# SUPPLEMENTARY FILES

## A novel *Roseobacter* phage possesses features of podoviruses, siphoviruses, prophages and gene transfer agents

Yuanchao Zhan[1], Sijun Huang[2], Sonja Voget[3], Meinhard Simon[4], Feng Chen[1,*]

1. Institution of Marine and Environmental Technology, University of Maryland Center for Environmental Science, USA
2. CAS Key Laboratory of Tropical Marine Bio-resources and Ecology, South China Sea Institute of Oceanology, Chinese Academy of Sciences, Guangzhou, China
3. Institute for Microbiology and Genetics. University of Göttingen, Germany
4. Institute for Chemistry and Biology of the Marine Environment, University of Oldenburg, Germany

* Correspondence: chenf@umces.edu

Keywords: Roseobacter, *Ruegeria pomeroyi,* phage, CbK-like phage, GTA

Running title: A novel roseophage

Fig. S1. The maximum likelihood phylogenetic tree of major capsid protein of bacteriophages. CbK-like phages, available roseophages, typical marine bacteriophages and Enterobacter phages were selected as references. Bootstrap = 500.

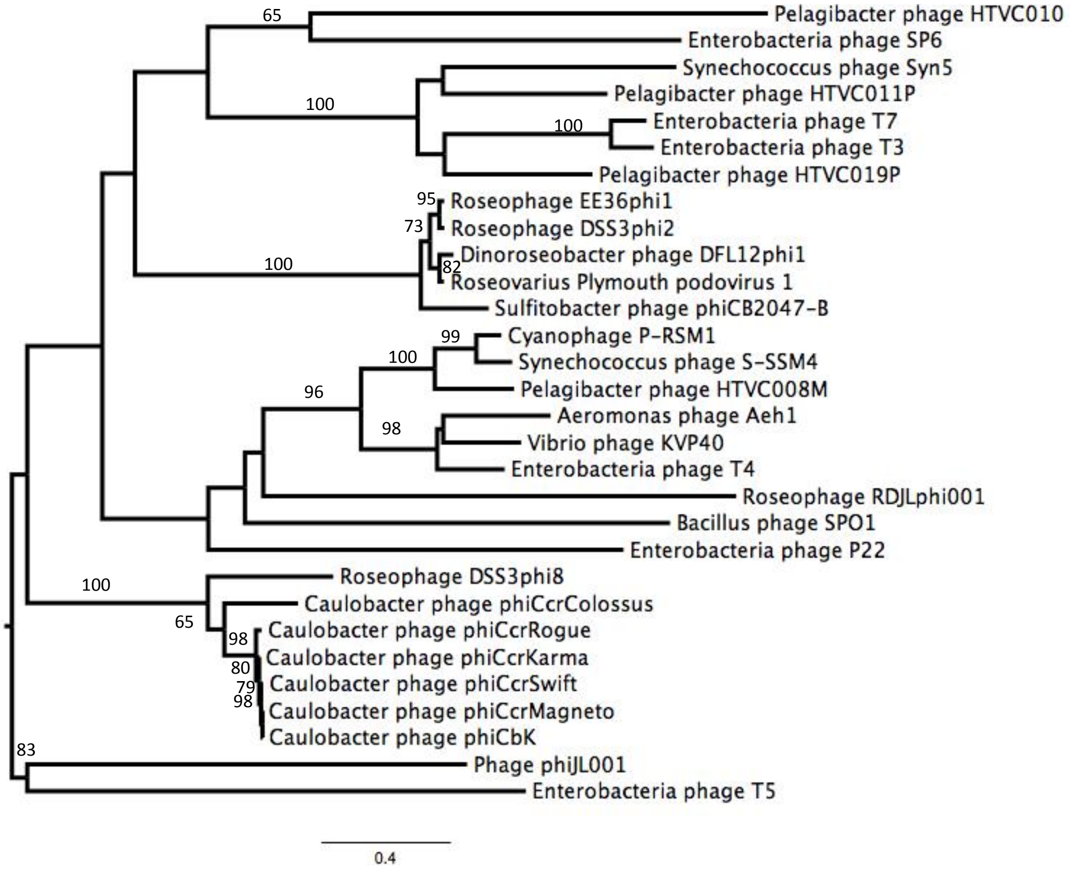

Fig. S2. The maximum likelihood phylogenetic tree of terminase large subunit of bacteriophages. CbK-like phages, available roseophages, typical marine bacteriophages and Enterobacter phages were selected as references. Bootstrap = 500.

