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REVIEW ARTICLE

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Microbial transformation of elements: the case of arsenic and selenium

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Abstract Microbial activity is responsible for the transformation of at least one third of the elements in the periodic table. These transformations are the result of assimilatory, dissimilatory, or detoxification processes and form the cornerstones of many biogeochemical cycles. Arsenic and selenium are two elements whose roles in microbial ecology have only recently been recognized. Known as "essential toxins", they are required in trace amounts for growth and metabolism but are toxic at elevated concentrations. Arsenic is used as an osmolite in some marine organisms while selenium is required as selenocysteine (i.e. the twenty-first amino acid) or as a ligand to metal in some enzymes (e.g. FeNiSe hydrogenase). Arsenic resistance involves a small-molecular-weight arsenate reductase (ArsC). The use of arsenic and selenium oxyanions for energy is widespread in prokaryotes with representative organisms from the Crenarchaeota, thermophilic bacteria, low and high G + C gram-positive bacteria, and Proteobacteria. Recent studies have shown that both elements are actively cycled and play a significant role in carbon mineralization in certain environments. The occurrence of multiple mechanisms involving different enzymes for arsenic and selenium transformation indicates several different evolutionary pathways (e.g. convergence and lateral gene transfer) and underscores the environmental significance and selective impact in microbial evolution of these two elements.

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Introduction

Microorganisms are involved in a variety of element transformations including a change in valence (i.e. oxidation/reduction) or chemical form (i.e. solid, liquid, gas). Many of these transformations are key steps in biogeochemical cycles. For example, the conversion of dinitrogen gas to organic nitrogen (in the form of ammonium) by nitrogen-fixing bacteria is crucial for communities in low-nitrogen environments and an important intermediate in the global nitrogen cycle. To date, over 40 elements (in their elemental form or their compounds) are known to be affected by microbial activity. These include the "major" (i.e. carbon, nitrogen, sulfur, oxygen, hydrogen, phosphorus), "minor" (i.e. magnesium, iron, calcium, potassium) and "trace" (i.e. manganese, molybdenum, tungsten, copper, nickel, selenium, and zinc) elements that make up a cell's chemistry. In addition, there are elements needed for specific structure (i.e. skeletal) or function (i.e. catalytic site of an enzyme). Their transformation may be the result of assimilatory processes in which an element is incorporated into cell biomass, dissimilatory processes in which transformation results in the generation of energy, or detoxification [71].

Arsenic and selenium are two elements whose significance in microbial ecology has only recently been recognized [57, 58, 71]. They have some characteristics in common, situated next to each other on the fourth period of the periodic table (As with atomic number 33 and Se with atomic number 34). Their most common chemical oxidation states, however, are different. The primary oxidation states for arsenic are As(V), As(III), As(0), and As(-III), while those for selenium are Se(VI), Se(IV), Se(0), and Se(-II). Both have been called "essential toxins" because they are required in trace amounts for growth and metabolism but are toxic at

high concentrations. They have similar modes of toxicity and are used as antagonists (i.e. arsenic is used for treatment of selenium poisoning and vice versa) [18, 67]. Events such as the loss of wildlife in the Kesterson National Wildlife Refuge due to selenium contamination [61], and the continuing devastation to the people of Bangladesh due to arsenic in their drinking water [49, 50] have promoted the investigation of the role microorganisms play in the mobilization and speciation of these two elements. The purpose of this review is to provide a brief overview of the microbial processes involved in the transformation of oxyanions of arsenic and selenium. Further information can be found in several recent reviews [48, 57, 58, 71] and two book volumes [15, 16].

Arsenic transformation

While arsenic has an historically infamous reputation as a poison [6], its biological uses are less well known. Arsenate is a chemical analog of phosphate and can uncouple mitochondrial oxidative phosphorylation [26]. Arsenite has a high affinity for thiol groups and affects respiration by binding to the vicinal thiols in pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase [52]. It has recently been shown to affect the function of the glucocorticoid receptor [34]. The methylated forms of arsenic, such as monomethylarsonic (MMA) and dimethylarsonic acid (DMA), have been thought to be less toxic and the main route of detoxification in mammals [8]. Recent studies, however, have revealed that not all mammals have methyl transferases [80], and that the methylated species can also have deleterious effects. Paradoxically, organoarsenicals (e.g., arsenobetaine, arsenocholine) are common in marine organisms [4], and while arsenic is added to chicken feed (i.e. Roxarsone) as a prophylactic against coccidial infections [11], it also promotes growth [52].

