A modeling study of ecosystem carbon and nutrient cycling following oil sands mining

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Oil sands in northern Alberta provide a valuable resource for the national and international production of gas and petroleum. However after this resource is extracted, industries must restore disturbed landscapes to a productivity equivalent to that of natural landscapes. Carbon and nitrogen cycling play important roles in the restoration of this productivity. To examine these roles, we compared modelled vs. measured effects of three different depths of mixed peat-mineral soil covers on ecosystem productivity, soil quality and salinity in a disturbed landscape at the South Hills site of the Syncrude mine in northern Alberta. We then compared the productivities of these landscapes with that of a natural landscape to determine the depth of soil cover required to restore the productivity of a reclaimed landscape to that of a natural one. These results are preliminary pending more detailed measurements of site and soil properties.

Single cell genomics of uncultured subsurface archaea

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Abstract

Microorganisms are dominant players in global biogeochemical cycling, and the marine subsurface contains many deeply-branching groups of archaea that have no cultured relatives.[1,2] Much of these archaea come from the Miscellaneous Crenarchaeotal Group (MCG) and the Marine Benthic Group D (MBG-D), which are globally distributed in anoxic environments. The phylogenetic identity of these archaea has only been established through genetic information in the 16S rRNA gene. Metabolic capacity, on the other hand, can be inferred by presence of functional genes that represent specific metabolic pathways. In order to link phylogenetic identity to metabolic capacity of these uncultured archaea, we sorted a single cell of each and sequenced the entire genome of each using a hybrid approach with 454 FLX and Illumina methods. We then compared this to abundance data in Aarhus Bay sediments to determine potential roles for these groups in marine non-seep sediments.

Out of the 56 single copy genes conserved in all cultured archaea, we found 14 and 29, MCG and MBG-D, respectively. A concatanation of these conserved genes provide support for an evolutionary grouping of the MCG within the mesophilic Crenarchaeota (or Thaumarchaeota) and the MBG-D within the Order Thermoplasmatales within the Euryarchaeota. MCG and MBG-D were found to comprise the bulk of the archaeal population, using qPCR as well as 454 FLX sequencing of archaeal 16S genes. The genomes of MCG and MBG-D contain nearly complete pathways for the tricarboxylic acid cycle, as well as transporters for externally-derived organic molecules. They both contain variations on pathways for amino acid degradation. These data support a heterotrophic lifestyle for uncultured archaea in the marine subsurface, as was predicted by bulk biomass isotopic ratios.[1] No evidence was found for commonly used inorganic terminal electron acceptors such as oxygen, sulfate, iron, or CO_2 (for methanogenesis). Therefore the physiology of MCG and MBG-D most likely diverges from those of their aerobic closest relatives.

[1] Biddle, J. F., et al. (2006) *PNAS* **103**, 3846-3851.
[2] Whitman, W.B., et al. (1998) *PNAS* **95**, 6578-6593.