

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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REFERENCES

1. Ast JC, Dunlap PV. 2005. Phylogenetic resolution and habitat specificity of members of the *Photobacterium phosphoreum* species group. *Environ. Microbiol.* 7:1641–1654. <http://dx.doi.org/10.1111/j.1462-2920.2005.00859.x>.
2. Al Ali B, Garel M, Cuny P, Miquel JC, Toubal T, Robert A, Tamburini C. 2010. Luminous bacteria in the deep-sea waters near the ANTARES underwater neutrino telescope (Mediterranean Sea). *Chem. Ecol.* 26:57–72. <http://dx.doi.org/10.1080/02757540903513766>.
3. Martini S, Al Ali B, Garel M, Nerini D, Grossi V, Pacton M, Casalot L, Cuny P, Tamburini C. 2013. Effects of hydrostatic pressure on growth and luminescence of a moderately-piezophilic luminous bacteria *Photobacterium phosphoreum* ANT-2200. *PLoS One* 8:e66580. <http://dx.doi.org/10.1371/journal.pone.0066580>.
4. Vallenet D, Belda E, Calteau A, Cruveiller S, Engelen S, Lajus A, Le Fèvre F, Longin C, Mornico D, Roche D, Rouy Z, Salvignol G, Scarpelli C, Thil Smith AA, Weiman M, Médigue C. 2013. Microscope—an integrated microbial resource for the curation and comparative analysis of genomic and metabolic data. *Nucleic Acids Res.* 41:D636–D647. <http://dx.doi.org/10.1093/nar/gks1194>.
5. Eloe EA, Lauro FM, Vogel RF, Bartlett DH. 2008. The deep-sea bacterium *Photobacterium profundum* SS9 utilizes separate flagellar systems for swimming and swarming under high-pressure conditions. *Appl. Environ. Microbiol.* 74:6298–6305. <http://dx.doi.org/10.1128/AEM.01316-08>.
6. Vezzi A, Campanaro S, D'Angelo M, Simonato F, Vitulo N, Lauro FM, Cestaro A, Malacrida G, Simionati B, Cannata N, Romualdi C, Bartlett DH, Valle G. 2005. Life at depth: *Photobacterium profundum* genome sequence and expression analysis. *Science* 307:1459–1461. <http://dx.doi.org/10.1126/science.1103341>.