



Original Article

## Isolation of arsenic-tolerant bacteria from arsenic-contaminated soil

Pattamaporn Aksornchu, Poonsuk Prasertsan and Vorasan Sobhon\*

Department of Industrial Biotechnology, Faculty of Agro-Industry,  
Prince of Songkla University, Hat Yai, Songkhla, 90112 Thailand

Received 26 December 2006; Accepted 30 October 2007

### Abstract

The disposal of toxic heavy metals such as arsenic posed high risk to the environment. Arsenite [As(III)], a reduced form of arsenic, is more toxic and mobile than arsenate [As(V)]. The aim of this work was to isolate arsenic-tolerant bacteria from contaminated soil collected in Ronphibun District, Nakorn Srithammarat Province, followed by screening these bacteria for their ability to adsorb arsenite. Twenty-four bacterial isolates were obtained from samples cultivated in basal salts medium plus 0.1% yeast extract and up to 40 mM sodium-arsenite at 30°C under aerobic condition. From these, isolates B-2, B-3, B-4, B-21, B-25 and B-27 produced extracellular polymeric-like substances into the culture medium, which may potentially be used in the bioremediation of arsenic and other contaminants. All isolates displayed arsenite adsorbing activities in the ranges of 36.87-96.93% adsorption from initial concentration of 40 mM sodium-arsenite, without any arsenic transforming activity. Five isolates with the highest arsenite adsorbing capacity include B-4, B-7, B-8, B-10 and B-13 which adsorbed 80.90, 86.72, 87.08, 84.36 and 96.93% arsenite, respectively. Identification of their 16S rDNA sequences showed B-7, B-8, and B-10 to have 97%, 99% and 97% identities to *Microbacterium oxydans*, *Achromobacter* sp. and *Ochrobactrum anthropi*, respectively. Isolates B-4 and B-13, which did not show sequence similarity to any bacterial species, may be assigned based on their morphological and biochemical characteristics to the genus *Streptococcus* and *Xanthomonas*, respectively. Thus, both isolates B-4 and B-13 appear to be novel arsenite adsorbing bacteria within these genera.

**Keywords:** arsenic, arsenic-tolerant bacteria, arsenite, bioadsorption

### 1. Introduction

Arsenic is a semi-metallic element, which may be found in a variety of form, viz. -3, 0, +3, +5 valencies. The most common arsenic species observed in the environment are the trivalent form arsenite [As(III)] and pentavalent form arsenate [As(V)]. Arsenate is often found co-precipitated with iron oxyhydroxide (FeOOH), which may be immobilized under acidic and moderately reducing conditions. Under reducing conditions, arsenic is found as arsenite which can co-precipitate with metal sulfides (Niggemyer *et al.*, 2001). In addition, numerous environmental factors also influence arsenic speciation in soil, such as pH, redox potential, the presence of other ions, organic matter content,

soil texture, fungal or bacterial activities (Turpinen *et al.*, 1999).

The sources of environmental arsenic may derived from various natural sources (i.e. weathered volcanic, marine sedimentary rocks, fossil fuels, minerals), water, air, living organisms and anthropogenic activities including mining, agricultural chemicals (e.g. pesticides, herbicides), wood preservatives, medicinal products, industry activities (Dowdle *et al.*, 1996; Stolz and Oremland, 1999; Liest *et al.*, 2000; Mandal and Suzuki, 2002).

The toxicity of different forms of arsenic decrease in the order: arsine>inorganic arsenite>organic arsenite>inorganic arsenate>organic arsenate>free arsenic (Mandal and Suzuki, 2002). Toxicity depends on factors such as physical state, gas, solution, or powder particle size, cell adsorption rate, elimination rate, and the nature of chemical substituents in the toxic compound (Anderson and Cook, 2004). The deleterious effects of arsenic to human health

\*Corresponding author.

Email address: vorasan.s@psu.ac.th

resulting from environmental contamination have been reported worldwide (Katsoyiannis *et al.*, 2002; Mandal and Suzuki, 2002). In Thailand, it was first reported from Ronphibun District in 1987, where local residents utilizing well-water were diagnosed with skin cancer. Soil and ground-water in the area were contaminated with up to 0.1% arsenopyrite and 100 times of the regulatory arsenic level of 0.01 mg/l in drinking water (Mandal and Suzuki, 2002).

