

## Note (Genome Announcement)

# Genome sequence of *Caballeronia sordidicola* strain PAMC 26577 isolated from *Cladonia* sp., an Arctic lichen species

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## 북극 지의류 *Cladonia* 종에서 분리한 *Caballeronia sordidicola* 균주 PAMC 26577의 유전체 서열 분석

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*Caballeronia sordidicola* strain PAMC 26577 was isolated from *Cladonia* sp., a lichen collected from Svalbard Archipelago in the Arctic Ocean. Draft genomic sequences of PAMC 26577 were determined using Illumina and 182 contigs were submitted to GenBank and N50 value was 159,226. The genome of PAMC 26577 was comprised of 8,334,211 base pairs and %G+C content was 59.4. The genome included 8 ribosomal RNA genes and 51 tRNA genes as non-coding sequences. Protein-coding genes were 8,065 in number and they included central metabolism genes as well as butanol/butyrate biosynthesis, polyhydroxybutyrate metabolism, serine cycle methylotrophy genes, and glycogen metabolism. Membrane transporters were more than two-hundreds in number, but sugar phosphotransferase system and TRAP transporters were lacking. PAMC 26577 lacked CRISPR-associated sequences and proteins. No transposable elements were observed and there were only limited number of phage remnant regions with 11 phage-related genes.

**Keywords:** *Caballeronia sordidicola*, *Cladonia*, Arctic, genome, lichen

Cultivable sixty eight isolates from polar lichen species were investigated by 16S rRNA phylogenetic analysis and they were affiliated with the phyla *Actinobacteria*, *Bacteroidetes*, *Deinococcus-Thermus*, and *Firmicutes* and with the classes *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria* (Lee *et al.*, 2014). The strain PAMC 26577 was originally deposited at Polar and Alpine Microbial Collection (Lee *et al.*, 2012) and it was reported that the strain PAMC 26577 was identified as *Burkholderia sordidicola* in the class *Betaproteobacteria* based on 16S rRNA sequence analysis, and the strain was associated with a *Cladonia* species in previous study (Lee *et al.*, 2014). Distinct phylogenetic lineage from the genus *Burkholderia*, *Caballeronia* has been proposed for isolates from soil, wastewater-treatment system, fungus, or moss (Dobritsa and Samadpour, 2016) and we will use *Caballeronia sordidicola* as a species name of the strain PAMC 26577 that was isolated from a lichen species (Lee *et al.*, 2014).

Here we report the draft genome sequence of the strain PAMC 26577 in this study (Table 1). Strain PAMC 26577 was isolated from a lichen, *Cladonia* sp. collected from Svalbard Archipelago in the Arctic Ocean (Lee *et al.*, 2014). The draft

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genome sequence was determined using Illumina and assembly software was Ray software (v.2.3.1) as we used in previous methods (Kim *et al.*, 2017); assembly of genome analysis were carried out with 23-mer search option with the longest N50 and largest contig numbers. Bedtools (bedtools genomecov; aka “genomeCoverageBed” v. 2.25.0) (Quinlan and Hall, 2010) was used to calculate genome coverage; Illumina reads aligned in \*.bam file corresponded to 59.4x coverage depth (Table 1). Contigs with no CDS features and contigs shorter than 500 base pairs were excluded. Finally 182 contigs were submitted to GenBank and N50 value was 159,226. The draft genome of PAMC 26577 was comprised of 8,334,211 base pairs with

59.4% G+C content.

The genome included 8,065 protein coding sequences by the methods described in the previous study (Kim *et al.*, 2017). The genome included 8 ribosomal RNA genes and 51 tRNA genes. Numbers of metabolic genes involved in central metabolism of carbohydrate, amino acid, nucleotides, vitamins, and cofactors indicated that PAMC 2657 may be a metabolic generalist affiliated with lichen species. More than seven-hundred carbohydrate-related genes could be annotated and genes for butanol/butyrate biosynthesis genes and polyhydroxybutyrate (PHB) metabolism were presented as it was found among some *Betaproteobacteria* (Garrity *et al.*, 2005). Propionyl-CoA/propionate metabolism genes were well-conserved. Ribulose monophosphate pathway was missing but serine cycle methylotrophy genes existed for the ability to fix C<sub>1</sub>-compound. Polysaccharide metabolism genes included glycogen utilization genes. PAMC 26577 genome presented glycogen synthases, glycogen phosphorylase, amyloamylase, branching and debranching enzymes of glycogen. Chitinase could not be found but N-acetylglucosamine-6-phosphate gene could be annotated. Ammonia and nitrate assimilatory genes were presented. Stress genes included heat shock and cold shock protein encoding sequences as well as osmotic and oxidative stress genes were more than a hundred in number. Membrane transporter genes existed more than two hundreds in number and they included ABC transporters for branched amino acids and peptides, cation metal transporters (Mg, Ni, Co, and Cu ions), Ton and Tol transporter system, protein secretion system Type I,II,IV,V,VI,VII. Sugar phosphotransferase system and TRAP transporter were lacking.

