**Genome Annotation of the Mycobacterium Phage Leston**

A newly isolated Mycobacterium Phage named Leston was annotated. This phage was isolated by Leslyann Mercier and Antonio Devine from the Univesity of Texas at El Paso. Its genome was sequenced at the Pittsburgh Bacteriophage Institute by Ilumina techonology. It has a genome shotgun coverage of 2224, a genome length of 61,808 bp and a GC content of 64.9%. It was characterized as a cluster K5 Siphoviridae bacteriophage.

The initial homology analysis of the whole sequence revealed a similarity of 98% with the Mycobacterium phage OkiRoe. A rapid annotation was performed using the PHAST tool [1] which identified 97 protein coding regions and 1 tRNA . We also did a manual annotation using gene prediction tools such as GeneMark and Glimmer, tRNA searching tools like tRNAscan and Aragorn and a gene verification process using BLAST yielding the same results as the PHAST output. The whole sequence was given to 9 groups of students of the phage hunter course at the University of Texas at El Paso in sections of 9,000 bp each with an overlap of 1,000 bp aproximately to perform a detailed annotation using DNAmaster and the annotation guide provided by PhagesDB. Each section of the genome was annotated by each group and a final annotation file was produced at the end by merging the files. For verification purposes the annotation was crosschecked in pairs of groups. 97 protein coding regions and a tRNA region were identified. Details of the annotations were written in the final DNAM5 file.

References

 [1] You Zhou, Yongjie Liang, Karlene Lynch, Jonathan J. Dennis, David S. Wishart “PHAST: A Fast Phage Search Tool” Nucl. Acids Res. (2011) 39(suppl 2): W347-W352 [doi:10.1093/nar/gkr485][PMID:21672955]