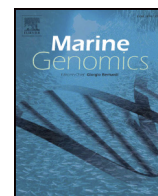




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Draft genome sequence of *Parvularcula oceani* JLT2013^T, a rhodopsin-containing bacterium isolated from deep-sea water of the Southeastern Pacific

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ABSTRACT

Parvularcula oceani JLT2013^T is a novel member of the genus *Parvularcula* within the order 'Parvularculales'. Here, we present the draft genome sequence of a deep-sea bacterium *P. oceani* JLT2013^T. The genome comprises 3,354,504 bp with a G + C content of 67.44% and includes 3141 protein-coding genes and 42 tRNA genes. The genome contains three genes encoding rhodopsin protein.

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1. Introduction

Rhodopsins are photoactive membrane-embedded opsins found in marine planktonic bacteria, archaea and eukaryotes (Béja et al., 2001; Man et al., 2003; Béja et al., 2000; Slamovits et al., 2011). Three types of microbial rhodopsins can be distinguished on the basis of their function: (1) proton/ion pump rhodopsin, it consists of a transmembrane protein bound to a retinal molecule and functions as a light-driven proton pump bacteriorhodopsin or an ion pump halorhodopsin (Blaurock and Stoekenius, 1971; Riedel et al., 2013); (2) sensory rhodopsins, sensory rhodopsins I and II function as the photoreceptors modulating the reversal frequency of the cell's flagellar motors (Hoff et al., 1997); and (3) light-harvesting xanthorhodopsin, a proton-pumping retinal protein/carotenoid complex and functions as an energy converter which transfers light energy from the carotenoid antenna to the retinal protein (Balashov et al., 2005). A large percentage of whole genome sequenced rhodopsin-containing bacteria were discovered in marine surface environments, yet little is known about deep-sea species (Béja et al., 2001; Man et al., 2003; Gómez-Consarnau et al., 2007). In the present study, we report the draft genome sequence of strain *Parvularcula oceani* JLT2013^T (= LMG 27362^T = CGMCC 1.12400^T) that was isolated from deep-sea water of the Southeastern Pacific (Li et al., 2014) (Table 1).

A summary of the genome project information was shown in Table 1. Putative protein-coding sequences were determined by

combining the prediction results of Glimmer 3.02 (Delcher et al., 2007). Functional annotation of CDS was performed by searching the NCBI non-redundant protein database and KEGG database. tRNA genes were predicted with tRNAScan-SE (Lowe and Eddy, 1997). Protein domain prediction and COG (Cluster of Orthologous Groups) assignment were performed by RPS-BLAST using NCBI CDD library (Marchler-Bauer et al., 2013).

The G + C content of strain JLT2013^T genome assembly was 67.44% (Table 2). A total of 3141 protein-coding sequences (CDSs) with an average length of 959 bp were determined occupying 98.40% of the genome, and distributed in 38 contigs. Defined biological functions were assigned to 2606 CDSs (81.64%) (Table 2). Among all the predicted genes, 2148 proteins (67.29%) were assigned to different COG categories (Table 2) and the functions of 993 proteins remained unknown. In strain JLT2013^T genome, 370 potential horizontal transferring elements were annotated via BLASTp against the ACLAME (v0.4) database (Lepplae et al., 2004).

The phylogenetic analysis performed using the amino acid sequence of proteorhodopsins, xanthorhodopsins and sensory-rhodopsins available in databases and those disclosed in the *P. oceani* JLT2013^T revealed one sensory rhodopsin gene and two xanthorhodopsins (Fig. 1). The genome of *P. oceani* JLT2013^T contained all the genes encoding proteins involved in retinal biosynthesis, including *idi* (encoding isopentenyl pyrophosphate D-isomerase), *crtE* (encoding geranylgeranyl pyrophosphate synthase), *crtZ* (encoding β-carotene hydroxylase), *crtW* (encoding β-carotene ketolase), *crtB* (encoding phytoene synthase), *crtI* (encoding phytoene dehydrogenase), and *crtY* (encoding lycopene

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Table 1

Classification, general features and genome sequencing project information for *Parvularcula oceani* JLT2013^T according to the MGS recommendations (Field et al., 2008).

MIGS ID	Property	Term
	Current classification	Domain <i>Bacteria</i> Phylum <i>Proteobacteria</i> Class <i>Alphaproteobacteria</i> Order <i>Parvularculales</i> Family <i>Parvularculaceae</i> Genus <i>Parvularcula</i> Species <i>Parvularcula oceani</i> Type strain JLT2013
	Gram stain	Negative
	Cell shape	Short rods
	Motility	Motile
	Sporulation	None
	Temperature range	Mesophile (10–40 °C)
	Optimum temperature	30 °C
	Carbon source	Varied
	Energy source	Heterotrophic
MIGS-6	Habitat	Marine
MIGS-6.3	Salinity	NaCl 0–9.0% (optimum, 3.0–6.0%)
MIGS-22	Oxygen	Aerobic
MIGS-15	Biotic relationship	Free living
MIGS-14	Pathogenicity	None
MIGS-4	Geographic location	Southeastern Pacific
MIGS-5	Sample collection time	Sep-11, 2013
MIGS-4.3	Depth	800 m
MIGS-4.4	Altitude	Not recorded
MIGS-31	Finishing quality	Improved-high-quality draft
MIGS-28	Libraries used	Shotgun
MIGS-29	Sequencing platforms	Roche 454 GS FLX
MIGS-31.2	Fold coverage	20.8X
MIGS-30	Assemblers	Newbler v. 7.3
MIGS-32	Gene calling method	Glimmer 3.02
	Database: IMG	2588254261
	NCBI project ID	254938
	GOLD ID	Gi0076057
	Project relevance	Environmental and biotechnological

cyclase). The *blh* gene encoding 15, 15'-β-carotene dioxygenase was detected but not found to be linked to any opsin genes in the genome of strain JLT2013^T.

