



## Genome announcement

# Complete genome sequence of *Burkholderia* sp. strain PAMC28687, a potential octopine-utilizing bacterium isolated from Antarctica lichen



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## ARTICLE INFO

## Article history:

Received 18 March 2016

Accepted 22 March 2016

Available online 23 March 2016

## Keywords:

*Burkholderia* sp. PAMC28687

Complete genome sequence

Octopine

Antarctica lichen *Useea* sp.

## ABSTRACT

We report the complete genome sequence of *Burkholderia* sp. PAMC28687, which was isolated from the Antarctica lichen *Useea* sp., for better understanding of its catabolic traits in utilizing octopine as a source of carbon/nitrogen between *Burkholderia* and lichen. The genome consists of three circular chromosomes with five circular plasmids for the total 6,881,273 bp sized genome with a G + C content of 58.14%.

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*Agrobacterium* is a genus of bacteria that utilizes opines as nutrient sources as well as signals in order to activate its quorum sensing to further promote virulence and opine catabolism (Subramoni et al., 2014). The production of opines by crown gall tumor tissues provides the inciting *Agrobacterium* strain with a selective growth substrate that favors its propagation like a 'opine concept' (Bevan and Chilton, 1982). The several genes suspected of being involved in opine metabolism such as *ooxA*, *ooxB*, *noxA*, and *noxB* were reported as membrane-associated oxidases (Zanker et al., 1994), and some groups also elucidated diverse octopine dehydrogenases that catalyzed a reversible oxidation-reduction reaction of several octopine-type opines from a few bacteria (Dairi and Asano, 1995; Watanabe et al., 2015). Members of the versatile genus *Burkholderia* occupy a wide range of ecological niches with many forming mutualistic associations with fungi and plants and some are endosymbionts in plant-associated insects (Compant et al., 2008). Nevertheless, until now, there have been no reports about utilization of octopine related with the genus *Burkholderia*. Therefore, we report the complete genome of lichen-associated *Burkholderia* sp. strain PAMC28687.

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*Burkholderia* sp. strain (available from Korea Polar Research Institute for Polar and Alpine Microbial Collection, KOPRI PAMC28687) was isolated from the lichen *Useea* sp. collected on Barton Peninsula, King George Island, Antarctica (62°13'S, 58°47'W). Genomic DNA was extracted from *Burkholderia* sp. PAMC28687 using a QIAamp DNA Mini Kit (Qiagen Inc., Valencia, CA), and the quantity and purity were determined using an Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA). Genome sequencing was performed using PacBio RS II single-molecule real-time (SMRT) sequencing technology (Pacific Biosciences, Menlo Park, CA). Ten-kilobase SMRTbell library inserts were sequenced using SMRT cells. Raw sequence data were generated from 67,217 reads and 1,129,705,382 bp that were *de novo* assembled using the hierarchical genome-assembly process (HGAP) protocol (Chin et al., 2013) and RS HGAP Assembly 2 in SMRT analysis version 2.3 software (Pacific Biosciences; <https://github.com/PacificBiosciences/SMRT-Analysis>).

The complete genome of *Burkholderia* sp. PAMC28687 is made up of three circular chromosomes of each 3,260,450 bp, 1,696,029 bp and 1,495,500 bp with 60.30%, 60.2% and 60.3% G + C content, and five circular plasmids of 286,935, 62,715, 52,585, 20,973 and 6086 bp, respectively. The complete circular chromosome was 5,503,156 bp with a G + C content of 65.2%. Coding DNA sequences (CDSs) were predicted and annotated using the Rapid Annotation using Subsystem Technology (RAST) server (Aziz et al., 2008). Predicted gene sequences were translated and searched against National Center for Biotechnology Information (NCBI)

**Table 1**  
Genome features of *Burkholderia* sp. PAMC28687.

Features	Chromosome 1	Chromosome 2	Chromosome 3	Plasmid 1	Plasmid 2	Plasmid 3	Plasmid 4	Plasmid 5
Genome size (bp)	3,260,450	1,696,029	1,495,500	286,935	62,715	52,585	20,973	6086
Contig numbers	1	1	1	1	1	1	1	1
G + C content (%)	60.13	60.19	60.27	57.06	57.39	57.33	56.44	56.31
Protein coding genes	2.991	1.509	1.397	277	60	51	22	9
rRNA genes	12	–	–	–	–	–	–	–
tRNA genes	49	–	–	–	–	–	–	–

non-redundant database, Clusters of Orthologous Groups (COG), and Kyoto Encyclopedia of Genes and Genomes (KEGG). A total of 5867 CDSs were predicted; the coding region accounted for 86.52% of the genome. In addition, 4 rRNA operon and 49 tRNA were predicted in the complete genome (Table 1).

Sequence analysis of the genome of *Burkholderia* sp. PAMC28687 revealed the presence of various genes which are associated to opine-utilizing catabolic traits. These genes are flavin-containing opine dehydrogenases (*odhABC*) cassette containing 2-oxoglutarate dehydrogenase (*odhA*, AX768\_08780), dihydrolipoamide S-succinyltransferase (*odhB*, AX768\_08775), and dihydrolipoamide dehydrogenase (*odhC*, AX768\_08770), which are responsible for the nopaline production in the presence of artificial electron acceptors; opine oxidase subunit A (*ooxA*, AX768\_20795, AX768\_27590), opine oxidase subunit B (*ooxB*, AX768\_16340, AX768\_20765, AX768\_20790, AX768\_20825), and opine oxidase subunit C (*ooxC*, AX768\_16335, AX768\_20800, AX768\_27595) that are involved in the opine catabolism as membrane-associated oxidases; ornithine cyclodeaminase (*ocd*, AX768\_01050, AX768\_21115) which are need for the production of L-proline via L-ornithine. The availability of the *Burkholderia* sp. PAMC28687 complete genome sequence provides the genetic basis about opines-related catabolism in the genus *Burkholderia* under Antarctica lichen-symbiont environment.

#### Nucleotide sequence accession numbers

The complete genome information of *Burkholderia* sp. PAMC28687 was deposited in GenBank under the accession numbers CP014505–CP014514.

#### Acknowledgements

This work was supported by the Antarctic organisms: Cold-Adaptation Mechanisms and its application grant (PE16070) funded by the Korea Polar Research Institute.

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