

PA-002:

Identification and genomic analysis of temperate *Pseudomonas* bacteriophage PstS-1 from the Japan Trench at a depth of 7000 m

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Viruses play important roles in aquatic ecosystems, but deep-sea bacteriophages remain largely unexplored. A temperate bacteriophage (termed vB-PstS-1) was identified from the psychrotolerant gammaproteobacterium *Pseudomonas stutzeri* 1-1-1b, which was isolated from hadopelagic water (depth of 7000 m) of the Japan Trench in the Northwest Pacific Ocean. The genome size of PstS-1 was 48,666 bp; its genome displayed a 59.8% G + C content and a total of 79 coding sequences were identified in its genome. The PstS-1 phage belongs to the family Siphoviridae, but its genomic sequence and organization are distinct from those of any other well-known Siphoviridae phage. The mosaic genomic structure of PstS-1 suggests the occurrence of genetic exchange between distinct temperate phages in deep-sea *Pseudomonas* populations. The PstS-1 genome also harbors three distinct sequence regions corresponding to spacers within a single clustered regularly interspaced short palindromic repeat (CRISPR) locus in the rhizosphere-associated diazotrophic *P. stutzeri* A1501 genome. The extension of these spacers to the soil environment and the presence of many homologs of both the hadal deep-sea phage PstS-1 and terrestrial *Pseudomonas* phages suggest the early co-evolution of temperate phages and their host genus *Pseudomonas* prior to the divergence of their habitational and physiological adaptation.

keywords:Temperate bacteriophage,Deep sea,Genome sequence,**Pseudomonas**