

COMPARATIVE GENOMIC ANALYSIS OF *PECTOBACTERIUM CAROTOVORUM* PHAGE P15_PC2B6 ISOLATED FROM CARROT FIELD SOIL

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Phylogenetic relationships play a significant role in the taxonomic identification of organisms. The classification helps in revealing the shared genomic and biological characteristics of an organism in comparison to its close relatives. Due to the recent advancement in next-generation sequencing technologies, the number of genomes deposited into public databases has dramatically increased. Among them, the taxonomic classification of bacterial viruses has reached a new level, where nucleotide and protein homologies are utilized to determine their phylogenetic relationships. In this study, the taxonomic relationship of *Pectobacterium carotovorum* phage P15_PC2B6, isolated from carrot field soils in the Badulla District, Sri Lanka, was determined using bioinformatic tools. In the VICTOR-generated phylogram of the annotated whole genome of P15_PC2B6 (Genbank Accession No: ON995367) with other known phage genomes of subfamily *Studiervirinae*, P15_PC2B6 clustered with the members of the genus *Unyawovirus*. Further, the phylogenetic reconstruction generated with the maximum-likelihood method using the amino acid sequences of RNA polymerase of the subfamily *Studiervirinae* demonstrated that the P15_PC2B6 grouped well with the known members of the genus *Unyawovirus*. Additionally, genome-wide comparisons employing TBLASTX homology of the P15_PC2B6 genome with the genomes of two members of the *Unyawovirus* genus, *Pectobacterium phages* phiPccP-1 and DU_PP_II, revealed that they shared a similar gene structure, indicating a closer relationship between them. Also, these phages shared closer average nucleotide identities (~91%) with the phage P15_PC2B6. The results of these comparative genomic analyses provide sufficient evidence for the placement of P15_PC2B6 within the genus *Unyawovirus* of the subfamily *Studiervirinae*.

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