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Complete genome sequence of *Runella* sp. ABRDSP2, a new mono-aromatic compounds degrading bacterium isolated from freshwater

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담수로부터 분리한 단환성 화합물 분해 미생물 *Runella* sp. ABRDSP2의 전장 유전체 서열

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The *Runella* sp. ABRDSP2, capable of degrading mono-aromatic compounds such as toluene, was isolated from freshwater. The whole genome, consisting of a circular single chromosome and three plasmids, was composed of total 7,613,819 bp length with 44.4% G+C contents and 6,006 genes. The genome of strain ABRDSP2 contains many aromatic hydrocarbon degrading genes such as monooxygenase, ring-cleaving dioxygenase, and catechol 1,2-dioxygenase. The complete genome reveals versatile biodegradation capabilities of *Runella* sp. ABRDSP2.

Keywords: *Runella*, bioremediation, mono-aromatic hydrocarbon degradation

The genus *Runella* was first proposed by Larkin and Williams (1978) and includes five recognized species. The member of genus *Runella* has been generally found in aquatic habitats such as activated sludge and these strains showed aerobic, chemoorganotrophic phenotypic characteristics and produced pale-pink pigmentation (Kim *et al*., 2017). The size of reported genome sequence of strains, belonging to genus *Runella*, is approximately 7.16 Mb encoding 5,826 genes with 44.8% G+C contents (NCBI database, https://www.ncbi.nlm.nih.gov/genome/71020). Here, we report the complete genome sequence of newly isolated bacterium, *Runella* sp. ABRDSP2, containing genes related with aromatic compounds degradation.

Runella sp. ABRDSP2 (= KACC 19854), capable of degrading aromatic hydrocarbons (benzene, phenol, toluene, and naphthalene), was isolated from freshwater. The genomic DNA was obtained from the cultivated cells on R2A agar during 2 days using the Wizard Genomic DNA Purification kit (Promega), following the protocol recommended by the manufacturer. The purified genomic DNA was completely sequenced by a combination of PacBio RSII and Illumina Hiseq 2500 sequencing. Briefly, the 20-kb sequencing library was constructed using a PacBio DNA Template Prep Kit 1.0 and analyzed by single-molecule real-time (SMRT) sequencing at Macrogen. *De novo* assembly of the sequencing reads was performed through the hierarchical genome assembly process (HGAP 2, version 2.3.0), and paired-end reads (101 bp) obtained from the Illumina sequencing were mapped on assembled contig for error correc-

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tions. The genome was annotated by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (Tatusova *et al*., 2016).

Total of 1,170,121,330 bp consisting 129,294 sequencing reads was yielded from PacBio sequencing and N_{50} value for the assembly was 7,432,530 bp. After *de novo* assembly and error correction, the whole genome of strain ABRDSP2 consisting of a circular single chromosome and three plasmids have been deposited in GenBank with the accession numbers of CP031030-CP031033. The circular maps representing the genome of strain ABRDSP2 (Fig. 1) were generated using the Web-based CGview program (Grant and Stothard, 2008). Sequencing depth of total four circular contigs is about 113.0 times and total contigs size, CDS, tRNA, rRNA, and G+C contents were estimated as shown in Table 1.

The genome of strain ABRDSP2 contained more than 27 oxygenase genes related with catalyzing oxidation of various organic compounds such as aromatic hydrocarbon. In particular, genes annotated as monooxygenase (WP_122930018.1), probably degrading of mono-aromatic compounds (such as benzene, phenol, and toluene) were identified. In addition, many other aromatic hydrocarbon metabolizing genes such as ring-cleaving dioxygenase (WP_122932451.1 and WP_122933798.1), homo-

