

## Insights into potential metabolisms of the cosmopolitan Miscellaneous Crenarchaeotal Group (MCG) from estuarine sediments using metagenomics

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The Miscellaneous Crenarchaeotal Group (MCG) represents a frequently detected and widespread phylum-level lineage of Archaea. Their members are as yet uncultivated and hence little is known about their metabolism or their biogeochemical role in the environment. Recently, single cell genomic sequencing of one MCG cell indicated a role in protein remineralization [1]. A characteristic feature of MCG is their wide intra-specific diversity. Up to 17 subgroups of MCG based on 16S rRNA sequences have been documented [2]. In order to expand the search on potential metabolisms of the MCG, sediment cores were sampled in the White Oak River estuary (North Carolina, USA) in October 2010; these sediments have been previously shown to be strongly enriched in members of the MCG. The archaeal diversity of these sediments was screened with 16S rRNA gene libraries, accompanied by detailed geochemical analysis. Apart from one shallow sediment sample (10 cmbsf) the MCG dominated all samples, and all 17 MCG subgroups were detected. A sample at 46 cmbsf was chosen for 454 pyrosequencing using genomic DNA. Sequence read assembly yielded approximately 34,000 contigs, 15 of which contained more than 6000 bp. Many of the top contigs belonged to the MCG Archaea. Of the ten 16S rRNA archaeal sequences retrieved from the reassembled contigs, nine were affiliated with MCG and belong to six different MCG subgroups. Metagenomic characterization of archaeal community members revealed a variety of novel organic matter utilization genes including; proteases, amino acid transporters, nucleases, and lipid degradation.

[1] Lloyd *et al.*. 2013. *Nature*. **496**, 215-218. [2] Kubo *et al.*. 2012. *ISME J.* **10**, 1949-65.

## A cyano-bacterial community as a possible agent of Ge accumulation in coal

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Quasi-synchronous hydrothermal activity is critical for high Ge contents in coal [1]. The mechanism of Ge accumulation remains unknown and has been suggested to be associated mainly with sorption from thermal waters bearing 100-150 ppb Ge.

We discuss the geochemistry of a cyanobacterial community at the Uro vent in the Baikal rift and compare element abundances in its waters with those in shale [2] and brown coal [1]. The Uro community contains 350 ppm Ge (average dry-weight contents, up to 1000 ppm), which is about that in the highest-Ge coal. The Uro thermal water composition is remarkable by elevated Be, Sr, Cs, Ga, Mo, and W. Trace elements in the community have implications for the general composition of the water but not for the abundances of elements in it. Bacteria may accumulate little (Cs, Rb, Mg, Sr, K, Ca, Si, V, U, Sb) or zero (Li, Na) amounts of some elements, or be poorer in others than the water (e.g., Mo and W). The living matter of the community hyper-accumulates Ge from water with only 3.4 ppm germanium. Thus, in order to infer the water composition from buried fossils (i.e., to do inversion), one has to take into account the mobility of elements, as well as their different sorption/accumulation by bacteria. The composition of the Uro community is typically thermophilic. Syngenetic hydrothermalism may induce formation of cyanobacterial mats, along with peat generation. Therefore, accumulation by the cyanobacterial community may be the agent responsible for high Ge in coal. As our study shows, Ge contents in the hot spring water may be not very high, within a few ppm.

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[1] Yudovich Ya.E. *Int. J. of Coal Geology*, 2003, **56**, 223–232. [2] Li *et al.*. *Geochemica et Cosmochimica Acta*, 1991, **55**, 3223-3240.