Several remediation techniques for arsenic removal have been applied, e.g., ion exchange, adsorption with activated alumina and activated carbon, ultrafiltration, reverse osmosis, and complexation with metal ions followed by coagulation. These methods required large amount of chemical reagents, for example, adsorption and ion exchange are expensive when use in the event of high concentration of heavy metal ions. Furthermore, the treated sludge may be contaminated with treatment reagents resulting in secondary environmental pollution. Due to this apparent disadvantage of the above physico-chemical treatments, novel techniques for the reduction of contaminant toxicity in concerted with minimizing cost have been proposed.

Biological remediation techniques, either using living/dead cells or biosynthesized molecules have been examined (Katsoyiannis *et al.*, 2002). Studies have shown that both plant and microorganism are able to accumulate metal ions via processes such as transportation across the cell membrane, biosorption onto cell wall, entrapment in extracellular capsule, precipitation, oxidation-reduction reaction and biosorption to extracellular polysaccharide (Malik, 2004). Hyperaccumulating plant species, such as *Pityrogramma calomelanos* and *Pteris vitta*, were shown to accumulate arsenic in the form of arsenate at the leaf section (Visoottiviseth *et al.*, 2002). Studies have reported the ability of algae, fungi and bacteria to transform arsenite to arsenate and vice versa during their growth (Macy *et al.*, 2000; Hasegawa *et al.*, 2001; Visoottiviseth and Panviroj, 2001). *Desulfomicrobium* sp. BenR-B has been shown to reduce arsenate to arsenite via enzyme arsenate reductase (Macy *et al.*, 2000). The mechanisms involved in the microbial transformation and removal of arsenic from the environment included adsorption via reduction reaction by *Desulfomicrobium* sp. BenR-B, oxidation/reduction reaction by *Trichoderma harzianum* AS11 and *Trichosporon mucoides* SBUG801, and methylation reaction by *Paenibacillus* sp. and *Pseudomonas* sp. (Macy *et al.*, 2000; Hofmann *et al.*, 2001; Jenkis *et al.*, 2003)

In this report, we describes the isolation, effect of arsenic on bacterial growth and identification of arsenic-tolerant bacteria from contaminated soil in the area surrounding arsenic landfill site and from area within the Phytoremediation Project site (collaborative effort between Mahidol University and Ronphibun Subdistrict).

## 2. Materials and Methods

### 2.1 Soil collection

Soil samples were collected from Ronphibun District, Nakorn Srithammarat Province, where soil, sediment, and ground water in the area have been contaminated with arsenic for many years by decades of tin mining activities (Mandal and Suzuki, 2002). Sample collecting sites were within the area of the Phytoremediation Project and area surrounding arsenic landfill. Subsurface soil (from 0-15 cm in depth) were collected, placed in plastic bag and kept on ice or at 4°C until further analysis.

The pH of soil sample was determined by shaking 10 g of soil in 20 ml of distilled water for 25 minutes followed by measurement with pH meter (model Delta 320, Mettler; UK).

### 2.2 Arsenic analysis by ICP-AES

One to two grams of soil samples were added to 10 ml 50% HNO<sub>3</sub>, heated and refluxed at 95°C for 10-15 min. The soil suspension was left at room temperature to cool, then added with 5 ml concentrated HNO<sub>3</sub> and refluxed for another 30 min at 95°C. This step was repeated one more time. The solution was evaporated until approximately 5 ml of the solution was left. After the solution cooled to room temperature, 2 ml deionized H<sub>2</sub>O and 3 ml 35% H<sub>2</sub>O<sub>2</sub> was added and heated to 95°C. The solution was cooled to room temperature and added with 7 ml warmed 35% H<sub>2</sub>O<sub>2</sub>. The solution was again cooled to room temperature, added with 5 ml concentrated HCl and 10 ml deionized H<sub>2</sub>O, and refluxed at 95°C for 15 min. The digested solution was filtered to remove residual particulates and then diluted to 100 ml with deionized H<sub>2</sub>O. Arsenic concentration was determined by Inductively Coupled Plasma-Atomic Emission Spectrometry (ICP-AES) (PerkinElmer, Inc.; USA).

### 2.3 Growth media for bacteria isolation

Two formulations of basal salt medium were used throughout this study. BSMY I used for the isolation of bacteria from arsenic contaminated soil samples contained (per liter): 1.0 g yeast extract, 0.3 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.14 g MgSO<sub>4</sub>·7H<sub>2</sub>O, 0.2 g CaCl<sub>2</sub>·2H<sub>2</sub>O, 0.1 g NaCl, 0.05 g KH<sub>2</sub>PO<sub>4</sub>, 0.05 g K<sub>2</sub>HPO<sub>4</sub>, 0.6 mg H<sub>3</sub>BO<sub>3</sub>, 0.17 mg CoCl<sub>2</sub>·6H<sub>2</sub>O, 0.09 mg CuCl<sub>2</sub>·2H<sub>2</sub>O, 0.1 mg MnCl<sub>2</sub>·4H<sub>2</sub>O, 0.22 mg ZnCl<sub>2</sub>, 10 g glucose in 1 liter of Tris-HCl buffer (pH 8.0) (Yamamura *et al.*, 2003).

