



# Complete Genome Sequence of the Lytic Giant Bacteriophage pT24 Infecting *Tenacibaculum* spp., Isolated from a Shrimp Culture Pond

Ho Viet Khoa,<sup>a</sup> Yuki Midorikawa,<sup>a</sup> Tsubasa Uchino,<sup>a</sup> Toshihiro Nakai,<sup>b</sup> Goshi Kato,<sup>a</sup> Hidehiro Kondo,<sup>a</sup> Ikuo Hirono,<sup>a</sup> Matthura Labaiden,<sup>c</sup> Sataporn Direkbusarakom,<sup>c</sup> Motohiko Sano<sup>a</sup>

School of Marine Science, Tokyo University of Marine Science and Technology, Tokyo, Japan<sup>a</sup>; Graduate School of Biosphere Science, Hiroshima University, Hiroshima, Japan<sup>b</sup>; School of Agricultural Technology, Walailak University, Nakhon Si Thammarat, Thailand<sup>c</sup>

**ABSTRACT** The lytic bacteriophage pT24, which infects *Tenacibaculum* spp., was isolated from the water of a whiteleg shrimp (*Litopenaeus vannamei*) culture pond in Thailand. This giant bacteriophage with myovirus morphology comprised 234,670 bp with 296 predicted genes.

The genus *Tenacibaculum* is a member of the family *Flavobacteriaceae* and is an abundant and important component of marine bacterial ecosystems (1–3). We isolated *Tenacibaculum* sp. T24—a Gram-negative, aerobic, gliding motile, long-rod bacterium that produces yellow pigment—from the water of a whiteleg shrimp (*Litopenaeus vannamei*) culture pond in Thailand. The lytic bacteriophage pT24 with myovirus morphology was isolated from the water of a shrimp-rearing pond in Thailand by screening on T24. Here, we report the complete genome sequence of phage pT24, which can infect the species *T. mesophilum* and *T. discolor*.

DNA of the phage was sequenced with the Illumina MiSeq platform using the Nextera XT library preparation kit and the MiSeq version 3 reagent kit (600 cycles). The sequence reads were imported into CLC Genomics Workbench version 9 (CLC bio) and *de novo* assembled. The obtained linear DNA sequences were confirmed by PCR, with a primer set designed at both ends of the sequence, followed by Sanger sequencing. The coding sequences (CDSs) were predicted by GeneMarkS (4), followed by annotation using Blast2GO (5); tRNAs were found using tRNAscan-SE version 2.0 (6).

In total, 1,182,866 reads were generated (1,290× coverage of the genome), and their average length was 255.84 bp. Phage pT24 had 234,670 bp of linear genomic DNA with a GC content of 28.85% and 4 tRNAs identified. A total of 296 CDSs were predicted, and among the 41 annotated genes were those encoding for DNA ligase, DNA helicase, DNA polymerase, large terminase protein, ribonucleotide reductase, DNA topoisomerase, RNA ligase, and thymidylate synthase. Twenty of the 41 annotated proteins revealed similarities to those of the “giant phage” *Sphingomonas* phage PAU (GenBank accession no. NC\_019521) (7) at 42.9 to 59.7% identity.

This is the first report of a *Tenacibaculum* phage genome sequence. This newly sequenced genome information will be useful for studies on the dynamics of phage-infecting environmental bacteria in shrimp culture ponds and on the interactions between phages and their hosts, as well as to clarify the impact of lytic phages on the microbial community structure in the pond.

**Accession number(s).** The complete genome sequence of bacteriophage pT24 was submitted to DDBJ/GenBank under the accession number [LC168164](https://doi.org/10.1128/genomeA.00081-17).

Received 24 January 2017 Accepted 9 May 2017 Published 6 July 2017

**Citation** Khoa HV, Midorikawa Y, Uchino T, Nakai T, Kato G, Kondo H, Hirono I, Labaiden M, Direkbusarakom S, Sano M. 2017. Complete genome sequence of the lytic giant bacteriophage pT24 infecting *Tenacibaculum* spp., isolated from a shrimp culture pond. *Genome Announc* 5:e00081-17. <https://doi.org/10.1128/genomeA.00081-17>.

**Copyright** © 2017 Khoa et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Motohiko Sano, [msano00@kaiyodai.ac.jp](mailto:msano00@kaiyodai.ac.jp).

H.V.K. and Y.M. contributed equally to this work.

## ACKNOWLEDGMENTS

This work was supported in part by a grant from the Japan Science and Technology Agency/Japan International Cooperation Agency, Science and Technology Research Partnership for Sustainable Development (JST/JICA, SATREPS), and by JSPS KAKENHI grant 26660170.

## REFERENCES

1. Kirchman DL. 2002. The ecology of *Cytophaga-Flavobacteria* in aquatic environments. *FEMS Microbiol Ecol* 39:91–100. <https://doi.org/10.1111/j.1574-6941.2002.tb00910.x>.
2. Habib C, Houel A, Lunazzi A, Bernardet JF, Olsen AB, Nilsen H, Toranzo AE, Castro N, Nicolas P, Duchaud E. 2014. Multilocus sequence analysis of the marine bacterial genus *Tenacibaculum* suggests parallel evolution of fish pathogenicity and endemic colonization of aquaculture systems. *Appl Environ Microbiol* 80:5503–5514. <https://doi.org/10.1128/AEM.01177-14>.
3. Suzuki M, Nakagawa Y, Harayama S, Yamamoto S. 2001. Phylogenetic analysis and taxonomic study of marine *Cytophaga*-like bacteria: proposal for *Tenacibaculum* gen. nov. with *Tenacibaculum maritimum* comb. nov. and *Tenacibaculum ovolyticum* comb. nov., and description of *Tenacibaculum mesophilum* sp. nov. and *Tenacibaculum amyolyticum* sp. nov. *Int J Syst Evol Microbiol* 51:1639–1652. <https://doi.org/10.1099/00207713-51-5-1639>.
4. Besemer J, Borodovsky M. 2005. GeneMark: Web software for gene finding in prokaryotes, eukaryotes and viruses. *Nucleic Acids Res* 33:W451–W454. <https://doi.org/10.1093/nar/gki487>.
5. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *J Mol Biol* 215:403–410. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2).
6. Lowe TM, Eddy SR. 1997. TRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res* 25:955–964. <https://doi.org/10.1093/nar/25.5.955>.
7. Ackermann HW, Auclair P, Basavarajappa S, Konjin HP, Savanurmath C. 1994. Bacteriophages from *Bombyx mori*. *Arch Virol* 137:185–190. <https://doi.org/10.1007/BF01311186>.