Genome sequence of *Caballeronia sordidicola* strain PAMC 26510 isolated from *Psoroma* sp., an Antarctic lichen

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남극 지의류에서 분리한 *Caballeronia sordidicola* 균주 PAMC 26510의 유전체 서열 분석

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Caballeronia sordidicola strain PAMC 26510 was isolated from *Psoroma* sp., a lichen material, collected from Barton Peninsula of King George Island in Antarctica. The draft genome sequence of PAMC 26510 consisted of 224 contigs and they was 7,872,143 base pairs with 59.7% G+C content. The genome included 7,580 protein coding sequences and 6 ribosomal RNA genes and 46 tRNA genes. The strain PAMC 26510 is also a metabolic generalist as we have observed in previous genomic studies in the arctic strain of *Caballeronia sordidicola*. The draft genomic sequences of PAMC 26510 had six CRISPR arrays on six contigs, and there were two clusters of CRISPR-associated genes that were linked with respective CRISPR arrays.

Keywords: Caballeronia sordidicola, Psoroma species, Antarctic, lichen

The strain PAMC 26510 was identified as *Burkholderia sordidicola* based on 16S rRNA sequence analysis and the strain was associated with a *Psoroma* species (Lee *et al.*, 2012,

2014). The genus Burkholderia contains animal and plant pathogenic species, endophytes, and legume nodulators as well as environmental bacteria in soil and water (Angus et al., 2014). However the Burkholderia was proposed for animal and plant pathogens and a new generic name Paraburkholderia was coined to include so-called environmental isolates by the molecular typing and phylogenetic analysis (Sawana et al., 2014). The Caballeronia genus was proposed to include twelve Burkholderia and Paraburkholderia species with distinct phylogenetic lineage from the main phylogenetic lineages of Burkholderia and Paraburkholderia (Dobritsa and Samadpour, 2016). Members of the genus Caballeronia has been isolated from soil, wastewater-treatment system, fungus, or moss (Dobritsa and Samadpour, 2016). So the strain PAMC 26510 was assigned from Burkholderia sordidicola to Caballeronia sordidicola during the genome analysis.

Here we report the draft genome sequence of the strain PAMC 26510 (Table 1). It was isolated from *Psoroma* sp., a lichen collected from Barton Peninsula of King George Island in the Antarctic (Lee *et al.*, 2014). The draft genome sequence was determined using Illumina and was assembled with Ray

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Item	Description	
Genome Assembly Data		
Assembly method	Ray v. 2.3.1	
Genome coverage	54.5x	
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 Penninsula	
Investigation_type	bacteria_archaea	
Isol_growth_condt	NA	
Lat_lon	-62.22605 -58.78356667	
Material	Lichen	
Project_name	Caballeronia sordidicola PAMC 26510	
Seq_meth	Illumina	
Experimental_factor	NA	
Depth	NA	
Alt_elev	NA	
Num_replicons	NA	
Ref_biomaterial	NA	
Source_mat_id	PAMC 26510	
Pathogenicity	NA	
Biotic_relationship	Symbiont	
Trophic_level	chemoheterotroph	
Rel_to_oxygen	aerobe	
Assembly_name	NA	
Finishing_strategy	draft;54.5x coverage; 224 contigs	
Annot_source	NA	

 Table 1. Caballeronia sordidicola strain PAMC 26510 genome assembly

 and its general features

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 (121,862 bp) and 225 contigs. Bedtools (bedtools genomecov; aka "genomeCoverageBed" v. 2.25.0) (Quinlan and Hall, 2010) was used to calculate genome coverage (Kim *et al.*, 2017) and aligned Illumina reads corresponded to 54.5x coverage depth (Table 1). Finally 224 contigs were submitted to GenBank and the draft genome of PAMC 26510 was comprised of 7,872,143 base pairs with 59.7% GC content. One contig was filtered because it was contaminant sequence with no hits to any known nucleotides in the GenBank database.

