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ABSTRACT BOOK

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Stenotrophomonas maltophilia, a potential multidrug resistant pathogen in Sri Lankan hot water springs

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Hot springs, natural habitats having extreme temperature conditions persist as reservoirs of evolving organisms. Microbes, a highly diverse group of organisms can colonize extreme environmental conditions owing to their genetic, ecological and species diversity. Organisms living in extreme temperature conditions are already evolved to encounter environmental challenges. This enables the organism to meet future selective pressures, specially, upon contact with antibiotics. There are several studies on microbes, but there has been no comprehensive metagenomics study on the microbial diversity of Sri Lankan hot springs. Hence, the study was conducted to gain a comprehensive insight into the microbial diversity of Sri Lankan hot springs. Water samples were collected from hot springs (40 °C - 54 °C) located at four locations (Mahapelessa, Wahawa, Mahaoya, and Nelumwewa) and one spring located at Digana (27 °C) as the control. Genomic DNA was extracted directly from the environmental samples using Boom's method. The extracted DNA was subjected to 16S metagenomics (Illumina Platform). The results were analyzed to identify organisms using GAIA: Metagenomics data analysis software. According to analysis it was observed that the hot spring microbiome consists of numerous human pathogens. Interestingly, *Stenotrophomonas maltophilia*, an emerging global opportunistic pathogen was found in all hot water springs (Mahapelessa: 4.431%, Wahawa: 3.934%, Mahaoya: 0.721%, and Nelumwewa: 0.006%) while no strains of *S. maltophilia* were observed in the control. To our knowledge, this is the first record on *S. maltophilia* existence in hot water springs in Sri Lanka. *S. maltophilia* is recorded as a multidrug-resistant nosocomial pathogen in immunocompromised patients with a significant fatality/ case ratio due to relatively limited treatment options. The pathogen can infect upon direct contact via bathing, ingestion and through contact with wounds. The possibility of acquiring resistance genes by the strains found in this study is high due to the fact of living in hot water springs where there is a high evolution rate. However, as pathogenicity varies

among different strains of the same species further studies are needed for better understanding. Further, the results emphasize the need for raising public awareness on this matter to prevent microbial infections associated with hot springs.