Two mechanisms for arsenic detoxification have been described. The first mechanism is methylation with either arsenate or arsenite being methylated. In higher eukaryotes, glutathione reduces arsenate to arsenite, which then accepts a methyl group from *S*-adenosylmethionine producing MMA or DMA [52]. An 85-kDa methyltransferase has been identified as mediating the last step [52]. In some bacteria, arsenite is first oxidized to arsenate by a specific enzyme, arsenite oxidase, with the arsenate subsequently methylated [5,19]. The second mechanism, which has been found in bacteria, yeast, and some lower eukaryotes, is the ArsC system [21, 31, 32, 69]. ArsC is a small-molecular-mass protein (13–15 kDa) that mediates the reduction of As(V) to As(III) in the cytoplasm. While As(III) is more toxic, it can be excreted via an As(III)-specific transporter, ArsB [69]. Although originally described as being plasmid borne, chromosomal loci have been found in over 25 species of bacteria, yeasts, and protoctists. While at least three distinct ArsC systems are believed to exist, the system has been best described in bacteria. The *ars* operon of plasmid R733 from *Escherichia coli* comprises *arsA*, *arsB*, *arsC*, *arsD* and *arsR*, whereas the chromosomal locus has only *arsB*, *arsC*, and *arsR* [21, 45]. A cysteine residue near the N-terminal of ArsC binds the arsenate, which is transformed to As(III) with electrons donated by reduced glutathione. As(III) is then expelled from the cytoplasm through an ATP-dependent arsenite transporter formed by ArsAB [45]. The *ars* operon in plasmid pI258 of *Staphylococcus aureus* contains only *arsB*, *arsC*, and *arsD* [31, 32]. In this case, reduced thioredoxin provides the electrons to reduce As(V), and arsenite is expelled from the cell via an ATP-independent ArsB [31, 32].

The widespread ability to utilize the transformation of arsenic oxyanions for the generation of energy has only recently been elucidated [48, 57, 58, 71] . Sixteen species of prokaryotes are known to have the ability to use arsenate as a terminal electron acceptor (Table 1). These include representatives from the Crenarchaeota, thermophilic bacteria, low and high G + C gram-positive bacteria, and Proteobacteria (Fig. 1).

To date, only the respiratory arsenate reductase from *Chrysiogenes arsenatis* has been studied in any detail [38]. A periplasmic enzyme, it is comprised of subunits of 87 and 29 kDa. N-terminal sequence data suggest that both subunits contain an iron-sulfur cluster, and metals analysis has confirmed the presence of Mo, Fe, and S [38]. The protein sequence and the presence of two pyranopterin cofactors per molybdenum atom places this protein in the DMSO reductase subfamily of mononuclear molybdenum enzymes [25]. It is most closely related to polysulfide reductase and formate dehydrogenase F [38]. The enzyme has an apparent K_m of 300 μM and can use benzyl viologen as an electron donor [38]. Initial investigations of the arsenate reductase from the haloalkaliphilic gram-positive bacterium *Bacillus selenitireducens* revealed similar characteristics. N-terminal sequence analysis indicates a 50% sequence identity and 85% similarity of both ArrA and ArrB subunits (Afkar and Stolz, unpublished results). In contrast, the putative arsenate reductase from *Sulfurospirillum barnesii* is membrane bound, consists of a single subunit (48 kDa) and has no metal associated with it (Newman et al., submitted manuscript). It has a comparable K_m of 200 μM, and NADH can also be used as an electron donor. Enzymological and immunological analyses further indicate that *S. barnesii* and related *Sulfurospirillum* species (*S. arsenophilum*, *S. deleyianum*) do not have a *Chrysiogenes*-type arsenate reductase.

The oxidation of arsenite to arsenate is used both for detoxification and for energy generation. Over thirty strains representing at least nine genera of arsenite oxidizing prokaryotes have been reported and include α-, *β*-, and *γ*-Proteobacteria, Deinocci (i.e. *Thermus*), and Crenarchaeota. Physiologically diverse, they include heterotrophic and chemolithoautotrophic species (Table 2).

While the majority of these organisms use oxygen, a *γ*-proteobacterium isolated from Mono Lake, Califor-

Table 1 Arsenate, selenate, and selenite respiring prokaryotes. *TEA* Terminal electron acceptor

