

Note (Genome Announcement)

Draft genome sequence of *Caballeronia sordidicola* strain PAMC 26633 isolated from an antarctic lichen, *Psoroma* species

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남극 지의류 *Psoroma* 종에서 분리한 *Caballeronia sordidicola* 균주 PAMC 26633의 초벌 유전체 서열 분석

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Here we report the draft genome sequence of the *Caballeronia sordidicola* strain PAMC 26633, isolated from *Psoroma* species, a lichen material from Barton Peninsula, King George Island in Antarctica. As we have observed in previous genomic studies in the genus *Caballeronia* from polar lichen, draft genomic sequences of PAMC 26633 had an assortment of genes of ecological importance and of biotechnical potentials, which include diverse metabolic genes for carbohydrates, amino acids, and genes for nitrogen/sulfur metabolisms, stress responses, membrane transporters, antibiotic resistance, and heavy metal resistance. CRISPR genes and sequences were not found and there were some phage remnants and transposons.

Keywords: *Caballeronia sordidicola*, *Psoroma*, Antarctic, genome, lichen

Polar and Alpine Microbial Collection got started (Lee *et al.*, 2012) and the strain PAMC 26633 was deposited as one of the 68 cultured PAMC strains from polar lichen samples (Lee *et al.*, 2014). The strain PAMC 26633 was identified as *Burkholderia sordidicola* based on 16S rRNA sequence analysis, and it was

associated with a *Psoroma* species in previous study (Lee *et al.*, 2014). However we would use *Caballeronia sordidicola* as a species name of the strain PAMC 26633 because it is included in the genus *Caballeronia* (Dobritsa and Samadpour, 2016) as we have done with previous genome analyses (Kim *et al.*, 2017).

Here we report the draft genome sequence of the strain PAMC 26633 (Table 1). Strain PAMC 26633 was isolated from a lichen collected from Barton Peninsula, King George Island in Antarctica (Lee *et al.*, 2014). The draft genome sequence was determined using the Illumina sequencing platform, and were assembled with Ray software (v.2.3.1) (Boisvert *et al.*, 2010). Assembly of genome analysis were carried out with 23-mer search option, which produced longest N50 and contigs as we did in previous genome analysis (Kim *et al.*, 2017). Illumina reads corresponded to 70.5x coverage depth (Table 1). Contigs with no CDS features and contigs shorter than 500 bp were excluded. Finally 307 contigs were submitted to GenBank and N50 value was 106,617. The draft genome of PAMC 26633 was comprised of 9,746,569 bp with 59.5% GC content (Table 2).

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Table 1. *Caballeronia sordidicola* strain PAMC 26633 genome assembly and contextual data

Item	Description
Genome Assembly Data	
Assembly Method	Ray v. 2.3.1
Genome Coverage	70.54X
Sequencing Technology	Illumina
MIGS Data	
Assembly	Ray v. 2.3.1
Biome	Lichen
Collection_date	2010-02-06
Env_package	Missing
Feature	Lichen
Geo_loc_name	Antarctica: South Shetland Islands, King George Island, Barton Peninsula
Investigation_type	Bacteria_archaea
Isol_growth_condt	NA
Lat_lon	62.22605 -58.783566667
Material	Lichen
Project_name	<i>Caballeronia sordidicola</i> PAMC 26633
Seq_meth	Illumina
Experimental_factor	NA
Depth	NA
Alt_elev	NA
Num_replicons	NA
Ref_biomaterial	NA
Source_mat_id	PAMC 26633
Pathogenicity	NA
Biotic_relationship	Symbiont
Trophic_level	Chemoheterotroph
Rel_to_oxygen	Aerobe
Assembly_name	NA
Finishing_strategy	Draft;70.54x coverage; 308 contig
Annot_source	NA

The genome included 9,390 protein coding sequences out of 9,446 genes (Table 2) that were annotated by RAST server and by the methods described in the previous study (Aziz *et al.*, 2008; Kim *et al.*, 2017). The genome included 8 ribosomal RNA genes and 48 tRNA genes (Table 2). The most abundant feature of metabolic categories classified by the RAST system included genes involved in central metabolisms as well as stress responses, membrane transporters, antibiotic resistances (resistance to fluoroquinolones and β -lactamases), and heavy metal resistances (arsenic, cadmium, chromium, copper, mercuric,

Table 2. *Caballeronia sordidicola* strain PAMC 26633 genome summary

Attribute	Value
Genome size (bp)	9,746,569
No. of Contigs	308
DNA G + C content	59.5%
Total genes	9,446
tRNA genes	48
rRNA genes	8
Protein-coding genes	9,390

and zinc ions). Among carbohydrate-related genes, pentose phosphate pathway and gluconeogenesis were feasible. Semi-phosphorylative Entner-Doudorff pathway existed due to 2-dehydro-3-deoxy-phosphogluconate aldolases [EC:4.1.2.14 and EC:4.1.2.55]. TCA cycle and pyruvate-metabolizing anerplerotic reactions and acetogenesis could be annotated. Fermentation of pyruvate into ethanol/acetate or formate was impaired but lactate may be formed. Butanoate fermentation was impaired but poly- β -hydroxybutyrate formation and utilization genes were present. Monosaccharides including L-arabinose, L-fucose, L-rhamnose, Inositol, and mannitol could not be utilized, but mannose, D-arabitol, D-sorbitol, erythritol, ribitol, and xylitol could be utilized by pentose phosphate interconverting enzymes. Genes for nitrogen metabolisms included assimilatory nitrate and nitrite reduction but, there was no denitrification genes nor nitrogen fixation genes. ATP: adenylyl sulfate 3'-phosphotransferase reaction (3'-Phosphoadenosine 5'-phosphosulfate [PAPS]-forming) was missing in assimilatory sulfate reduction system, but this process was shunted by PAPS-forming dissimilatory adenylyl sulfate reductase reaction.

The ABC transporter genes were 95 in number and they were transporters for amino acids, dipeptides, oligopeptides, and phosphorus salts. Protein secretion systems were diversely presented (type I, II, and IV~VIII) except for type III. There was no sugar phosphotransferase system gene. Genes for potassium homeostasis, nitrogen, phosphate, and iron regulation could be found. Genes of diverse metabolic enzymes of the strain PAMC 26633 could be observed for lichen-dwelling bacterial genomes collected around polar environments (Kim *et al.*, 2017; Yang *et al.*, 2017a, 2017b). We used the CRISPRDetect program analysis (Biswas *et al.*, 2016) and there was no contig that had clustered regularly interspaced short palindromic

repeat (CRISPR) from the draft genome sequences of the strain PAMC 26633. There are 14 phage-related genes and transposable element genes could be annotated.

Nucleotide sequence accession numbers

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession MTHB00000000. The version described in this paper is version MTHB01000000.

적 요

본 연구에서 남극 킹 조지 섬 인근에서 채집한 지의류 *Psoroma* 종에서 분리한 *Caballeronia sordidicola* 균주 PAMC 26633의 초벌 유전체를 분석하였다. 이전의 연구를 통한 극지방의 지의류에 공생하는 *Caballeronia* 속 세균의 유전체와 마찬가지로 생물공학 및 생태학적으로 활용가능성 있는 다양한 유전자를 발견할 수 있었다. 이는 다양한 대사 관련 유전자를 포함하며, 탄수화물, 아미노산, 질소/황 대사, 스트레스, 세포막 수송체, 항생제 및 중금속 내성에 관련이 있었다. 파아지와 트랜스포존 유전자가 소수 있었으며, CRISPR 관련 유전자 및 서열은 발견되지 않았다.

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