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Corresponding Faculty Member: Urszula Golebiewska (ugolebiewska@qcc.cuny.edu)



Shan He

Analysis of the genome of BelmontSKP

Shan He, Sana Ahmed, Amy Ajsiviniac, Japdeep Chhokar, Ali Chohan, Gabriel Fattakhov, Diana Idrovo, Zannat Khan, Minji Kwon, Nabila Laghzioui, Alyssa Malave, Lenny Naspud, Sakina Niazy, Sarah O'Leary, Maymona Obaid, Ishany Rahman, Christopher Scott, Gurjeet Singh, Raymond Tang, Fiza Zahid, Urszula P Golebiewska

The Queensborough Community College SEA-PHAGES class of Fall 2020 was very thankful for the opportunity to adopt BelmontSKP. BelmontSKP was first discovered in the soils near Lake Wylie, North Carolina in 2019, by Sarah Lewin from Queens University of Charlotte. It is a double-strand DNA virus and was isolated using Microbacterium foliorum. BelmontSKP has a genome of 41665-base-pairs. We used PhagesDB, Glimmer, GeneMarkS, Starterator, Protein BLAST, HHPred, Phamerator, DNAmaster, Aragorn, tRNAScanSe and TMHMM to identify and analyze its genes. We predicted that BelmontSKP has 72 genes including 69 protein-encoding genes and 3 tRNA genes. Out of the 69 protein-ecoding genes, 36 do not have predicted functions. According to Protein BLAST and Phamerator, the closest relative to Belmont SKP is phage AnnaLie, another member of the Cluster EB. After further examining the genome with both Aragorn and tRNAScanSe, we identified that Gene 68,69,70 of BelmontSKP are tRNA genes. Gene 68 codes for tRNA of anti-codon GUU corresponding to Asparagine; Gene 69 codes for tRNA of anti-codon CUG corresponding to Glutamine, and Gene 70 codes for tRNA of anti-codon CUU corresponding to Lysine. BelmontSKP is a member of cluster EB, that includes 39 other phages. The average presence of tRNA in this cluster is 1 gene per species. BelmontSKP so far has the highest number of tRNA genes in the cluster. But that might change because most members of this cluster are still waiting to be annotated.