

# Complete Genome Sequence of *Brevibacterium linens* BS258, a Potential Marine Actinobacterium for Environmental Remediation via Microbially Induced Calcite Precipitation

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## Abstract

*Brevibacterium linens* BS258 is a urease positive actinobacterium isolated from marine sediment of China Yellow Sea, which demonstrated to have strong capability of calcite precipitation and bioremediation of heavy metal pollution. Here, we report the complete genome sequence of this strain, which might provide a lot of valuable information for environmental remediation, wastewater treatment and atmospheric CO<sub>2</sub> sequestration.

**Keywords:** Complete genome; *Brevibacterium linens*; Remediation

## Introduction and Results

Microbially induced carbonate precipitation (MICP), a widespread process among microorganisms, has been widely exploited in biotechnology, with applications in the remediation of metal contaminated soil and groundwater [1,2], long-term atmospheric CO<sub>2</sub> sequestration [1], the strengthening and consolidation of soil and sand [3], the reduction of the porosity of geological formations [4], the protection and repair of concrete and cement structures [5], and the conservation of monumental calcareous stones [6]. This kind of carbonate precipitation is often associated with pathway of the nitrogen cycle, especially ammonification of amino acids, nitrate reduction and urea degradation [7]. However, the exact role of bacteria in this process remains unclear. Actinobacterium *Brevibacterium linens* BS258 is a urease positive strain isolated from marine sediment of China Yellow Sea. Our previous study demonstrated that *B. linens* BS258 had strong capability of calcite precipitation, and could effectively remove heavy metal ions such as manganese and strontium. The genome sequence of *B. linens* BS258 will provide further understanding about the potential biotechnological applications

In order to understand properties of *B. linens* BS258 and exploit its potentials, the whole genome was sequenced by PacBio single molecule real time sequencing technology with a 10 kb SMRTbell library. A total of 92,575 long reads (1,330,998,188 bp) were obtained where the N50 Read Length was 20,542 bp. Reads were assembled using SMRT Analysis 2.3.0. Coding genes were annotated by Prokaryotic Genome Annotation Pipeline (PGAP) version 2.10 software on NCBI ([https://www.ncbi.nlm.nih.gov/genome/annotation\\_prok/](https://www.ncbi.nlm.nih.gov/genome/annotation_prok/)) and Rapid Annotation using Sub-system Technology (RAST: <http://rast.nmpdr.org/>) server [8]. Additional functional annotation was performed with 5 databases, they are KEGG (Kyoto Encyclopedia of Genes and Genomes) [9], COG (Cluster of Orthologous Groups) [10], NR (Non-redundant Protein Database), GO (Gene Ontology) [11] and Swiss-Prot [12]. The tRNA genes and rRNA genes were annotated with tRNAscan-SE v1.23 [13] and rRNAmmer 1.2 [14], respectively.

The genome of *B. linens* BS258 consists of one circular chromosome of 3,862,244 bp with a 64.16% G+C content. The genome contained 3437 genes with the total length of 3,452,700 bp, which makes up 89.4% of genome. 47 tRNA genes and 12 rRNA genes were detected (Table 1). Total of 1921 genes were classified into 20 Clusters of Orthologous

Groups (COG) categories, and 137 genes were identified to be related with inorganic ion transport and metabolism. Additionally, 6 genes were found to be involved in urea catabolic process, and 3 genes involved in CO<sub>2</sub> fixation. The information of these genes was probably associated with precipitation of various metal ions and CO<sub>2</sub> fixation in the meanwhile, which will be helpful for environmental remediation, wastewater treatment and atmospheric CO<sub>2</sub> sequestration. The genome sequence of *B. linens* BS258 enables further studies in accessing its biotechnological characteristics.

## Nucleotide Sequence Accession Number

The complete genome sequence of *B. linens* BS258 was deposited in GenBank with the accession number CP014869.

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Features	Value
Genome size (bp)	3,862,244
G+C content (%)	64.16
Predicted genes	3437
rRNAs	12
tRNAs	47

Table 1: General genome features of *Brevibacterium linens* BS258.

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