BSMY II used to study growth phase of bacteria in cultivation medium that added arsenic solution contained (per liter): 1.0 g yeast extract, 0.25 g NH<sub>4</sub>Cl, 0.62 g MgCl<sub>2</sub>·6H<sub>2</sub>O, 0.15 g CaCl<sub>2</sub>·2H<sub>2</sub>O, 1.0 g NaCl, 0.14 g KH<sub>2</sub>PO<sub>4</sub>, 0.5 g KCl, 0.06 mg H<sub>3</sub>BO<sub>3</sub>, 0.12 mg CoCl<sub>2</sub>·6H<sub>2</sub>O, 0.015 mg

$\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$ , 0.1 mg  $\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$ , 0.22 mg  $\text{ZnCl}_2$ , 10 g glucose in 1 liter of deionized water adjusted to pH 6.8 with  $\text{NaHCO}_3$  (modified from Kuai *et al.*, 2001).

Growth media were sterilized by autoclaving at 121°C for 15 minutes. Sodium-arsenite [Na-As(III)] was filter sterilized and added to the medium for the initial concentration of 5, 10, 20 and 40 mM.

#### 2.4 Isolation and characterization of arsenic-tolerant bacteria

Two grams of each soil sample was dissolved in 20 ml 0.9% NaCl and shaken for 3 minutes. Then 5 millilitres of soil suspension was inoculated into 50 ml BSMY I containing 5 mM sodium-arsenite and incubated at room temperature on rotary shaker at 120 rpm for 3 days. Five milliliters of culture was transferred into fresh BSMY I medium containing 10 mM sodium-arsenite, and transferred twice into new medium that was supplemented with 20 and 40 mM sodium-arsenite. After growth was observed, 0.1 ml of culture was spreaded on BSMY agar that contained 40 mM sodium-arsenite and incubated at 30°C for 3 days. Bacterial isolates that could tolerate the highest arsenite concentration were selected and identified by their morphological features and biochemical properties.

#### 2.5 Effect of arsenic on bacterial growth

The selected bacterial strains were inoculated into BSMY II with 40 mM sodium-arsenite and then incubated at 30°C, 150 rpm for 5 days. Samples were collected every 6-12 hours for the measurement of growth and arsenic concentration. Growth was determined via total protein by Lowry's method ( $A_{750}$ ) and arsenic concentration ( $A_{880}$ ) was determined spectrophotometrically. Determination of arsenic concentration in culture medium was performed with the method provided by Dhar *et al.* (2004). The effect of arsenic on growth was shown by extrapolating cell growth data and arsenic concentration data together.

#### 2.6 Identification of bacteria isolates

##### 1) Morphological characteristic

Bacteria isolates were grown in BSMY I with the addition of 40 mM sodium-arsenite and incubated at 30°C until either turbidity or colony was observed. Gram stain and cell morphology was investigated under microscope (1000x magnification).

##### 2) Biochemical properties

Biochemical properties of the isolates were tested according to Bergey's Manual of Systematic Bacteriology (Krieg, 1984). The following properties were determined: motility, nitrite reduction, indole test,  $\text{H}_2\text{S}$  production, methyl

red test, citrate utilization, starch hydrolysis, liquefaction, catalase test, oxidase test, oxidation/fermentation test (O/F), acid production from carbohydrates: glucose, lactose, sucrose.

#### 3) 16S rDNA sequence analysis

Five isolates which showed the highest arsenic adsorption capacity was chosen for further identification by 16S rDNA sequence analysis. The genomic DNA was extracted from each isolate by boiling and freezing method (modified from Yamada *et al.*, 2002). Three milliliters of culture broth was centrifuged at 10,000 rpm for 5 min. Supernatant was decanted and cell pellet was washed with 300  $\mu\text{l}$  of Tris-EDTA buffer (pH 7.0). Cell suspension was centrifuged at 10,000 rpm for 5 min and resuspended into 300  $\mu\text{l}$  of Tris-EDTA buffer (pH 7.0). The suspension was placed in boiling water for 10 min and immediately cooled on ice-bath for 5 min. This step was repeated 3 times.

