

Draft Genome Sequence of the Moderately Halophilic Gammaproteobacterium *Halomonas anticariensis* FP35^T

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***Halomonas anticariensis* strain FP35^T is a moderately halophilic bacterium isolated from a soil sample taken from Fuente de Piedra, a saline wetland in the province of Málaga (Spain), which produces an exopolysaccharide and quorum-sensing signaling molecules of the type *N*-acylhomoserine lactone. We report here the draft genome sequence of this gammaproteobacterium.**

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Halomonas anticariensis FP35^T was isolated from saline soil at Fuente de Piedra, Málaga, in southern Spain (1). It is a Gram-negative, heterotrophic, aerobic rod and is motile by peritrichous flagella. This moderately halophilic organism has a respiratory metabolism, being able to grow in media with 0.5% to 15% (wt/vol) NaCl (optimal growth at 7.5% [wt/vol] NaCl). It excretes significant quantities of an exopolysaccharide (EPS) at the early stationary growth phase. This EPS is composed mainly of glucose, mannose, and galacturonic acid and produces solutions of low viscosity and pseudoplastic behavior. Moreover, it also has a high capacity for binding cations and has incorporated considerable quantities of sulfates, which is highly unusual in bacterial polysaccharides (2). This bacterium has also been reported to produce *N*-acylhomoserine lactones, which are signal molecules in quorum-sensing (QS) systems (3). We have characterized this system at the genetic level and found that it is composed of the *luxR* and *luxI* homologues *hanR*, believed to be the transcriptional regulator gene, and *hanI*, the autoinducer synthase gene (4). Furthermore, we have demonstrated that the *H. anticariensis* FP35^T QS system is regulated by a two-component system, suggesting its integral involvement in the intercellular communication strategies of this moderately halophilic bacterium (5). In addition, we recently demonstrated that the QS system is widespread within the *Halomonadaceae* family (6). *H. anticariensis* FP35^T belongs to the class *Gammaproteobacteria* within the family *Halomonadaceae* (7). *Halomonas* is one of the genera most frequently isolated from hypersaline habitats by conventional-culture techniques (8). Nevertheless, the ecological roles that *Halomonas* species play in these habitats and their relationships with other halophilic and non-halophilic microorganisms are still unknown.

Little genome data are currently available from this group of bacteria. In this study, we report the draft genome sequence of *H. anticariensis* strain FP35^T, which was obtained using high-throughput Illumina HiSeq paired-end (PE) sequencing technology. The raw data obtained were subjected to treatment, including several steps of data filtering. Then, we performed *de novo* assembly using SOAPdenovo version 1.05 (9), generating 45 contigs that

were further joined into 21 scaffolds. The assembled draft genome comprises 5,067,645 bases at 34.4-fold coverage and has a G+C content of 58.54%. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html) was employed for gene annotation. The tRNA and rRNA genes were predicted with tRNAscan-SE (10) and RNAmmer (11), respectively. A total of 4,652 putative protein-coding genes (CDSs) or open reading frames (ORFs) were predicted. Furthermore, the strain FP35^T contains a total of 61 tRNA genes and one rRNA operon.

The draft genome information reported in the present study might be valuable for future studies to investigate the role of the quorum-sensing regulatory system in the adaptation to high salinities in hypersaline environments.

Nucleotide sequence accession numbers. The *H. anticariensis* strain FP35^T whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [ASTJ00000000](https://accession.ncbi.nlm.nih.gov/ASTJ00000000). The version described in this paper is the first version, accession no. [ASTJ01000000](https://accession.ncbi.nlm.nih.gov/ASTJ01000000).

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REFERENCES

- Martínez-Cánovas M, Béjar V, Martínez-Checa F, Quesada E. 2004. *Halomonas anticariensis* sp. nov., from Fuente de Piedra, a saline-wetland wildfowl reserve in Malaga, southern Spain. *Int. J. Syst. Evol. Microbiol.* 54:1329–1332.
- Mata JA, Béjar V, Llamas I, Arias S, Bressollier P, Tallon R, Urdaci MC, Quesada E. 2006. Exopolysaccharides produced by the recently described halophilic bacteria *Halomonas ventosae* and *Halomonas anticariensis*. *Res. Microbiol.* 157:827–835.
- Llamas I, Quesada E, Martínez-Cánovas MJ, Gronquist M, Eberhard A, González JE. 2005. Quorum sensing in halophilic bacteria: detection of

- N*-acyl-homoserine lactones in the exopolysaccharide-producing species of *Halomonas*. *Extremophiles* 9:333–341.
4. Tahrioui A, Quesada E, Llamas I. 2011. The *hanR/hanI* quorum-sensing system of *Halomonas anticariensis*, a moderately halophilic bacterium. *Microbiology* 157:3378–3387.
 5. Tahrioui A, Quesada E, Llamas I. 2013. Genetic and phenotypic analysis of the GacS/GacA system in the moderate halophile *Halomonas anticariensis*. *Microbiology* 159:462–474.
 6. Tahrioui A, Schwab M, Quesada E, Llamas I. 2013. Quorum sensing in some representative species of *Halomonadaceae*. *Life* 3:260–275.
 7. de la Haba RR, Sánchez-Porro C, Ventosa A. 2011. Taxonomy, phylogeny, and biotechnological interest of the family *Halomonadaceae*, p 27–64. In Ventosa A, Oren A, Ma Y (ed), *Halophiles and hypersaline environments*. Springer, Heidelberg, Germany.
 8. Ventosa A, Mellado E, Sánchez-Porro C, Márquez MC. 2008. Halophilic and halotolerant micro-organisms from soils, p 87–115. In Dion P, Nautiyal CS (ed), *Microbiology of extreme soils*. Springer, Heidelberg, Germany.
 9. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu S-M, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam T-W, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *GigaScience* 1:18. doi:10.1186/2047-217X-1-18.
 10. 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.
 11. Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res.* 35:3100–3108.