By using the CRISPRDetect program analysis (Biswas *et al.*, 2016), there were no contigs that have clustered regularly interspaced short palindromic repeat (CRISPR) sequence of the strain PAMC 26577. No CRISPR-associated proteins could be annotated and no transposable elements were observed. There are phage remnant regions demarcated with 11 phage-related genes and they included four independent of phage tail genes.

#### Nucleotide sequence accession number(s)

This Whole Genome Shotgun project *Caballeronia sordidicola* strain PAMC 26577 has been deposited at DDBJ/ENA/GenBank under the accession NBTZ00000000. The version described in this paper is version NBTZ01000000.

**Table 1.** *Caballeronia sordidicola* strain PAMC 26577 genome assembly and its general features

Item	Description
Genome Assembly Data	
Assembly method	Ray v. 2.3.1
Genome coverage	59.4x
Sequencing technology	Illumina
MIGS Data	
Assembly	Ray v. 2.3.1
Biome	Lichen
Collection_date	2010-07-13
Env_package	missing
Feature	Lichen
Geo_loc_name	Europe: Norway, Svalbard
Investigation_type	bacteria_archaea
Isol_growth_condt	NA
Lat_lon	78.9121 11.95143333
Material	Lichen
Project_name	<i>Caballeronia sordidicola</i> PAMC 26577
Seq_meth	Illumina
Experimental_factor	NA
Depth	NA
Alt_elev	NA
Num_replicons	NA
Ref_biomaterial	NA
Source_mat_id	PAMC 26577
Pathogenicity	NA
Biotic_relationship	Symbiont
Trophic_level	chemoheterotroph
Rel_to_oxygen	aerobe
Assembly_name	NA
Finishing_strategy	draft;59.4x coverage; 182 contig
Annot_source	NA

## 적 요

*Caballeronia sordidicola* 균주 PAMC 26577은 다산 기지 근처에서 채집된 지의류인 *Cladonia* 종에서 분리되었다. Illumina 방식으로 분석한 균주 PAMC 26577의 초안 유전체 서열은 182개의 콘티그로 이루어졌으며, N50값은 159,226 염기쌍 길이에 해당하였다. 초안 유전체로 총 8,334,211 염기쌍을 확인하였으며, 59.4% G+C 함량을 나타냈다. 유전체는 단백질을 코딩하지 않는 8개의 rRNA 유전자와 51개의 tRNA 유전자를 포함하였다. 8,065개의 단백질 유전자는 기본 대사 과정뿐 아니라 부탄올/부티르산 생합성, 폴리하이드록시부티르산 대사, serine cycle methylotrophy 및 글라이코젠 대사 유전자들을 가지고 있었다. 2백개 이상의 막 전달 단백질은, 인산화 전달 시스템과 TRAP 전달시스템이 부재하였다. PAMC 26577은 CRISPR 관련 서열 및 단백질이 없었으며, 파아지 유전자의 감염흔적으로 인한 11개의 파아지 관련 유전자를 찾아낼 수 있었다.

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## References

- Biswas, A., Staals, R.H.J., Morales, S.E., Fineran, P.C., and Brown, C.M.** 2016. CRISPRDetect: A flexible algorithm to define CRISPR arrays. *BMC Genomics* **17**, 356.
- Dobritsa, A.P. and Samadpour, M.** 2016. Transfer of eleven species of the genus *Burkholderia* to the genus *Paraburkholderia* and proposal of *Caballeronia* gen. nov. to accommodate twelve species of the genera *Burkholderia* and *Paraburkholderia*. *Int. J. Syst. Evol. Microbiol.* **66**, 2836–2846.
- Garrity, G.M., Bell, J.A., and Lilburn, T.** 2005. Class II. Betaproteobacteria class. nov., pp. 575–922. *Bergey's manual® of systematic bacteriology*, Springer.
- Kim, J., Kwon, K.K., Kim, B.K., Hong, S.G., and Oh, H.M.** 2017. Genome sequence of *Caballeronia sordidicola* strain PAMC 26592 isolated from an arctic lichen species. *Korean J. Microbiol.* **53**.
- Lee, Y.M., Kim, G., Jung, Y.J., Choe, C.D., Yim, J.H., Lee, H.K., and Hong, S.G.** 2012. Polar and Alpine Microbial Collection (PAMC): a culture collection dedicated to polar and alpine microorganisms. *Polar Biol.* **35**, 1433–1438.
- Lee, Y.M., Kim, E.H., Lee, H.K., and Hong, S.G.** 2014. Biodiversity and physiological characteristics of Antarctic and Arctic lichen-associated bacteria. *World J. Microbiol. Biotechnol.* **30**, 2711–2721.
- Quinlan, A.R. and Hall, I.M.** 2010. BEDTools: a flexible suite of utilities for comparing genomic features. *Bioinformatics* **26**, 841–842.