The 16S rDNA from the extracted DNA was amplified by PCR using 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-ACGGCTACCTTGTTACGACTT-3') primers. The reaction mixtures composed of 5  $\mu\text{l}$  10xPCR buffer, 0.2 mM dNTPs, 1  $\mu\text{M}$  each primer, 5  $\mu\text{l}$  DNA template, 2.5 units *Taq* DNA polymerase and sterile deionized water to a final volume of 50 ml. PCR profile was as follows: initial denaturation at 94°C for 3 min, followed by 25 cycles of denaturation (94°C, 1 min), annealing (50°C, 45 sec), extension (72°C, 2 min), and final extension at 72°C for 10 min. PCR product was purified by QIAquick PCR Purification Kit (QIAGEN, Inc.). DNA sequences were performed by Macrogen, Inc. (South Korea). The 16S rDNA gene sequences were BLAST searched against GenBank database (<http://www.ncbi.nlm.nih.gov/>) and phylogenetic analysis was performed using Treeview software (Page, 1996).

### 3. Results and Discussion

#### 3.1 Arsenic and pH analyses of soil samples

A total of 25 soil samples were collected from areas within the Phytoremediation Project and area surrounding landfill containing arsenic contaminated soil. The pH and arsenic concentrations of collected soils were determined and found in the range of 5.39-8.19 and 42.14-1,010.96 ppm (or mg/kg soil), respectively (Table 1). Soils from the Phytoremediation Project had shown a more neutral pH (7.22-8.19) and slightly lower arsenic concentration (42.14-613.13 ppm) than soils from area surrounding arsenic-landfill, which had a slightly acidic pH of 5.39-7.20 and higher arsenic concentration (73.17-1,010.96 ppm). The arsenic levels shown here are relatively similar to those observed by Suwanmanee (1990), which reported arsenic concentration in the ranges of 50-5,300 mg/kg soil from samples obtained in the same vicinity. Arsenic concentration

Table 1. Arsenic concentration and pH value of the soil samples

Sample area	pH	Total arsenic concentration (mg As/kg soil)
Area within the Phytoremediation Project		
Site-1	7.35	123.52
Site-2	7.97	168.44
Site-3	7.88	102.15
Site-4	7.53	157.33
Site-5	7.71	140.07
Site-6	7.85	130.95
Site-7	7.22	42.14
Site-8	7.43	65.96
Site-9	8.00	94.76
Site-10	7.90	108.18
Site-11	7.95	140.77
Site-12	8.13	86.02
Site-13	7.51	613.13
Site-14	7.39	56.37
Area surrounding landfill containing arsenic contaminated soil		
Site-15	6.90	154.19
Site-16	6.95	73.17
Site-17	5.82	195.62
Site-18	7.02	91.49
Site-19	5.39	180.42
Site-20	5.58	102.00
Site-21	6.65	199.77
Site-22	6.72	132.43
Site-23	6.72	367.65
Site-24	6.26	1010.96
Site-25	7.20	641.94

and species are generally influenced by pH and redox potential of soil, soil texture, type of parent rock, organic matter and cation exchange capacity of soil (Mandal and Suzuki, 2002). Thus, arsenate is often the dominant species in aerobic environment or acidic soil and can absorb to organic matters. Sandy soil usually contains lower arsenic level as opposed to soil with high organic contents.

### 3.2 Isolation of arsenic-tolerant bacteria from contaminated soils

Indigenous bacteria from arsenic contaminated soils were firstly enriched in BSMY I broth with increased sodium-arsenite concentrations of 5, 10, 20 and 40 mM. The cultivated samples were then screened for arsenic-tolerant bacteria in BSMY I agar with the addition of 40 mM sodium-arsenite. In all, 45 bacterial strains were isolated from BSMY I medium at different sodium-arsenite concentrations, with 24 bacterial strains able to grow in the presence of 40 mM sodium-arsenite. This result suggested that the isolates may have developed metal resistance systems in an attempt to protect sensitive cellular components. It was observed that

