

Bioinformatic Analysis of the Flathead Lake Monster Bacteriophage

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The Flathead Lake Monster (FLM) bacteriophage was noted to have an abnormally-long tail upon its discovery. Once its genome was sequenced, this research sought out to identify the 117 FLM gene products using the BLASTp sequence alignment algorithm. This resulted in the discovery of five genes that are considered to be novel to the FLM. A specific gene within the FLM genome called the tape measure gene (TMG) was further analyzed once it was identified based on homology with other phages. Previous literature has suggested that a longer TMG can manifest itself as a longer bacteriophage tail length. This observation led to the hypothesis that a long tail length should yield a correspondingly-long TMG within the FLM. The bioinformatic investigation involved comparing the FLM tail length and FLM tape measure gene length to other phages. The results found that the FLM does not have an abnormally long TMG when compared to how long its tail is, indicating that the FLM is an anomaly when compared to other phages. Future examination of phage mosaicism may yield more information as to why the FLM tail length is abnormally long.