Species	Phylogeny	TEA	Reference
Pyrobaculum aerophilum	Crenarchaeota	Arsenate, selenate	[29]
Pyrobaculum arsenicum	Crenarchaeota	Arsenate, selenate	[29]
Thermus sp. HR13	Thermus	Arsenate	[20]
Chrysiogenes arsenatis	Chrysiogenes	Arsenate	[42]
Salana multivorans	Gram +, high G+C	Selenate	[78]
Bacillus selenitireducens	Gram +, low G+C	Arsenate, selenite	[73]
Bacillus arsenicoselenatis	Gram +, low G+C	Arsenate, selenate	[73]
Bacillus sp. JMM-4	Gram +, low G+C	Arsenate	[65]
Bacillus sp. HT-1	Gram +, low G+C	Arsenate	[24]
Clostridium sp. OhILAs	Gram +, low G+C	Arsenate	(A. Dawson, J. Lisak, and J.F. Stolz, unpublished)
Desulfitobacterium sp. OhF2	Gram +, low G+C	Selenate	(T. Kuchan, J. Lisak, and J.F. Stolz, unpublished)
Desulfitobacterium sp. GBFH	Gram +, low G+C	Arsenate	[51]
Desulfotomaculum auripigmentum	Gram +, low G+C	Arsenate	[47]
Selenihalanaerobacter schriftii	Halanaerobacter	Selenate	[74]
Bordetella petrii	β-Proteobacteria	Selenate	[77]
Thauera selenatis	β-Proteobacteria	Selenate	[41]
Aeromonas hydrophila	γ-Proteobacteria	Selenate	[36]
Citrobacter sp. TCA-1	γ-Proteobacteria	Selenate	[24]
Shewanella sp.	γ-Proteobacteria	Arsenate	(Venkateswaran, K., D. Newman, and K.H. Nealson, unpublished)
JSA	γ-Proteobacteria	Selenate	(T. Sakaguchi, E.Tamiya, and K.Yokoyama, unpublished)
TSA	γ-Proteobacteria	Selenate	(T. Sakaguchi, E.Tamiya, and K.Yokoyama, unpublished)
AK4OH1	γ-Proteobacteria	Selenate	[37]
Ke4OH1	γ-Proteobacteria	Selenate	[37]
Desulfomicrobium sp. Ben-RB	δ-Proteobacteria	Arsenate	[43]
Wolinella succinogenes	ϵ-Proteobacteria	Selenate	(M.A. Rasmussen and T.L. Giblin, unpublished)
Wolinella succinogenes R-1	ϵ-Proteobacteria	Arsenate, selenate	[24]
Sulfurospirillum barnesii	ϵ-Proteobacteria	Arsenate, selenate	[40, 55,72]
Sulfurospirillum arsenophilum	ϵ-Proteobacteria	Arsenate	[2,72]

nia, strain MLHE-1, oxidizes arsenite under anoxic conditions using nitrate as the terminal electron acceptor [59]. The physiological role of arsenite oxidation in the most well studied organism, *Alcaligenes faecalis* (which has recently been shown to belong to the genus *Achromobacter* [64]), has been subject to debate. While considered a heterotroph in some reports, studies have shown the presence of a periplasmic electron transfer chain consisting of arsenite oxidase, azurin (a copper-containing protein), cytochrome *c*, and cytochrome *c* oxidase [5,60]. The significance of this is that its arsenate oxidase has been purified [5] and its crystal structure determined [14]. A mononuclear molybdenum enzyme belonging to the DMSO class, it is structurally similar to the periplasmic nitrate reductase (NapA) from *Desulfovibrio desulfuricans* [14]. Comprising two subunits, the catalytic subunit (~85 kDa) contains molybdenum bound to two pterin cofactors and a [3Fe-4S] cluster. The associated subunit (~14 kDa) presumably functions as an electron shuttle and has a Rieske-type [2Fe-2S] cluster, a feature that is unique among molybdenum enzymes [14]. In addition, unlike other members of the DMSO reductase family, the molybdenum center is not coordinated by any endogenous protein ligand. Whether these will be common characteristics of all arsenite oxidases remains to be determined.

Arsenic is an important factor in biogeochemical cycling. While not considered an abundant element, it can reach significant concentrations in hydrothermal, sulfidic, evaporitic, and iron-hydroxide-rich environments [79]. Arsenate-respiring bacteria affect the speciation and mobilization of arsenic as they have been shown to release arsenite from sediments [3, 33] and ferrihydrite [81], as well as grow on arsenate-containing minerals (i.e. Scorodite) [47]. The discovery of chemolithoautotrophic arsenite oxidizers suggests that they could contribute to the overall carbon budget of microbial communities in arsenic-rich environments [27, 56, 59, 63, 64]. Arsenate respiration has been linked to the mineralization of ~14% of the photosynthate fixed during meromixis in Mono Lake, California [56]. The rates of arsenate respiration were so significant that they indicated a need for microbial oxidation and led to the discoveries of the anaerobic arsenite oxidizer and a robust arsenic cycle in the lake [56,59].

Selenium tranformation

Selenium is similar to arsenic in many respects. Selenium is an analog of sulfur and substitutes for sulfur in thiols. In high doses it causes respiratory distress, is

