

# Profiling of Microbial Communities from High Altitude Permafrost Affected Soil with Next-Generation Sequencing

Ahmad Ali and Archana Chauhan \*

Department of Zoology, Panjab University,  
Sector 14, Chandigarh, India 160014  
E-mail: [archie.chauhan@gmail.com](mailto:archie.chauhan@gmail.com)

---

**Background:** *Permafrost covers over 25% of the exposed land surface of the Northern Hemisphere and hosts a diversity of microbes proposed to be unique to cold habitats. These frozen soils represent a largely understudied genetic resource. Climate change due to global warming has a significant impact on permafrost thawing which in turn promote microbial carbon turnover with a positive feedback on greenhouse gases. In this study we attempted to get an insight into the microbiome of the high-altitude permafrost affected soil from the Changthang region of Ladakh through 16S rRNA amplicon sequencing.*

**Results:** *Bioinformatics analysis of the sequences clearly reveals that the phylum Proteobacteria, Actinobacteria, Acidobacteria, Bacteroidetes, Verrucomicrobia, Chloroflexi, Gemmatimonadetes and Nitrospirae dominated the permafrost soil microflora in the samples with slight difference in their relative abundance. Various classes of phylum Actinobacteria such as Acidimicrobiia, Actinobacteria, and Thermoleophilia were also observed in the samples. Further, the analysis of the sequence also shows that the phylum Thaumarchaeota and Euryarchaeota were the dominant archaeal phyla in the soil samples. Deeper analysis of the samples clearly showed that Methanosaeta followed by Methanobacterium were the dominant genera in the soil cores which are dominant acetoclastic methanogen.*

**Significance:** *Climate change due to global warming results in permafrost thawing which in turn increase microbial activity and microbial degradation of permafrost organic carbon. Our result suggested that the extreme terrestrial environments are excellent niches for specialized microorganisms belonging to the domains of Bacteria and Archaea. The micro organisms thriving in this soil have the potential to degrade the organic carbon sequestered in the permafrost of this region.*

**Keywords:** *Microbiome, Permafrost, Illumina sequencing, bacteria, 16S rRNA.*