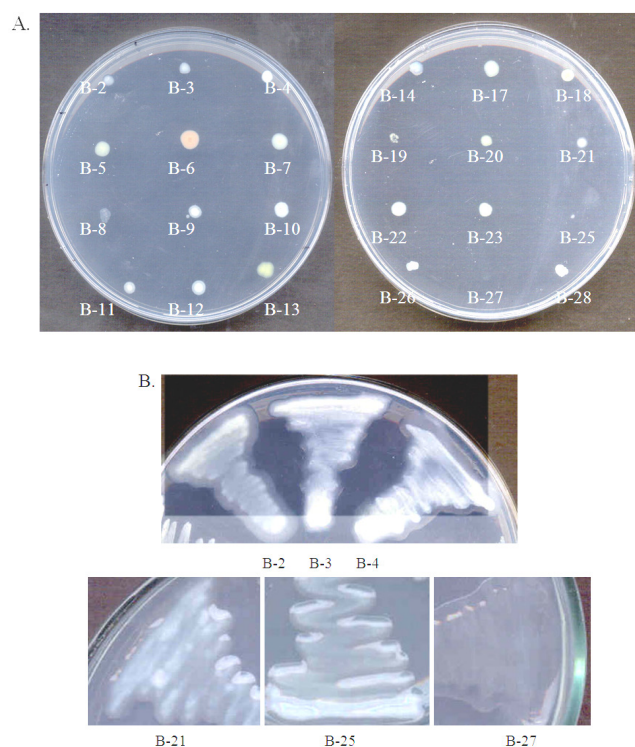


Figure 1. (A) Bacterial isolates grown on BSMY I agar supplemented with 40 mM sodium-arsenite at 30°C for 3 days. (B) Isolates with extracellular polymeric-like substance surrounding the colonies when grown on BSMY I agar supplemented with 40 mM sodium-arsenite at 30°C for 3 days.

most bacterial isolates had an off-white color, circular-shaped, translucent colony with flat plateau and smooth surface. Some isolates also had pale-orange (B-10 and B-19), pink (B-6 and B-18), yellow (B-9, B-13, B-20 and B-22) or colorless colonies (B-8 and B-11) (Figure 1A). Further observation indicated that five isolates (B-2, B-3, B-4, B-21, B-25 and B-27) produced extracellular polymeric-like substance, which may consisted of polysaccharide, protein or nucleic acid with functional group capable of binding to metal ion (Figure 1B). In general, microbial ability to grow at high metal concentration is found coupled with a variety of specific mechanisms of resistance and environmental factors. Mechanisms of resistance by microorganism include microbial surface sorption, enzymatic transformation, precipitation by oxidation/reduction reaction, and biosynthesis of metal binding proteins or extracellular polymers, whereas environmental factors may include the surrounding pH and redox potential, metal speciation, soil particulates, and soluble organic matters (Srinath *et al.*, 2002; Zoubilis *et al.*, 2004).

### 3.3 Effect of arsenic on bacterial growth

All 24 selected isolates showed increase lag and exponential phases of growth when grown in BSMY II with





grow at higher metal concentration than Gram positive bacteria. According to their observed morphological and biochemical characteristics, four isolates (B-6, B-17, B-22 and B-27) were designated to genus *Enterobacter*, three isolates (B-7, B-8 and B-21) to genus *Neisseria*, eight isolates (B-2, B-3, B-9, B-10, B-14, B-25, B-26 and B-28) to genus *Pseudomonas*, four isolates (B-5, B-18, B-20 and B-23) to genus *Staphylococcus*, two isolates (B-4 and B-19) to genus *Streptococcus*, two isolates (B-11 and B-12) to genus *Xanthobacter* and one isolate (B-13) to genus *Xanthomonas*.

Five isolates, i.e., B-4, B-7, B-8, B-10 and B-13, which displayed high arsenic adsorption capacity, were further identified by 16S rDNA analysis. The DNA extracts from each isolate were amplified with 27F-1492R primers and found to provide PCR products of 1,460-bp (data not shown). The PCR fragments were analyzed and the resulting 16S rDNA sequences indicated that the nearest phylogenetic relative of isolates B-7, B-8 and B-10 are *Microbacterium oxydans* (97% identity, 707/724), *Achromobacter* sp. (99% identity, 1378/1379) and *Ochrobactrum anthropi* (97% identity, 1106/1134), respectively (Figure 3). Although the above 16S rDNA analyses placed these isolates in a different genus than those identified by biochemical tests, it must be remember that DNA analysis provides us with the ability to clarify microorganism identity at species level opposed to

group or genus level by biochemical tests. In resolving these differences in identity, the biochemical characteristics of *Microbacterium oxydans*, *Achromobacter* sp. and *Ochrobactrum anthropi* were reviewed and found to be as follows: *Microbacterium oxydans* is an aerobic bacterium which produces acid from sucrose, cannot utilized Simmons' citrate for growth, catalase-positive, oxidase and methyl red-negative (Schumann *et al.*, 1999). *Achromobacter* sp. is an obligated aerobic Gram-negative bacterium which produces acid from sucrose or hydrolyzed starch, reduces nitrate to nitrite, does not liquefy gelatin, does not produced H<sub>2</sub>S and indole, and is oxidase-positive (Chester and Cooper, 1979). *Ochrobactrum anthropi* is an aerobic Gram-negative bacterium which produces acid from glucose, reduces nitrate to nitrite, and is oxidase- and catalase-positive (Laura *et al.*, 1996; Moller *et al.*, 1999). The above characteristics are identical to those observed from isolates B-7, B-8 and B-10 (Table 2). Thus, confirming the results obtained via 16S rDNA analyses.

