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Genome Sequences of Two Temperate Phages, Φ CB2047-A and Φ CB2047-C, Infecting *Sulfitobacter* sp. Strain 2047

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We announce the complete genome sequences of two temperate *Podoviridae*, *Sulfitobacter* phages Φ CB2047-A and Φ CB2047-C, which infect *Sulfitobacter* sp. strain 2047, a member of the *Roseobacter* clade. This is the first report of temperate podophage infecting members of the *Sulfitobacter* genus of the *Roseobacter* clade.

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We report here the genomes of two lysogenic *Podoviridae*, phages Φ CB2047-A and Φ CB2047-C, infecting *Sulfitobacter* sp. strain 2047, a member of the *Roseobacter* clade of marine bacteria. This is the first report of temperate *Podoviridae* infecting members of the *Sulfitobacter* genus of the *Roseobacter* clade. The two podophages were isolated from an induced algal bloom mesocosm study in Raunefjorden, Norway, using standard plaque assay techniques (1, 2), and were sequenced by the Broad Institute under the Gordon and Betty Moore Foundation's Marine Phage, Virus, and Virome Sequencing Project. An average sequencing coverage of $\approx 30\times$ was obtained for both phages. Genome annotations were done using the RAST annotation server (3) and tRNAscan-SE search server (4). Translated peptides from the phage genomes were used as BLASTp queries to the NCBI nonredundant protein sequence database to manually curate possible gene functions and identify the nearest phage or prophage relatives. The CoreGenesUniqueGenes (CGUG) genome analysis tool (5) was used to identify gene homologues and assign core genes that are shared with other closely related phages.

Phage Φ CB2047-A is 40,929 bp, with a G+C content of 58.8%. A total of 73 open reading frames (ORFs) were identified in phage Φ CB2047-A. Phage Φ CB2047-C is 40,931 bp, with a G+C content of 59%. A total of 73 ORFs were identified in phage Φ CB2047-C. Phages Φ CB2047-A and Φ CB2047-C are nearly identical at the nucleotide level, except for a $\sim 2,000$ -bp region encoding a T5orf172 domain-containing protein (PF10544) and RusA-like endodeoxyribonuclease in Φ CB2047-A and five hypothetical proteins in Φ CB2047-C, where they share no sequence similarity. Φ CB2047-A and Φ CB2047-C share greatest sequence similarity to Φ EBPR podovirus 2, an uncultured phage from an enhanced biological phosphorus removal reactor (6). CGUG analysis identified 17 highly homologous genes (BLASTp threshold score, 85) between Φ CB2047-A and Φ CB2047-C and Φ EBPR podovirus 2. Both Φ CB2047-A and Φ CB2047-C have a DNA Bre-C like integrase to integrate in the host genome and lysis/

lysozyme proteins with glycosyl hydrolase and peptidoglycan binding domains predicted to be involved in host cell lysis cells. Phages Φ CB2047-A and Φ CB2047-C also show relatedness to the temperate *Myxococcus* phage Mx8 (accession no. NC_003085), with protein homology existing within the terminase gene and several putative tail-fiber genes.

In contrast to other known roseophages, the genomes of Φ CB2047-A and Φ CB2047-C do not contain genes showing strong homology to currently described DNA polymerases, thymidylate synthases, ribonucleotide reductases, and deoxycytidine deaminases (7). The absence of well-characterized replication/nucleotide metabolism genes indicates that Φ CB2047-A and Φ CB2047-C may rely heavily on host resources for nucleotide production to generate new virions or possibly use novel replication and nucleotide metabolism proteins. Also absent from the genomes of Φ CB2047-A and Φ CB2047-C are homologs to known DNA methylases, which are frequently present in other temperate relatives (8), including Φ EBPR podovirus 2 (accession no. AEI70896.1). The genomes of Φ CB2047-A and Φ CB2047-C encode homing endonucleases (HNH_3 domain [Pfam13392]), which may be beneficial to the host and/or offer a competitive advantage to the phage by cleaving the DNA of other closely related competing phages during mixed infections (9).

Nucleotide sequence accession numbers. The whole-genome sequences of *Sulfitobacter* phages Φ CB2047-A and Φ CB2047-C were deposited in GenBank under the accession no. [HQ332142](https://www.ncbi.nlm.nih.gov/nuccore/HQ332142) and [HQ317384](https://www.ncbi.nlm.nih.gov/nuccore/HQ317384), respectively.

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