

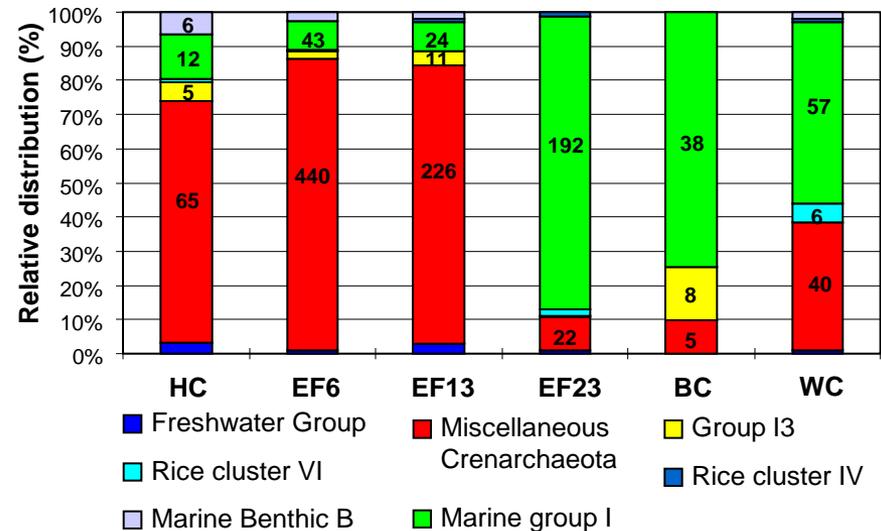
Archaeal Communities in Surface Stream Sediments

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DOE/Office of Science/Biological & Environmental Research

- Archaeal communities were characterized by pyrosequencing, from sites on the Oak Ridge Reservation, including mercury contaminated East Fork Poplar Creek (labeled as EF's in the figure), a uranium contaminated Bear Creek (BC) and a nitrate contaminated White Oak Creek (WC), as well from uncontaminated Hinds Creek (HC).
- Community diversity was decreased significantly in the most contaminated EF23, BC and WC sites.
- Most of the sequences belonged to the Crenarchaeota (70%). Clear differences were observed in the distribution of the Crenarchaeota sequences among the sampling sites.
- Marine Group I, including the ammonia oxidizer *Nitrosopumilus maritimus*, was the dominant group in both mercury and uranium/nitrate contaminated sites. The uranium contaminated site also contained a high concentration of nitrate, thus Marine Group I may play a role in the nitrogen cycle at this site.

Crenarchaeota community structures within each sampling site.



Porat et al., (2010) Microbial Ecology, *in press*.

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How anthropogenic sources of heavy metal contamination impact on the diversity of archaeal communities in surface streams? A team of scientists from Oak Ridge National Laboratory (ORNL) has characterized archaeal communities from mercury and uranium contaminated freshwater stream sediments and compared to those present in an uncontaminated stream located in the vicinity of Oak Ridge, TN. They determined the distribution of the Archaea by pyrosequencing analysis of the V4 region of 16S rRNA amplified from twelve sediment samples. Crenarchaeota composed 76 % of the 1,670 archaeal sequences and the remaining 24 % were from Euryarchaeota. Phylogenetic analysis further classified the Crenarchaeota as a Freshwater Group, Miscellaneous Crenarchaeota group, Group I3, Rice Cluster VI and IV, Marine Group I and Marine Benthic Group B; and the Euryarchaeota into Methanomicrobiales, Methanosarcinales, Methanobacteriales, Rice Cluster III, Marine Benthic Group D, Deep Sea Hydrothermal Vent Euryarchaeota 1 and Eury 5. Both hydrogen- and acetate- dependent methanogens were found in all samples. Most of the groups (with 60 % of the sequences) described in this study were not similar to any cultivated isolates, making it difficult to discern their function in the freshwater microbial community. A significant decrease in the number of sequences, as well as in the diversity of archaeal communities was found in the contaminated sites. The Marine Group I, including the ammonia oxidizer *Nitrosopumilus maritimus*, was the dominant group in both mercury and uranium/nitrate contaminated sites. The uranium contaminated site also contained a high concentration of nitrate, thus Marine Group I may play a role in nitrogen cycle.

Reference: Porat, I., Vishnivetskaya, T.A., Mosher, J.J., Brandt, C.C., Yang, Z., Brooks, S.C., Liang, L., Drake, M.M., Podar, M., Brown, S.D., and Palumbo, A.V. (2010) Characterization of Archaeal Community in Contaminated and Uncontaminated Surface Stream Sediments. *Microbial Ecology*, *in press*.

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