



Defining Conditions for Maximizing Bioreduction of Uranium

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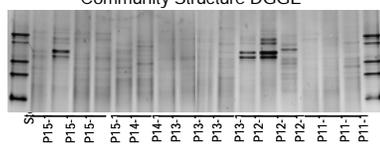
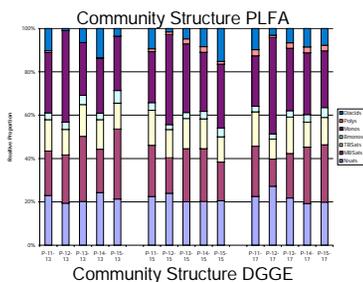
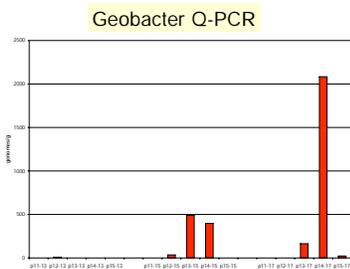
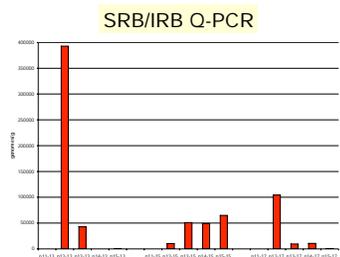
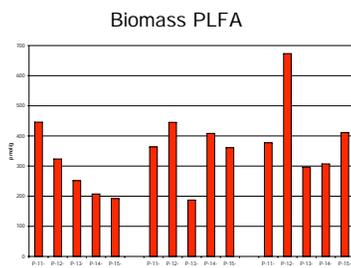
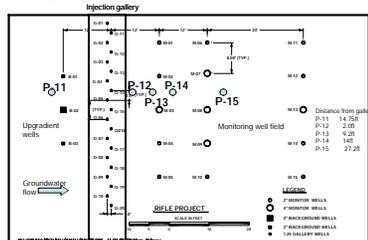


UMTRA Old Rifle Biostimulation Sediment Data

Correlations between modifying electron donor and acceptor accessibility, the in-situ microbial community, and bioreduction of Uranium at the FRC and UMTRA research sites indicated that significant modifications in the rate, amount and by inference the potential stability of immobilized Uranium are feasible in these environments. The in-situ microbial community at these sites was assessed with a combination of lipid and real-time molecular techniques providing quantitative insights of effects of electron donor and manipulations.

Increased (9mM in 2003 vs 3mM 2002) donor amendment at the Old Rifle site resulted in the stimulation of anaerobic conditions downgradient of the injection gallery. Biomass within the test plot increased relative to the control well at 17'. Q-PCR specific for IRB/SRB showed increased copy numbers within the test plot and was the highest at the injection gallery. Q-PCR specific for *Geobacter* sp. showed increased copy numbers within the test plot but further downgradient from the injection gallery than the SRB/IRB. DNA and Lipid analysis confirm changes in the microbial community structure due to donor addition. See also the PNNL (Long) and UMMASS (Anderson) posters for more information about this site.

Rifle Site 2003 Sediment Core Collection Positions



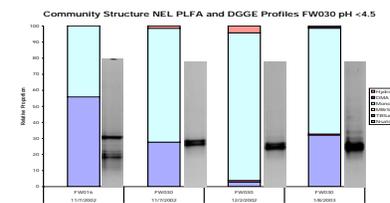
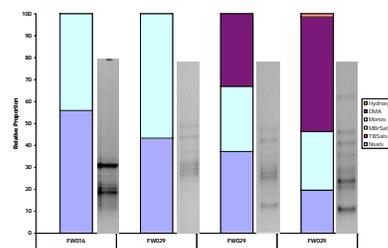
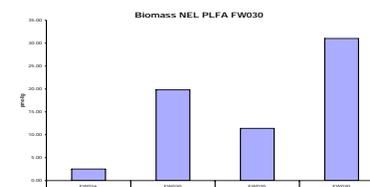
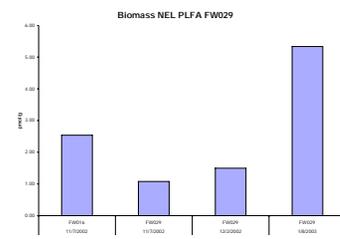
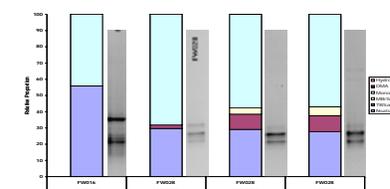
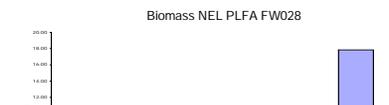
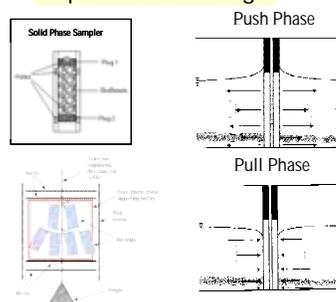
Comparison of DGGE profile of direct DNA PCR amplification and cDNA amplified from total RNA

Ask about 13C donors
Quinones and
Ferrihydrite!

Oak Ridge FRC Time Course Push-Pull Experiments

Previous microcosm tests conducted with sediment from FRC Area 1 showed little activity at low (<4.0) pH. It was hypothesized that repeated electron donor amendments would stimulate in-situ microbial activity and moderate the low pH. The push-pull experiments were performed utilizing coupons containing powder activated carbon (PAC) beads deployed in wells. These coupons were recovered at one, two, and three month intervals and results are currently being compared to analyses of sediments recovered from these same sites. Microbial biomass on the coupons increased throughout the time of deployment. Non ester-linked phospholipid fatty acid (NPLFA) profiles in the low pH wells were dominated by monounsaturates in the first month. However by the third month more diverse NPLFA profiles were evident. Genetic community profiling by 16S rDNA showed distinct differences between control and test wells. Sequences related to Rhizobium, Caulobacter, Chromobacterium, and Bosea dominated the control well. Sequences recovered from low pH test wells included Burkholderia, Alcaligenes, Desulfosporosinus, Azoarcus, and Rhodanobacter. Community structure as monitored by 16S rDNA changed over time with the appearance of Cytophaga, Clostridia and Desulfotomaculum in the test wells by the third month.

Experimental Design



Conclusions: Understanding the changes in the microbial community structure and function due to the rate and type of donor addition can aid stakeholders when deciding on remedial options. More work must be done in the area of monitoring/forecasting/modeling of microbial community response to donor stimulation in order to streamline the process.