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Draft genome sequence of *Pseudoalteromonas* sp. meg-B1 isolated from marine sediment

Soo-Je Park[1*] and Sewook Park[2]

[1]*Department of Biology, Jeju National University, Jeju 63243, Republic of Korea*
[2]*Food Microbiology Division, Ministry of Food and Drug Safety, Cheongju 28159, Republic of Korea*

해양퇴적물로부터 분리된 *Pseudoalteromonas* sp. meg-B1의 유전체 분석

박수제[1*] · 박세욱[2]

[1]제주대학교 생물학과, [2]식품의약품안전처 식품의약품안전평가원 미생물과

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Pseudoalteromonas sp. meg-B1 belonging to *Gammaproteobacteria* was isolated from marine sediment in Jeju island. Here, we report the draft genome sequence of strain meg-B1 with a size of approximately 4.15 Mbp and a mean G + C content of 41.2%. The draft genome included 3,606 coding sequences, and 9 ribosomal RNA and 94 transfer RNA genes. In the draft genome, genes (e.g. choline dehydrogenase) involved in the accumulation of compatible solutes required for survival in marine environments have been identified.

Keywords: *Pseudoalteromonas*, genome, marine sediment

The genus *Pseudoalteromonas* was first reported by Gauthier *et al*. (1995) which was classified into a member of the *Gammaproteobacteria*. To date, there are validated 53 species isolated mostly from marine environment (http://www.bacterio.net/pseudoalteromonas.html). The genus *Pseudoalteromonas* has been identified as ubiquitous marine bacterium and chemoheterotrophic metabolism. They are Gram-stain negative, aerobic or facultative anaerobic, rod-shaped. Also, they need sodium ion for growth, and possess ubiquinone-8 (Q-8) as respiratory quinone (Ivanova *et al.*, 2014). Here, we describe the draft genome sequence and annotation of *Pseudoalteromonas* sp. meg-B1 isolated from marine sediment in Jeju island, the Republic of Korea.

Strain meg-B1 was cultured in 50 marine broth (Difco) medium at 30°C in the incubator shaker at 200 rpm. The extraction of genomic DNA (gDNA) was conducted according to the manufacturer's instructions by a commercial DNA extraction kit (GeneAll Biotechnology. Co. Ltd.). The concentration and purity of the DNA was determined by a DS-11+ spectrophotometer (DeNovix Inc.). An Illumina Miseq sequencer (Illumina) was used to conduct the whole-genome shotgun sequencing. A reads passed filtering a total of 3.42 Gb (ca. 710X in depth) in sequenced reads used into scaffold assembly. The trimming of the resulting nucleotide sequences and assembling *de novo* were accomplished by SPAdes (v.3.11.1) (Bankevich *et al.*, 2012). Finally, 13 scaffolds were obtained in this study. To estimate genome completeness and quality, we used checkM (Parks *et al.*, 2015). The resulting assembled sequences were annotated by NCBI Prokaryotic Genome Annotation Pipeline with GeneMarkS + version 4.5, using the best-placed reference protein method (Angiuoli *et al.*, 2008). The draft genome size of the strain meg-B1 is *ca*. 4.15 Mb with 41.2% G + C content. CheckM estimated genome completeness at 99.83% with 0.51% contamination and no strain heterogeneity.

***For correspondence.** E-mail: sjpark@jejunu.ac.kr;
Tel.: +82-64-754-3524; Fax: +82-64-756-3541

The genome includes 3,632 coding sequences (CDSs), and 9 ribosomal RNA and 94 transfer RNA genes (Table 1). Among them, 1,997 CDSs were matched in KEGG database (55.4% of total CDSs), in which most of them were affiliated into protein families: genetic information processing category. We found that various genes involved in hydrolytic extracellular enzymes (α -amylase, glucoamylase, chitinase, α - and β -glucosidase, protease, α -trehalase, alkaline phosphatase) were identified in the genome. Genes involved in assimilatory sulfate reduction (CysNSCHJI) were completely identified in the genome. Moreover, we found that genes (e.g. choline dehydrogenase) involved in the accumulation of compatible solutes required for survival in marine environments have been identified. On the other hand, the strain meg-B1 appeared to harbor genes responsible for 17 two-component regularity systems including EnvZ-OmpR (osmotic stress response). Unexpectedly, 10 ATP-binding cassette transporters were only identified in the genome, despite strain meg-B1 has been isolated under a heterotrophic condition.

