CONSIDER FOR TALK

11th Annual SEA Symposium Abstract

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Old Westbury NY

Corresponding Faculty Member: Christos Noutsos (noutsosc@oldwestbury.edu)

mechanisms of Genome Expansion in Phages

Iman Raja, Fernando Nieto, Christos Noutsos

Bacteriophages are viral organisms that propagate through the infection of bacterial hosts. Their ability to do so is influenced by the amount of DNA within their capsid. This indicates the presence of evolutionary pressures, leading towards gene-creating mutations. In this project, the mechanisms of genome expansion are studied that could potentially lead to new phage strains. Three modes of genome expansion were noted: Expansion of existing genes by inteins, Insertions of newly encoded genes, and *de novo* genes. For further investigation, models were developed. For the first mode, certain phams unique to each Cluster were repeatedly expanding among aligned pairs. After being tested for Synonymous/Non-synonymous substitutions, seven showed neutral/negative selection while two demonstrated neutral/positive selection. For the second mode, Insertions, the developed hypothesis indicates that the observed new genes were part of an ancestral phage that may have been passed down through positive selection. For the third mode, de novo genes were noticed throughout the phage genomes due to a few nucleotide deletions in their sequences. When those deletions were filled in, the genes disappeared. Overall, several factors causing genome expansion among Bacteriophages were revealed.