

Draft Genome Sequence of Strain JLT2015^T, Belonging to the Family *Sphingomonadaceae* of the *Alphaproteobacteria*

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Strain JLT2015^T was isolated from the southeastern Pacific, as a representative of a new genus of the family *Sphingomonadaceae* of the *Alphaproteobacteria*. Here, we present the draft genome sequence of strain JLT2015^T, which provides insight into the oligotrophic strategy of this organism.

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Strain JLT2015^T (LMG27364, CGMCC1.12401) was isolated from surface waters (depth, 100 m) in the southeastern Pacific using previously described dilution-to-extinction culturing with rich organic medium (1). The phylogenetic analysis using 16S rRNA gene sequences showed that strain JLT2015^T was most closely related to a member of the family *Sphingomonadaceae*, *Novosphingobium pentaromativorans* (2), with 94.7% sequence similarity. Members of the *Sphingomonadaceae* are characterized by a smaller cell size than copiotrophic bacteria and display an oligotrophic strategy with low rates of growth in the nutrient-limited marine environment (3). Here, we report the draft genome sequence of strain JLT2015^T.

The nucleotide sequence was determined using a 454 GS FLX sequencer. Assembly was performed using the Newbler 2.3 program. A total of 194,762 reads were obtained, which represented a 32.8-fold coverage of the genome. The strain JLT2015^T draft genome sequence contained 3,253,993 bp distributed in 38 contigs, with a G+C content of 64.2%. The assemblies were uploaded to the automated annotation platform on the Rapid Annotation using Subsystems Technology (RAST) server (4). A total of 3,058 protein-coding sequences with an average length of 950 bp were determined, occupying 89.33% of the genome. Among all the proteins predicted to be encoded, 2,370 proteins (77.5%) were assigned to different Clusters of Orthologous Groups (COG) categories (5). In addition, 1,494 genes (53.4%) were involved in 173 different pathways. The genome contained 48 tRNA genes and 4 rRNA operons.

Genes putatively encoding a carbon monoxide dehydrogenase were present in the genome. Genes encoding proteins involved in biosynthesis and export of extracellular or capsular polysaccharides were identified. Strain JLT2015^T contained abundant TonB-dependent transporter genes in the genome, which allow bacteria to take up scarce resources from nutrient-limiting environments (6). Strain JLT2015^T was predicted to have complete Embden-Meyerhof-Parnas, pentose-phosphate, and Entner-Doudoroff pathways. Strain JLT2015^T possessed genes responsible for assimilation of *N*-acetylglucosamine as a carbon source. Genes for a high-affinity phosphate transporter and a *pho* regulon for sensing

of environmental inorganic phosphate availability were present. Genes for ammonium transporters, nitrate reductase, and sulfate reductase were also present in the strain JLT2015^T genome.

Comparison with genome sequences available in RAST (4) showed that *Sphingomonas* sp. strain SKA58 (score, 501), *Sphingomonas wittichii* RW1 (score, 490), and *Sphingobium japonicum* UT26S HTCC2559 (score, 462) were the closest neighbors of strain JLT2015^T.

Nucleotide sequence accession numbers. The strain JLT2015^T shotgun genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession number [AMRV00000000](https://www.ncbi.nlm.nih.gov/nuccore/AMRV00000000). The version described in this paper is the first version, [AMRV01000000](https://www.ncbi.nlm.nih.gov/nuccore/AMRV01000000).

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REFERENCES

1. Connon SA, Giovannoni SJ. 2002. High-throughput methods for culturing microorganisms in very-low-nutrient media yield diverse new marine isolates. *Appl. Environ. Microbiol.* 68:3878–3885.
2. Sohn JH, Kwon KK, Kang JH, Jung HB, Kim SJ. 2004. *Novosphingobium pentaromativorans* sp. nov., a high-molecular-mass polycyclic aromatic hydrocarbon-degrading bacterium isolated from estuarine sediment. *Int. J. Syst. Evol. Microbiol.* 54:1483–1487.
3. Lauro FM, McDougald D, Thomas T, Williams TJ, Egan S, Rice S, DeMaere MZ, Ting L, Ertan H, Johnson J, Ferreira S, Lapidus A, Anderson I, Kyrpides N, Munk AC, Detter C, Han CS, Brown MV, Robb FT, Kjelleberg S, Cavicchioli R. 2009. The genomic basis of trophic strategy in marine bacteria. *Proc. Natl. Acad. Sci. U. S. A.* 106:15527–15533.
4. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75.
5. Tatusov RL, Galperin MY, Natale DA, Koonin EV. 2000. The COG database: a tool for genome-scale analysis of protein functions and evolution. *Nucleic Acids Res.* 28:33–36.
6. Tang K, Jiao N, Liu K, Zhang Y, Li S. 2012. Distribution and functions of TonB-dependent transporters in marine bacteria and environments: implications for dissolved organic matter utilization. *PLoS One* 7:e41204.