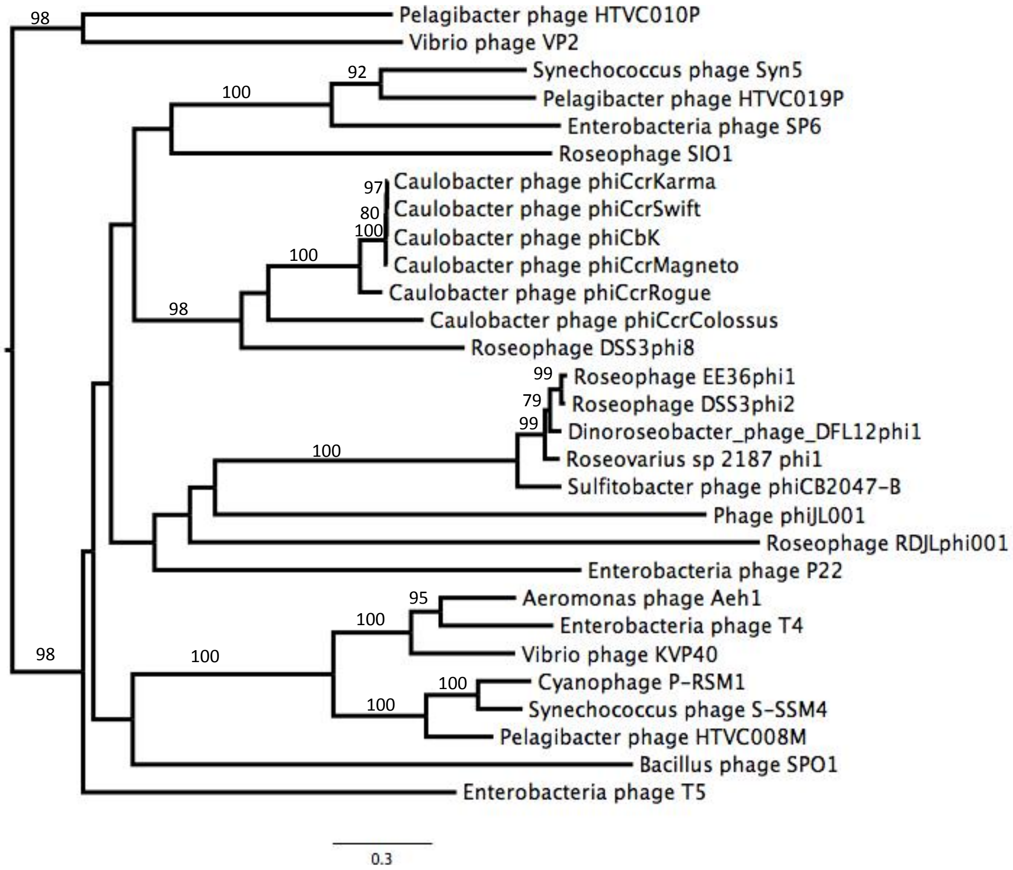

Table S1. Description of characterized ORFs of phage DSS3Φ8 and its kinship with the CbK-like phages

| Orf Name | Start | End | Length of amino acid | Strain | Description | Homolog to CbK-like phage* |
|---|---|---|---|---|---|---|
| DSS3P8_gp023 | 18900 | 19313 | 138 | + | putative aminoacyl-tRNA hydrolase | + |
| DSS3P8_gp027 | 20891 | 22531 | 547 | + | putative portal protein | + |
| DSS3P8_gp030 | 23245 | 24051 | 269 | + | hypothetical protein | + |
| DSS3P8_gp031 | 24249 | 25175 | 309 | + | putative major capsid protein | + |
| DSS3P8_gp032 | 25238 | 25642 | 135 | + | putative minor capsid protein | + |
| DSS3P8_gp034 | 26831 | 26205 | 209 | - | transcriptional regulator | |
| DSS3P8_gp035 | 26995 | 27222 | 76 | + | hypothetical protein | + |
| DSS3P8_gp038 | 27889 | 28794 | 302 | + | PhoH-like protein | + |
| DSS3P8_gp039 | 28794 | 29312 | 173 | + | hypothetical protein | + |
| DSS3P8_gp043 | 30791 | 32251 | 487 | + | major tail tube protein | + |
| DSS3P8_gp044 | 32406 | 32855 | 150 | + | pre-tape measure chaperone protein | + |
| DSS3P8_gp046 | 33256 | 38733 | 1826 | + | phage tail length tape-measure protein | + |
| DSS3P8_gp047 | 38775 | 40121 | 449 | + | GTA Orf12 | + |
| DSS3P8_gp049 | 41202 | 42116 | 305 | + | GTA Orf12 | |
| DSS3P8_gp050 | 42113 | 44173 | 687 | + | GTA Orf13 | |
| DSS3P8_gp051 | 44173 | 44622 | 150 | + | GTA Orf14 (NlpC/P60 family cell wall peptidase) | + |
| DSS3P8_gp052 | 44612 | 48403 | 1264 | + | GTA Orf15 | |
| DSS3P8_gp056 | 52579 | 53370 | 264 | + | N-acetylmuramoyl-L-alanine amidase | |
| DSS3P8_gp063 | 58220 | 57705 | 172 | - | Deoxyuridine 5'-triphosphate nucleotidohydrolase | |
| DSS3P8_gp064 | 58526 | 58290 | 79 | - | putative glutaredoxin protein | |
| DSS3P8_gp065 | 60286 | 58583 | 568 | - | Ribonucleotide reductase, alpha subunit | |
| DSS3P8_gp066 | 61294 | 60314 | 327 | - | Ribonucleotide reductase, beta subunit | |
| DSS3P8_gp069 | 63042 | 62089 | 318 | - | thymidylate synthase | |

