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Draft Genome Sequence of Meropenem-Resistant *Pseudomonas peli* CJ30, Isolated from the Han River, South Korea

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대한민국 한강에서 분리된 메로페넴 내성 *Pseudomonas peli* CJ30의 유전체 서열 초안

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Meropenem-resistant *Pseudomonas peli* CJ30 was isolated from the Han River, South Korea. The genome of strain CJ30 comprising 4,919,106 bp with a G + C content of 60.0% was assembled to nine contigs. The draft genome sequence contained 5,411 protein-coding genes, 18 rRNA genes, and 70 tRNA genes. Strain CJ30 contained bla_{SFC-3} and ampC β-lactamase gene.

Keywords: *Pseudomonas peli*, genome, Han River, meropenem resistance, β-lactamase

The genus *Pseudomonas* is one of the most diverse and complex bacterial genera and widespread in various environmental habitats. Most of members are aerobic, Gram-staining-negative, and rod-shaped and have one or more polar flagella. Furthermore, the genome sequences of 166 validly published strains showed an average of genome size and G + C content were 5.63 Mbp and 61.2%, respectively [1].

β-Lactam antibiotics, such as cephalosporins and carbapenems, are the most frequently used for the treatment of bacterial infections in clinical settings. Carbapenem antibiotics, such as meropenem, biapenem, ertapenem, and doripenem, have a broad spectrum of antibacterial activity and are slightly more effective against Gram-negative bacteria than Gram-positive bacteria [2]. β-Lactamases are the major resistance mechanism for the β-lactam antibiotics in Gram-negative bacteria and are classified into four classes based on structural similarities (class A, B, C, and D). Extended-spectrum β-lactamases (ESBLs)- and carbapenemase-producing *Enterobacteriaceae* are a global issue of clinical importance. Awareness of the impact of ESBL- and carbapenemase-producing *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and other gram-negative

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bacteria has also increased in recent years. In addition, a large number of *Pseudomonas*-derived cephalosporinases family belonging to ampC β-lactamase, are clinically important and have been reported from the genus *Pseudomonas* in recent years [3].

In this study, meropenem-resistant *Pseudomonas peli* strain CJ30 was isolated from the Han River, South Korea (37°32'2.06"N 127°2'15.63"E) and the draft genome sequence of the strain is reported.

The genomic DNA of strain CJ30 was extracted using FastDNA™ Spin Kit for Soil (MP Biomedicals) and prepared for sequencing using Ligation Sequencing Kit SQK-LSK109 (Oxford Nanopore, UK) following the manufacturer's protocols. Whole genome sequencing was performed using the Oxford Nanopore MinION (R9.4.1 FLO-MIN106, Oxford Nanopore) sequencing platform. Raw reads of nanopore sequencing were pre-processed by trimming and filtering out low-quality reads using Filtlong v0.2.1 (https://github.com/rrwick/Filtlong). The genome was assembled and polished using Miniasm and Racon implemented by Unicycler v0.5.0 [4]. To improve the draft genome sequence, we performed an additional polishing step using medaka (https://github.com/nanoporetech/medaka). Genome completeness was evaluated using BUSCO v5.3.2 [5] and CheckM2 v1.0.0 [6]. Average nucleotide identity (ANI) value was calculated by the OrthoANIu algorithm [7]. Protein-coding genes (CDS), rRNA genes and tRNA genes were predicted using Prodigal v2.6 [8], bacterial covariance models using Pfam database [9], and tRNA-scan-SE [10], respectively. Functional annotation of genome sequence was performed based on three UniProt Reference Cluster databases using bakta v 1.6.1 [11]. Antibiotic resistance genes were predicted using NCBI Antimicrobial Resistance Gene Finder v3.11.2 [12]. The antibiotic susceptibility of strain CJ30 was tested by the disk diffusion assay using antibiotic impregnated disks (Lioflchem, Italy) including amoxicillin (10 μg), cephalexin (30 μg), and meropenem (10 μg).

Table 1. Genome feature of *Pseudomonas peli* CJ30.

Feature	Value
Genome size (bp)	4,919,106
G + C ratio (%)	60.0
N_{50}	4,548,428
Number of	
contigs	9
CDSs	5411
rRNA genes (5S, 16S, 23S)	18 (3, 3, 3)
tRNA genes	70

The sequencing depth was 173.17 × coverage and the completeness of genome assembly were determined to be 97.7% and 100.0% based on BUSCO and CheckM2, respectively. The genome size of strain CJ30 was 4,919,106 bp comprising nine contigs with a G + C content of 60.0%. The genome sequence contained 5,411 CDSs, 18 rRNA genes (six rRNA operons) and 70 tRNA genes (Table 1). The 16S rRNA sequence similarity of strain CJ30 with *Pseudomonas peli* DSM 17833^T was 100% and the ANI value between strain CJ30 and *P. peli* DSM 17833^T was 96.6% indicating that strain CJ30 can be identified as *P. peli*. Based on the annotated genes from the draft genome sequence of strain CJ30, the genes related to central carbon metabolism systems including glycolysis, citric acid cycle and pyruvate metabolism was conserved in the genome. In addition, two β-lactamase genes, bla_{SFC-3} and ampC β-lactamase gene, were present in the genome. These results are in accordance with phenotypic resistance to amoxicillin, cephalexin and meropenem. In particular, SFC β-lactamase gene which was reported to confer resistance to carbapenems in *Serratia fonticola* was first discovered in the *Pseudomonas* genome [13]. AmpC -lactamase gene was known to confer resistance to 1st generation cephalosporins and penicillins [14].

요 약

메로페넴에 내성을 갖는 *Pseudomonas peli* CJ30 균주가 대한민국의 한강에서 분리되었다. CJ30 균주의 유전체는 크기가 4,919,106 bp이고 G + C 함량이 60.0%인 아홉 개의 contig로 조립되었다. CJ30 균주의 유전체 서열은 5,411개의 단백질 코딩 유전자, 18개의 rRNA 유전자 및 70개의 tRNA 유전자를 포함하였다. 균주 CJ30에는 bla_{SFC-3} 및 ampC β-락타마아제 유전자가 포함되어 있습니다.

Nucleotide Sequence Accession Number(s)

Pseudomonas peli CJ30 the draft genome sequence has been deposited to the DDBJ/EMBL/GenBank under the accession number JARODB000000000.
The version described in this paper is version JARODB010000000.

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Conflict of Interest

The authors have no financial conflicts of interest to declare.

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