

Pechrada Jareonmit 2011: Transformation and Detoxification of Arsenic Compounds by Soil Microorganisms. Doctor of Philosophy (Soil Science), Major Field: Soil Science, Department of Soil Science. Thesis Advisor: Assistant Professor. Kannika Sajjaphan, Ph.D. 208 pages.

The study of the shift in the microbial community structure in heavily arsenic contaminated soils and slightly arsenic contaminated soils located in Amphoe Dan Chang, Suphan Buri Province was determined by denaturing gradient gel electrophoresis (DGGE). Band pattern analysis obtained from this study indicated that the microbial community was not significantly different in two kinds of soils. Phylogenetic analysis obtained by excising and sequencing six bands indicated that the soils were dominated by *Arthobacter* sp. and *Proteobacteria* sp. In the isolation of arsenic resistance bacteria, two hundred and sixty-two bacterial isolates were obtained from arsenic contaminated soils. Majority of the arsenic resistant isolates were found to be gram-negative. Minimum inhibitory concentration (MIC) study showed that all of the isolated bacteria were more resistant to arsenate than to arsenite. In the course of this study, some of the bacterial isolates were found resist in medium containing up to 1,500 mg/L of arsenate and arsenite. All strains were also evaluated for resistance to eight antibiotics. Correlations analysis of antibiotic resistance patterns could be categorize the isolates into 100 unique groups indicating high diversity relation among all isolates. Isolates from each antibiotic resistance group were further characterized using the repetitive element-PCR (rep-PCR) DNA fingerprinting technique with ERIC primers. The genetic relatedness of the 100 bacterial fingerprints showed that these 100 groups of bacteria could be divided into four major clusters with 5-99% similarity. Moreover, the presence of arsenic resistant genes (*ars*) was also identified among the arsenic-resistant isolates using PCR and 30% of one hundred isolates were found to be carrying *arsC* gene encoding arsenic reductase enzyme. One hundred arsenic resistant bacterial isolates were obtained from arsenic contaminated soils. The agar plate screening assay was used to determine if isolates had the ability to transform arsenite and arsenate. The results showed that 95 isolates were capable of arsenate reduction on agar plates. None of bacterial isolates oxidized arsenite to arsenate under the growth conditions tested, but the isolates grew in the presence of high concentrations of arsenite. Only 13 of 100 tested isolates could transform high level of arsenate (33-69 μ M) when tested using molybdenum blue method. Partial sequence analysis of 16S rDNA genes indicated that the isolates belonged to two broad taxonomic group i.e. *Firmicutes* and the *Proteobacteria*. Ten isolates were assigned to four species in the genus *Bacillus*, and three isolates belonged to two species in the genera *Enterobacter* and *Ochrobactrum*. Taken together these results indicated that phylogenetically diverse bacteria isolated from arsenic contaminated soils in an old tin mine area in Thailand have the ability to transform arsenate to arsenite.

Student's signature

Thesis Advisor's signature