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Genome Announcements

Complete genome sequence of the aerobically denitrifying thermophilic bacterium *Chelatococcus daeguensis* TAD1

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ABSTRACT

Chelatococcus daeguensis TAD1 is a thermophilic bacterium isolated from a biotrickling filter used to treat NO_x in Ruiming Power Plant, located in Guangzhou, China, which shows an excellent aerobic denitrification activity at high temperature. The complete genome sequence of this strain was reported in the present study. Genes related to the aerobic denitrification were identified through whole genome analysis. This work will facilitate the mechanism of aerobic denitrification and provide evidence for its potential application in the nitrogen removal.

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Denitrification conducted by many organisms plays a critical role in the nitrogen cycle, which is conventionally considered to be occurred anaerobically. However, some microorganisms were found to have the capacity of aerobic denitrification, such as *Klebsiella pneumoniae* CF-S9,¹ *Vibrio diabolicus* SF16,² *Anoxybacillus contaminans* HA,³ *Pseudomonas tolaasii* Y-11,⁴ *Cupriavidus* sp. S1⁵ and so on. Due to much higher growth rate than autotrophs and capability of utilizing various substrates, these bacteria have attracted more and more attention. Nevertheless, the aerobic denitrification mechanism with respect to functional genes has not been

clarified. In addition, the research on the aerobic denitrification mechanism at high temperature was seldom reported. *Chelatococcus daeguensis* TAD1 that can use a variety of carbon sources to denitrify aerobically at high temperature was isolated from a biotrickling filter used to treat NO_x in Ruiming Power Plant, located in Guangzhou, China.⁶ In order to gain insights about genetic elements involved in aerobic denitrification properties and to further identify the nitrogen removal activity of this strain, we performed genome sequencing and hereby present the complete genome sequence of *C. daeguensis* TAD1.

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Table 1 – Features of *Chelatococcus daeguensis* TAD1 genome.

Attributes	Values
Genome size (bp)	4,095,174
GC content (%)	68.34
Plasmid	1
rRNAs	6
tRNAs	48
ncRNA	55
CDSs	3889

Genomic DNA from TAD1 was extracted with standard genomic DNA isolation methods. Sequencing was performed using the PacBio RS II (Pacific Biosciences, USA) by constructing a 20 kb insert library at NOVOGENE (Beijing, China), and 366,577,965 bp were generated from 57,631 subreads. The N50 subread sequence length was 8695 bp. For sequence assemblies, SMRT Analysis Software (Pacific Biosciences, USA) was used. One complete circular chromosome and one complete circular plasmid were generated. Genome annotation was performed using GeneMarkS software (<http://topaz.gatech.edu/>).

The complete genome sequence of TAD1 consists of a circular 3.56 Mb chromosome and a circular 0.5 Mb plasmid, with GC contents of 67.85% and 68.12%, respectively (Table 1). The count of predicted protein-coding sequences is 3889, and the genome comprises 48 tRNA genes and 6 tRNA operons (Table 1). We identified four genes (*napA*, *nirK*, *norB* and *nosZ*) involved in the aerobic denitrification, encoding nitrate reductase, nitrite reductase, nitric oxide reductase and nitrous oxide reductase, respectively. As a facultative thermophile, the strain TAD1 grows optimally at 45–50, and possesses a good performance of nitrogen removal.^{7,8} It is well known that emissions from some industries, especially in Power Plant where the temperature of flue gas (NO_x) is high and a certain concentration of oxygen exists in NO_x, are harmful to those microorganisms at room temperature, indicating that thermophilic bacteria are necessary for the efficient nitrogen removal under aerobic conditions. Therefore, the genes relating to the aerobic denitrification activity of this strain were enough to evaluate its application in those industries with high temperature of emissions.

The complete genome sequence of *C. daeguensis* TAD1 will enrich the sources of thermostable denitrifying enzymes, facilitate the aerobic denitrification mechanism and eventually exhibit basic information for wider exploitation of this strain in nitrogen removal.

The complete genome sequence of *C. daeguensis* TAD1 was deposited at GenBank under accession number CP018095–CP018096. This strain has been deposited in China General Microbiological Culture Collection Center (CGMCC no. 5226).

Conflict of interest

We declare that we have no conflict of interest.

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