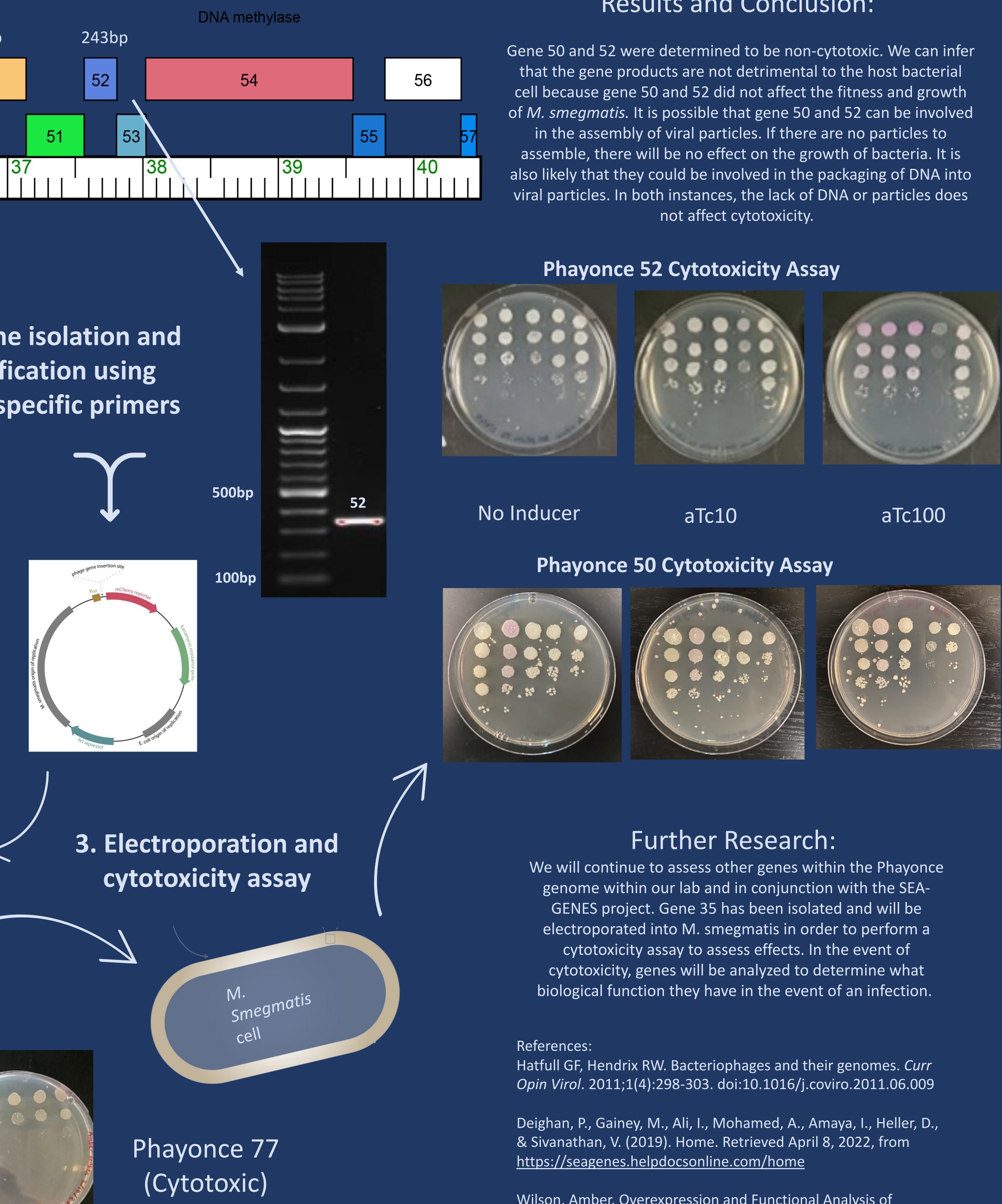
Coastal Carolina University's SEA-**GENES** lab selected mycobacteriophage Phayonce, whose genome is comprised of 77 genes. Using PCR, genes 50 and 52 were amplified.

