Article

Poseidonibacter ostreae sp. nov., Isolated from the Gut of *Ostrea* from the Seomjin River

Kiwoon Baek, Sumin Jang, Eu Jin Chung, Shi Hyun Ryu and Ahyoung Choi *

Nakdonggang National Institute of Biological Resources (NNIBR),
Sangju 37242, Republic of Korea; backy8575@nnibr.re.kr (K.B.); als089@nnibr.re.kr (S.J.);
eujenee@nnibr.re.kr (E.J.C.); bubo94@nnibr.re.kr (S.H.R.)
* Correspondence: aychoi@nnibr.re.kr; Tel.: +82-54-530-0891; Fax: +82-54-530-0899

Table S1. Genome statistics of strains SJOD-M-6[T], SJOD-M-5, and SJOD-M-33 and their related strains of species of genus *Poseidonibacter*.

Strains: 1, SJOD-M-6[T]; 2, SJOD-M-5; 3, SJOD-M-33; 4, *P. parvus* LPB0137[T]; 5, *P. antarcticus* SM1702 [T]; 6, *P. lekithochrous* DSM 100870[T].

Abbreviations: [a], data obtained from this study; [b], from GenBank.

Features	1[a]	2[a]	3[a]	4[b]	5[b]	6[b]
Sequencing platform	Illumina Novaseq	Illumina Novaseq	Illumina Novaseq	PacBio	Illumina MiSeq	PacBio + Illumina MiSeq
Assembler	Unicycler	Unicycler	Unicycler	SMRT Analysis v2.3	ABySS v.2.0.2	Newbler v. 2.6
Estimated genome size (bp)	2,858,436	2,958,551	3,206,717	2,866,429	2,919,928	3,568,672
Number of contigs	162	156	182	1	57	1
Coverage	1668.0 ×	1827.0 ×	1795.0 ×	421.0 ×	782.0 ×	410.0 ×
Contig N_{50}	55,001	49,062	47,531	2,866,429	260,053	343,594
Number of rRNA genes	3	3	3	19	14	24
Number of tRNA genes	44	42	45	65	46	82
DNA G+C mol%	27.5	27.5	27.6	27.7	27.1	28.2
Accession number	WFKI00000000	WFKJ00000000	WFKK00000000	CP019070	RCWF00000000	CP054052

