

Genome Announcement

Complete genome of a denitrifying *Halioglobus* sp. RR3-57 isolated from a seawater recirculating aquaculture system

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순환여과양식시스템으로부터 분리된 *Halioglobus* sp. RR3-57의 유전체 분석

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Halioglobus sp. RR3-57 was isolated from a biofilter of a seawater recirculating aquaculture system and its complete genome sequence was obtained using the PacBio RS II platform. Two circular contigs were assembled and considered as a chromosome and a plasmid (size of 4,847,776 bp and 155,799 bp, and G+C content of 57.5% and 53.2%, respectively). Genomic analysis showed RR3-57 had 18 denitrification-related genes and an incomplete prophage.

Keywords: *Halioglobus*, complete genome, denitrification, seawater recirculating aquaculture system

Recirculating aquaculture systems (RASs) are closed-loop aquaculturing facilities where waste water from rearing tanks is removed by mainly microbial community and nitrogenous compounds are degraded and transformed by nitrifying and denitrifying bacteria in biofilters (Leonard *et al.*, 2000). In that process, nitrate is reduced to nitrogen (N₂) or nitrous oxide (N₂O) through a process called denitrification (Ward, 1996). For identification of denitrifying bacteria, bacteria were isolated from biofilters in a seawater RAS operated in National Institute of Fisheries Science (NIFS), Busan, South Korea (Lee *et al.*,

2016). Bacterial strains were cultivated on a modified denitrification medium (Wu *et al.*, 2013) at 25°C for 7 days. Among isolated strains, a Gram-negative, aerobic bacterium, the strain RR3-57 showed 96.2% of 16S rRNA gene similarity with *Halioglobus pacificus* S1-72^T. The genomic DNA of the *Halioglobus* sp. RR3-57 was extracted and purified using MagAttract[®] High-Molecular-Weight Genomic DNA Kit (QIAGEN) and PacBio RS II platform (Pacific Biosciences) was used for whole genome sequencing. Sequence reads obtained were assembled by PacBio Hierarchical Genome Assembly Process (HGAP, Version 3.0) and two contigs were generated (Chin *et al.*, 2013). Total 5,003,575 bp were obtained with two circular structures representing a chromosome and a plasmid (Fig. 1). Total 4,599 coding sequences including 43 tRNAs and 6 rRNAs were annotated by the Rapid Annotation using Subsystem Technology (RAST) pipeline (Aziz *et al.*, 2008). The genome of *Halioglobus* sp. RR3-57 (contig 1) encoded 37 predicted nitrogen metabolism-related genes and among them, 18 genes were associated with denitrification, such as respiratory nitrate reductase, cytochrome cd1 nitrite reductase and nitric oxide reductase which reduce nitrate to nitrite, nitrite to nitric oxide and nitric oxide to dinitrogen oxide sequentially. However, nitrous oxide reductase gene was missing.

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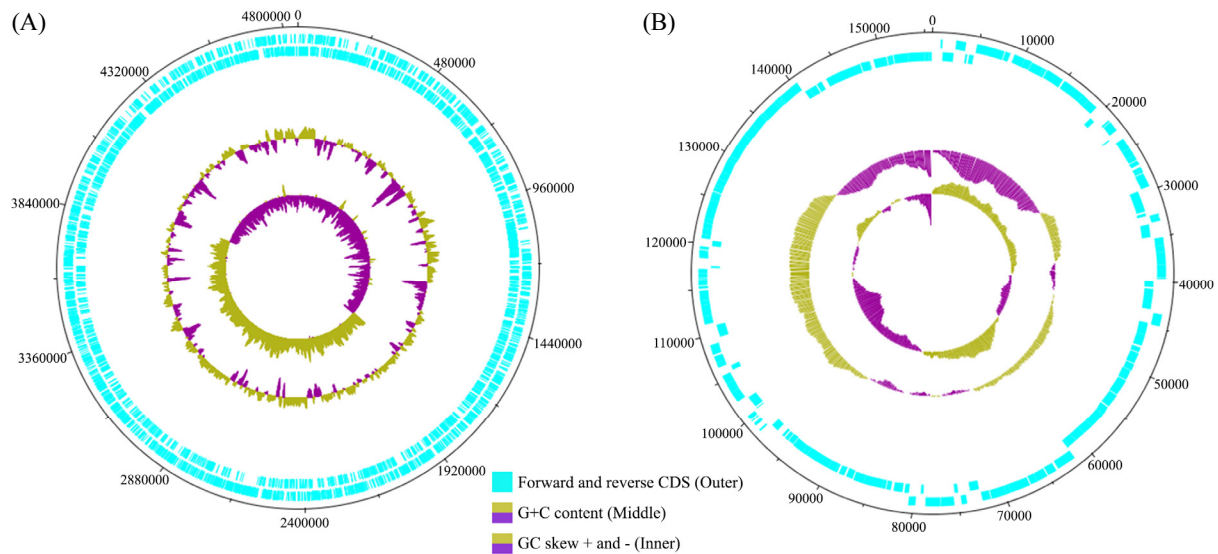


Fig. 1. Circular map of contig 1 (A), contig 2 (B). Marked characteristics are shown from outside to the center: CDS on forward strand, CDS on reverse strand, GC content, and GC skew.

Table 1. Genome features of *Halioglobus* sp. RR3-57

Genome features	Value	Value
Contig	1	2
Sequencing depth (X)	285	315
Genome size (bp)	4,847,776	155,799
G+C content (%)	57.5	53.2
Protein coding sequences	4,410	140
tRNAs	43	0
rRNAs	6 ^a	0
Coding percentage ^b	89.6	82.0

^a Two operons of 16S rRNA genes

^b (Total length for coding sequences)/(length of each contig)

The PHAge Search Tool (PHAST) web server was used to identify prophage (Zhou *et al.*, 2011) and one incomplete prophage was detected with 13.2 kb in size and 47.8% G+C content containing 13 CDS.

Complete genome analysis of *Halioglobus* sp. RR3-57 will provide us a useful approach for understanding nitrogen metabolism in the RAS, but also additional tests will be required to fully appreciate this strain.

Acknowledgements

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Accession numbers of *Halioglobus* sp. RR3-57

The strain was deposited in KCTC under the deposit number KCTC 52652. The sequences for the chromosome and the plasmid of *Halioglobus* sp. RR3-57 are accessible in GenBank under the accession number CP019046 and CP019045, respectively.

적 요

Halioglobus sp. RR3-57는 해수순환여과양식시스템의 생물여과조에서 순수분리되었으며, PacBio RS II 서열분석법을 이용하여 전체 유전체 서열이 해독되었다. 그 결과 길이 4,847,776 bp, G+C함량 57.5%인 염색체와 155,799 bp, 53.2%인 플라스미드로 구성된 유전체 서열을 획득하였다. 유전체 분석결과 탈질작용에 관련된 18개의 유전자와 불완전한 프로파지(prophage)로 추정되는 유전자서열이 확인되었다.

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