Data in Brief

Deciphering the microbiota of Tuwa hot spring, India using shotgun metagenomic sequencing approach

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Abstract

Here, we report metagenome from the Tuwa hot spring, India using shotgun sequencing approach. Metagenome consisted of 541,379 sequences with 98.7 Mbps size with 46% G + C content. Metagenomic sequence reads were deposited into the EMBL database under accession number ERP009321. Community analysis presented 99.1% sequences belong to bacteria, 0.3% of eukaryotic origin, 0.2% virus derived and 0.05% from archaea. Unclassified and unidentiﬁed sequences were 0.4% and 0.07% respectively. A total of 22 bacterial phyla include 90 families and 201 species were observed in the hot spring metagenome. Firmicutes (97.0%), Proteobacteria (1.3%) and Actinobacteria (0.4%) were reported as dominant bacterial phyla. In functional analysis using Cluster of Orthologous Group (COG), 21.5% drops in the poorly characterized group. Using subsystem based annotation, 4.0% genes were assigned for stress responses and 3% genes were ﬁt into the metabolism of aromatic compounds. The hot spring metagenome is very rich with novel sequences afﬁliated to unclassiﬁed and unidentiﬁed lineages, suggesting the potential source for novel microbial species and their products.

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Keywords:
Hot spring
Metagenome
Shotgun sequencing
Community analysis
Functional analysis

Direct link to deposited data

http://www.ebi.ac.uk/ena/data/view/ERP009321

Culturability of microorganisms in extreme habitats is usually very poor, which creates the need to explore the culture-independent tech-
65 °C and water is alkaline with high salt and minerals content. Visitor and local community often take the bath due to its therapeutic belief. The bottom of the reservoir has hard rocks and photosynthetic microbes thrive in the water column. To the best of our knowledge, the microbial diversity and biogeological study of Tuwa hot water springs has not yet been investigated. The present research is the first investigation to describe the microbial diversity by metagenomics approach.

The water sample was collected in thermos bottle and transported to the laboratory for the physicochemical analysis. The microbial community DNA from the hot spring water was isolated and purified by silica spin columns using HiPura™ water DNA isolation kit (MB547; Hi-Media, Mumbai, India). Isolated metagenomic DNA was subjected to the sequencing after the testing of quality and purity using agarose gel electrophoresis and spectrophotometer. Shotgun metagenomic sequencing was performed with an Ion Torrent PGM platform using Ion Express Template 300 chemistry on a 318 chip as per the manufacturer’s instructions. Analysis and annotation of output data were carried out by MG-RAST, an online server using default parameter [8].

During the sampling of water from Tuwa hot springs, pH was reported ranging from 8.2 to 9.0 and conductivity was 19 μS/cm. The elemental composition of hot spring water (mg/L) showed the Sodium 19.93, Potassium 14.5, Calcium 0.5, Chloride 15.8 and Sulphate 1.83, Carbonate 2.4 and Bicarbonate 0.4. The output data encompassed a total of 541,379 sequences comprised of 98,773,736 bps with 46% G + C content. The microbial community analysis revealed predominance of domain bacteria (99.1%), followed by unclassified sequences (0.4%) eukaryota (0.3%), viruses (0.2%), unidentified sequences (0.07%), and archaea (0.05%).

At phyla level, a total of 22 diverse microbial phyla together with unclassified category were depicted in the metagenome. Most abundant
sequences affiliated to bacterial phyla were Firmicutes (97.0%) followed by Proteobacteria (1.3%) and Actinobacteria (0.4%). Whereas Ascomycota (0.08%) and Chordata (0.08%) were abundant eukaryotic phyla and prominent archaeal phylum was Euryarchaeota (0.05%). Metagenomes comprised a total of 90 families with the abundant existence of Bacillaceae (94.6%) followed by Paenibacillaceae (0.4%) and Clostridiaceae (0.4%). At the species level, the most common bacterial species reported were Bacillus licheniformis (40%) and Bacillus subtilis (26%) (Fig. 1). Thermophilic alkaline serine protease producing B. licheniformis was reported from the same territory at Unnai hot spring, India [9].

Functional analysis was also performed using MG-RAST server. Out of the 350,069 sequences that exceeded quality control, 263,997 sequences (75.4%) produced a total of 170,681 predicted protein coding regions. Of these 170,681 predicted protein features, 127,064 (74.4%) of features have been assigned an annotation using at least one of the protein databases (M5NR) and rest of 25.6% of features have no significant similarities to the protein database.

In the functional annotation, a total of 218,926 features were assigned to functional categories with COG approach and 47,049 sequences (75.4%) produced a total of 170,681 predicted protein coding regions. Of these 170,681 predicted protein features, 127,064 (74.4%) of features have been assigned an annotation using at least one of the protein databases (M5NR) and rest of 25.6% of features have no significant similarities to the protein database.

The study presented a considerable microbial diversity and offers insights into microbial community composition, distribution and abundance. A number of DNA sequences remained taxonomically and functionally unanswered representing potentially novel microorganisms and genes in the hot spring.

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