Bacterial productivity in a cyanide-contaminated aquifer

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Heterotrophic bacterial productivity and microbial cell density were examined in groundwater from nine wells in a cyanide-contaminated aquifer in the 200 Area at the US Department of Energy's Hanford Site in southeastern Washington State. Tritiated leucine (^{3}H-Leu) uptake served as a proxy for heterotrophic, aerobic bacterial productivity, and cell density was determined by nucleic acid staining followed by epifluorescence microscopy.

Results show that the ^{3}H-Leu uptake assay is a valid tool to assess productivity of heterotrophic groundwater bacteria, confirming recent attempts to adapt the technique from surface waters to aquifers [1-3]. Bacterial productivity, as indicated by ^{3}H-Leu uptake, varied widely, both among wells that had high historical or recent cyanide (CN^-) concentrations and among wells that had low CN^- values. Standing microbial biomass, as indicated by microscopic cell counts, varied less, and was generally greater than that observed in a similar study at Hanford for a uranium-affected aquifer [1].

Even though CN^- is a potential microbial inhibitor, our results suggest that CN^- contamination in the 200 Area aquifer has not likely limited microbial biomass production. Rather, other geochemical factors likely drive bacterial productivity in the aquifer. Consequently, our results suggest that CN^- contamination is unlikely to inhibit microbially facilitated *in situ* attenuation and degradation of co-contaminants in the aquifer, under either bioremediation or monitored natural attenuation scenarios. Alternate microbial probing, such as anaerobic tritiated leucine uptake for anaerobic bacteria and carbon-14 labelled bicarbonate incorporation for autotrophs, might provide a more complete assessment of the bacterial productivity of the aquifer, and could provide additional information on factors limiting bacterial productivity, including contaminants such as cyanide and iron cyanide species.

[1] Konopka *et al*. (2013) *Microb. Ecol.* **66**, 889-896. [2] Velasco Ayuso *et al.* (2010) Geomicrobiol. J. **27**, 409-423. [3] Wilhartitz *et al.* (2009) FEMS Microb. Ecol. **68**, 287-299.