Figure S1. Circular map of the Poseidonibacter sp. strain SJOD-M-6^T genome. From outside to the center; the colored bands in ring 1 represent contigs; ring 2 represents the annotated genes on the forward strand (color determined by COG category); ring 3 shows the annotated genes on the reverse strand (color determined by COG category); ring 4 displays the RNA genes (rRNAs are displayed in red and tRNAs are displayed in purple); ring 5 shows the GC skew (higher-than-average values are displayed in green, while lower-than-average values are displayed in red) and ring 6 shows the GC ratio (higher-than-average values in blue and lower-than-average values in yellow).
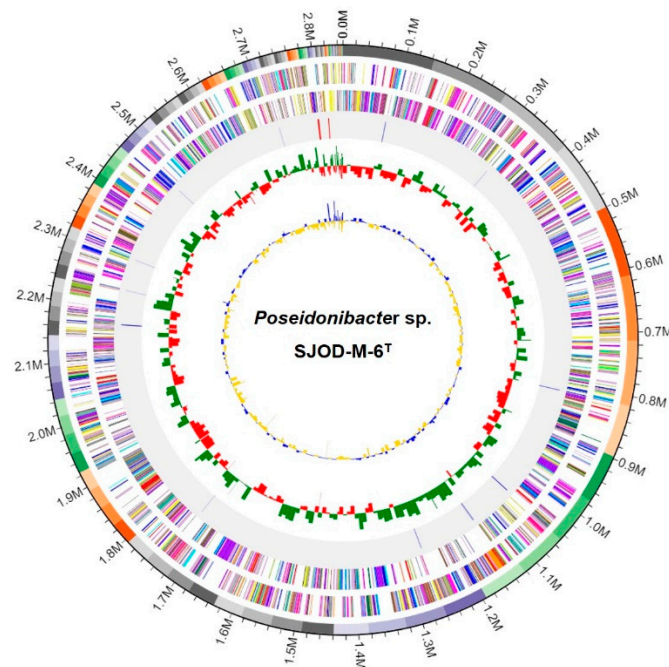
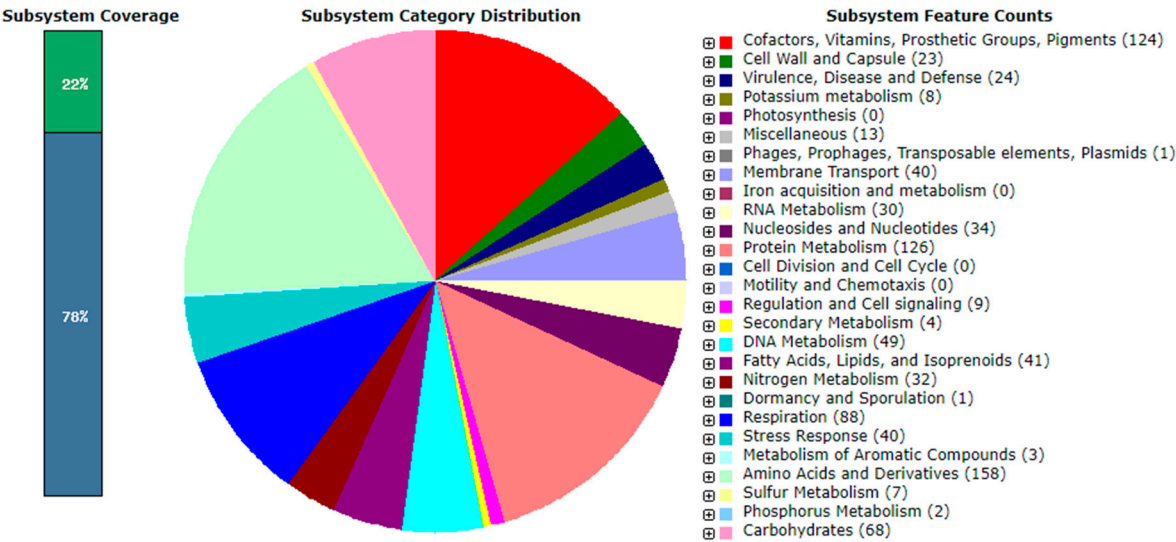**Figure S2.** Subsystem category distribution of strain SJOD-M-6^T based on the RAST annotation server (https://rast.nmpdr.org/) (accessed on 25 May 2023).

Subsystem Coverage

22%

78%

Subsystem Category Distribution

Subsystem Feature Counts

- Cofactors, Vitamins, Prosthetic Groups, Pigments (124)
- Cell Wall and Capsule (23)
- Virulence, Disease and Defense (24)
- Potassium metabolism (8)
- Photosynthesis (0)
- Miscellaneous (13)
- Phages, Prophages, Transposable elements, Plasmids (1)
- Membrane Transport (40)
- Iron acquisition and metabolism (0)
- RNA Metabolism (30)
- Nucleosides and Nucleotides (34)
- Protein Metabolism (126)
- Cell Division and Cell Cycle (0)
- Motility and Chemotaxis (0)
- Regulation and Cell signaling (9)
- Secondary Metabolism (4)
- DNA Metabolism (49)
- Fatty Acids, Lipids, and Isoprenoids (41)
- Nitrogen Metabolism (32)
- Dormancy and Sporulation (1)
- Respiration (88)
- Stress Response (40)
- Metabolism of Aromatic Compounds (3)
- Amino Acids and Derivatives (158)
- Sulfur Metabolism (7)
- Phosphorus Metabolism (2)
- Carbohydrates (68)

Figure S3. COG functional classification of proteins in strain SJOD-M-6^T genome.

