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Draft genome sequence of *Aurantimonas coralicida* DM33-3 isolated from Amundsen Sea Polynya

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아문젠해 폴리냐로부터 분리된 *Aurantimonas coralicida* DM33-3의 유전체 분석

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Here, we report the draft genome sequence of *Aurantimonas coralicida* DM33-3 isolated from Amundsen Sea Polynya. The genome size is 4,620,302 bp, 4,415 coding sequences, one rRNA operon (additionally two 5S ribosomal RNA genes), and 45 tRNA genes. Genes related to manganese oxidation and thiosulfate oxidation are also included in the genome. The genome harbors genes coding for enzymes having varying affinities to oxygen and nitrate reduction. This showed that strain DM33-3 might play the potential role in biogeochemical cycling (manganese, sulfur and nitrogen cycle) in the Amundsen Sea Polynya.

Keywords: *Aurantimonas coralicida*, Antarctica, Polynya

Manganese is an abundant element in the Earth's crust and plays a key role in biogeochemical cycles. Some microorganisms are known to be associated with the manganese cycle. Recently, the first chemolithotrophic manganese oxidizer was isolated, and its genomic properties were reported (Yu and Leadbetter, 2020). Previously, only heterotrophic manganese-oxidizing bacteria were known (Nealson, 2006). One strain, *Aurantimonas manganoxydans* SI85-9A1, is a known heterotrophic Mn(II) oxidizer that produces Mn(III/IV) oxides (Dick *et al.*, 2008). The genus *Aurantimonas* has been isolated from various environments such as deep-sea sediment (Li *et al.*, 2017), marine (Anderson *et al.*, 2009), cave (Jurado *et al.*, 2006), coral (Denner *et al.*, 2003), root (Liu *et al.*, 2016), and air (Weon *et al.*, 2007). DM33-3 was isolated from a water column of the Amundsen Sea Polynya, Antarctica. For preparation of inoculum, microbial cells from the seawater were collected under vacuum through a sterile membrane filter (pore diameter of 0.2 μm, Adcantec Tokyo) and was incubated in marine broth (Difco) at 15°C. To obtain isolate, the enrichment culture was spread on marine agar 2216 (MA; Difco). Among the colonies, a bacterial strain was isolated and purified. Its cells were routinely cultured at 25°C on MA and deposited at the Korea Culture Type Collection (KCTC) as KCTC 72499.

DNA was extracted using a DNeasy Blood & Tissue Kit (Qiagen) for genome sequencing. The DNA library was prepared using the TruSeq DNA Nano kit and the genome sequencing was performed using Illumina Hiseq 6000 at Microgen. Automated annotation was performed using the

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Table 1. Genomic features of *Aurantimonas coralicida* DM33-3 and related strains

Description	*A. coralicida* DM33-3	*A. coralicida* DSM14790	*A. manganoxydans* SI85-9A1
Size (bp)	4,620,302	4,615,647	4,325,257
GC content	66.6	66.7	66.7
Number of contigs	49	38	35
Number of coding genes	4,415	4,275	3,650
rRNA (5S, 16S, 23S)	3, 1, 1	3, 1, 5	3, 3, 3
tRNA	45	48	50
Accession number	JACSGS010000000	ATXK01000000	AAPJ01000000

NCBI Prokaryotic Genome Annotation Pipeline. Bacterial universal primers 27F and 1492R were used to amplify 16S rRNA gene sequence (Lane, 1991). The similarity of 16S rRNA gene was conducted using EzBioCloud (Yoon *et al.*, 2017). 16S rRNA gene analysis revealed that the isolate had 100% similarity with *Aurantimonas coralicida* DSM14790. Digital comparisons of genomic sequence of strain DM33-3 and DSM14790, ANI and AAI were analyzed by JSpiecesWS and compareM, respectively. The ANI and AAI values were 97.8% and 96.1%, respectively. Based on the value of species boundaries (Konstantinidis and Tiedje, 2005; Konstantinidis *et al.*, 2006), strain DM33-3 is considered a new strain of *Aurantimonas coralicida.*

The genomic size of *Aurantimonas coralicida* DM33-3 is 4,620,302 bp with 49 scaffolds and 66.6% of the G + C content. The coverage of the genome is 286.0×. Total genes are predicted to be 4,423, with one ribosomal operon (Table 1). The genome has complete glycolysis and TCA cycle. Similar to *Aurantimonas manganoxydans* SI85-9A1, the manganese oxidizer, duplicate manganese-oxidizing related gene cluster (H9Q09_15580 - 15610 and H9Q09_20460 - 20480) and RubisCO (H9Q09_17670 - 17675) are found in this genome. However, the function of RubisCO in *A. manganoxydans* SI85-9A1 is unclear (Caspi *et al.*, 1996). Strain DM33-3 contains the sox gene cluster (SoxGTRSVWXYZABCD; H9Q09_00175 - 00235). These genes are also found in the genome of DSM14790. This might support the growth of strain DM33-3 with thiosulfate oxidation in the environment.

The genome includes one cytochrome *bd*-type quinol oxidase (H9Q09_17750 - 17755; high affinity for oxygen), two cbb_3-type cytochrome *c* oxidases (H9Q09_01970 - 02005 and H9Q09_21295 - 21310; high affinity for oxygen), and three cytochrome *c* oxidases (H9Q09_04305 - 04310, H9Q09_12435 - 12455, and H9Q09_21985 - 22005; low affinity for oxygen). Compared with DSM 14790, the genome of strain DM33-3 had an additional cbb_3-type cytochrome *c* oxidase. Furthermore, genes related to respiratory nitrate reductase (H9Q09_21845 - 21860) are observed in this genome, which are absent in the genomes of *A. manganoxydans* SI85-9A1 and *A. coralcida* DSM14790. This shows that strain DM33-3 might live at various oxygen levels and under anaerobic conditions. The genome also contains heavy metal detoxification systems such as arsenic reductase (H9Q09_03245 - 03260) and mercury reductase (H9Q09_09930 - 09945).

Taken together, strain DM33-3 may adapt various environments by thiosulfate oxidation, a wide range of oxygen respiration, and heavy metal detoxification compared to previous isolates. Thus, this report provides new insights into the ecology of manganese-oxidizing groups from the Amundsen Sea Polynya.

Nucleotide sequence accession number(s)

The genome of *Aurantimonas coralicida* DM33-3 has been deposited in NCBI under accession number JACSGS0100 00000. Strain DM33-3 is deposited at KCTC as KCTC 72499.

적 요

아문젠해 폴리냐로부터 분리한 *Auramtimonas coralicida* DM33-3 균주의 유전체 정보를 제공한다. 이 유전체는4,620,302 bp, 4,415개의 단백질 코딩 유전자, 1개의 rRNA 오페론, 45개의 rRNA를 가진다. 망간과 티오황산염 산화 유전자가 발견되었다. 또한 다양한 산소 친화도를 가지는 말단산화 효소와 질산염

환원 효소를 암호화하는 유전자를 포함하고 있다. 이는 아문젠 해 폴리냐에서 DM33-3 균주가 생지화학적 순환(망간, 황, 질소 순환)에 다양한 잠재적 역할을 할 수 있음을 보여 준다.

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Conflict of Interest

The authors have no conflicts of interest to report.

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