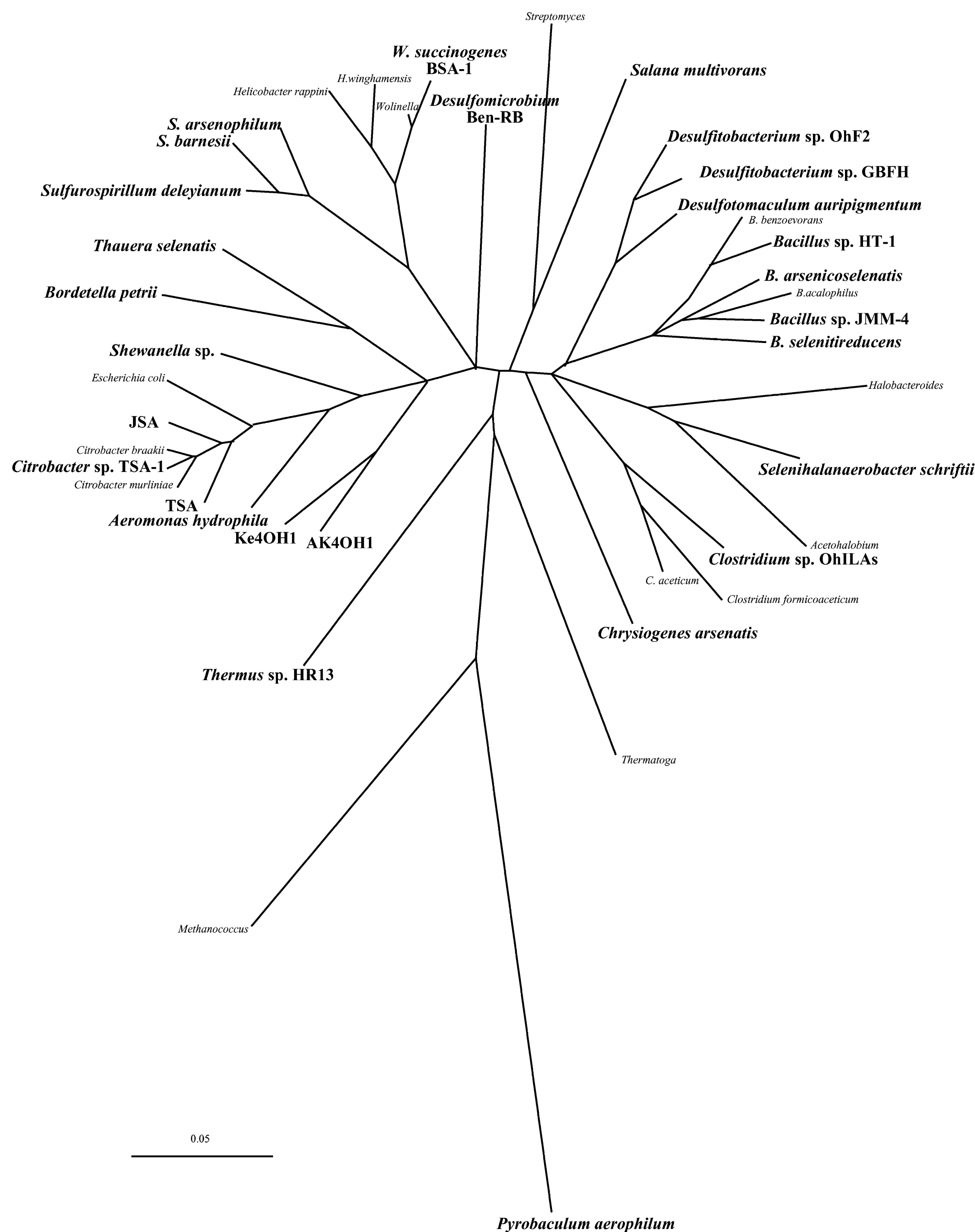

Fig. 1 Phylogenetic tree of prokaryotes that respire arsenic and selenium oxyanions constructed using distance matrix analysis (PAUP) [74]. Organisms not in bold type and in a smaller font are non-arsenic and non-selenium respiring species that were added to help define specific branches

teratogenic, and has clinical manifestations (e.g., blind staggers, alkali disease) [23, 28]. Trace amounts, however, are essential and it is often added to livestock feed [23]. The common biological forms are selenocysteine (the twenty-first amino acid) and selenomethionine. Selenocyteine is encoded by its own tRNA and provides the selenium in glycine reductase, formate dehydrogenase, and NiFeSe hydrogenase [17, 23, 46]. Selenium is assimilated in yeast and plants via the sulfur assimilation pathway [12,23]. Selenate is activated by ATP sulfurylase and subsequently converted to selenomethione [12]. While a similar mechanism has been proposed for prokaryotes, some studies have suggested specific mechanisms for the uptake of selenate and selenite [9, 10]. The reaction of selenite with glutathione produces selenodiglutathione. Selenodiglutathione and its subsequent reduction to glutathioselenol are key intermediates in the transformation of selenium [76].

Several different mechanisms are known for the detoxification of selenium. As with arsenic, methylation via a methyltranferase is a common mode of removal in eukaryotes [22] and prokaryotes [23]. Again, the reactivity of glutathione and other reduced species (i.e. dithiothreitol) with selenium creates a number of different intermediates. Selenocystine can be reduced to hydrogen selenide by reduced glutathione via selenocysteine-glutathione selenenyl sulfide [66]. Another strategy for detoxification is the reduction of selenite to elemental selenium. Selenium deposits may collect in the cytoplasm [7, 35], periplasm, or extracellularly [73, 74]. The phototrophic bacterium *Rhodospirillum rubrum* has

Table 2 Representative arsenite oxidizing prokaryotes. *TEA* Terminal electron acceptor, *NR* non-respiratory

Species	Phylogeny	TEA	Reference
Achromobacter "Alcaligenes" faecalis	β-Proteobacteria	NR	[60]
Agrobacterium albertimagni AOL15	α-Proteobacteria	NR	[62]
MLHE-1	γ-Proteobacteria	Nitrate	[59]
NT-26	α-Proteobacteria	Oxygen	[64]
Pseudomonas putida	γ-Proteobacteria	NR	[1]
Pseudomonas arsenitoxidans	γ-Proteobacteria	Oxygen	[30]
Thermus aquaticus	Thermus	NR	[19]
Thermus thermophilus	Thermus	NR	[19]
Thermus sp. HR13	Thermus	NR	[20]

been shown to expel elemental selenium across the plasma membrane and cell wall [35].

