|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Cyanophage** | **Gene** | **Forward primer (5’ to 3’)** | **Reverse primer (5’ to 3’)** | **References** |
| P-HM1 | *gp18* | CGAAGCGAATGAGTATTTAACAACCAAT | AGAAACTTGAGTTCCTACAGTTGTTGTGCCA | Current study |
| P-HM2 | *gp43* | CAGTAGATGTTCCAAAGGAGTATGCGTTG | CTTCTCTAGTTCTTTAGTAGGTGTCTTTTGATAC | Current study |
| P-SSM2 | *pstS* | GGCAGGAGGAAGACTAAGTGG | CTCTTCACCTTGGCAATATCC | [1] |
| P-SSP7 | *DNApol* | AAACACTTCCGCCCTTACCT | CTGCAACGAAAGGGAATTGT | [2] |
| P-GSP1 | *talC* | CGCTGACTTGATACAAGACTTAGGC | GCTTGGTCTATCCATAGCTTACCG | Current study |

**Supplementary Table 1**. PCR primers used in this study

Quantitative PCR primers

|  |  |  |  |
| --- | --- | --- | --- |
| **Cyanophage genus/gene** | **Forward primer (5’ to 3’)** | **Reverse primer (5’ to 3’)** | **References** |
| T4-like/g20 portal protein | GTAGWATWTTYTAYATTGAYGTWGG | ARTAYTTDCCDAYRWAWGGWTC | [3] |
| T7-like/DNA polymerase | CCNAAYYTNGSNCARGT | TCRTCRTGNAYRAANGC | [4] |
|  | CCNAAYYTNGSNCARGTNCC | TGNWRYTCRTCRTGNAYRAA | [5] |
| TIM5-like/DNA polymerase | GAYWSNYWYGCNTAYAAYGA | TGNWRYTCRTCRTGNAYRAA | [4] |

Primers used to screen and sequence cyanophages isolated from the South China Sea

**Supplementary References**

1. Zeng, Q. and S.W. Chisholm, *Marine viruses exploit their host's two-component regulatory system in response to resource limitation.* Curr Biol, 2012. **22**(2): p. 124-128.

2. Lindell, D., et al., *Genome-wide expression dynamics of a marine virus and host reveal features of co-evolution.* Nature, 2007. **449**(7158): p. 83-6.

3. Sullivan, M.B., et al., *Portal protein diversity and phage ecology.* Environ Microbiol, 2008. **10**(10): p. 2810-23.

4. Dekel-Bird, N.P., et al., *Host-dependent differences in abundance, composition and host-range of cyanophages from the Red Sea.* Environ Microbiol, 2015.

5. Dekel-Bird, N.P., et al., *Diversity and evolutionary relationships of T7-like podoviruses infecting marine cyanobacteria.* Environ Microbiol, 2013.