

## Draft genome sequence of a marine *Flavobacteria Flagellimonas eckloniae* DOKDO 007<sup>T</sup>

Yong Min Kwon<sup>1</sup>, Patra Ajit Kumar<sup>1</sup>, Sang-Jin Kim<sup>1,2</sup>, and Kae Kyoung Kwon<sup>2\*</sup> 

<sup>1</sup>National Marine Biodiversity Institute of Korea, Seocheon 33662, Republic of Korea

<sup>2</sup>Marine Biotechnology Research Center, Korea Institute of Ocean Science and Technology, Pusan 49111, Republic of Korea

## 해양 *Flavobacteria Flagellimonas eckloniae* DOKDO 007<sup>T</sup>의 유전체 염기서열 해독

권용민<sup>1</sup> · Patra Ajit Kumar<sup>1</sup> · 김상진<sup>1,2</sup> · 권개경<sup>2\*</sup> 

<sup>1</sup>국립해양생물자원관, <sup>2</sup>해양생명공학연구센터 한국해양과학기술원

(Received October 22, 2018; Revised November 8, 2018; Accepted November 8, 2018)

*Flagellimonas eckloniae* DOKDO 007<sup>T</sup>, isolated from the rhizosphere of the marine algae *Ecklonia kurome* collected from Dokdo Island, South Korea, is a marine *Flavobacteria* belonging to the family *Flavobacteriaceae*. The genome consists of 4,132,279 bp, 3,527 coding sequences with 37.85% G + C contents and two contigs in one scaffold chromosome. This strain contains a gene encoding proteorhodopsin, as well as other retinal biosynthesis genes, allowing it to utilize sunlight as an energy source. The strain contained only few segment of flagellar constructing gene cluster and this is not consistent with genus name *Flagellimonas*, therefore, revision of the genus name is required.

**Keywords:** *Flagellimonas eckloniae*, genome sequence, marine *Flavobacteria*, proteorhodopsin

The genus *Flagellimonas* is a part of the family *Flavobacteriaceae*, one of the major phylogenetic lineages within the phylum *Bacteroidetes* (Garrity and Holt, 2001). *Flavobacteria* play a pivotal role in the photometabolic system in marine environments (Fuhrman *et al.*, 2008). The genus *Flagellimonas*

was proposed by Bae *et al.* (2007), with the description of *Flagellimonas eckloniae* as the type species and recently emended by Choi *et al.* (2018) with a new species *F. aquimarina* and combination with the genus *Spongiibacterium* Yoon and Oh 2012. The strain DOKDO 007<sup>T</sup> is an orange-pigmented, aerobic, Gram-negative, rod-shaped marine *Flavobacteria*, which was isolated from the rhizosphere of the marine macroalgae *Ecklonia kurome* and collected along the seashore of Dokdo Island, South Korea (Bae *et al.*, 2007). Therefore, addition of the information on the draft genome to the data on the genus *Flagellimonas* provides an opportunity for comparative genome analyses and serves as a resource for understanding the evolution and molecular mechanisms for adaptation of *Flagellimonas* species in the rhizosphere of the marine macroalgae.

The DOKDO 007<sup>T</sup> genome sequencing was undertaken using PacBio RS II single-molecule real-time (SMRT) sequencing technology. A 10-kb insert library was constructed and sequenced, yielding > 161.8 × average genome coverage. *De novo* assembly of the 136,261 reads (668,421,644 bp in total) was conducted using the hierarchical genome-assembly process pipeline of SMRT Analysis v2.2.0. Open reading frames were predicted using the National Centre for Biotechnology Information

\*For correspondence. E-mail: kkkwon@kiost.ac.kr;  
Tel.: +82-51-664-3371; Fax: +82-51-955-3981

Prokaryotic Genomes Annotation Pipeline and the genome was submitted to the Integrated Microbial Genomes server of the Joint Genome Institute for Cluster of Orthologous Groups (COG) analysis.

The draft genome of *Flagellimonas eckloniae* DOKDO 007<sup>T</sup> consists of 4,132,279 bp, with 37.85% GC content and two contigs in one scaffold chromosome without plasmids (Table 1). The coding regions cover 90.38% of the genome (3,734,922 bp) and encode 3,527 proteins (Table 1); of these, 1,903 (53.28%) were assigned to COGs. The most abundant COG category was ‘General function prediction only’ (207 proteins), followed by ‘Translation, ribosomal structure, and biogenesis’ (177 proteins) and ‘Amino acid transport and metabolism’ (170 proteins). Additionally, the genome encodes 142 pseudo-genes, 6 rRNAs, and 38 tRNAs with a single rRNA operon (Table 1).

The genome analysis of strain DOKDO 007<sup>T</sup> revealed the presence of a green light-absorbing proteorhodopsin (PR) of 242 amino acid residues. Several important residues necessary for energy generation are conserved among rhodopsins, including Asp97, Glu108, and Lys216 (Béjà *et al.*, 2000; Man *et al.*, 2003; Fuhrman *et al.*, 2008). The PR sequence of DOKDO 007<sup>T</sup> is closest to that of the *Muricauda pacifica* DSM 25027<sup>T</sup> with 90% sequence identity according to BLAST analysis. Additionally, the *blh* gene encoding a 15,15'-β-carotene dioxygenase was located adjacent to the PR gene, similar to the genes in other PR-containing *Bacteroidetes* genomes and putative

retinal-producing biosynthetic pathway genes (Béjà *et al.*, 2000; Teramoto *et al.*, 2003; Gómez-Consarnau *et al.*, 2007; Kimura *et al.*, 2011). One of the remarkable feature is that only few no. of flagellar construction related genes were detected from the genome sequence and this was consistent with the result of Choi *et al.* (2018). Therefore, emendation of the genus name “*Flagellimonas*” is required.