The use of selenium oxyanions, primarily selenate, as terminal electron acceptors is also widespread among prokaryotes, with at least two species of Crenarchaeota and fifteen species of bacteria (Fig. 1, Table 1). The respiratory selenate reductase from *Thauera selenatis* has been purified and characterized, and the genes encoding it cloned and sequenced [39, 68]. A heterotrimeric enzyme composed of subunits of 96, 40 and 23 kDa, it contains Mo, Fe, and S and has a visible spectrum indicative of a cytochrome b_{558} [68]. Located in the periplasm, it has a K_m for selenate of 16 μM. The *ser* operon contains four open reading frames, *serA*, *serB*, *serC*, and *serD* [39]. serA is the molybdenum-containing catalytic subunit. A member of the DMSO class of mononuclear molybdenum enzymes, it is most closely related to the membrane-bound nitrate reductase (NarG) of *Haloarcula marismortuii* (Stolz, unpublished data). serB contains four iron-sulfur cluster-binding sites while the serC is the putative cytochrome b_{558}. Similar to the function of narJ, serD may be a chaperone protein [39]. The enzyme has been crystallized recently, but its structure has yet to be elucidated [44].

Selenate respiring bacteria may also influence the speciation and mobility of selenium in the environment. Microbially driven selenate reduction, which has been found in a wide range of sediment types, results in the precipitation of elemental selenium [53, 54, 70]. While the remobilization of selenium through oxidation does occur, the rates are three to four orders of magnitude less than the reductive part of the cycle [13]. Thus unlike arsenic, microbial activity actually removes selenium from the environment.

Conclusions

Arsenic and selenium represent two examples of element transformation by prokaryotes. Prokaryotes with the ability to methylate, oxidize, or reduce inorganic and organic species of arsenic and selenium are widespread in nature and not confined to contaminated environments. This suggests that arsenic and selenium are more important in microbial ecology than previously recognized. The occurrence of multiple mechanisms for arsenate reduction is an indication of convergent evolution, whereas the presence of similar terminal reductases in distantly related species is suggestive of horizontal gene transfer. In addition, the phylogenetic diversity of species that can metabolize these two elements suggests that they are significant selective agents in microbial evolution.

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References

1. Abdrashitova, SA, Mynbaeva BN, Ilyaletdinov AN (1981) Oxidation of arsenic by the heterotrophic bacteria *Pseudomonas putida* and *Alcaligenes eutrophus*. Mikrobiologya 50:41–45
2. Ahmann, D, Roberts AL, Krumholz LR, Morel FMM (1994) Microbe grows by reducing arsenic. Nature 371:750
3. Ahmann, D, Krumholz LR, Hemond H, Lovley DR, Morel FMM (1997) Microbial mobilization of arsenic from sediments of the Aberjona Watershed. Environ Sci Technol 31:2923–2930
4. Almela C, Algora S, Benito V, Clemente MJ, Devesa V, Suner MA, Velez D, Montoro R (2002) Heavy metal, total arsenic, and inorganic arsenic contents of algae food products. J Agric Food Chem 50:918–923
5. Anderson GL, Williams J, Hille R (1992) The purification and characterization of arsenite oxidase from *Alcaligenes faecalis*, a molybdenum-containing hydroxylase. J Biol Chem 267:23674–23682
6. Azcue JM, Nriagu JO (1994) Arsenic, historical perspectives. In: Nriagu JO (ed.) Arsenic in the environment. Vol 26. Wiley & Sons, New York, NY, pp 1–16
7. Bebien M, Chauvin JP, Adriano JM, Grosse S, Verméglio A (2001) Effect of selenite on growth and protein synthesis in the phototrophic bacterium *Rhodobacter sphaeroides*. Appl Environ Microbiol 67:4440–4447
8. Bode AM, Dong Z (2002) The paradox of arsenic: molecular mechanisms of cell transformation and chemotherapeutic effects. Crit Rev Oncology Hematol 42:5–24
9. Brown TA, Shrift A (1980) Assimilation of selenate and selenite by *Salmonella typhimurium*.Can J Microbiol 26:671–675
10. Brown TA, Shrift A (1982) Selective assimilation of selenite by *Escherichia coli*. Can J Microbiol. 28:307–310
11. Czarnecki GL, Baker DH (1982) Roxarsone toxicity in the chick as influenced by dietary cysteine and copper and by experimental infection with *Eimeria acervulina*. Poult Sci 61:516–23
12. de Souza MP, Lytle CM, Mulholland MM, Otte ML, Terry N (2000) Selenium assimilation and volatilization from dimethylselenonioproprionate by Indian mustard. Plant Physiol 122:1281–1288.
13. Dowdle PR, Oremland RS (1998) Microbial oxidiation of elemental selenium in soil slurries and bacterial cultures. Environ Sci Technol 32:3749–3755
14. Ellis PJ, Conrads T, Hille R, Kuhn P (2001) Crystal structure of the 100 kDa arsenite oxidase from *Alcaligenes faecalis* in two crystal forms at 1.64 and 2.06 A. Structure 9:125–132

