

# Genome Sequence of *Photobacterium mandapamensis* Strain *svers.1.1*, the Bioluminescent Symbiont of the Cardinal Fish *Siphamia versicolor*<sup>∇</sup>

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***Photobacterium mandapamensis* is one of three luminous *Photobacterium* species able to form species-specific bioluminescent symbioses with marine fishes. Here, we present the draft genome sequence of *P. mandapamensis* strain *svers.1.1*, the bioluminescent symbiont of the cardinal fish *Siphamia versicolor*, the first genome of a symbiotic, luminous *Photobacterium* species to be sequenced. Analysis of the sequence provides insight into differences between *P. mandapamensis* and other luminous and symbiotic bacteria in genes involved in quorum-sensing regulation of light production and establishment of symbiosis.**

*Photobacterium mandapamensis* (Gammaproteobacteria, Vibrionaceae) is the bioluminescent symbiont of the cardinal fish *Siphamia versicolor*. The fish harbors a dense population of the bacterium in a ventral light organ and uses the bacterial light to attract zooplankton prey. The light organ begins to form early in larval development, through a proliferation and differentiation of intestinal epithelial cells, and it becomes colonized by *P. mandapamensis* after further larval development (2, 4–8, 11, 14). The specificity of the association and the ability to culture larvae of the fish (5, 8) establish a foundation for experimental analysis of how this vertebrate animal acquires, accommodates, and functions cooperatively with its bacterial symbiont. To begin gaining insight into the genetic interactions underlying the *P. mandapamensis*–*S. versicolor* association, we sequenced the genome of *P. mandapamensis* strain *svers.1.1*. This is the first genome of a symbiotic, luminous *Photobacterium* species to be sequenced.

The genome of *svers.1.1* was sequenced using the Roche 454 GS FLX titanium platform; 310,304 single-end reads and 195,674 paired-end reads were obtained (8-kb fragments), with approximately 36-fold coverage. The sequence reads were initially assembled with GS Assembler software into 31 contigs (>500 bp).

The draft genome is 4,564,780 bp in total, with a G+C content of 40.76%. The *svers.1.1* genome contains two circular chromosomes (as determined by a pulsed-field gel electrophoresis [PFGE] analysis; data not shown), as found in other *Vibrionaceae* (10). Identification of protein-coding sequences (CDSs) was carried out using the Microbial Genome Annotation Pipeline (MiGAP) (12) with additional information provided by Manatee (IGS Annotation Service [http://manatee.sourceforge.net]). A total of 4,026 CDSs were identified. The

genome contains at least six rRNA operons and at least 74 tRNAs.

Comparisons were made to genome sequences of other *Vibrionaceae* to screen for *P. mandapamensis* genes involved in quorum-sensing regulation of bioluminescence and in symbiosis. A single, vertically inherited *lux-rib* operon, *luxCDABEFG-ribEBHA* (3, 13), was present in the *svers.1.1* genome, as were homologs of the regulatory genes *cyaA* and *crp* and certain *Vibrio harveyi* quorum-sensing-regulatory genes, *luxO*, *luxS*, *luxU*, and *cqsA*. In contrast, homologs of other *V. harveyi* quorum-sensing-regulatory genes, *luxR*, *luxL*, *luxM*, *luxN*, *luxP*, *luxQ*, and *cqsS*, and *Aliivibrio* (*Vibrio*) *fischeri* quorum-sensing-regulatory genes, *luxR*, *luxI*, and *ainS*, were absent. Furthermore, homologs of *A. fischeri* genes involved in bioluminescent symbiosis with the squid *Euprymna scolopes*, *sypG*, *htrB1*, and *rscS* (1, 9, 15), were also not present in the *svers.1.1* genome. These results indicate that quorum-sensing control of luminescence, as well as other cellular functions, in *P. mandapamensis* differs significantly from that in other *Vibrionaceae*. Furthermore, bacterial genes involved in the symbiotic interactions between *P. mandapamensis* and the fish *S. versicolor* are likely to be substantially different from those involved in the *A. fischeri* symbiosis with the squid *E. scolopes*.

**Nucleotide sequence accession numbers.** The 31 contig sequences of *P. mandapamensis* strain *svers.1.1* were deposited in DDBJ under accession numbers BACE01000001 to BACE01000031.

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