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University of Lagos

Lagos

Corresponding Faculty Member: Imade Nsa (insa@unilag.edu.ng)



Habeeb Aderolu

Big3, a close relative of MrGordo

Emmanuella Omolade, Oyindamola Akinyemi, Kafayat Razaaq, Taiwo Ogunfile, Blessing Omolere, Maryam Saliu, Habeeb Aderolu, Nzube Ekpunobi, Seun Bamisaye, Ayodeji Odunsi, Imade Nsa, Tenny Egwuatu, Ganiyu Oyetibo, Matthew Ilori

Big3 is a siphoviridae phage isolated from an enriched soil sample in Richmond,VA by Brandon Brown-Ruffin at Virginia Union University in 2016. Its genome was found to be 53442 bp in length and assigned to Cluster A, subcluster A1. Programs used for annotation include DNA Master, NCBI BLAST Phamerator, Starterator, GeneMark, HHPred and Gene Content Similarity (GCS) Tool. On annotation, we found 91 called ORFS, 49 had known functions, the expected mosaic patterns in the gene order of sub-cluster A1, and no tRNAs. About 56% were reverse genes, no orpham genes, 26% of the start sites began with GTG, 5.5% with TTG and others with ATG. Big3’s annotation revealed a very strong resemblance to another temperate phage MrGordo isolated by Sean Kearney at Purdue University. Using the GCS tool, Seventy-eight phams were common to both with a GCS of 85.72% and fifty out of the 78 shared phams had the exact same ORF length. They were identical in their gene sizes of their tape measure, Lysin B, portal, capsid maturation protease, integrase, endonuclease VII proteins to name a few. They had the exact order of gene functions including the programmed translational frameshift at the tail assembly chaperone except that MrGordo had a split primase, only one terminase, more structural proteins but no superinfection immunity and helix-turn-helix binding domain proteins. On the other hand, Big3 had more minor tail proteins, small and large terminase subunits and membrane proteins. In addition, the largest ORF in Big3 was the large terminase subunit (2712 bp) followed by the tape measure protein (2472 bp), whereas, for MrGordo, tape measure (2472 bp) was the largest.