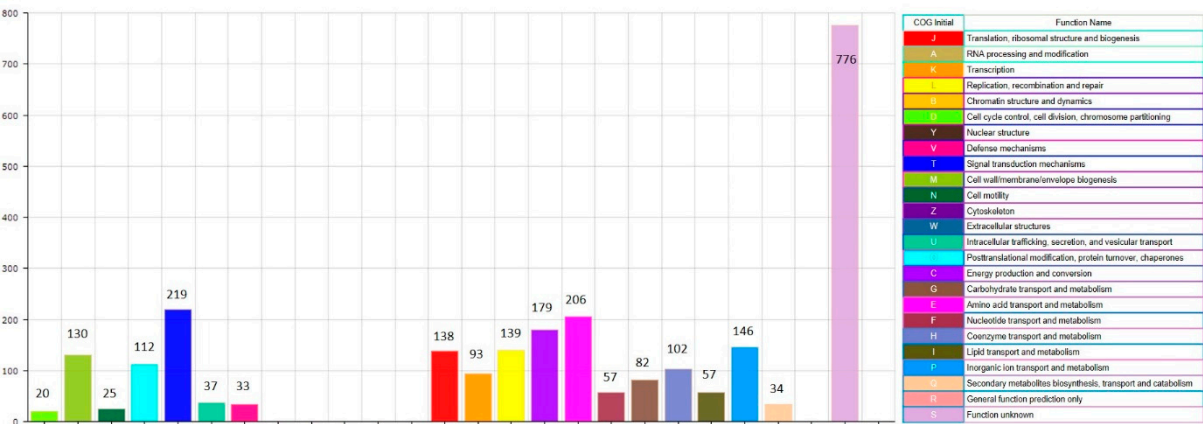| COG Initial	Function Name
J	Translation, ribosomal structure and biogenesis
A	RNA processing and modification
K	Transcription
L	Replication, recombination and repair
B	Chromatin structure and dynamics
D	Cell cycle control, cell division, chromosome partitioning
Y	Nuclear structure
V	Defense mechanisms
T	Signal transduction mechanisms
M	Cell wall/membrane/envelope biogenesis
N	Cell motility
Z	Cytoskeleton
W	Extracellular structures
U	Intracellular trafficking, secretion, and vesicular transport
O	Posttranslational modification, protein turnover, chaperones
C	Energy production and conversion
G	Carbohydrate transport and metabolism
E	Amino acid transport and metabolism
F	Nucleotide transport and metabolism
H	Coenzyme transport and metabolism
I	Lipid transport and metabolism
P	Inorganic ion transport and metabolism
Q	Secondary metabolites biosynthesis, transport and catabolism
R	General function prediction only
S	Function unknown

Figure S4. Venn diagram representing the core orthologous and unique genes for strains SJOD-M-6^T and closely related type strains.
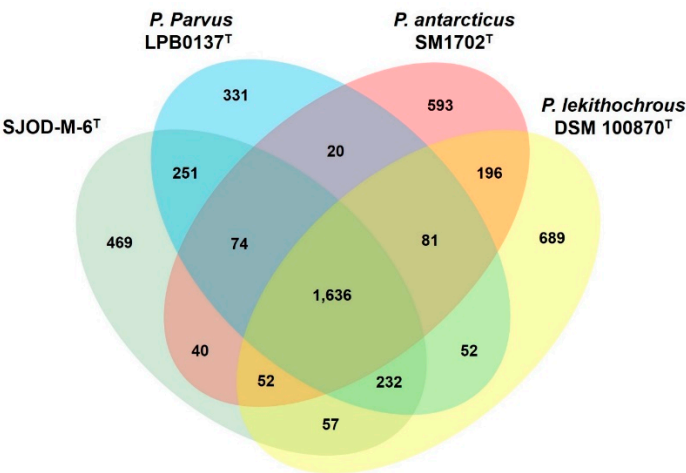