In contrast, the 16S rDNA sequences of isolates B-4 and B-13 did not show similarity to any bacterial species suggesting that both may be novel arsenic absorbing strains. Based on their morphological and biochemical characteristics, isolates B-4 and B-13 were assigned to the genus *Streptococcus* and *Xanthomonas*, respectively (Figure 3).

The diversity of bacteria isolates is rather typical as

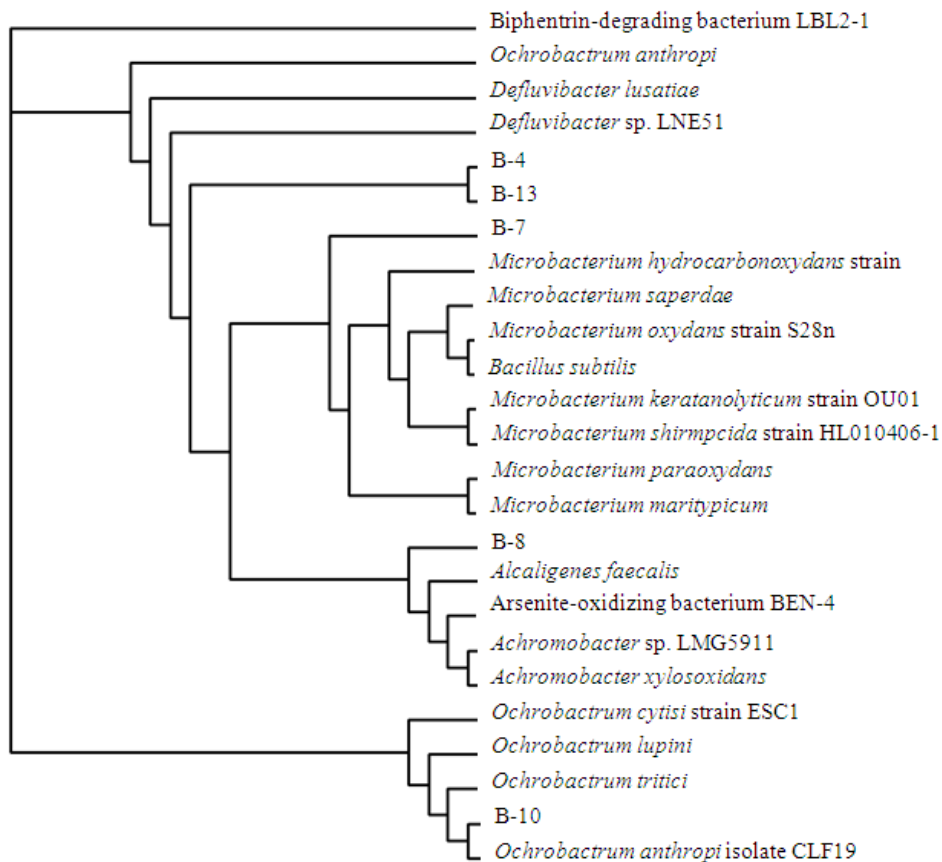


Figure 3. Phylogenetic analysis of arsenic-tolerant bacterial isolates B-4, B-7, B-8, B-10 and B-13.

difference of source and physico-chemical properties of arsenic contaminated samples have been shown to provide different bacteria isolates, such as *Acinetobacter*, *Aeromonas*, *Aureobacterium*, *Bacillus*, *Escherichia*, *Klebsiella*, *Micrococcus*, *Pseudomonas*, *Rhodococcus* and *Stenotrophomonas* (Clausen, 2000; Anderson and Cook, 2004).