The genome included 7,580 protein coding sequences annotated by the methods described in the previous study (Kim et al., 2017). Annotation of some genes of interest was confirmed using BLAST search tool against National Center for Biotechnology Information (NCBI) database. The genome had 6 ribosomal RNA genes (four 5S rRNA genes) and 46 tRNA genes. Major genes covered varieties of enzymes involved in metabolism of carbohydrate, amino acid, nitrogen/sulfur, aromatic compound, and vitamins. Glucose metabolism genes included Embden-Meyerhof-Parnas Pathway, Entner-Doudoroff Pathway, and Pentose phosphate pathway. Glycogen or starch metabolic genes and maltose phosphorylase and β-phosphoglucomutase were presented. Chitobiose could not be utilizable but Nacetylglucosamine could be processed by deacetylase and deaminases to glucose. PAMC 26510 had two kinds of lactate dehydrogenases that can form D-lactate and L-lactate from pyruvate from carbohydrate metabolisms. Acetyl-CoA fermentation to butyric acid is impaired because butanoyl-CoA dehydrogenase was missing for crotonyl-CoA that was converted from acetyl-CoA. Propanoate could be metabolized to succinate through propanoyl-CoA formation. Environmental response genes and regulators included stress response proteins, membrane transporters, antibiotic resistance genes, multidrug resistance efflux pumps, and heavy metal resistances. Twenty three phage-related genes were observed and there were three regions with transposable elements. Overall metabolic features were not different from PAMC26592 from the same species with poles apart location and different host lichen (Kim et al., 2017). By using the CRISPRDetect program for CRISPR array analysis (Biswas et al., 2016), there are several contigs that have clustered regularly interspaced short palindromic repeat (CRISPR) sequence on them, which is differentiating PAMC 26510 from previous arctic strain PAMC 26592 that had no CRISPR array (Kim et al., 2017). There are six CRISPR arrays by CRISPRDetect program and two contigs shared the same spacer sequences (GenBank Accessions: NBTY01000155.1 and NBTY01000222.1) (Table 2). CRISPR-related protein genes were adjacent to two contigs respectively (NBTY01000120.1 and NBTY01000155.1).

