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Bacterial community structure of paddy fields as influenced by heavy metal contamination

Sherlyn Tipayno¹, Sandipan Samaddar², Poulami Chatterjee², MD Abdul Halim² and Tongmin Sa^{2*}

¹ *College of Arts and Sciences, Benguet State University, La Trinidad, Philippines*

² *Department of Environmental and Biological Chemistry, Chungbuk National University, Cheongju, South Korea*

Abstract

Heavy metal pollution of agricultural soils affects land productivity and has impact on the quality of surrounding ecosystem. Soil microbial community parameters are used as reliable indices for assessing quality of agricultural lands under metal stress. This study investigated bacterial community structure of polluted and undisturbed paddy soils to elucidate soil factors that are related to alteration of bacterial communities under conditions of metal pollution. No obvious differences in the richness or diversity of bacterial communities were observed between samples from polluted and control areas. The bacterial communities of three locations were distinct from one another, and each location possessed distinctive set of bacterial phylotypes. The abundances of several phyla and genera differed significantly between study locations. Variation of bacterial community was mostly related to soil general properties at phylum level while at finer taxonomic levels concentrations of arsenic and lead were significant factors. According to results of bacterial community functional prediction, the soil bacterial communities of metal polluted locations were characterized by more abundant DNA replication and repair, translation, transcription and nucleotide metabolism pathway enzymes while amino acid and lipid metabolism as well as xenobiotic biodegradation potential was reduced. Our results suggest that the soil microbial communities had adapted to the elevated metal concentrations in the polluted soils as evidenced by changes in relative abundances of particular groups of microorganisms at different taxonomic resolution levels, and by altered functional potential of the microbial communities.

Keywords: Pyrosequencing, Metal contamination, Paddy field, Bacterial diversity

Corresponding author*

Tongmin Sa

Address: Chungdae-ro 1, Seowon-Gu, Cheongju, Chungbuk 28644, South Korea

Tel: +82-43-261-2561, Fax: +82-43-271-5921

E-mail: tomsa@chungbuk.ac.kr