#### 4. Conclusion

It was found that all soil samples collected from the Phytoremediation Project and Arsenic landfill were contaminated by arsenic at a level of 15-fold higher than that found in terrestrial soil (1.5-3 ppm). From the soil samples, 45 bacterial isolates were able to grow in BSYM I with 5 mM sodium-arsenite and twenty-four isolates were able to grow with the addition of 40 mM sodium-arsenite. Sixteen isolates were aerobic, Gram-negative, and rod-shaped bacteria. Six isolates were aerobic, Gram-positive, and coccoid-shaped bacteria. Two isolates were aerobic, Gram-negative, coccoid-shaped bacteria. Six isolates, B-2, B-3, B-4, B-21, B-25 and B-27, produced extracellular polymeric-like substance onto the agar medium. This occurrence may result in the removal of arsenite by adsorption to the extracellular polymeric-like substance even at a low cellular biomass of isolates B-21, B-25 and B-27. In the case of isolates B-2, B-3 and B-4 the mechanisms of both cellular adsorption and extracellular polymeric-like substance adsorption may play a combined role in arsenite removal, as shown by the relatively high arsenite removal of more than 75% compared to only 45% by isolates B-21, B-25 and B-27.

Based on biochemical characteristics, all twenty-four isolates were assigned to either genus *Enterobacter*, *Neisseria*, *Pseudomonas*, *Staphylococcus*, *Streptococcus*, *Xanthobacter* or *Xanthomonas*. However, 16S rDNA sequence analysis of five isolates, B-4, B-7, B-8, B-10 and B-13, which showed the highest removal of arsenite from growth medium, suggested a different genus identity. The 16S rDNA sequence analyses of isolates B-7, B-8 and B-10 indicated that they belong to/or are closely related to *Microbacterium oxydans*, *Achromobacter* sp. and *Ochrobactrum anthropi*, respectively. While 16S rDNA sequence analyses of isolates B-4 and B-13 did not show close sequence similarity to any bacterial species in the GenBank database. Therefore, based on their morphological and biochemical characteristics, isolates B-4 and B-13 may be novel arsenic absorbing strains belonging in the genus *Streptococcus* and *Xanthomonas*, respectively. Analysis of arsenite and arsenate levels during cultivation revealed that all isolates displayed arsenite adsorbing activities during either exponential or stationary phases of growth without the presence of any arsenic transforming activity. Bioadsorption of arsenite was found to be in the ranges of 36.87-96.93% from the initial concentration of 40 mM sodium-arsenite. The ability of the isolates which do not produce extracellular polymeric-like substance to remove large amount of arsenite from the cultivation medium are probably due solely to the cellular adsorption mechanism.

In order to fully appreciate the arsenic remediation potential of these five selected isolates, further studies on the use of viable or non-viable biomass as adsorbing material, optimizing the bioadsorption conditions, the possible recycling of this bioadsorbing material, and optimizing of the adsorbing and desorbing conditions need to be investigated.

#### Acknowledgement

This work was supported by Graduate School funding, Prince of Songkla University and Thailand Research Fund-Master Research Grants 2004 (TRF-MAG) (Grant# MRG475S070). We would also like to express our sincere gratitude to Professor Dr. Pornsawan Visoottiviseth for giving us permission to access the Phytoremediation Project for sample collection.

#### References

- Anderson, C. and Cook, G. M. 2004. Isolation and characterization of arsenate-reducing bacteria from arsenic-contaminated sites in New Zealand. *Curr. Microbiol.* 48, 341-347.
- Chester, B. and Cooper, L. H. 1979. *Achromobacter* species (CDC Group V<sub>d</sub>): morphological and biochemical characterization. *J. Clin. Microbiol.* 9, 425-436.
- Clausen, C. A. 2000. Isolation metal-resistant bacteria capable of removing copper, chromium and arsenic from treated wood. *Water Manage. Res.* 18, 264-268.
- Dhar, R. K., Zheng, J., Rubenstone, J. and Geen, A. V. 2004. A rapid colorimetric for measuring arsenic concentrations in groundwater. *Analytica Chimica Acta.* 526, 203-209.
- Dowdle, P. R., Laverman, A. and Oremland, R. S. 1996. Bacterial dissimilatory reduction of arsenic (V) to arsenic (III) in anoxic sediments. *Appl. Environ. Microbiol.* 62, 1664-1669.
- Hasegawa, H., Sohrin, Y., Seki, K., Sato, M., Norisuye, K., Naito, K. and Matsui, M. 2001. Biosynthesis and release of methylarsenic compound during the growth of fresh water algae. *Chemosphere.* 43, 265-272.
- Katsoyiannis, I., Zouboulis, A., Althoff, H. and Bartel, H. 2002. As(III) removal from groundwaters using fixed-bed upflow bioreactors. *Chemosphere.* 47, 325-332.
- Krieg, R. N. 1984. *Bergey's Manual of Systematic Bacteriology.* Williams & Wilkins, Baltimore, pp. 837-942.
- Kuai, L., Nair, A. A. and Polz, M. F. 2001. Rapid and simple method for the most-probable-number estimation of arsenic-reducing bacteria. *Appl. Environ. Microbiol.* 67, 3168-3173.
- Laura, D., Socio, G. D., Frassanito, R. and Rotilio, D. 1996. Effects of atrazine on *Ochrobactrum anthropi* membrane fatty acids. *Appl. Environ. Microbiol.* 62, 2644-2646.
- Leist, M., Casey, R. J. and Caridi, D. 2000. The management of arsenic wastes: problems and prospects. *J. Haz.*

