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Complete genome sequence of *Tamlana* sp. UJ94 degrading alginate

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알긴산을 분해하는 세균 *Tamlana* sp. UJ94의 완전한 유전체 서열

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Tamlana sp. UJ94 isolated from seawater can degrade alginate. To identify the genomic basis of this activity, the genome was sequenced. The genome was composed of 4,116,543 bp, 3,609 coding sequences, and 35.2 mol% G + C content. A BLASTp search predicted the presence of 9 alginate lyases as well as 6 agarases, 5 amylases, 4 carrageenases, 1 cellulase, 4 pectate lyases, and 7 xylanases, indicating its ability to degrade diverse polysaccharides. The genome of strain UJ94 is a source of polysaccharide-degrading enzymes for bioconversion processes.

Keywords: *Tamlana* sp., alginate lyase, bioconversion, carbohydrate-active enzyme, polysaccharide

Strain UJ94 was isolated from seawater collected from Uljin, Republic of Korea on April 26, 2017. Analysis of the 16S rRNA gene sequence indicated that strain UJ94 has high sequence similarity with the type strain of *Tamlana agarivorans* JW-26^T (98.4%), *T. sedimentorum* KMM 9545^T (96.1%), and *T. crocina* HST1-43^T (95.4%). The neighbor-joining phylogenetic tree also showed that strain UJ94 formed a cluster with *T. agarivorans* JW-26^T (data not shown). Therefore, we designated strain UJ94 as *Tamlana* sp. UJ94. Strain UJ94 can degrade alginate, as observed by the halo zone on a marine agar (BD) plate containing 1% (w/v) sodium alginate after cultivation at 30°C for 7 days. To date, 4 genomes of *Tamlana* species have been published in the NCBI genome database; however, only the genome of *Tamlana* sp. UJ94 has been sequenced completely. To provide a genomic basis for alginate degradation, we conducted genomic analysis of strain UJ94.

Genomic DNA was isolated from cells grown on marine agar at 30°C for 2 days using a Wizard Genomic DNA isolation kit (Promega). The 20-Kbp sequencing library was constructed using a PacBio DNA Template Prep Kit 1.0. The library was sequenced using 8-well-SMART Cell v3 in PacBio RSII. Sequencing data were assembled with PacBio SMRT Analysis 2.3.0 using the HGAP2 protocol. Library construction and sequencing were performed by ChunLab, Inc. Sequencing depth was 319.14X. The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline. The genome was deposited to NCBI GenBank (accession number CP025938).

The genome of strain UJ94 consists of a single circular chromosome composed of 4,116,543 bp (4,116,543 of N_{50} and 1 of L_{50}), 3,609 coding sequences, 3 copies of 5S, 16S, and 23S rRNAs, and 44 tRNAs with a 35.2 mol% of G + C content (Table 1). The CAZy database (www.cazy.org) was used to analyze the genome of strain UJ94, which revealed many carbohydrate-active enzymes such as 87 glycoside hydrolases, 64 glycosyltransferases, and 26 polysaccharide lyases (Lombard *et al.*, 2014). BLASTp search predicted 9 alginate lyases, as

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Table 1. General feature and MIGS information of *Tamlana* sp. UJ94 genome

Attribute	Value
Genome Size (bp)	4116543
G + C content (%)	35.2
Total genes	3609
Protein-coding genes	3433
RNA	
rRNA	3, 3, 3 (5S, 16S, 23S)
tRNA	44
ncRNA	4
Pseudogenes	119
investigation_type	bacteria
lat_lon	36°45'35.44" N, 129°28'11.23" E
geo_loc_name	South Korea
collection_date	2017-04-26
env_biome	marine biome (ENVO:00000447)
env_feature	marine water body (ENVO:00001999)
env_material	sea water (ENVO:00002149)
source_mat_id	KCTC 62451, NBRC 113234
biotic_relationship	free living
trophic_level	chemoorganotroph
rel_to_oxygen	aerobe
seq_meth	PacBio RSII
assembly	PacBio SMRT Analysis 2.3
finishing_strategy	complete; 319.14X;1
annot_source	NCBI PGAP

* NCBI accession number is CP025938

expected. Additionally, the genome contained 6 agarases, 5 amylases, 4 carrageenases, 1 cellulase, 4 pectate lyases, and 7 xylanases (BLASTp cutoff values were *E*-value < 10^{-10} and sequence similarity > 25%), suggesting the ability to degrade diverse polysaccharides. Genes related to the regulation, uptake, and metabolism of polysaccharides are often co-localized in the genomic loci of the phylum *Bacteroidetes*, known as polysaccharide-utilization loci (PUL) (Grondin *et al.*, 2017). PULDB predicted 20 PULs in the genome of strain UJ94 (Terrapon *et al.*, 2018). One of the PULs, a 22.1-kb region (1,146,465 to 1,168,568) containing 11 genes (C1A40_05190 to C1A40_05240), is thought to function in alginate metabolism. This region harbors 4 alginate lyases, 1 transcriptional regulator, 2 transporters, 3 hypothetical protein-coding genes, and 1 pseudogene.

Polysaccharide-degrading enzymes have gained attention because of their potential in the bioconversion of polysaccharides into renewable energy sources and biochemical commodities (Trincone, 2011). Genes coding for polysaccharide-degrading enzymes from the genome of *Tamlana* sp. UJ94 would have potential use for such industrial applications.

적 요

Tamlana sp. UJ94는 해수로부터 분리되었으며 알긴산을 분해할 수 있다. 알긴산 분해 관련 특성을 이해하기 위해 이 세균의 유전체를 분석하였다. UJ94의 유전체는 4,116,543 bp의 크기로 3,609개의 코딩서열을 가지고 있으며 35.2 mol%의 G + C 함량을 가진다. BLASTp 검색 결과 9개의 alginate lyase 외에도 6개의 agarase, 5개의 amylase, 4개의 carrageenase, 1개의 cellulase, 4개의 pectate lyase, 7개의 xylanase의 존재가 예측되어 UJ94의 다양한 다당류 분해 능력을 암시하였다. *Tamlana* sp. UJ94의 유전체는 생물전환 공정에 사용할 수 있는 다당류 분해 유전자를 제공할 수 있을 것이다.

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