

Metagenomics insight into effects of a heavy metal resistance in hot spring environments adjacent to Huang-gang Creek

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Huang-gang Creek, a popular spa area in Taiwan originating from Tatun Volcano Group, is known to contain high concentration of various aquatic heavy metals such as iron, aluminum, manganese, sulfides, sulfosalts and arsenic. Since aquatic microbial communities interact with the environmental chemicals intensively, by investigating their interactions, it provides a useful strategy to deal with the pollution of environmental heavy metal. In this study, the aquatic samples and biofilms from Huang-gang Creek and Beitou Creek were collected. Next generation sequencing (NGS) was carried out to examine the metagenomics of uncultured microbial community in these samples. The metagenomics were further clustered into operational taxonomic units (OTUs) to analyze relative abundance, heatmap of OTUs, and principal coordinates analysis (PCoA). Our results show that the phyla of Proteobacteria and Actinobacteria are most abundant in all samples. Metallibacterium, a genus of microbe which is resistant to acid, is found in areas of high sulfosalts. Microbes of Bangiophyceae are prolific in the tributary and downstream of the river, suggesting a high nutrition source in these areas. Our data provided an example of kinetic interaction of microbial communities with environmental ingredients.