NITYII 0001200 1 2 200 34	Contig (Accession)	Position	Repeat	%identity	Spacer	Repeat sequence	Spacer sequence	Insertion/Deletion
NBTY0000201 2 00 34 0.00000000000000000000000000000000000	NBTY01000120.1	1	32	100	34		CATGCCACCGTACCCATGCCACCGTAATTTAGAT	[position]
Image: Section of the sectio		67	32	100	34		GAGCGGGCAATCGACGAGGTTCGAAGACCGGGGA	
98 92 90 93 94 95 94 95 94 95 94 95 94 95 94 95 94<		133	32	100	35		TCAAACTGGACTTCGGACAAATCGATTTCGACGGT	
9/7 27 00 9/4		200	32	100	35		GGTTGCTAGGGCGTGGGGCATACGCAAAACGCAAC	
937 937 938 <td></td> <td>267</td> <td>32</td> <td>100</td> <td>34</td> <td></td> <td>ACCTCGGCTTTAGAGGATGCAGCGAAAGCCGGAC</td> <td></td>		267	32	100	34		ACCTCGGCTTTAGAGGATGCAGCGAAAGCCGGAC	
Horis Jong Jong <thjong< th=""> Jong Jong <th< td=""><td></td><td>333</td><td>32</td><td>100</td><td>36</td><td></td><td>TATAGGTTCGACGCGCTACTCTGGGTCTACATATTC</td><td></td></th<></thjong<>		333	32	100	36		TATAGGTTCGACGCGCTACTCTGGGTCTACATATTC	
448 42 100 34		401	32	100	35		AGAGCACGGCCAACTCGTCCGACTACGGTCGTAGC	
94 32 100 33		468	32	100	34		CGCTGCCGACCGTATTGTCGATGAGGTGATCGAG	
99 30 100 35		534	32	100	33		CAATCCGGCCAGTTTCTCGGCGCCATCGTGGTA	
64 32 100 0 Control contro control contro control contro control control contro control con		599	32	100	33		CGCGCATTTCACCGCCGATATCGTTGCCTATGA	
171 32 100 0 GTTCAACCCAACGGGCCCGTGAAAAGCGGTGGGGAAAGCGGTGGGGAAGGGGGGGG		664	32	100	35		GATGGTAGCCGTTGCCGTTGAATCAAACGAATGGT	
NITYUUUUUUUU III 3 3 OPTICALCOADCOCCURAGUAGECEURGANAGECEURG 969 3 100 35		731	32	100	0			
NBT 100001.201 912 31 100 33	NDTW01000120 1	0725	32	100	35	GTTTCAACCCACGCGCCCGTGAAGAGCGCGAC		
Here 1 100 34	NB1Y01000120.1	9/25	31	100	35			
979 31 100 35		9659	21	100	34 24			
Main Main <th< td=""><td></td><td>0520</td><td>31</td><td>100</td><td>35</td><td></td><td></td><td></td></th<>		0520	31	100	35			
998 31 100 36		9463	31	100	34		GCTTGATCTCACGCGCGCGCGCGCGCGCGCGCGCGCGCGC	
931 31 98 35		9398	31	100	36		GCCGCCCGCAAAAAACAAGCTGTTGATTGACTACGA	
905 91 948 95 9		9331	31	100	35		CGACAATTCGTCGAGACGTGCGATACATCGGCTAA	
9/99 31 100 56		9265	31	96.8	35	C	TGAATTGTTGCTGGCCTTGGCTATCGCCAAAGCGC	
912 31 100 56		9199	31	100	36		ACCATCATGGCCGCGTGTGTGGACTCAGGCGGGCAC	
905 31 100 35		9132	31	100	36		GCCACTGGCCGGGGCTGTAGCGAAGCCATTTACACC	
Bit volume St.1 0		9065	31	100	35		TATCGGGGCCTATGGGTGTATGGCAGCAAGCCGTT	CGCGGGTG
III 31 98.7 35 GTCGCCTCCTCACGGCGCCTGGGTGGGTGGGTGGGTGGGT		8991	31	87.1	0	ATG		[9039]
NBTV01000155.1 505 28 100 32 Accesses Accesses <td></td> <td>12</td> <td>31</td> <td>98.7</td> <td>35</td> <td>GTCGCGTCCTCACGGGCGCGTGGGTTGAAAC</td> <td></td> <td></td>		12	31	98.7	35	GTCGCGTCCTCACGGGCGCGTGGGTTGAAAC		
S1515 28 100 32 TGACGATACACCAAGCGGGGATCTGTCAGCCCC NBTY0100022.1 1 26 9.29 32 GTTTGCTGCCGCAAGGCAGCCCGGGAGGAGGCAGGCGAGTCGGAAGGCAGCTGGATCA NBTY0100022.1 1 26 9.29 32	NBTY01000155.1	55095	28	100	32		AACCAGACACCACGCAGCGCAAAAAACATGGG	
5215 22 78.6 0		55155	28	100	32		TGACGATACACCAAGCGCGGATCTGTCAGCCC	
NBTY01000222.1 3 2 9TTTGCTGCCGCACAGGCACGGCACGGCACAGGCACAGGCACAGGCACAGGCACAGGCACAGGCACGGCACAGGCACGGCACAGGCACGGCACAGGCACGCACGGCACGGCACGCACGGCACGGCACGCACGGCACGGCACGCACGGCACGGCACGCACGGCACGGCACGCACGGCACGGCACGCACGGCACGCACGGCACGCACGGCACGCACGGCACGGCACGCACGGCACGCACGGCACGCACGGCACGGCACGCACGGCACGCACGGCACGCACGCACGGCACGGCACGCACGGCACGCACGCACGGCACGCACGCACGCACGGCACGCACGCCACGGCACGGCACGCCCGGCACGGCACGCCCGACGCACGCCACGCCACGGCACGACG		55215	22	78.6	0			
NBTY01000222.1 1 2.6 9.29 32		3	28	92.9	32	GTTTGCTGCCGCACAGGCAGCTCAGAAA		
Hom Second	NBTY01000222.1	1	26	92.9	32		ATGAGGATCGTGGACGGCACGTCTACCAACTT	
H19 28 100 32 GTCTTCCTCAACGACATAGCAGCGCCCATCG 179 28 100 32 ACCCCGAGGAGGCGAGGAGCTTGGGCGCCCATCG 239 28 100 32 ACCCCGAGGGGGGGGGGGGCGCACCCATCGGCGCCA 399 28 100 32 TCCAGCAGGGGGGCGCCCACCCTTGGCGGCGCCCCA 399 28 100 32 TCCAGCAGGCGGCCCGCCCCCCCCCCCCCCCCCCCCCCC		59	28	100	32		AGCGCGGCGTCATCGAAATGCAACTCGATGTA	
Image: Note of the second se		119	28	100	32		GTCTTGCTCAACGACATAGCAGCGCCCGATCG	
239 28 100 32		179	28	100	32		ACCCCGAAGGCATCGAAAAATTGAAGCCCATT	
299 28 100 32		239	28	100	32		ACAAACATATCGACCGATCAGCGCGTGGCCGC	