15. Frankenberger WTJr, Engberg RA (eds) (1998) Environmental chemistry of selenium. Marcel Dekker, New York
16. Frankenberger WT Jr (ed) (2001) Environmental chemistry of arsenic. Marcel Dekker, New York
17. Garcin E, Vernede X, Hatchikian EC, Volbeda A, Frey M, Fontecilla-Camps JC (1999) The crystal structure of a reduced [NiFeSe] hydrogenase provides an image of the activated catalytic center. Struct Fold Des 7:557–566
18. Gebel T (2000) Confounding variables in the environmental toxicology of arsenic. Toxicology 144:155–162
19. Gihring TM, Druschel GK, McCleskey RB, Hamers RJ, Banfield JF (2001) Rapid arsenite oxidation by *Thermus aquaticus* and *Thermus thermophilus*: field and laboratory observations. Environ Sci Technol 35:3857–3862
20. Gihring TM, Banfield JF (2001) Arsenite oxidation and arsenate respiriation by a new *Thermus* isolate. FEMS Microbiol Lett 204:335–340
21. Gladysheva TB, Oden KL, Rosen BP (1994) Properties of the arsenate reductase of plasmid R773. Biochemistry 33:7288–7293
22. Hassoun BS, Palmer IS, Dwivedi C (1995) Selenium detoxification by methylation. Res Commun Mol Pathol Pharmacol 90:133–142
23. Heider J, Boeck A (1993) Selenium metabolism in microorganisms. Adv Microbiol Physiol 35:71–109
24. Herbel MJ, Switzer Blum J, Hoeft SH, Cohen SM, Arnold LL, Lisak J, Stolz JF, Oremland R. (2002) Dissimilatory arsenate reductase activity and arsenate-respiring bacteria in bovine rumen fluid, hamster feces, and the termite hindgut. FEMS Microbiol Ecol 41:59–67
25. Hille R (1996) The mononuclear molybdenum enzymes. Chem Rev 96:2757-2816
26. Hindmarsh JT (2000) Arsenic, its clinical and environmental significance. J Trace Elem Exp Med 13:165–172
27. Hoeft SE, Lucas F, Hollibaugh JT, Oremland RS (2002) Characterization of microbial arsenate reduction in the anoxic bottom waters of Mono Lake, California. Geomicrobiol J 19:23–40
28. Hoffman DJ (2002) Role of selenium toxicity and oxidative stress in aquatic birds. Aquatic Toxic 57:11–26
29. Huber R, Sacher M, Vollmann A, Huber H, Rose D (2000) Respiration of arsenate and selenate by hyperthermophilic Archaea. Syst Appl Microbiol 23:305–314
30. Ilyaletdinov AN, Abdrashitova SA (1981) Autotrophic oxidation of arsenic by a culture of *Pseudomonas arsenitoxidans*. Mikrobiologya 50:197–204
31. Ji, G, Silver S (1992) Reduction of arsenate to arsenite by the ArsC protein of the arsenic resistance operon of *Staphylococcus aureus* plasmid pI258. Proc Nat Acad Sci 89:9474–9478
32. Ji G, Garber EAE, Armes LG, Chem CM, Fuchs JA, Silver S (1994) Arsenate reductase of *Staphylococcus aureus* plasmid pI258. Biochemistry 33:7294–7299
33. Jones CA, Langner HW, Anderson K, McDermott TR, Inskeep WP (2000) Rates of microbially mediated arsenate reduction and solubilization. Soil Sci Soc Am J 64:600–608
34. Kaltreider RC, Davis AM, Lariviere JP, Hamilton JW (2001) Arsenic alters the function of the glucocorticoid receptor as a transcription factor. Environ Health Perspect 109:245–251
35. Kessi J, Ramuz M, Wehrli E, Spycher M, Bachofen R (1999) Reduction of selenite and detoxification of elemental selenium by the phototrophic bacterium *Rhodospirillum rubrum*. Appl Environ Microbiol 65:4734–4740
36. Knight VK, Blakemore R (1998) Reduction of diverse electron acceptors by *Aeromonas hydrophila*. Arch Microbiol 169:239–248
37. Knight VK, Nijenhuis I, Kerhof LJ, Haeggblom MH (2002) Degradation of aromatic compounds coupled to selenate reduction. Geomicrobiol J 19:77–86
38. Krafft T, Macy JM (1998) Purification and characterization of the respiratory arsenate reductase of *Chrysiogenes arsenatis*. Eur J Bioch 255:647–653
