

## Genome Announcement

# Genome sequence of the strain RR3-28 isolated from a seawater recirculating aquaculture system and related to the genus *Nitratireductor*

Eun Soo Noh<sup>1</sup>, Young-Sam Kim<sup>2</sup>, Da-Eun Lee<sup>2</sup>, and Kyoung-Ho Kim<sup>2\*</sup>

<sup>1</sup>Biotechnology Research Division, National Institute of Fisheries Science, Busan 46083, Republic of Korea

<sup>2</sup>Department of Microbiology, Pukyong National University, Busan 48513, Republic of Korea

## 해수순환여과양식시스템에서 분리된, *Nitratireductor* 속과 관련된 균주 RR3-28의 유전체 서열

노은수<sup>1</sup> · 김영삼<sup>2</sup> · 이다은<sup>2</sup> · 김경호<sup>2\*</sup>

<sup>1</sup>국립수산과학원 생명공학과, <sup>2</sup>부경대학교 미생물학과

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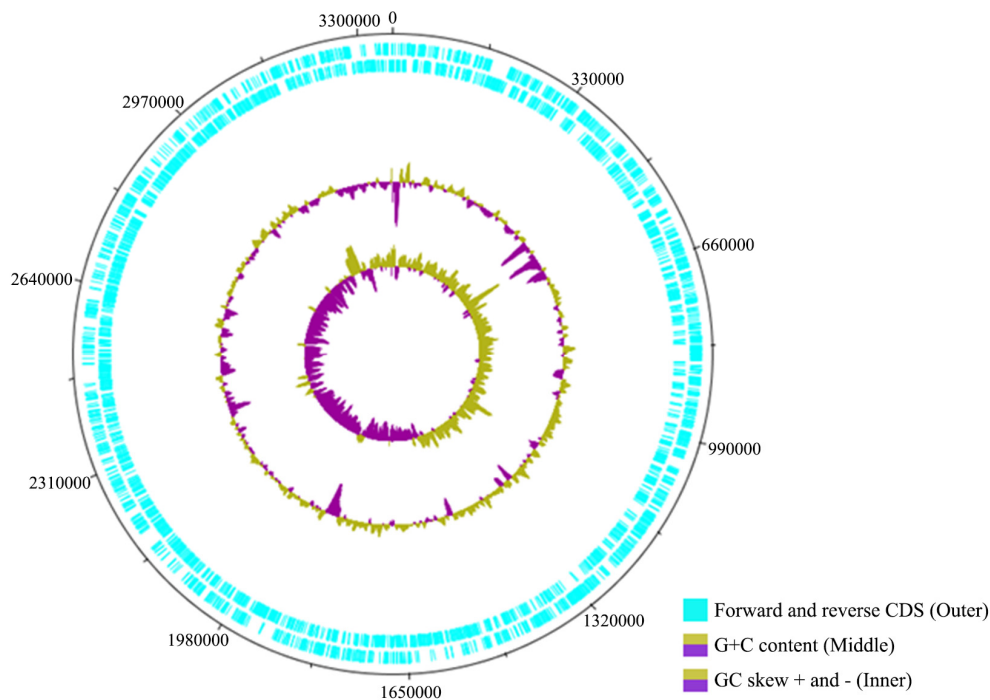
Complete genome sequences were retrieved from the strain RR3-28 that was isolated from a seawater recirculating aquaculture system and related to the genus *Nitratireductor*. The genome sequence consists of a single, circular chromosome of 3,357,577 bp with 58.6% G+C content. The genome was identified to contain twenty-one genes related to denitrification and one intact prophage.

**Keywords:** *Nitratireductor*, genome sequencing, recirculating aquaculture system, RR3-28

Inland aquaculture systems are less affected by sea environments. However, they are not completely independent of sea environments because of massive seawater requirements. The recirculating aquaculture system (RAS) is a sea-independent aquaculture system which recirculates used seawater without additional supplement to the system. In the RAS, eliminating toxic nitrogen byproducts such as ammonia and nitrate which are generated by farmed fish is the most important process and this process is mainly done by nitrifying and denitrifying

bacteria in biofilters (Leonard *et al.*, 2000). As a part of surveying denitrifying bacteria, we isolated a Gram-negative, aerobic, and nitrate-reducing bacterium RR3-28 from a biofilter in a seawater RAS operated in National Institute of Fisheries Science (NIFS), Busan, South Korea (Lee *et al.*, 2016) using a modified denitrification medium (Wu *et al.*, 2013) after incubation at 25°C for 7 days. The strain RR3-28 showed 95.5% of 16S rRNA sequence similarity with *Nitratireductor basaltis* J3<sup>T</sup>. Genomic DNA extraction of RR3-28 was done using MagAttract<sup>®</sup> High-Molecular-Weight Genomic DNA Kit (QIAGEN) and genome sequencing was performed by PacBio RS II platform (Pacific Biosciences). A total of 133,792 sequence reads was obtained and assembled using PacBio Hierarchical Genome Assembly Process (HGAP, Version 3.0) (Chin *et al.*, 2013). Single contig was 3,357,577 bp in length, and the G+C content was 58.6%. Rapid Annotation using Subsystem Technology (RAST) pipeline (Aziz *et al.*, 2008) estimated total 3,458 protein coding sequences, 3 rRNAs (1 copy of rRNA operon) and 41 tRNAs (Table 1). Twenty-one genes were associated with denitrification metabolism among thirty four nitrogen metabolism-related genes. An intact prophage sequence was also detected with 15.8 kbps in size and 61.2%

\*For correspondence. E-mail: kimkh@pknu.ac.kr;  
Tel.: +82-51-629-5611; Fax: +82-51-629-5619



**Fig. 1.** Circular map of the *Nitratireductor* sp. RR3-28. Marked characteristics are shown from outside to the center: CDS on forward strand, CDS on reverse strand, GC content, and GC skew.

**Table 1.** General genomic features of the strain RR3-28

Genomic features	Value
Contig	1
Sequencing depth (X)	153
Genome size (bp)	3,357,577
G + C content (%)	58.6
Protein coding sequences	3,458
tRNAs	41
rRNAs	3

G+C content encoding 22 CDSs by PHAge Search Tool (PHAST) (Zhou *et al.*, 2011).

The complete genome of the strain RR3-28 will contribute to understanding of nitrogen metabolism and denitrification process in the RAS, however, additional studies will be necessary to understand this strain.

#### Accession numbers of *Nitratireductor* sp. RR3-28

KCTC deposit number of *Nitratireductor* sp. RR3-28 is KCTC 52649 and the complete genome sequence can be accessed under the accession number CP019044 in GenBank.

## 적 요

해수순환여과양식시스템에서 분리된 *Nitratireductor* 속과 관련된 균주 RR3-28의 전체 유전체 서열을 해독하였다. 그 유전체는 3,357,577 bp, 58.6% G+C 함량을 가진 하나의 원형의 염색체로 구성되었다. 유전체 분석을 통해 21개의 탈질대사 관련 유전자와 하나의 온전한 프로파지도 확인되었다.

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