Alig 28 100 32 TTGCAGCGACAGCTTTGTCGATGATGTC 8 28 99.3 0 C. C Image: Comparison of the		299	28	100	32		AGAAGCCGAGGAGAGCTTTGAGGTGGCCGCCA	
Ho 28 97.3 0 Interference 8 28 97.8 32 GTTGCTGCCGCACAGGCAGCTCAGAAA NBTY01000194.1 56456 31 100 32 ATCATCTGTGAGGAGCGGCCCGCATCGTC 56519 31 100 33 TTCATGTAGGGACCCGCCTATTGTGGGGCGCCCTTTTT 56544 31 100 36 ACTTGAGCCCCCTATTGTGGGGGGGGGGGGGGGGGGGGG		359	28	100	32		TGCAGCAGCCCGACAGCTTTGTCGATGATGTC	
NBTY01000194.1 5645 51.0 52.0 FITECTOCCCALAGOCACCICANAGC NBTY01000194.1 56456 31 100 32		419	28	89.5	22			
NBT010001-A1 542	NRTV01000194.1	0 56456	20 31	97.0 100	32	GIIIGCIGCCGCACAGGCAGCICAGAAA	ATCATCTCCTCCACCACCCCCCCATCCTC	
5633 31 100 33	NB1101000194.1	56519	31	100	34		TTCATGTAAGCGGACCACTCATCGCCGCTCTTTT	
56648 31 100 35		56584	31	100	33		GATATTCGGTGCCGGCGTGGTTTCTGGGGACGG	
56714 31 100 36 AGCTTGCCTGATATGTGAGTATCGCCGCGCCCCCCCC 56781 31 100 36 GATGACAGTGACCGGCGGGGGGGGGGGGGGGGGGGGGCCCACGGGCC 56848 31 100 35 GTCGACGGCCGTAGCCGGGCGTGACCGGGGCGAAACG 56914 31 100 34 TTGCAACGGTCGCCGTTGACCGCGGCGCAACGGCGACGAACG 56980 31 100 34 GCAAGAAACTGGCGGGGCCCAACGGCGGCGAGGGGGG 57104 31 100 34 GCAAGAAACTGGCGGGGCCCAACGGCGGCGAGGGGGGGGG		56648	31	100	35		AGCTTGAGGCCCCTATCTATATGGGCGTTGAAACC	
56781 31 100 36		56714	31	100	36		AGCTTGCCTGATATGTGAGTATCCGCCGCCTCCGCC	
56848 31 100 35		56781	31	100	36		GATGACAGTGACCGGCGCGGGAGTGGCACCAGGCAC	
56914 31 100 35		56848	31	100	35		GTCGACGGCCGTAGCCGGGTTGATCTTGCCGCGCT	
56980 31 100 34 TTGCATCCAAAGCCCGTTGAGCCAATAAGCCGAC 57045 31 100 34 GCAAGAAACTCGCGCGGGCTCCACCGGCGTGAGGT 57110 31 100 35 GACACAGTCAGCAACTAGACGTCACCGCGCCCGAG 57176 30 96.8 0 GACACAGTCAGCAACTAGACGTCACCGCGCCCGAG 57206 31 64.5 4 CG.T.ATC.C.CCT GTGG Deletion [57241] 57214 31 100 36		56914	31	100	35		GTCCAAGCGGTCGCCAGTCTTCAACGTGCCAAACG	
57045 31 100 34		56980	31	100	34		TTGCATCCAAAGCCCGTTGAGCCAATAAGCCGAC	
57110 31 100 35		57045	31	100	34		GCAAGAAACTCGCGCGGCTCCACCGGCGTGAGGT	
57176 30 96.8 0		57110	31	100	35		GACACAGTCAGCAAACTAGACGTCACGCGCCCGAG	
57206 31 64.5 4 CG.TT.ATC.C.CCT GTGG Deletion [57241] 57241 31 100 36		57176	30	96.8	0		-	Deletion [57206]
57241 31 100 36		57206	31	64.5	4	CG.TT.ATC.CCT	GTGG	Deletion [57241]
57308 31 100 0		57241	31	100	36		GCCGCCCGCAAAAAACAAGCTGTTGATTGACTACGA	
15 31 97.4 30 GTCGCGTCCTCACGGGCGCGTGGGTTGAAAC NBTY01000066.1 123058 32 100 36 TTCAATAGTTCAATGTTCATTAACCTCCCAATAAGC 122900 32 100 36 CATGCGAGCCACCGTAATCGGTCCGCCCGATACCG 122922 32 100 35 CATGCGAGCAATCGGCGCGTCATCAGTTCGGCCGGGC 122855 32 96.9 35 TTCAATAGTCCAACCTGACGCGGCGGTGACGGGGGGCAA 122788 32 100 35 TGCAACGCTCGACAACGGCGGATGCGGTTATCACG 122781 32 100 34 TTCCAATAGTTCACGGTGTCATCGGGGTGCAAAGG 122721 32 100 34 TTCCAATGGCGCGTGAAGGTGCGATCAAGGTCGAAAGG 122655 32 90.6 0 TTCCAATCAGGCGTGTGAAAG 122655 32 98.2 35 GTCGCGCTCTCACGGCGCGGGTGTGGTGTGAACG		57308	31	100	0			
NB1Y01000006.1 123058 52 100 36 TTCAATAGTTCAATAGTTCAATTAACCTCCCAATAAGC 122900 32 100 36 CATGCGAGCCACCCGTAATCCGTCCGCCCGATACCG 122922 32 100 35 CATGCGAGCCACCCGTAATCCGTCCGCCGATACCG 122855 32 96.9 35 TTCAATAGCTCGACCACGGAGCAACCTGACGCGGTGACGGGGAGCAA 122788 32 100 35 TGCCAACGCTCGACAACGGCGATGCGGTTATCACG 122711 32 100 34 GTGGGCAATATCTACGGTGTCATCGGGATCAAAG 122655 32 90.6 0 A.C.G. C C [122625] 7 32 98.2 35 GTCGCGCTCTTCACGGGGGTGTGAGCG C [122625]		15	31	97.4	30	GTCGCGTCCTCACGGGCGCGTGGGTTGAAAC		
122990 32 100 36 CATGCGAGCCACCCGTAATCCGTCCGGCGCGTAACCG 122922 32 100 35 GAATCCAGCAACCCGTAATCCGTCCGGCGCGGC 122855 32 96.9 35 TGAAGCGCATCAACCTGACGCGGGGGCGCGCGGGGGGGGG	NBTY01000066.1	123058	32	100	36			
122722 32 100 35 GAATCCAGCAATGCGCGTCATCAGTTCGGGGCGCGGG 122855 32 96.9 35 TGAAGCGCATCAACCTGACGCGGGGGGGGGGGGGGGGGG		122990	32	100	36 25	•••••		
122055 32 90.7 55 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		122922	32 32	06.0	35 35			
122721 32 100 34		122633	32	100	35	· · · · · · · · · · · · · · · · · · ·	I GAAGUGUAI CAAUUIGUUGGTGAUGGAGUAA	
122655 32 90.6 0		122700	32	100	34		GTGGGCAATATCTACGGTGTCATCGCGATCAAAGGCCGAATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAATCAAAGGCCGAAAGGGCCGAATCAAAGGCCGAACGAA	
7 32 98.2 35 GTCGCGCTCTTCACGGGCGCGTGGGTTGAAAC		122655	32	90.6	0	A C C		C [122625]
		7	32	98.2	35	GTCGCGCTCTTCACGGGCGCGTGGGTTGAAAC	!	- [-22020]

