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Complete genome sequence of *Flavivirga eckloniae* ECD14^T isolated from a seaweed *Ecklonia cava*

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감태(*Ecklonia cava*)에서 분리한 *Flavivirga eckloniae* ECD14^{T}의 유전체 서열 분석

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The genome of *Flavivirga eckloniae* ECD14^T isolated from a seaweed *Ecklonia cava* was sequenced. The genome comprises a single circular 5,665,358 bp chromosome with a G + C content of 33.9%, 4,647 total genes, 4,595 protein-coding genes, 44 pseudo genes, and 52 RNA genes. CRISPER genes and sequences were not found and there were some phage remnants and transposons. This strain contains alginate lyase and β-glucosidase genes responsible for the degradation of seaweed polysaccharides.

Keywords: *Flavivirga eckloniae*, alginate lyase, genome sequence, seaweed

The genus *Flavivirga* was first proposed by Yi *et al*. (2012), as a member of the family *Flavobacteriaceae*, class *Flavobacteria*, phylum *Bacteroidetes*, and encompasses four species with validly published names (LPSN, http://www.bacterio.net/). The members of the genus *Flavivirga* were isolated from marine environments such as seawater and seaweed (Lee *et al*., 2017). Members of the genus *Flavivirga* are Gram-strain-negative, aerobic, non-spore-forming, and rod-shaped with DNA G + C contents of 27~33 mol% and require sea salts for growth.

Alginate and cellulose are widely distributed in the cell wall of marine algae such as *Ecklonia cava* (Kim *et al*., 2016; Yagi *et al*., 2018). Many kinds of marine bacteria including *Vibrio*, *Shewanella*, *Paenibacillus*, and *Bacillus* were known to excrete alginate lyase and cellulase (Kim *et al*., 2016; Wang *et al*., 2017; Yagi *et al*., 2018; Zhu *et al*., 2018). These enzymes were known to decompose the dead algae in the marine environments and also concerned to produce bioactive oligosaccharides in industry (Kim *et al*., 2016; Wang *et al*., 2017).

Flavivirga eckloniae ECD14^T was isolated from a seaweed *Ecklonia cava* collected from the South Sea, Republic of Korea and showed the degradation activity of seaweed polysaccharides alginate and cellulose (Lee *et al*., 2017). Thus, we determined the complete genome sequence of *Flavivirga eckloniae* ECD14^T (= KCTC 52352^T) and identified the presence of genes responsible for the degradation of seaweed polysaccharides. There were no whole genome sequence data on bacteria belonging to the genus *Flavivirga*.

The genomic DNA was extracted from the stationary phased cells using a Wizard genomic DNA isolation kit (Promega).

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Table 1. Genome statistics of *F. eckloniae* ECD14^T

Attribute	Values
Genome size (bp)	5,665,358
G + C content (%)	33.9
No. of contigs	1
No. of total genes	4,647
No. of coding sequences (CDS)	4,595
No. of pseudogenes	44
No. of rRNAs (5S, 16S, 23S)	6 (2, 2, 2)
No. of tRNAs	42
No. of ncRNAs	4

The whole genome of ECD14^T was determined using Pacific Biosciences (PacBio) RSII platform (Pacific Biosciences). Sequencing data were assembled with PacBio SMRT analysis using the HGAP2 protocol (Pacific Biosciences; Chin *et al.*, 2013). The annotation of each CDS was made through National Center for Biotechnology Information prokaryotic genome Annotation Pipeline (Tatusova *et al.*, 2016). Identification of clustered regularly interspaced short palindromic repeat (CRISPR) sequences was predicted by application CRISPRFinder program online (http://crispr.i2bc.paris-saclay.fr/Server/; Grissa *et al.*,