The strain meg-B1 contains further antibiotic resistance genes, including those for, AmpC type β -lactamase (class C), chloramphenicol (*catA*), virginiamycin (*vat*), cationic antimicrobial peptide (*pgtE*). Despite the genome was incomplete genome sequence, clustered regularly interspaced short palindromic repeat (CRISPR) finder (Grissa *et al.*, 2007) found one questionable CRISPR sequence (224 in length) in the genome. Unexpectedly, one intact prophage regions were identified by PHAST (Zhou *et al.*, 2011), in which 46 CDSs were observed within the length of 42.1 kb. The percentage of GC of the region was 44.0%.

Table 1. ***Pseudoalteromonas*** **sp. meg-B1 genome assembly and its general features**

Item	Description
Genome Assembly Data	
Assembly Method	SPAdes v. 3.11.1
Genome Coverage	710X
Sequencing Technology	Illumina MiSeq
Genome features	
Size (Mbp)	4.15
GC content (%)	41.2
No. of total predicted genes	3,739
No. of total coding sequences	3,632
No. of coding sequences	3,606
rRNA (23S, 16S, 5S)	9 (3, 1, 5)
tRNA	94

Accession number

The whole genome shotgun project of the strain meg-B1 (= KCCM 43285) has been deposited at DDBJ/ENA/GenBank under the accession QGQU00000000. The version described in this paper is version QGQU01000000.

적 요

*Gammaproteobacteria*에 속하는 *Pseudoalteromonas* sp. meg-B1을 제주도 해양 퇴적물로부터 분리하였다. 본 연구에서는 대략 4.15 Mb의 크기와 41.2%의 평균 G+C 함량을 가진 meg-B1 균주의 완전한 유전체를 보고한다. 유전체는 3,606개의 코딩 서열, 9개의 리보솜 RNA 및 94개의 전사 RNA 유전자가 존재하며, 한 개의 완전한 프로파지 영역이 발견되었다. 본 유전체는 해양환경에서 생존하기 위한 삼투화합성 용질 합성과 관련된 유전자(예, choline dehydrogenase)들이 확인되었다.

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References

Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, *et al.* 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. *OMICS* **12**, 137–141.

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, *et al.* 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J. Comput. Biol.* **19**, 455–477.

Gauthier G, Gauthier M, and Christen R. 1995. Phylogenetic analysis of the genera *Alteromonas*, *Shewanella*, and *Moritella* using genes coding for small-subunit rRNA sequences and division of the genus *Alteromonas* into two genera, *Alteromonas* (emended) and *Pseudoalteromonas* gen. nov., and proposal of twelve new

species combinations. *Int. J. Syst. Bacteriol.* **45**, 755–761.

Grissa I, Vergnaud G, and Pourcel C. 2007. CRISPRFinder: a web tool to identify clustered regularly interspaced short palindromic repeats. *Nucleic Acids Res.* **35**, W52–57.

Ivanova EP, Ng HJ, and Webb HK. 2014. The family *Pseudoalteromonadaceae*, pp. 575–582. *In* Rosenberg E, DeLong EF, Lory S, Stackebrandt E, and Thompson F. (eds.), The prokaryotes: Gammaproteobacteria. Springer, Berlin, Heidelberg, Germany.

Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, and Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res.* **25**, 1043–1055.

Zhou Y, Liang Y, Lynch KH, Dennis JJ, and Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res.* **39**, W347–352.