Data in Brief

Bacterial diversity of Murlen National Park located in Indo-Burman Biodiversity hotspot region: A metagenomic approach

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Pairend end Illumina Mi-Seq sequencing of 16S rRNA gene amplicon was carried out to study the bacterial community in the soil of Murlen National Park located in Indo-Burman Biodiversity hotspot region. Metagenome consisted of 302,416 reads with 151.81 Mb data and G + C content of 56.48%. More than 85% sequence was having a Phred score N=Q30 and individual sequence length was 251 bp. Metagenome sequence data are available at NCBI under the Bioproject database with accession no. SRP057136. Community metagenomics revealed a total of 1802 species belonging to 29 different phyla dominated by Acidobacteria (39.45%), Proteobacteria (26.95%) and Planctomycetes (7.81%). Our data detected a wide group of bacterial community which will be useful in further isolating and characterizing the economic importance of bacteria from this region.

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followed by Proteobacteria (26.95%), Planctomycetes (7.81%), Actinobacteria (7.18%), Bacteroidetes (6.65%), Chloroflexi (4.11%) and Nitrospirae (3.33%). However, 0.51% of the reads were not classified at the phylum level (Fig. 1). The analysis identified 100 bacterial orders dominated by iii1–15 (23.94%), Rhizobiales (13.97%), Actinomycetales (5.83%), Solibacterales (5.06%), Burkholderiales (4.83%), Saprospirales (4.61%), Nitrospirales (3.33%), Gemmatales (3.40%), Ellin6513 (2.94%), Thermogemmatisporales (2.74%) and Acidobacteriales (2.55%). A total of 138 genus were detected and the most dominating among them were DA101 (7.02%), followed by Gemmata (1.03%), Candidatus Xiphinematobacter (1.02%), and Rhodoplanes (0.92%). However, 84.44% reads were not identified at the genus level which suggested that the uniqueness and unidentified bacterial community structure might lead to reveal novel bacterial populations with some unique properties (Supplementary Fig. 1).

Our study, which is the first to study bacterial communities using high-throughput methods in Murlen national forest soil, a pristine reserve forest, revealed the presence of diverse bacterial population. This will be helpful in cataloging and describing the bacteria diversity of the forests of Mizoram that needs to be conserved and simultaneously could be the habitat for large number of economically important microbes.

Metagenome sequence data are available at NCBI Accession No. SRP057136.

Competing interests

The authors declare that there are no competing interests.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.gdata.2015.04.025.

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