

Draft Genome Sequence of *Pontibacter* sp. nov. BAB1700, a Halotolerant, Industrially Important Bacterium

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***Pontibacter* sp. nov. BAB1700 is a halotolerant, Gram-negative, rod-shaped, pink-pigmented, menaquinone-7-producing bacterium isolated from sediments of a drilling well. The draft genome sequence of the strain, consisting of one chromosome of 4.5 Mb, revealed vital gene clusters involved in vitamin biosynthesis and resistance against various metals and antibiotics.**

Pontibacter is a unique genus of phylum *Bacteroidetes* discovered by Nedashkovskaya et al. in 2005 (10). Since the discovery of the genus, 10 novel species have been reported with validly published names: *Pontibacter actiniarum* (10), *Pontibacter ake-suensis* (19), *Pontibacter korensis* (18), *Pontibacter niistensis* (6), *Pontibacter roseus* (12), *Pontibacter xinjiangensis* (15), *Pontibacter rhizosphera* sp. nov. (11), *Pontibacter salisaro* sp. nov. (9), *Pontibacter populi* (16), and *Pontibacter lucknowensis* sp. nov. (8). All members of the genus possess menaquinone-7 (MK-7) as their predominant respiratory quinone (4, 15); MK-7 is a very essential form of vitamin K-2 for the human body and contributes alone and in combination with other factors to bone health (2, 13, 14, 17). It cannot be produced by human beings, but some microbes can produce it (3). Due to their ability to produce MK-7, members of the genus *Pontibacter* are of interest for genomic research. Therefore, *Pontibacter* sp. nov. BAB1700 was subjected to whole-genome sequencing, which can be beneficial to understanding the functional genomics of this organism and the genus as a whole.

The bacterium was isolated from sediments of a drilling well in a saline area of Gandhidham, Gujarat, India (23°1'50"N, 70°12'31"E), by using the traditional dilution plating method. Preliminary characterization revealed that *Pontibacter* sp. nov. BAB1700 was a Gram-negative, pink-pigmented, and halotolerant (salinity tolerance of up to 10% NaCl) organism.

Whole-genome sequencing of the strain was done with a high-throughput Ion Torrent personal genome machine with Ion Torrent Server (Torrent suite Version 1.5.1). Following the manufacturer's protocol, 13.25× coverage data and a total of 559,880 mate-paired reads (lowest read of 120 bp and highest read with 203 bp) were obtained. *De novo* assembly was performed using the MIRA-3 assembler (version 3.4.0.1-1). The automatic annotation of the genome was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), which utilizes GeneMark, Glimmer, and tRNAscan-SE searches (5), and using the RAST server (1) with the SEED database (7).

The total length of the genome was found to be 4,568,473 bp, which were distributed in 267 contigs having nucleotide sequences of more than 500 bp (scaffold $N_{50} = 28,778$). The G+C content was 49%. The chromosome of *Pontibacter* sp. nov. BAB1700 harbored 347 subsystems having 4,044 protein-coding genes, 43 transfer RNAs, and 3 ribosomal RNAs. Six gene clusters were attributed to menaquinone-7 and phyloquinone biosynthesis. Gene clusters for resistance to various antibiotics, such as acriflavine and fluoroquinolones, and heavy metals, including co-

balt, zinc, cadmium, chromium, and arsenic, were predicted. A unique gene involved in one-carbon metabolism by tetrahydropyrimidines was also identified within the genome.

The present study not only suggests that *Pontibacter* sp. nov. BAB1700 is an important model organism for understanding its role as a vitamin-producing and metal-reducing bacterium but also facilitates future bioengineering efforts for this pigment-producing bacterial species. To the best of our knowledge, this is the first report on the genome sequence of a *Pontibacter* species. Thus, the genome of strain BAB1700 represents a unique phylogenetic node and provides considerable insights for functional and comparative genomic study of the species, as well as the genus.

Nucleotide sequence accession number. The draft genome sequence of *Pontibacter* sp. nov. BAB1700 has been deposited at GenBank under accession number [AKIS000000000](https://www.ncbi.nlm.nih.gov/nuccore/AKIS000000000).

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