Figure S5. Phylogenomic tree based on concatenated multiple-alignment of 82 genes showing the relationship between SJOD-M-6^T and members of the family *Arcobacteraceae*. The tree was generated using UBCG2 pipeline with the concatenation of 82 gene sequences. GenBank accession numbers are shown in parentheses. Percentage bootstrap values are shown at the branch points. The tree was rooted with *Hydrogenimonas thermophila* EP 1551^T (FOXB00000000). The Bar represents 0.05 substitutions per nucleotide position.
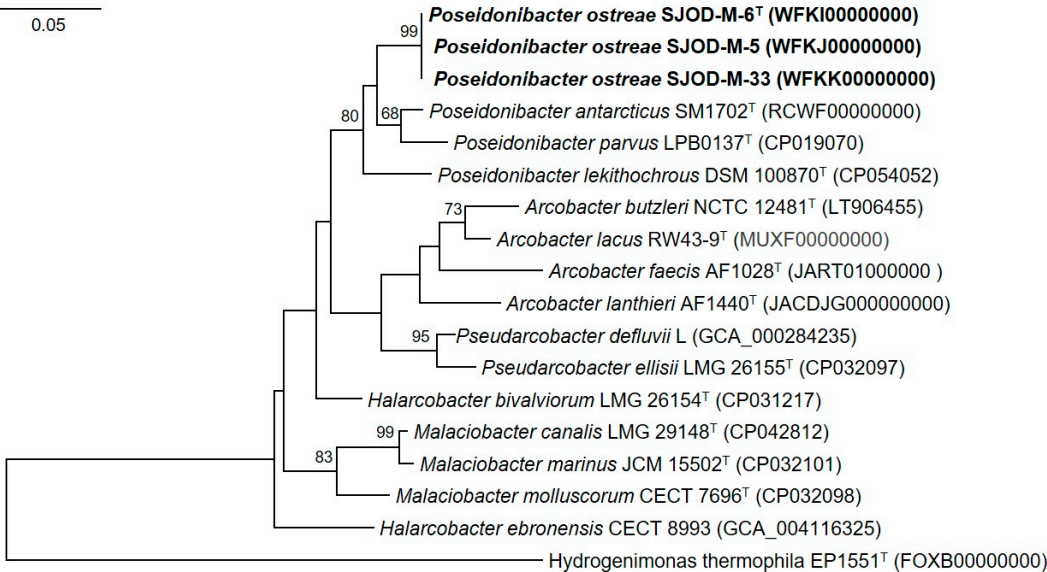
Figure S6. Transmission electron micrograph of negatively stained cells of strain SJOD-M-6[T]. Bar, 200 nm.
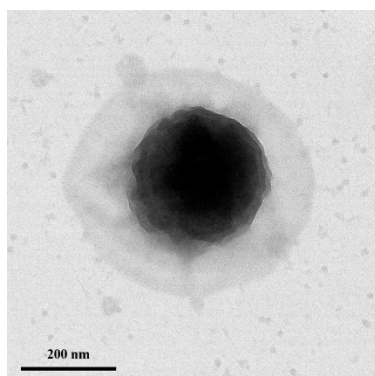

Figure S7. Two-dimensional thin-layer chromatogram showing polar lipids of SJOD-M-6[T], which were stained with a phosphomolybdic acid solution for total lipids (A), spraying zinzadze reagent (molybdenum blue spray reagent, 1.3%) for phospholipids (B), and 0.2% ninhydrin solution for aminolipids (C), α-naphthol solution for glycolipids (D), respectively. Abbreviations: PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PL1–2, unidentified phospholipids; AL, unidentified aminolipid.; APL, unidentified aminophospholipid.