| | | | | | | |
|---|---|---|---|---|---|---|
| DSS3P8_gp073 | 64502 | 64056 | 149 | - | CMP deaminase | |
| DSS3P8_gp074 | 65130 | 64504 | 209 | - | deoxynucleotide monophosphate kinase | |
| DSS3P8_gp075 | 65763 | 65164 | 200 | - | nucleotide pyrophosphohydrolase | |
| DSS3P8_gp077 | 67519 | 66083 | 479 | - | putative RecD-like helicase | + |
| DSS3P8_gp080 | 69964 | 68831 | 378 | - | hypothetical protein | + |
| DSS3P8_gp083 | 73119 | 70885 | 745 | - | putative T7-like Pol I DNA polymerase | + |
| DSS3P8_gp084 | 73756 | 73187 | 190 | - | type II restriction endonuclease PvuII | |
| DSS3P8_gp087 | 76912 | 75092 | 607 | - | DNA helicase | + |
| DSS3P8_gp090 | 78404 | 77403 | 334 | - | RnlB RNA ligase2 | |
| DSS3P8_gp094 | 80893 | 79604 | 430 | - | Phage rIIB lysis inhibitor | |
| DSS3P8_gp095 | 83066 | 80919 | 716 | - | Phage rIIA lysis inhibitor | |
| DSS3P8_gp098 | 83904 | 84551 | 216 | + | putative tyrosine recombinase | + |
| DSS3P8_gp099 | 84567 | 85118 | 184 | + | polynucleotide kinase | |
| DSS3P8_gp104 | 86488 | 86895 | 136 | + | cell wall hydrolase | |
| DSS3P8_gp105 | 86975 | 88219 | 415 | + | RNA ligase | |
| DSS3P8_gp107 | 88728 | 89186 | 153 | + | proteasome subunit beta | |
| DSS3P8_gp110 | 89882 | 90913 | 344 | + | bifunctional nicotinamide mononucleotide adenylyltransferase/ ADP-ribose pyrophosphatase | |
| DSS3P8_gp112 | 91272 | 92681 | 470 | + | nicotinate phosphoribosyltransferase | |
| DSS3P8_gp113 | 92816 | 93973 | 386 | + | DNA ligase | |
| DSS3P8_gp117 | 98440 | 98613 | 58 | + | hypothetical protein | + |
| DSS3P8_gp119 | 99460 | 98840 | 207 | - | Type I secretion protein | |
| DSS3P8_gp122 | 101454 | 100585 | 290 | - | transposase | |
| DSS3P8_gp129 | 104376 | 103924 | 151 | - | phage prohead protease | |
| DSS3P8_gp131 | 104890 | 104570 | 107 | - | thioredoxin | |
| DSS3P8_gp136 | 107556 | 106381 | 392 | - | poly(A) polymerase | |
| DSS3P8_gp139 | 108496 | 108095 | 134 | - | hypothetical protein | + |

| | | | | | | |
|---|---|---|---|---|---|---|
| DSS3P8_gp141 | 109574 | 108939 | 212 | - | putative metallophosphatase | |
| DSS3P8_gp181 | 121519 | 119435 | 695 | - | hypothetical protein | + |
| DSS3P8_gp182 | 122100 | 121516 | 195 | - | hypothetical protein | + |
| DSS3P8_gp187 | 124081 | 123674 | 136 | - | putative chaperone protein DnaJ | |
| DSS3P8_gp199 | 129170 | 129763 | 198 | + | hypothetical protein | + |
| DSS3P8_gp200 | 129760 | 130302 | 181 | + | putative RNaseH-like domain protein | + |
| DSS3P8_gp205 | 131324 | 131575 | 84 | + | terminase small subunit | |
| DSS3P8_gp206 | 131562 | 132086 | 175 | + | terminase small subunit | |
| DSS3P8_gp207 | 132083 | 133732 | 550 | + | putative terminase large subunit | + |

*: + in the column indicates that the top tBLASTx hit of respective gene is one of CbK-like phages.