39. Krafft T, Bowen A, Theis R, Macy JM (2000) Cloning and sequencing of the genes encoding the periplasmic cytochrome b containing selenate reductase of *Thauera selenatis*. DNA Sequence 10:365–377
40. Laverman AM, Switzer Blum J, Schaefer JK, Phillips EJP, Lovley DR, Oremland RS (1995) Growth of strain SES-3 with arsenate and other diverse electron acceptors. Appl Environ Microbiol 61:3556–3561
41. Macy J.M, Rech S, Auling G, Dorsch M, Stackebrandt E, Sly LI (1993) *Thauera selenatis* gen. nov., sp. nov., a member of the beta subclass of Proteobacteria with a novel type of anaerobic respiration. Int J Syst Bacteriol 43:135–142
42. Macy JM, Nunan K, Hagen KD, Dixon DR, Harbour PJ, Cahill M, Sly LI (1996) *Chrysiogenes arsenatis*, gen. nov., sp. nov., a new arsenate-respiring bacterium isolated from gold mine wastewater. Int J Syst Bacteriol 46:1153–1157
43. Macy JM, Santini JM, Pauling BV, O'Neill AH, Sly LI (2000) Two new arsenate/sulfate reducing bacteria: mechanisms of arsenate reduction. Arch Microbiol 173:49–57
44. Maher MJ, Macy JM (2002) Crystallization and preliminary X-ray analysis of the selenate reductase from *Thauera selenatis*. Acta Cryst 58:706–708
45. Martin P, DeMel S, Shi J, Gladysheva T, Gatti DL, Rosen BP, Edwards BFP (2001) Insights into the structure, solvation, and mechanism of ArsC arsenate reductase, a novel arsenic detoxification enzyme. Structure 9:1071–1081
46. Menon NK, Peck HD Jr, Le Gall J, Przybyla AE (1987) Cloning and sequencing of the genes encoding the large and small subunits of the periplasmic (NiFeSe) hydrogenase of *Desulfovibrio baculatus*. J Bacteriol 169:5401–5407
47. Newman DK, Kennedy EK, Coates JD, Ahmann D, Ellis DJ, Lovley DR, Morel FMM (1997) Dissimilatory arsenate and sulfate reduction in *Desulfotomaculum auripigmentum* sp. nov. Arch Microbiol 168:380–388
48. Newman DK, Ahmann D, Morel FMM (1998) A brief review of microbial arsenate respiration. Geomicrobiol J 15:255–268
49. Nickson R, McArthur J, Burgess W, Ahmed KM, Ravenscroft P, Rahman M (1998) Arsenic poisoning of Bangladesh groundwater. Nature 395:398
50. Nickson RT, McArthur JM, Ravenscroft P, Burgess WG, Ahmed KM (2000) Mechanism of arsenic release to groundwater, Bangladesh and West Bengal. Appl Geochem 15:403–413
51. Niggemyer A, Spring S, Stackebrandt E, Rosenzweig RF (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
52. NRC (1999) National Research Council Report: Arsenic in Drinking Water. National Academy Press, Washington, DC
53. Oremland RS, Steinberg NA, Maest AS, Miller LG, Hollibaugh JT (1990) Measurements of in situ rates of selenate removal by dissimilatory bacterial reduction in sediments. Environ Sci Tech 24:1157–1164
54. Oremland RS, Steinberg NA, Presser TS, Miller LG (1991) In situ bacterial selenate reduction in the agricultural drainage systems of western Nevada. Appl Environ Microbiol 57:615–617
55. Oremland RS, Switzer Blum J, Culbertson CW, Visscher PT, Miller LG, Dowdle P, Strohmaier FE (1994) Isolation, growth, and metabolism of an obligately anaerobic, selenate-respiring bacterium, strain SES-3. Appl Environ Microbiol 60:3011–3019
56. Oremland RS, Dowdle PR, Hoeft S, Sharp JO, Schaefer JK, Miller LG, Switzer Blum J, Smith RL, Bloom NS, Wallschlaeger D (2000) Bacterial dissimilatory reduction of arsenate and sulfate in meromictic Mono Lake, California. Geochem Cosmochem Acta 64:3073–3084
57. Oremland RS, Stolz JF (2000) Dissimilatory reduction of selenate and arsenate in nature. In: Lovley DR (ed) Environmental microbe – metal interactions. ASM Press, Washington, DC, pp 199–224

58. Oremland R.S, Newman DK, Kail BW, Stolz JF (2001) Bacterial respiration of arsenate and its significance in the environment. In: Frankenberger WTJr (ed) Environmental chemistry of arsenic. Marcel Dekker, New York, pp 273–295
59. Oremland RS, Hoeft SE, Santini JM, Bano N, Hollibaugh RA, Hollibaugh JT (2002) Anaerobic oxidation of arsenite in Mono Lake water and by a facultative, arsenite-oxidizing chemoautotroph, strain MLHE-1. Appl Environ Microbiol 68:4795–4802
60. Osborne FH, Ehrlich HL (1976) Oxidation of arsenite to arsenate by a soil isolate of *Alcaligenes*. J Appl Bacteriol 41:295–305
61. Presser TS (1994) The Kesterson effect. Environ Manag 18:437–454
62. Salmassi TM, Venkateswaren K, Satmomi M, Nealson KH, Newman DK, Hering JG (2002) Oxidation of arsenite by *Agrobacterium albertimagni*, AOL15, sp. nov. from Hot Creek, California. Geomicrobiol J 19:53–66
63. Santini JM, Sly LI, Schnagl RD, Macy JM (2000) A new chemolithoautotrophic arsenite-oxidizing bacterium isolated from a gold mine: phylogenetic, physiological, and preliminary biochemical studies. Appl Environ Microbiol 66:92–97
64. Santini JM, Sly LI, Wen A, Comrie D, de Wulf-Durand P, Macy JM (2002) New arsenite-oxidizing bacteria isolated from Australian gold mining environments—phylogenetic relationships. Geomicrobiol J 19:67–76
65. Santini JM, Stolz JF, Macy JM (2002) Isolation of a new arsenate-respiring bacterium—physiological and phylogenetic studies. Geomicrobiol J 19:41–52
66. SayatoY, Nakamuro K, Hasegawa T (1997) Selenium methylation and toxicity mechanism of selenocystine. Yakugaku Zasshi 117:665–672
67. Schrauzer GN (1976) Selenium and cancer: a review. Bioinorg Chem 5:275–281
68. Schroeder I, Rech S, Krafft T, Macy JM (1997) Purification and characterization of the selenate reductase from *Thauera selenatis*. J Biol Chem 272:23765–23768
69. Silver S, Ji G, Bröer S, Dey S, Dou D, Rosen BP (1993) Orphan enzyme or patriarch of a new tribe: the arsenic resistance ATPase of bacterial plasmids. Mol Microbiol 8:637–642
70. Steinberg NA, Oremland RS (1990) Dissimilatory selenate reduction potentials in a diversity of sediment types. Appl Environ Microbiol 56:3550–3557
71. Stolz JF, Oremland RS (1999) Bacterial respiration of arsenic and selenium. FEMS Microbiol Rev 23:615–627
72. Stolz JF, Ellis DJ, Switzer Blum J, Ahmann D, Lovley DR, Oremland RS (1999) *Sulfurospirillum barnesii* sp. nov., *Sulfurospirillum arsenophilus* sp. nov., and the *Sulfurospirillum* clade in the Epsilon Proteobacteria. Int J Syst Bacteriol 49:1177–1180.
73. Switzer Blum J, Bindi AB, Buzzelli J, Stolz JF, Oremland RS (1998) *Bacillus arsenoselenatis* sp. nov., and *Bacillus selenitireducens* sp. nov.: two haloalkaliphiles from Mono Lake, California, which respire oxyanions of selenium and arsenic. Arch Microbiol 171:19–30
74. Switzer Blum J, Stolz JF, Ohren A, Oremland RS (2001) *Selenihalanaerobacter shriftii* gen. nov. sp. nov., a halophilic anaerobe from Dead Sea sediments that respires selenate. Arch Microbiol. 175:208–219
75. Swofford DL (1998) PAUP*. Phylogenetic analysis using parsimony (*and other methods) version 4. Sinauer, Sunderland, Massachusetts
76. Turner RJ, Weiner JH, Taylor DE (1998) Selenium metabolism in *Escherichia coli*. Biometals 11:223–227
77. von Wintzingerode F, Schattke A, Siddiqui RA, Rösick U, Göbel UB, Gross R (2001) *Bordetella petrii*. sp. nov., isolated from an anaerobic bioreactor, and emended description of the genus *Bordetella*. Int J Syst Evol Microbiol 51:1257–1265
78. Von Wintzingerode F, Göbel UB, Siddiqui RA, Rösick U, Schumann P, Frühling A, Rohde M, Pukall R, Stackebrandt E (2001) *Salana multivorans* gen. nov., sp. nov., a novel actinobacterium isolated from an anaerobic bioreactor and capable of selenate reduction. Int J Syst Evol Microbiol 51:1653–1661
79. Welch AH, Westjohn DB, Helsel DR, Wanty RB (2000) Arsenic in ground water of the United States: occurrence and geochemistry. Groundwater 38:589–604
80. Wildfang E, Radabaugh TR, Aposhian HV (2001) Enzymatic methylation of arsenic compounds. IX. Liver arsenite methyltransferase and arsenate reductase activities in primates. Toxicology 168:213–221
81. Zobrist J, Dowdle PR, Davis JA, Oremland RS (2000) Mobilization of arsenite by dissimilatory reduction of adsorbed arsenate. Environ Sci Technol 34:4747–4753