Thanyaporn Ruangdech 2014: Effect of Heavy Metal Contaminated Rhizosphere of *Chromolaena odorata* (L.) on Microbial Community Structure Using Metagenomics. Master of Science (Environmental Science), Major Field: Environmental Science, Department of Environmental Science. Thesis Advisor: Associate Professor Kannika Sajjaphan, Ph.D. 99 pages.

A metagenomics approach was used to assess the impacts of cadmium and zinc contamination on rhizobacterial population of *Chromolaena odorata* (L.). Twelve rhizosphere soil samples were obtained from Phra That Pha Daeng District, Mae Sot, Tak Province. Bacterial communities were characterized using the V6 hypervariable region of the 16S rDNA gene using Illumina next-generation sequencing technology. Among 54,026 unique OTUs identified, 99.74% were classified as bacteria, 0.26% were classified as archaea and 0.0001% could not be assigned to a kingdom. At all sites, several dominant phyla were observed including *Proteobacteria, Actinobacteria, Acidobacteria, Fimicutes* and *Bacteroidetes*. These five Phyla accounted for 89.17% of all OTUs identified among all sites, and only two OTUs could not be classified in a Phylum. Nonparametric Shannon and Shanon diversity index indicated that the low Cd contaminated soil had higher species diversity than the high Cd contaminated soil at significant level ($P<0.05$). Bacteria resistant to Cd and Zn (a total of 96 isolates) were obtained from each sample and were used to analyze patterns of gene function by using MICs. All 1,152 MIC values of individual isolates were analyzed by using BioNumeric software. The results showed that more than 26.7% of the bacteria were resistant to cadmium at concentrations up to 320 mg/L and only 2.3% of bacteria were resistant to zinc at concentration up to 3,200 mg/L. The MICs analyses indicated that cadmium and zinc resistance decreased with increasing cadmium and zinc concentrations and those bacteria resistant to Cd and Zn at the same level of concentration may contain the same group of genes. PCR reactions were performed to identify *czcD, czrC, nccA, cadA* and *cadB*. However, the genes were not detected.

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