- Mat. 76, 125-138.
- Macy, J. M., Santini, J. M., Panling, B. V., O'Neil, A. H. and Sly, L. I. 2000. Two new arsenate/sulfate-reducing bacteria: Mechanisms of arsenate reduction. *Arch. Microbiol.* 173, 49-57.
- Malik, A. 2004. Metal bioremediation through growing cell. *Environ. Int.* 30, 261-278.
- Mandal, B. K. and Suzuki, K. T. 2002. Arsenic around the world: a review. *Talanta.* 58, 201-235.
- Moller, L. V. M., Arends, J. P., Harmsen, J. M., Talens, A., Terpstra, P. and Slooff, M. J. H. 1999. *Ochrobactrum intermedium* infection after liver transplantation. *J. Clin. Microbiol.* 37, 241-244.
- Niggemyer, A., Spring, S., Stackebrandt, E. and Rosenzweig, R. F. 2001. Isolation and characterization of a novel As(V)-reducing bacterium: Implications for arsenic mobilization and the genus *Desulfitobacterium*. *Appl. Environ. Microbiol.* 67, 5568-5580.
- Page, R. D. M. 1996. TREEVIEW: An application to display phylogenetic trees on personal computers. *Comp. Appl. Biosci.* 12, 357-358.
- Schumann, P., Rainey, F. A., Buyghardt, J., Stackebrandt, E. and Weiss, N. 1999. Reclassification of *Brevibacterium oxydans* (Chetalin and Second 1966) as *Microbacterium oxydans* comb. nov. *Int. J. Syst. Bacteriol.* 49, 175-177.
- Srinath, T., Verma, T., Ramteke, P. W. and Garg, S. K. 2002. Chromium (VI) biosorption and bioaccumulation by chromate resistant bacteria. *Chemosphere.* 48, 427-435.
- Stolz, J. F. and Oremland, R. S. 1999. Bacterial respiration of arsenic and selenium. *FEMS Microbiol. Rev.* 23, 615-627.
- Suwanmanee, A. 1990. The distribution of arsenic in environment Ronpiboon district, Nakhon Srithammarat province. Master of Science Thesis in Environmental Management. Prince of Songkla University.
- Turpinen, R., Pantsar-Kallio, M., Häggblom, M. and Kairesalo, T. 1999. Influence of microbes on the mobilization, toxicity and biomethylation of arsenic in soil. *Sci. Total Environ.* 236, 173-180.
- Visoottiviseth, P., Francesconi, K. and Sridochan, W. 2002. The potential of Thai indigenous plant species for the phytoremediation of arsenic contaminated land. *Environ. Pollut.* 118, 453-461.
- Visoottiviseth, P. and Panviroj, N. 2001. Selection of fungi capable of removing toxic arsenic compounds from liquid medium. *Sci. Asia.* 27, 83-92.
- Wang, C. L., Michels, P. C., Dawson, S. C., Kitisakkul, S., Baross, J. A., Keasling, J. D. and Clark, D. S. 1997. Cadmium removal by a new strain of *Pseudomonas aeruginosa* in aerobic culture. *Appl. Environ. Microbiol.* 63, 4075-4078.
- Yamada, Y., Makimura, K., Mirhendi, H., Ueda, K., Nishiyama, Y., Yamaguchi, H. and Osumi, M. 2002. Comparison of difference methods for extraction mitochondrial DNA from human pathogenic yeast. *JPN J. Infect. Dis.* 55, 122-125.
- Yamamura, S. Ike, M. and Fujita, M. 2003. Dissimilatory arsenate reduction by a facultative anaerobe, *Bacillus* sp. strain SF-1. *J. Biosci. Bioeng.* 96, 454-460.
- Yilmaz, E. I. 2003. Metal tolerance and biosorption capacity of *Bacillus circulans* strain EB1. *Res. Microbiol.* 154, 409-415.
- Zouboulis, A. I., Loukidou, M. X. and Matis, K. A. 2004. Biosorption of toxic metals from aqueous solutions by bacteria strains isolated from metal-polluted soils. *Process Biochem.* 39, 1-8.