CONSIDER FOR TALK

2024 SEA Symposium Abstract

McGill University

Montreal

Corresponding Faculty Member: Patrick Lypaczewski (patrick.lypaczewski@mcgill.ca)

Genome Annotations of phages CabbageMan and SJReid

Reem Araji, Maiya Hernandez-Morrison, Natalie Abuelsamen, Orthy Aiyana, Taline Bawab, Laura Camelo Valera, Andrew Dayton, Lucie Droin, Brenna Fox, Eirc Gojan, Chloe Nyiligira, Jesse Shapiro, Patrick Lypaczewski

Many genes encoded by bacteriophages have been identified and their functions have been assigned thanks to the field of bioinformatics. However, most of them are still unknown. Two bacteriophages, CabbageMan and SJReid, were discovered by students enrolled in a course offered by McGill University in partnership with SEA-PHAGES. The course allows students to discover novel phages. The follow-up course is involved in annotating bacteriophage genomes. During this course, the genomes of CabbageMan and SJReid were fully and partially annotated, respectively, using a range of bioinformatics tools. The results were corroborated by fellow classmates. Some of the tools used include SEA-PHAGES website (guiding principles), HHPred, DNA Master, Aragorn, tRNA scan-SE, DeepTMHMM, GeneMark, PhagesDB, NCBI and DNA Master (BLASTp), Starterator, and Phamerator. Our analysis revealed that CabbageMan shares high similarity with phages in the FE cluster, in particular Corgi, Noely, and Idaho. 72% of CabbageMan’s genes had strong BLASTp hits (e-value < 10^-4), with 7 novel genes. Phage SJReid, an FC cluster phage, shares little similarity to phages within this cluster. This phage contains 354 genes, including 27 reverse genes and 26 tRNAs. Both CabbageMan and SJReid exhibit distinct features, presenting the opportunity for the discovery of novel phage genes.