### Strain and nucleotide sequence accession numbers

The draft genome sequence of *Flagellimonas eckloniae* DOKDO 007<sup>T</sup> has been deposited at DDBJ/EMBL/GenBank under accession number LCTZ00000000. The strain is available from Marine & Extreme Bioresource Collection ([http://www.megrc.re.kr/mebic/mebic\\_11/eng/html/intro\\_mebic.asp](http://www.megrc.re.kr/mebic/mebic_11/eng/html/intro_mebic.asp)), under the code MEBiC01917<sup>T</sup>.

## 적 요

*Flavobacteriaceae*에 속하는 해양 *Flavobacteria*인 *Flagellimonas eckloniae* DOKDO 007<sup>T</sup>은 독도에서 서식하는 조류(*Ecklonia kurome*)에서 분리되었다. DOKDO 007<sup>T</sup>균주의 유전체는 4,132,279 bp 크기로 3,527개의 코딩 서열과 37.85%의 GC 함량을 가지며, 하나의 스케폴드에서 두 개의 콘티그로 구성되어 있다. 이 균주는 태양광을 에너지원으로써 이용할 수 있는 여러 레티날 생합성 유전자들과 마찬가지로 프로테오로돕신을 인코딩하는 유전자를 함유하고 있다. 속명과는 달리 편모 형성에 관여하는 유전자가 충분하지 못한 것을 감안하여 속명의 개정이 필요하다.

## Acknowledgements

This work was supported by the MABIK in-house program (2018M00600) and the KIOST in-house program (PE99622). We thank Marine & Extreme Bioresource Collection (MEBiC) at KIOST for providing marine *Flavobacteria* isolate.

## References

Bae SS, Kwon KK, Yang SH, Lee HS, Kim SJ, and Lee JH. 2007. *Flagellimonas eckloniae* gen. nov., sp. nov., a mesophilic

**Table 1.** General features of *Flagellimonas eckloniae* DOKDO 007<sup>T</sup>

Features	Chromosome
Genome size (bp)	4,132,279
DNA coding region (bp)	3,734,922
GC content (%)	37.85
Contig	2
Plasmid	0
Protein coding genes	3,527
rRNA (5S, 16S, 23S)	6 (2, 2, 2)
tRNA	38
ncRNA	1
Genes with functional prediction	2,703
Genes assigned to COGs	1,903
Genes with Pfam domains	2,721
Genes with signal peptides	349
Genes with transmembrane helices	789
Pseudo genes	142

marine bacterium of the family *Flavobacteriaceae*, isolated from the rhizosphere of *Ecklonia kurome*. *Int. J. Syst. Evol. Microbiol.* **57**, 1050–1054.

- Béjà O, Aravind L, Koonin EV, Suzuki MT, Hadd A, Nguyen LP, Jovanovich SB, Gates CM, Feldman RA, Spudich JL, et al.** 2000. Bacterial rhodopsin: evidence for a new type of phototrophy in the sea. *Science* **289**, 1902–1906.
- Choi S, Lee JH, Kang JW, Choe HN, and Seong CN.** 2018. *Flagellimonas aquimarina* sp. nov., and transfer of *Spongiibacterium flavum* Yoon and Oh 2012 and *S. pacificum* Gao *et al.* 2015 to the genus *Flagellimonas* Bae *et al.* 2007 as *Flagellimonas flava* comb. nov. and *F. pacifica* comb. nov., respectively. *Int. J. Syst. Microbiol.* **68**, 3266–3272.
- Fuhrman JA, Schwalbach MS, and Stingl U.** 2008. Proteorhodopsins: an array of physiological roles? *Nat. Rev. Microbiol.* **6**, 488–494.
- Garrity GM and Holt JG.** 2001. The road map to the manual, pp. 119–166. In Boone DR, Castenholz RW, and Garrity GM. (eds.), Bergey's manual of systematic bacteriology, 2nd edn, vol. 1, Springer, New York, USA.
- Gómez-Consarnau L, González JM, Coll-Lladó M, Gourdon P, Pascher T, Neutze R, Pedrós-Alió C, and Pinhassi J.** 2007. Light stimulates growth of proteorhodopsin-containing marine *Flavobacteria*. *Nature* **445**, 210–213.
- Kimura H, Young CR, Martinez A, and DeLong EF.** 2011. Light-induced transcriptional responses associated with proteorhodopsin-enhanced growth in a marine flavobacterium. *ISME J.* **5**, 1641–1651.
- Man D, Wang W, Sabehi G, Aravind L, Post AF, Massana R, Spudich EN, Spudich JL, and Béjà O.** 2003. Diversification and spectral tuning in marine proteorhodopsins. *EMBO J.* **22**, 1725–1731.
- Teramoto M, Takaichi S, Inomata Y, Ikenaga H, and Misawa N.** 2003. Structural and functional analysis of a lycopene L-monocyclase gene isolated from a unique marine bacterium that produces myxol. *FEBS Lett.* **545**, 120–126.