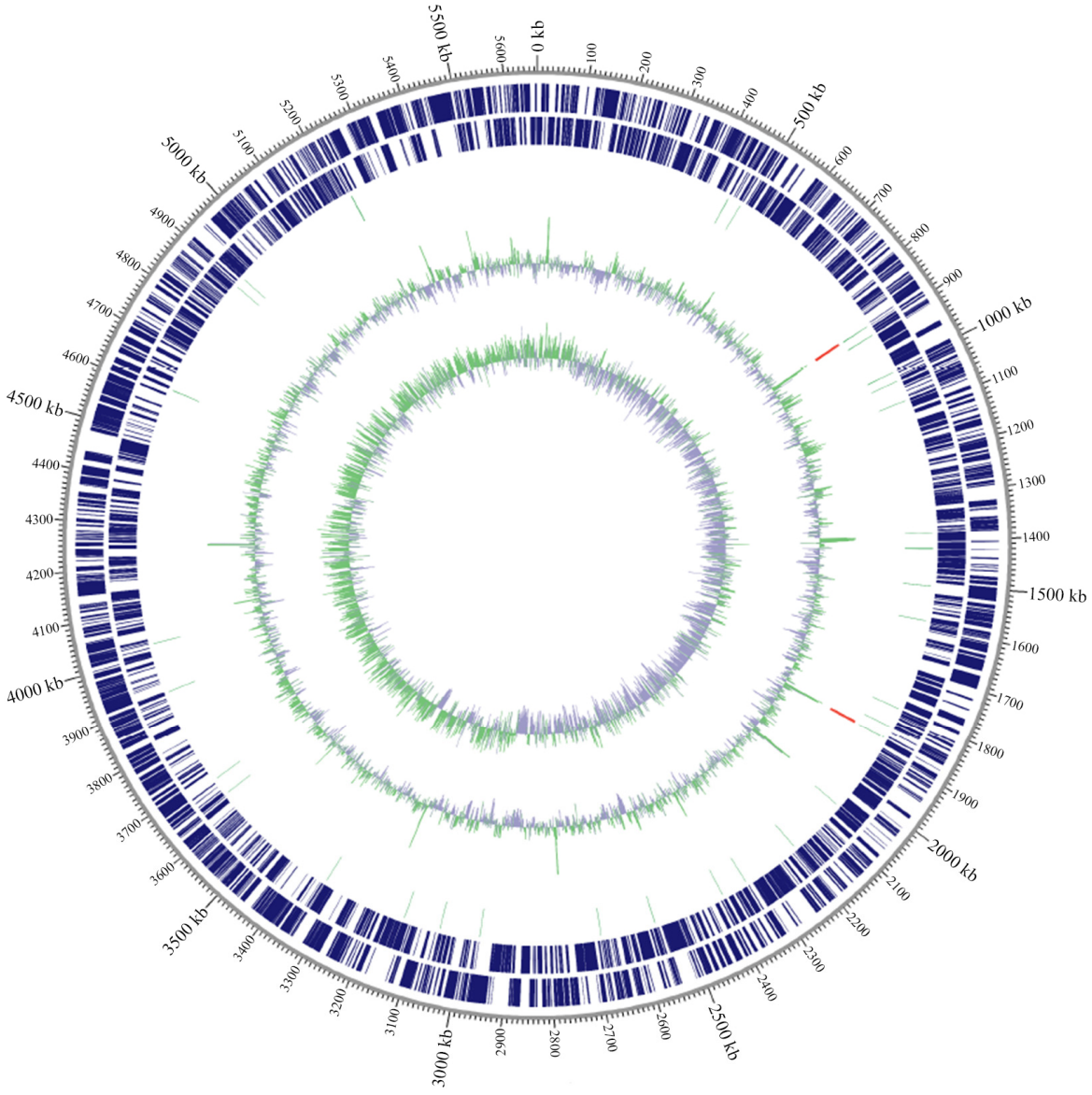

Fig. 1. Graphical circular map of *F. eckloniae* ECD14^T. Marked characteristics are shown from outside to the center; CDS on forward strand, CDS on reverse strand, tRNA, rRNA, GC content, and GC skew.

2007).

The genome statistics are described in Table 1. The complete genome of strain ECD14^T was composed of a single circular chromosome and did not contain any plasmid DNA. The 5,665,358 bp genome with a G + C content of 33.93% contained 4,595 coding regions (CDS), 44 pseudogenes, and 52 RNA genes (6 rRNA genes, 42 tRNA genes, and 4 non-coding RNA genes) based on NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) (Fig. 1). The pseudogenes make stop codon in the middle of nucleotides sequences that encode proteins. There were no contigs that had CRISPR which originates from, matched the corresponding parts of viral DNA and provided the cleaving site of Cas-proteins (Makarova *et al*., 2011). Five phage-related genes and transposable element genes could be annotated. The genome revealed the presence of two alginate lyases and five β-glucosidases, which involved in the degradation of alginate and cellulose, respectively. Also a monooxygenase gene associated with antibiotic biosynthesis and a gene related to the degradation of microcystin were found.

