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10th Annual SEA Symposium Abstract

Universidad Autónoma de Nuevo León

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Comparative genomics of recently annotated mycobacterium phage genome: Target.

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The mycobacterium phage Target possesses a genome sequence of 49097 bp, GC% of 63.6, and the overhang sequence: CGGATGGTAA. It belongs to the subcluster A1 and it´s morphotype´s characteristic of the Siphoviridae group. 39 of its genes do not have an assigned function. The annotated sequence resulted in 85 genes annotation, some of which have been mentioned as necessary for the viral lifecycle, specifically the Mycobacterium spp. Some of the features in the genes include the characteristic scaffolding assembly protein that contains a frame shift, which follows the coding sequence of a fusion protein, and some others as the terminase, HNH endonuclease, lysine A and B, several minor tail proteins, etc. Comparative genomics methods were applied to the Target´s genome, including phylogenetical relations with other genomes of the same cluster and subcluster, so we could observe the Target´s divergence when compared to other viruses, taking the terminase sequence as the base for its construction and exploring the similarity of the genome nucleotide sequence against other mycobacteriophages. Also synteny was studied in other phylogenetic related phage´s genomes. After we could see all this characteristics and relations together we can infer that there must be some adaptive advantage conferred, that explains the conservation of this particular gene order.