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Diversity and Relative Abundance of Industrially Important Enzyme Producing Microbial Genera in Hot Springs in Sri Lanka

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Thermal tolerant enzyme producing bacteria can be successfully used in industrial settings to minimize environmental impacts caused by excess use of chemical catalysts in production chains. Hot springs are a major habitat for extremophiles which produce extremozymes. Characterization and identification of microbial community in hot springs provide an initial platform for identification of extremophilic microorganisms for industrial applications. In the present study, the diversity and relative abundance of industrially important enzyme producing microbial genera in hot springs in Sri Lanka was studied. Water samples were collected from surface and bottom of the hot springs. Temperature, conductivity, pH and Dissolved Oxygen (DO) were measured at the site using portable meters. To analyse microbial community (bacteria and archaea) of hot springs, extracted DNA was sequenced through 16s rDNA amplicon sequencing on Illumina MiSeq platform. Sequencing data were analyzed using Mother V. 1.42 software. METAGENassist web server tool was used to predict the metabolic functional diversity of the bacterial and archaeal communities. The temperature of the hot springs were ranged from 33.7 ^{0}C to 55.4 ^{0}C where conductivity, pH and DO levels were reneged from 801 to 1507 µS/cm, 7.20 to 8.27 and 1.05 – 3.5 mg/L respectively. The microbial communities of the hot springs were mostly comprised of Bacteria and Archaea. Bacteria was the dominant component respectively 99% and only <1% Archaea. *Chloflexus, Rubelllimicrobium, Acinetobacter, Pseudomonas, Methylobacterium, Tepidimonas, Rheinheimera, Flavobacterium,* and *Vogesella* were the major bacteria genera recorded in all hot springs. The metabolic inference analysis of the microbial community of hot springs comprised of dinitrogen-fixing bacteria, lignin degraders, nitrogen and sulfate reducers, nitrogen fixation bacteria, sulfur reducers, denitrifying bacteria, cellulose degraders and sugar fermentors. Thus the results of the present study implied that the hot springs could be a useful source of bacteria for future industrial perspectives. Further studies are in progress along with a metagenomic analysis.

Keywords: Hot springs; Community analysis; Extremophiles; NGS analysis; Biotechnological Prospects