

# Genome Sequence of Luminous Piezophile *Photobacterium phosphoreum* ANT-2200

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**Bacteria of the genus *Photobacterium* thrive worldwide in oceans and show substantially varied lifestyles, including free-living, commensal, pathogenic, symbiotic, and piezophilic. Here, we present the genome sequence of a luminous, piezophilic *Photobacterium phosphoreum* strain, ANT-2200, isolated from a water column at 2,200 m depth in the Mediterranean Sea. It is the first genomic sequence of the *P. phosphoreum* group. An analysis of the sequence provides insight into the adaptation of bacteria to the deep-sea habitat.**

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*Photobacterium* is one of the major genera of the family *Vibrionaceae* and is widespread in marine environments. Previously, the name *Photobacterium phosphoreum* was used to refer to various species. Recent multilocus fine-scale phylogenetic analysis has resolved three distinct species in the *P. phosphoreum* group: *Photobacterium phosphoreum*, *Photobacterium iliopiscarium*, and *Photobacterium kishitani* (1). Among them, *P. phosphoreum* and *P. kishitani* are luminous, and *P. kishitani* is the only species found in the light organs of deep-sea fishes. None of the *P. iliopiscarium* strains analyzed emit light. *P. phosphoreum* ANT-2200 is a piezophilic species isolated from the Mediterranean Sea at a depth of 2,200 m (2, 3). To gain insight into the genetic traits underlying the differences among the three closely related species of the *P. phosphoreum* group dwelling in different environments, we sequenced the genome of *P. phosphoreum* ANT-2200.

The ANT-2200 whole-genome shotgun sequence was obtained using the Illumina technology. Mate-paired (MP) and paired-end (PE) libraries were created with 8-kb and 350-bp insert sizes, respectively. The sequencing was performed on a MiSeq instrument with paired read lengths of 150, leading to 90- and 180-fold coverage for the MP and PE data, respectively. These data were assembled using Velvet 1.0 (<http://www.ebi.ac.uk/~zerbino/velvet>), and to reduce the number of undetermined bases, GapCloser (<http://soap.genomics.org.cn/soapdenovo.html>) was used on the scaffold sequences, with the PE reads. The annotation was performed using the MicroScope platform (<https://www.genoscope.cns.fr/agc/microscope/home/index.php>) (4).

The whole-genome draft of *P. phosphoreum* ANT-2200 consists of 25 contigs assembled into 19 scaffolds, for a total of

5,107,216 bp with 38.89% G+C content. A total of 4,667 coding DNA sequences were predicted, as well as 36 miscellaneous RNAs, 6 disrupted rRNA operons, and 168 tRNA genes.

Among the NCBI genomic reference sequences, the top 11 that were homologous to the *P. phosphoreum* ANT-2200 genome are from 6 *Photobacterium* genomes with decreasing *E* values, in the following order: *P. leiognathi* subsp. *mandapamensis* svers.1.1 (accession no. NZ\_DF093598.1), *P. leiognathi* Irivu.4.1 (accession no. NZ\_DF196819.1), *P. angustum* S14 (accession no. NZ\_CH902602.1), *P. profundum* SS9 (accession no. NC\_006370.1), *Photobacterium* sp. strain SKA34 (accession no. NZ\_CH724145.1), *P. angustum* S14 (accession no. NZ\_CH902604.1), *P. leiognathi* subsp. *mandapamensis* svers.1.1 (accession no. NZ\_DF093594.1), *P. leiognathi* Irivu.4.1 (accession no. NZ\_DF196811.1), *Photobacterium* sp. SKA34 (accession no. NZ\_CH724147.1), *P. angustum* S14 (accession no. NZ\_CH902603.1), and *P. profundum* 3TCK (accession no. NZ\_CH724136.1). A synton of the *luxLCDABFEG-ribEBHA* luminous genes was found in the ANT-2200 genome and is perfectly conserved in the genome of *P. leiognathi* subsp. *mandapamensis* svers.1.1. As a trait of adaptation to the deep-sea habitat, the genome of the piezophilic *P. profundum* strain SS9 contains 2 sets of flagellar genes functioning under different pressures and viscosities (5). ANT-2200 bears two sets of flagellar genes that are highly conserved compared to those from SS9. Furthermore, SS9 has multiple *torA* genes encoding trimethylamine *N*-oxide reductases, one of them being upregulated by high hydrostatic pressure (6). Interestingly, the genome of *P. phosphoreum* ANT-2200 has four copies of *torA*, including the counterpart of the pressure-

upregulated *torA*. The genome of *P. phosphoreum* ANT-2200 will be used as the first representative of the *P. phosphoreum* group in studies of the evolution of luminous bacteria and adaptation of bacteria to the deep-sea habitats.

**Nucleotide sequence accession numbers.** The genome sequence of *P. phosphoreum* ANT-2200 was deposited in EMBL under accession no. [CCAR010000001](#) to [CCAR010000025](#).

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