Strain JLT2013^T was predicted to possess complete central carbon metabolic pathways, including glycolysis, the pentose phosphate pathway, the Entner–Doudoroff pathway and tricarboxylic acid cycle. The genome contained genes for type IV secretion/conjugal transfer systems, TonB-dependent transporter systems and genes for cobalt–zinc–cadmium resistance. A cluster of genes encoding pilin and the assembly and secretion machinery for type IV pili was present.

Table 2

Genome statistics of *Parvularcula oceani* JLT2013^T.

Attribute	Value	% of total
Genome size (bp)	3,354,504	100.00
DNA coding region (bp)	3,071,614	91.57
DNA G + C content (bp)	2,262,237	67.44
Number of contigs	38	
Total genes	3192	100.00
RNA genes	51	1.60
rRNA operons	1	0.03
tRNA genes	42	1.32
Protein-coding genes	3141	98.40
Genes with function prediction	2606	81.64
Genes assigned to COGs	2148	67.29
Genes assigned Pfam domains	2669	83.62
Genes with signal peptides	411	12.88
Genes with transmembrane helices	717	22.46

2. Nucleotide sequence accession numbers

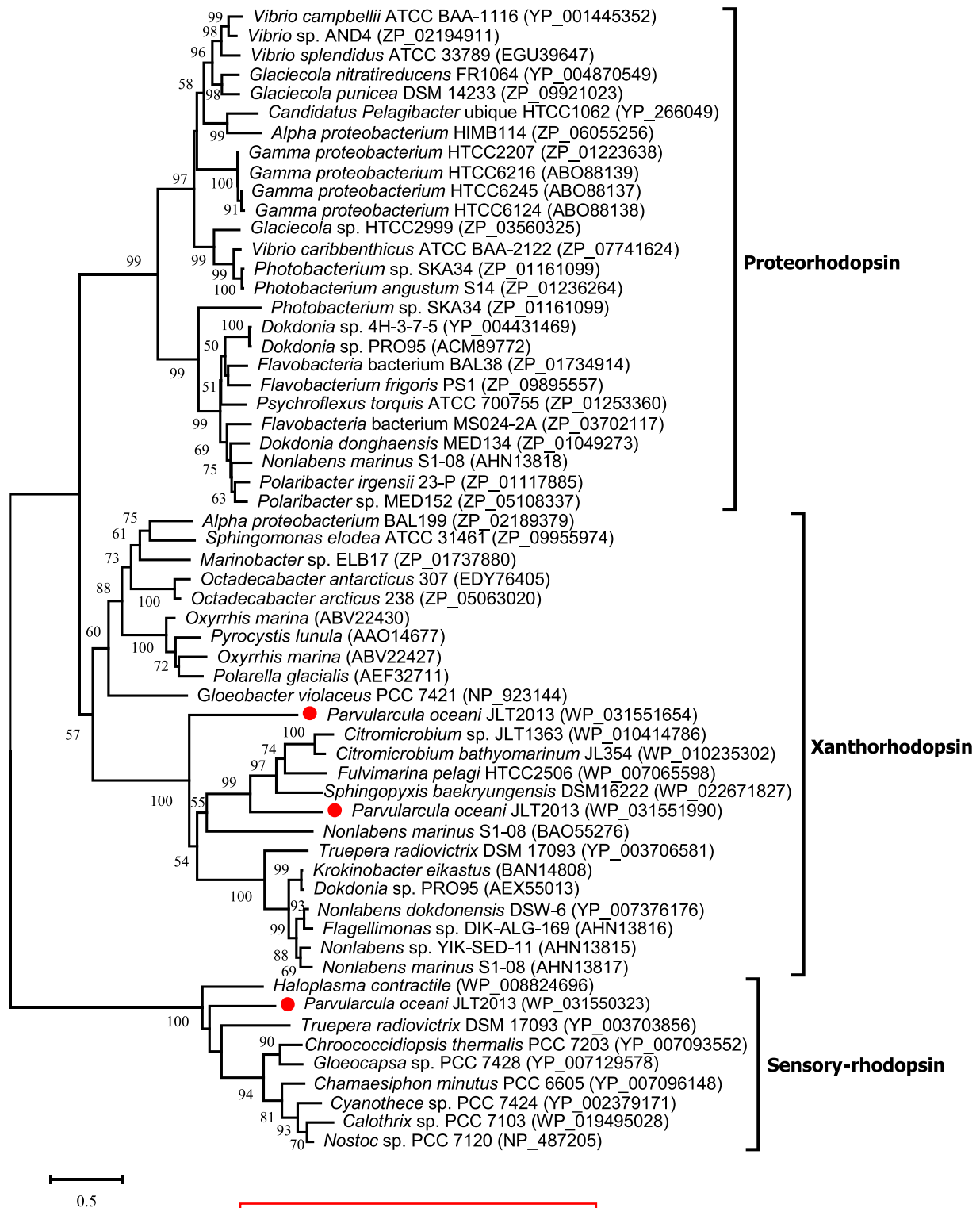
The bacterium *P. oceani* JLT2013^T shotgun genome sequence has the GenBank accession no. JPHU00000000. The version described in this paper is the first version, LOCUS JPHU01000000.

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Fig. 1. Unrooted phylogenetic tree of microbial rhodopsin amino acid sequences. The three rhodopsin genes (WP_031550323, WP_031551654 and WP_031551990) encoded by the *P. oceani* JLT2013^T genome are indicated by red circles. The scale bar shows the number of amino acid substitutions per site. Bootstrap values below 50% are not shown (1000 replications). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)