CONSIDER FOR TALK

2021 SEA Symposium Abstract

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Selective pressure in a region of Raythefirefly a DB cluster gemone

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A Bacteriophage is a virus and is considered an obligated parasitic organism requiring a host to propagate and move to the next generation. We are working with RayTheFireFly that requires a bacteria as a host the Gordonia terae. RaytheFirefly is a Cluster DB genome, 45,754 basepairs long. It has a 66.94% GC Content. Raythefirefly has 73 genes, with 12 on the reverse strand and 61 on the forward strand. Utilizing NCBI’s blastn we found the closest genome to Raythefirefly called Dmitri genome that belongs to cluster DB.The 5 prime site of the genomes are relatively similar to one another up to position 25800nt . From 25800nt to 33700nt in RaytheFirefly the two genomes match poorly an indication this region is under strong selection. There are 15 genes in this region in RayTheFireFly genome. In this presentation we study the evolution rates of those genes