Proceedings of the NATIONAL CONFERENCE ON MULTIDISCIPLINARY RESEARCH VIRTUAL 2020 POSTGRADUATE SYMPOSIUM

"Inspiring Sri Lankan Youth for Tomorrow's Science"



NCMR 2020 08th October 2020



Organized by the Young Scientists' Association, National Institute of Fundamental Studies, Sri Lanka



Main Sponsor:





Diversity of phylum Proteobacteria in four hot springs of Sri Lanka based on 16S rRNA metagenomic analysis

D.G.S.N. Samarasinghe¹, R.P. Wanigatunge², D.N. Magana-Arachchi^{1*}

¹National Institute of Fundamental Studies, Hantana Road, Kandy ²Department of Plant and Molecular Biology, Faculty of Science, University of Kelaniya

*dhammika.ma@nifs.ac.lk

Sri Lanka harbours several hot springs, but majority of them are not yet explored for microorganisms and require comprehensive studies to unravel their unknown and untapped phylogenetic and functional diversity. The aim of this study was to perform metagenomics analysis on four major hot springs located in Sri Lanka to reveal the diversity and distribution of Proteobacteria. Water samples were collected from four hot springs (40 °C-54 °C) located at Mahapelessa, Wahawa, Mahaoya, and Nelumwewa. Genomic DNA was extracted from the water samples using modified Boom's method and was subjected to 16S rRNA metagenomic sequencing using Illumina platform. The results were analyzed using GAIA: Metagenomics data analysis software to identify bacteria (Operational taxonomic units/ OTU) and to determine their relative abundance. OTU analysis was carried out with a cut-off similarity value at 97%. The 16S rRNA gene amplicon of V3-V4 region metagenome sequencing revealed a unique taxonomic diversity of the resident thermophilic Proteobacteria communities in those hot springs. Proteobacteria was dominant in all sampled hot springs; Mahapelessa (57.4%), Wahawa (46.7%), Mahaoya (86.3%) and Nelumwewa (47.7%), with 78 genera belonging to 6 classes; Alphaproteobacteria (44.9%), Betaproteobacteria (33.3%), Gammaproteobacteria (14.1%), Deltaproteobacteria (3.85%), Hydrogenophilalia (2.56%) and Epsilonproteobacteria (1.28%). Among them Burkholderi acepacia and Stenotrophomonas maltophilia were the most abundant species recorded in all hot springs. Seven different bacterial species were unique to Wahawa and three species were unique to Mahaoya. Vogesella perlucida and Vibrio fluvialis were detected only in Nelumwewa and Mahapelessa hot springs, respectively. Nitrogen fixing bacteria; Azospirillum halopraeferens, Bradyrhizobium liaoningense, and Bradyrhizobium elkanii; Sulphate reducing bacterium Desulfovibrio alkalitolerans were also identified. Hydrogenophilus hirschii, Hydrogenophilus thermoluteolus and Petrobacter sp. were recorded and they were known as thermophiles in previous studies. This is the first report of a high resolution profile of proteobacteria diversity in Sri Lankan hot springs.

Keywords: Proteobacteria, hot springs, 16S metagenomics