Data in Brief 6 (2016) 53–67

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Digital data for Quick Response (QR) codes of thermophiles to identify and compare the bacterial species isolated from Unkeshwar hot springs (India)

Bhagwan N. Rekadwad *, Chandrahasya N. Khobragade

School of Life Sciences, Swami Ramanand Teerth Marathwada University, Nanded, Maharashtra 431606, India

ARTICLE INFO

Article history:
Received 8 May 2015
Received in revised form
16 September 2015
Accepted 16 November 2015
Available online 24 November 2015

Keywords:
DNA bank
DNA signatures
Microbial diversity informatics
Thermal springs

ABSTRACT

16S rRNA sequences of morphologically and biochemically identified 21 thermophilic bacteria isolated from Unkeshwar hot springs (19°85′N and 78°25′E), Dist. Nanded (India) has been deposited in NCBI repository. The 16S rRNA gene sequences were used to generate QR codes for sequences (FASTA format and full Gene Bank information). Diversity among the isolates is compared with known isolates and evaluated using CGR, FCGR and PCA i.e. visual comparison and evaluation respectively. Considerable biodiversity was observed among the identified bacteria isolated from Unkeshwar hot springs. The hyperlinked QR codes, CGR, FCGR and PCA of all the isolates are made available to the users on a portal https://sites.google.com/site/bhagwanrekadwad/.

Specifications Table

Subject area	*Biology*
More specific subject area	*Microbial diversity Informatics*

* Corresponding author.
E-mail address: rekadwad@gmail.com (B.N. Rekadwad).

http://dx.doi.org/10.1016/j.dib.2015.11.035

Type of data	*Text file, sequences, table, Quick Response Codes (QR Codes), Chaos Game representation (CGR) and Chaos Game Representation of Frequencies (FCGR), neighbor joining(NJ) plot and Principal Component Analysis (PCA) images*
How data was acquired	*Amplified Biosystems Model 3730 XI (96 capillary) DNA sequencer*
Data format	*Raw and analyzed*
Experimental factors	*DNA fragments were obtained using slightly modified Phenol-Chloroform method.*
Experimental features	*Genomic DNA fragmented and then sequenced using Sanger's dideoxy DNA sequencing method using Amplified Biosystems DNA sequencer. 16SrRNA gene sequences were used to create QR codes using DNA BarID software.*
Data source location	*Unkeshwar* (19°85′N and 78°25′E), *School of Life Sciences, Swami Ramanand Teerth Marathwada University, Nanded, India* (19°6′N and 78°17′E).
Data accessibility	1. *Raw data is available through NCBI's BioSample database* (www.ncbi.nlm.nih.gov/nuccore). *BioSample IDs include JN392966-JN392971, KC120909-KC120919, KM KM998072-KM998074 and KP053645.* 2. *Data is with this article made available to users* a. *Each isolates have two hyperlinked QR codes, CGR, FCGR.* b. *Names of isolates, Accession Numbers, QR codes, CG and PCR, FCGR and PCA of isolates made available on internet on website created by us* https://sites.google.com/site/bhagwanrekadwad/

Value of the data

- Microbial community isolated from Unkeshwar hot spring has enormous biotechnological applications. Generated digital information is a limelight for identification and comparison of newly isolated microorganisms.
- This digitization of 16S RNA sequences of thermophiles were carried out first time by us from Unkeshwar hot spring and made available to users.
- This generated digital information provides a baseline to any researchers by reducing time and cost on identification and comparison of bacterial diversity in hot springs.
- The DNA sequence data digitization is a standard, fast and reliable tool for identification of microorganisms up to species level using short DNA sequences.

1. Experimental design, materials and methods

The Sanger's dideoxy method was adopted for DNA sequencing. 16S rRNA gene sequence analysis was carried out to confirm the identity of bacteria using morphological and biochemical tests. The bacterial cultures were enriched in a nutrient agar medium and the DNA was extracted using a phenol–chloroform method with slight modification. The method was modified as follow. About 2 mL of cell pellet from each enrichment culture of isolate was suspended in extraction buffer containing (100 mM Tris–HCl, pH 8.0, 100 mM Na_2EDTA (pH 8.0) and Proteinase K (Nitrogen, USA) at the final concentration of 100 mg/mL. The resulting mixture was incubated at 55 °C for 2 h with continuous