The strain *Flavivirga eckloniae* ECD14^T is available at KCTC 52352^T and JCM 31797^T.

Nucleotide sequence accession number

The genome sequence of *Flavivirga eckloniae* ECD14^T has been deposited in NCBI GenBank under accession number CP025791.

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적 요

대한민국 남해에서 채집한 해조류 감태(*Ecklonia cava*)로부터 분리한 *Flavivirga eckloniae* ECD14^T 균주의 유전체서열을 분석하였다. 균주 ECD14^{T}의 유전체는 G + C 비율이 33.9%이며, 4,647개의 유전자와 4,595개의 단백질 코딩 유전자, 44개의 위유전자, 52개의 RNA 유전자를 포함한 단일 원형 염색체로 구성되었으며 그 크기는 2,371,912 bp였다. 파아지와 트랜스포존 유전자가 존재하며, CISPR array 관련 유전자 및 서열은 발견되지 않았다. 균주 ECD14^{T}는 해조 다당의 분해에 관여하는 alginate lyase와 β-glucosidase 유전자를 가지고 있었다.

References

Chin, C.S., Alexander, D.H., Marks, P., Klammer, A.A., Drake, J., Heiner, C., Clum, A., Copeland, A., Huddleston, J., Eichler E., *et al.* 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat. Methods* **10**, 563–569.

Grissa, I., Vergnaud, G., and Pourcel, C. 2007. CRISPRFinder: a web tool to identify clustered regularly interspaced short palindromic repeats. *Nucleic Acids Res*. **35**, W52–W57.

Kim, B.M., Park, J.H., Kim, D.S., Kim, Y.M., Jun, J.Y., Jeong, I.H., and Chi, Y.M. 2016. Effects of the polysaccharide from the sporophyll of brown alga *Undaria pinnatifida* on serum lipid profile and fat tissue accumulation in rats fed a high-fat diet. *J. Food Sci*. **81**, H1840–H1845.

Lee, J.H., Kang, J.W., Choe, H.N., and Seong, C.N. 2017. *Flavivirga eckloniae* sp. nov. and *Flavivirga aquimarina* sp. nov., isolated from seaweed *Ecklonia cava*. *Int. J. Syst. Evol. Microbiol.* **67**, 3089–3094.

Makarova, K.S., Haft, D.H., Barrangou, R., Brouns, S.J.J., Charpentier, E., Horvath, P., Moineau, S., Mojica, F.J.M., Wolf, Y.I., Yakunin, A.F., *et al.* 2011. Evolution and classification of the CRISPR-Cas systems. *Nat. Rev. Microbiol*. **9**, 467–77.

Tatusova, T., DiCuccio, M., Badretdin, A., Chetvernin, V., Nawrocki, E.P., Zaslavsky, L., Lomsadze, A., Pruitt, K.D., Borodovsky, M., and Ostell, J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res.* **44**, 6614–6624.

Wang, M., Chen, L., Zhang, Z., Wang, X., Qin, S., and Yan, P. 2017. Screening of alginate lyase-excreting microorganisms from the surface of brown algae. *AMB Express* **7**, 74.

Yagi, H., Fujise, A., Itabashi, N., and Ohshiro, T. 2018. Characterization of a novel endo-type alginate lyase derived from *Shewanella* sp. YH1. *J. Biochem*. **163**, 341–350.

Yi, H., Cho, J.C., and Chun, J. 2012. *Flavivirga jejuensis* gen. nov., sp. nov., and *Flavivirga amylovorans* sp. nov., new members of the family *Flavobacteriaceae* isolated from seawater, and emended descriptions of the genera *Psychroserpens* and *Lacinutrix*. *Int. J. Syst. Evol. Microbiol.* **62**, 1061–1068.

Zhu, X., Li, X., Shi, H., Zhou, J., Tan, Z., Yuan, M., Yao, P., and Liu, X. 2018. Characterization of a novel endo-type alginate lyase derived from *Shewanella* sp. YH1. *J. Biochem*. **163**, 341–350.