


DATA NOTE

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# Draft genome sequence of *Paenibacillus* sp. EZ-K15 isolated from wastewater systems

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## Abstract

**Objectives:** *Paenibacillus* species, belonging to the family *Paenibacillaceae*, are able to survive for long periods under adverse environmental conditions. Several *Paenibacillus* species produce antimicrobial compounds and are capable of biodegradation of various contaminants; therefore, more investigations at the genomic level are necessary to improve our understanding of their ecology, genetics, as well as potential biotechnological applications.

**Data description:** In the present study, we describe the draft genome sequence of *Paenibacillus* sp. EZ-K15 that was isolated from nitrocellulose-contaminated wastewater samples. The genome comprises 7,258,662 bp, with a G+C content of 48.6%. This whole genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession PDHM00000000. Data demonstrated here can be used by other researchers working or studying in the field of whole genome analysis and application of *Paenibacillus* species in biotechnological processes.

**Keywords:** *Paenibacillus* sp., Genome sequencing, Draft genome assembly and annotation, Wastewater

## Objective

*Paenibacillus* species, belonging to the family *Paenibacillaceae*, are rod-shaped Gram-positive or Gram-variable endospore forming aerobic or facultatively anaerobic bacteria, which are able to survive for long periods under adverse environmental conditions. Bacteria belonging to the genus *Paenibacillus* can be isolated from a wide range of environments including humans, animals, plants and the environment [1, 2]. Many species of *Paenibacillus* genus synthesize antimicrobial compounds that can be used as pesticides as well as in medicine, and many species produce enzymes important in bioremediation related technologies. *Paenibacillus* strains can be successfully applied for contaminants removal from a variety of wastewater systems. Also, several *Paenibacillus* strains can be involved in hydrolysis of cellulose and hemicellulose, lignin depolymerization and degradation of various textile dyes, polyvinyl alcohol, diesel fuel, bitumen,

polycyclic aromatic hydrocarbons, benzene and other compounds [2]. Hence, more studies at the genomic level are important to clarify our understanding of their ecology, genetics, as well as potential biotechnological applications. Thus, *Paenibacillus* sp. EZ-K15 was isolated from nitrocellulose-contaminated wastewater systems, Kazan, Republic of Tatarstan, Russia [3]. These industrial wastes produce high levels of wastewaters polluted with multifarious dissolved chemical compounds and nitrocellulose particles. Therefore, isolation of bacteria which are able to transform various adverse pollutants and their genome analysis are of high importance for the creation of effective bioremediation strategies [4, 5].

## Data description

*Paenibacillus* sp. EZ-K15 was isolated from nitrocellulose-contaminated wastewater environments, Kazan, Republic of Tatarstan, Russia [3]. The bacterium optimally grown on Luria agar at + 30 °C had been cultivated for 1–2 days. Genomic DNA of the bacterial strain EZ-K15 was extracted using a FastDNA spin kit (#116540600; MP Biomedicals) and a Super FastPrep-1 homogenizer (#116011500; MP Biomedicals) as detailed

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