Table 2. CRISPR array list from draft genome of C. sordidicola strain PAMC 26510 in this study: (.) consensus sequences, (-) missing sequences

Korean Journal of Microbiology, Vol. 53, No. 2

Nucleotide sequence accession number(s)

This whole genome shotgun project has been deposited under the accession NBTY00000000 at GenBank. The version described in this paper is version NBTY 01000000 (NBTY 01000001-NBTY01000224). Small subunit rRNA sequence of *Caballeronia sordidicola* strain PAMC 26510 was deposited at GenBank under accession number KJ606826 according to previous study.

적 요

Caballeronia sordidicola 균주 PAMC 26510은 남극 킹조 지섬의 바톤반도에서 채집된 지의류인 Psoroma sp.에서 분리 되었다. 균주 PAMC 26510의 초안 유전체 서열은 224개의 콘 티그로 이루어졌으며, 총 7,872,143 염기쌍은 59.7% G+C 함 량을 나타냈다. 유전체는 7,580개의 단백질 유전자, 6개의 rRNA 유전자와 46개의 tRNA 유전자를 포함하였다. 균주 PAMC 26510는 이전에 연구한 Caballeronia sordidicola에 속 하는 북극 균주와 마찬가지로 대사능력에 있어서 광범위한 능 력을 가지고 있는 것으로 여겨진다. PAMC 26510의 초안 유전 체는 6개의 CRISPR arrays를 각각의 콘티그 상에 가지고 있으 며, 이중 두 개의 콘티그 상에 CRISPR-관련 유전자가 연결되 어 있었다.

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