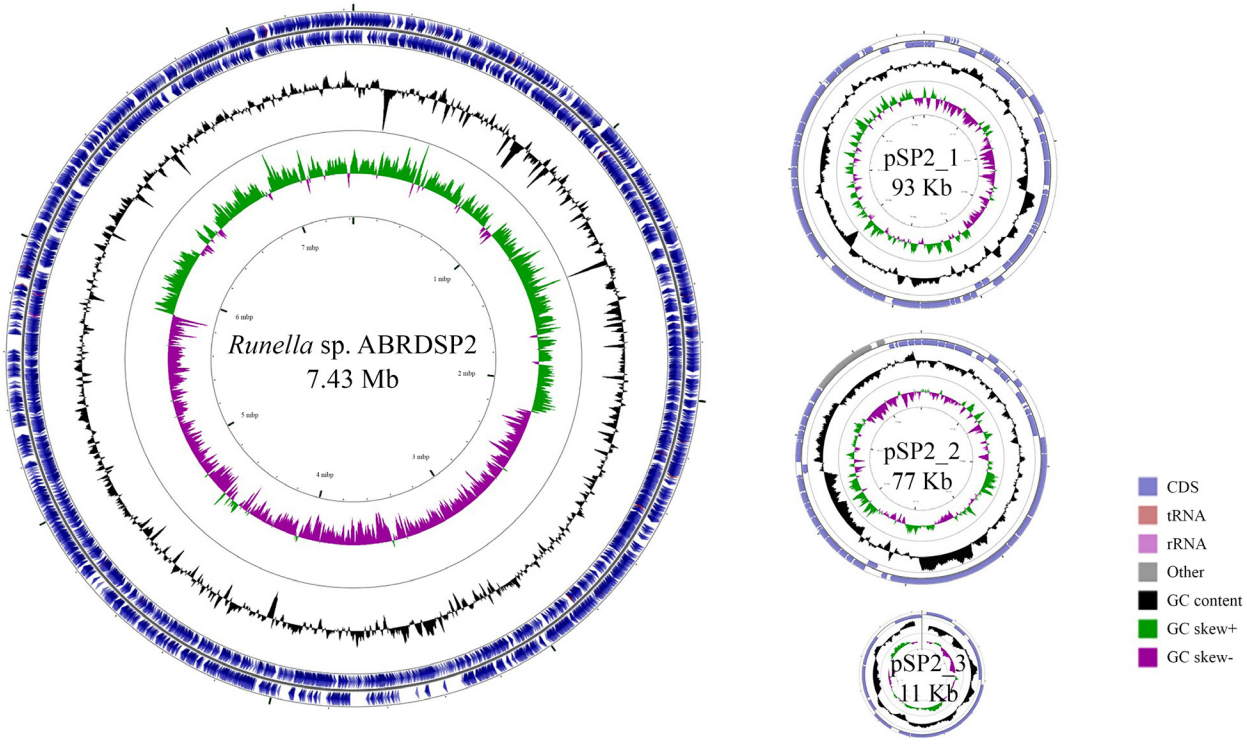

Fig. 1. Graphical circular maps of the chromosome and plasmids of *Runella* sp. ABRDSP2. Circles illustrate the following characteristics from the outside to the center: (1) coding sequences on forward strand, (2) coding sequences on reverse strand, (3) Transfer RNAs (tRNAs), (4) ribosomal RNAs (rRNAs), (5) GC content, and (6) GC skew.

Table 1. General genomic features of the *Runella* sp. ABRDSP2

Feature	Chromosome	pSP2_1	pSP2_2	pSP2_3
GenBank accession	CP031030	CP031031	CP031032	CP031033
Genome size (bp)	7,432,530	93,030	76,966	11,293
G+C content (%)	44.6	38.4	40.6	35.9
Number of Coding Sequence (CDS)	5,891	59	45	11
Number of tRNA genes	44	-	-	-
Number of rRNA (5S, 16S, 23S) genes	9	-	-	-

gentisate 1,2-dioxygenase (WP_122930416.1), catechol 1,2-dioxygenase (WP_122930014.1), protocatechuate 3,4-dioxygenase (WP_122934357.1 and WP_122930784.1), and hydroxybenzoate 3-monooxygenase (WP_122930782.1), were also found. The complete genome reveals versatile biodegradation capabilities of *Runella* sp. ABRDSP2 and will provide insights into the bioremediation of contaminated aquatic environment by strain ABRDSP2.

Nucleotide sequence accession number

The whole-genome sequence was deposited in GenBank under accession number NZ_CP031030-CP031033.

적 요

페놀과 같은 단환성 화합물을 분해하는 미생물인 *Runella* sp. ABRDSP2 균주는 담수로부터 분리되었다. 원형으로 완성된 하나의 chromosome과 3개의 plasmid로 구성된 유전체는 GC 함량이 44.4%인 총 7,613,819 bp의 크기를 나타내며 6,006개의 유전자를 인코딩하고 있다. ABRDSP2 균주는 monooxygenase, ring-cleaving dioxygenase 및 catechol 1,2-dioxygenase 등의 다수의 방향성 탄화수소를 분해하는 유전자를 함유하고 있다. 이런 전장 유전체는 *Runella* sp. ABRDSP2 균주가 다양한 생분해능력이 있음을 나타낸다.

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