CONSIDER FOR TALK

2023 SEA Symposium Abstract

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Evolution rates of actinobacteria viruses' genes in the DB cluster

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Genome sequence analysis has transformed every aspect of bacterial biology by improving our understanding of bacteria's genetics, physiology, and evolutionary development. Actinobacteria viruses are key components in shaping the evolution and ecology of life on Earth. This is a result of their high rates of evolution, ability to integrate into the genomes of other organisms, and relentless selection for mechanisms of host resistance and immunity. Evolutionary rates are used to describe the dynamics of change in a lineage across many generations.

Our main objective is to analyze the changes in the bacteriophage genome. Phages are genetic organisms that undergo mutations and natural selection, which alters the DNA structure. To comprehend the evolutionary dynamics of modern phages, comparative genomic analyses are helpful. In our genome there were areas with high similarity, we used these areas to calculate the evolutionary rates in those regions. We compared these regions to ones with less similarity. The most effective method to analyze the evolutionary rates for our genome is with Maximum likelihood (ML). We will support the analysis with phylogenetic trees. The length of the tree, or the anticipated total number of nucleotide substitutions per site on the phylogeny, is a measure of the evolutionary pace. Both fixed trees with predetermined branch lengths and random trees with branch lengths derived from a cladogenesis model were used to mimic DNA sequence data.