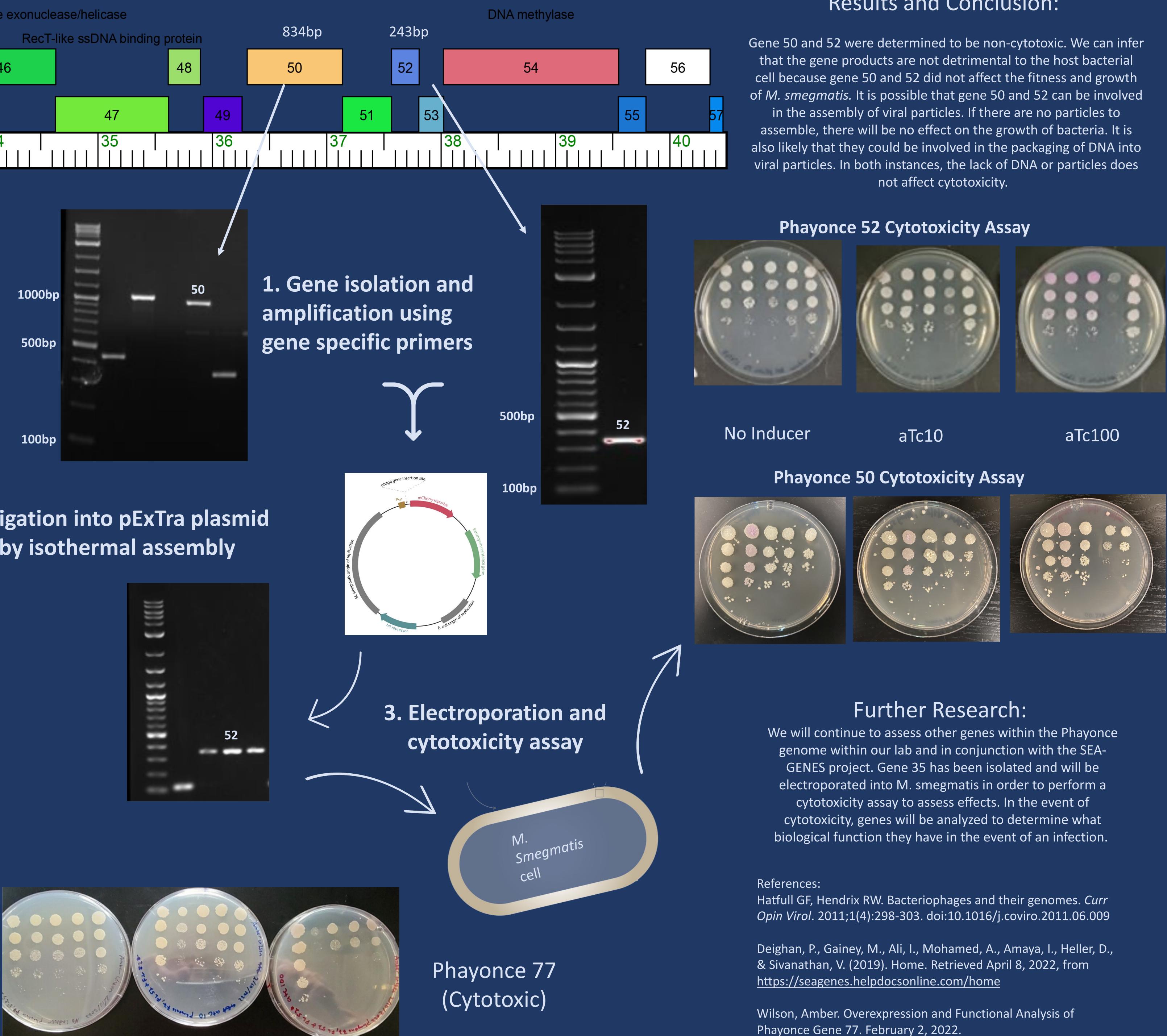
Cloning and Overexpression of Phayonce Genes to Assess Cytotoxicity in Mycobacterium Smegmatis Abbey Montoya, Olivia Sundman, Dr. Daniel Williams, Dr. Michael Pierce

Department of Biology









Results and Conclusion: