

Arsenic Mobility is Mediated by Bacterial Reduction in New Jersey Shallow Groundwater

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Introduction

The mobilization of arsenic bound to aquifer sediments is a source of contamination in groundwater in New Jersey. Deep Coastal Plain sediments have average As concentrations of 15-23 mg/kg [1,2], and As concentrations of 26 mg/kg have been recorded in shallow glauconitic sediments[3]. In a prior study [3] we demonstrated that As reducing bacteria promote As release and mobility in groundwater at a New Jersey Coastal Plain site. We have expanded this study to investigate the potential for microbial As mobilization beneath the streambeds at two other sites, Six Mile Run and Pike Run, in the New Jersey Piedmont. Groundwater at the Six Mile Run site has an As concentration of 27 µg/L, which is in excess of the 5µg/L limit set by the NJDEP, while the As concentration at the Pike Run site is 2.1 µg/L.

Methods:

Groundwater was sampled on gaining reaches of Pike Run and Six Mile Run in the New Jersey Piedmont Physiographic Province, and inoculated into anaerobic microcosms with acetate as a carbon source and As(V) as an electron acceptor. Arsenic reduction was monitored by HPLC. Groundwater was filtered on site, and DNA was extracted from the filters for amplification and cloning of the 16S rRNA gene and the arsenate respiratory reductase gene, *arrA*, a biomarker for As(V) respiration [4]. 16S rRNA gene sequence data was analyzed using ARB [5] and the SILVA 108 NR 16S rRNA gene database [6]. *arrA* gene sequence analysis was performed using ARB [6]. Operational Taxonomic Unit (OTU) analysis was performed with mothur [7].

Results and Conclusions

Microcosms developed from Six Mile Run groundwater reduced 1 mM of As(V) to As(III) in 30 days, while microcosms from Pike Run did not reduce As. Based on a 97% similarity cutoff, 10 OTUs unique to Six Mile Run were identified, and 11 OTUs unique to Pike Run were identified. The sites shared 4 OTUs out of the 25 sequenced, suggesting that distinct bacterial communities were present at each site. Based on the *arrA* gene, distinct arsenic respiring communities were identified at each site, with 8 unique OTUs found at Six Mile Run, and 11 unique OTUs shared at Pike Run. Globally, the *arrA* sequences recovered from both Pike Run and Six Mile Run are most similar to those recovered from the Meuse River in France, and distinct from those recovered from marine environments. Our findings demonstrate that while the *arrA* gene may indicate the presence of As reducing organisms, microcosm studies are necessary to predict microbial As reduction and mobilization from sediments.

[1] Dooley (1998) *The New Jersey Geological Survey Technical Memorandum 98-1*. [2] Dooley (2001) *N. J. Geological Survey Investigation Report* [3] Mumford *et al.* (2012) *Water Res. In Review* [4] Malasarn *et al.* (2004) *Science* **306**, 455. [5] Ludwig *et al.* (2004) *Nucleic Acids Res* **32**, 1363-1371, [6] Pruesse *et al.* (2007) *Nucleic Acids Res* **35**, 7188-7196 [7] Schloss *et al.* (2009) *Appl Env Microb* **75**, 7537-7541

Combining macroscopic invasion percolation with mass transfer to model bubble-facilitated transport of VOCs in groundwater

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Gas bubbles present in otherwise water-saturated porous media can affect the transport of volatile organic compounds (VOCs) in groundwater. The partitioning of VOCs to gas bubbles, with the bubbles acting as a variable-volume sink, can retard VOC transport, and can also affect the transport of other volatile species (e.g., dissolved atmospheric or biogenic gases). If sufficient gas volumes exist for bubbles to be vertically mobilized, the transport is also affected by the creation of an additional mass transport pathway – the buoyant advection of the bubbles – which can carry mass away from regions with higher aqueous concentration to those with lower aqueous concentration, resulting in mass partitioning from the bubble back to the aqueous phase. This type of transport has been observed in a variety of systems, including: the natural attenuation of hydrocarbon plumes, the expansion of trapped gases above non-aqueous phase liquid (NAPL) sources, and remediation by in situ thermal treatment.

In these types of systems, where the expansion and mobilization of the gas bubbles is controlled by the mass transfer between the aqueous phase and the trapped gas phase, it is important to model both the partitioning of multiple volatile species and the subsequent discontinuous bubble flow as mass transfer and immiscible displacement occur over similar time scales. One promising approach is the use of macroscopic invasion percolation (MIP) to model gas movement, combined with continuum-scale simulation of aqueous-phase transport and mass transfer between phases. The MIP routine can be modified to include gravity for biased vertical growth, as well as fragmentation and mobilization to reproduce bubble behaviour, provided that gridblock sizes are less than a critical length scale required for mobilization. Here, simulations of VOC transport in the presence of mobilized gas bubbles were compared to an intermediate-scale laboratory flow cell experiment, where non-monotonic changes in concentrations were observed at higher-than-expected elevations above a dense non-aqueous phase liquid (DNAPL) pool. Additional simulations that investigated the potential role of bubbles during in situ thermal remediation showed greater mass removal from a targeted heating area due to bubble formation and mobilization. Finally, a third set of simulations investigated bubble-facilitated transport of VOCs in heated and unheated, heterogeneous systems.