JETIR.ORG ISSN: 2349-5162 | ESTD Year : 2014 | Monthly Issue

JOURNAL OF EMERGING TECHNOLOGIES AND INNOVATIVE RESEARCH (JETIR)

An International Scholarly Open Access, Peer-reviewed, Refereed Journal

Draft genome sequence of *Bacillus Subtilis subsp. subtilis* DJ9192 isolated from Waste Water Treatment plant

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ABSTRACT

We report the draft genome sequence of *Bacillus subtilis subsp. subtilis* DJ9192 isolated from Rajkot Municipality Corporation (RMC) wastewater sewage treatment plant of Rajkot city in Gujarat, a state of India, located on the country's western coast. The genome assembly comprised 4,240,940bp with a GC content of 43.54% and 4262 protein-coding sequences.

The non-degradable nature of conservative plastics roots in many environmental difficulties. So, it is essential to recognize the bacteria that can degrade the toxic substances and alter them into recyclable plastics.[1]

To resolve the above-stated problems of artificial plastic & the hazardous effect of phenol, one effective organism ***Bacillus Subtilis subsp. subtilis*** **DJ9192** isolated from Raiya Waste Water Treatment plant, Rajkot, Gujarat, India.

To acquire the genome sequence, The random soil sample was taken by performing a random sampling method from Raiya Waste Water Treatment Plant, Rajkot. (N $22^0$18'12'', E 70^0 44'17'') The isolate was isolated by using a serial dilution technique with the spread plate technique [2]. A microbial genomic DNA was extracted from a pure single colony from 1% Glucose medium after 48 hours of Incubation at 45^{oc} temperature [3] by using QIAGEN DNeasy Blood & Tissue Kit (as per manufacturer directives) [4] The single end genome sequencing of the isolate was accomplished using the ion 316 chip and 400bp chemistry on an Ion Torrent PGM platform per the manufacturer's directives. The sequence reads obtained were assembled using GS De Novo Assembler v. 2.6, with default parameters resulting in a draft genome of 4,240,940 bp comprising 8 contigs and an N50 size of 7,58,988 bp. The GC content of 43.54 % was found in the whole sequence calculated using SeqinR package RStudio version.R.3.6.[5]

The genome coverage of the assembled contigs was 40.27x. The genome alignment result using BLAST against an NCBI genome database gave 98% identity with the *Bacillus subtilis subsp. subtilis* strain (6). The gene annotation and screening for RNA were done using the GeneMarkS-2+ with 4.12. annotation software revision. (7) confirmed to have 64 RNA molecules. The genome revealed the presence of 4,262 coding sequences (CDS), Apart from these, the draft genome of the strain will be assumed to help in revealing genetic & proteomics features in the production of Polyhydroxy butyrate and degradation of phenol aromatic components [8][9][10]

Nucleotide sequence accession numbers JACVER000000000. The genome sequence has been deposited in DDBJ/ENA/GenBank under the accession number JACVER000000000. The version defined in this paper is the first version JACVER000000000. Bio project submitted with accession PRJNA661285, Biosample SAMN16051102.

FUNDING INFORMATION

This research received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

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