

Plan Overview

A Data Management Plan created using DMPTool

Title: Bacteriophage genomics

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Bacteriophage genomics

My lab is currently in possession of 40 *Paenibacillus larvae* phage genomes awaiting annotation. The genomes were obtained from collaborators at Brigham Young University using standard bacteriophage culturing techniques. We expect to receive more *Paenibacillus larvae* phage genomes from our collaborators over the duration of the award.

We will isolate and sequence bacteriophage DNA as part of an undergraduate course on discovery of bacteriophages of the U.S. Southwest. Bacteriophages will be isolated using standard bacteriophage culturing techniques. The DNA will be sequenced using Illumina sequencing technology and assembled using the Geneious 10.0 software.

We will use the TargeTron technology to generate edited *Paenibacillus larvae* phage genomes for the purposes of our experiments.

We will generate a novel tool for bacteriophage genome annotation.

All DNA sequencing data, complete genomes, and edited genomes will be in .fasta format

All data and data management will be the responsibility of the PI

All complete, annotated, novel bacteriophage genomes will be uploaded to GenBank immediately prior to publication and made publically available to the scientific community. All complete, annotated, novel bacteriophage genomes will also be published in the journal Genome Announcements.

The completed software will be freely available for download by the scientific community from a dedicated website indefinitely . A community wiki will be created for the software. The software will be actively maintained, updated and expanded indefinitely.

All complete, annotated, novel bacteriophage genomes uploaded to GenBank will be publically available by the scientific community indefinitely. There are no HIPAA or IRB related issues with the data

All DNA sequencing data and complete bacteriophage genomes will be stored indefinitely on the PI's computer and on three external hard drives as backup storage.
