

# Improvement of passive treatment of mine influenced water using genomics

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# Objectives:

Passive treatment is one way of cleaning up mine influenced water so that it can be re-used or discharged safely into the environment. The word passive means that treatment of the water is accomplished with natural geochemical and biological processes. This is done by constructing a system of subsurface and surface flow ponds where the mine water percolates through organic rich material containing microbes that help to remove metals and other chemicals such as sulphate. Some metals and chemicals are removed when the water flows in a vertical direction beneath the surface where there is no oxygen, and other metals are removed when water flows through surface ponds with plants.

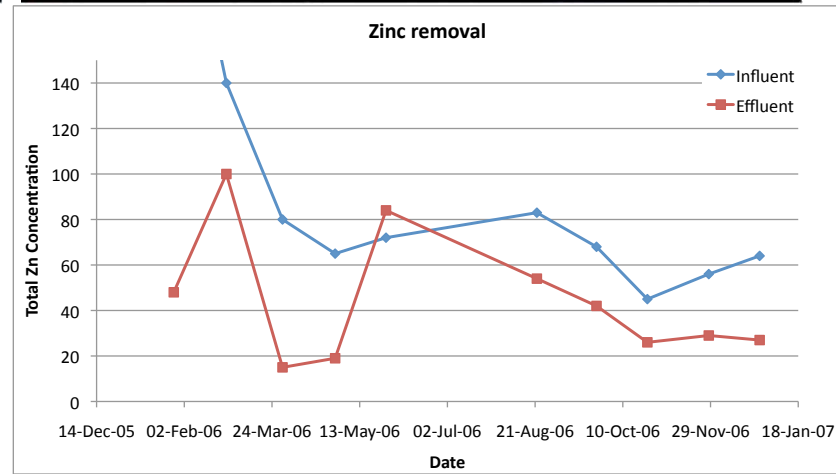
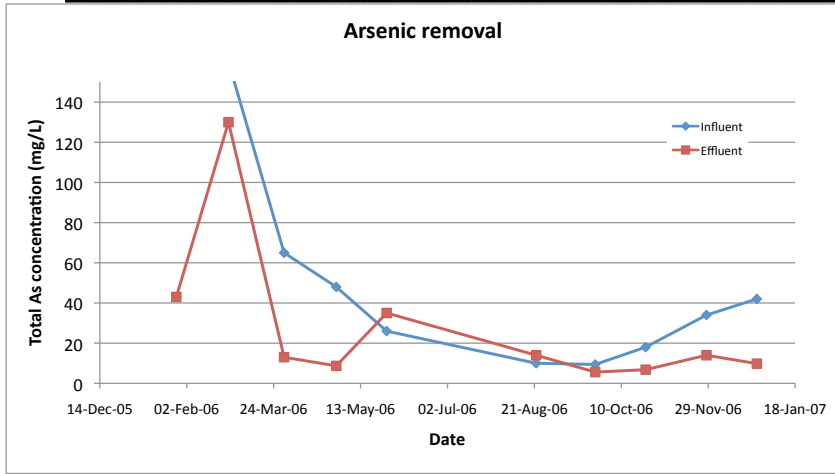
Because the biological mechanisms taking place inside these passive treatment systems are so complex, we have a hard time understanding when they are working or not. To make passive treatment systems more reliable, we need a way of monitoring which microbes are indicative of a successful treatment system. We are attempting to accomplish this by sequencing the genomes of the microbes in operating passive treatment systems.



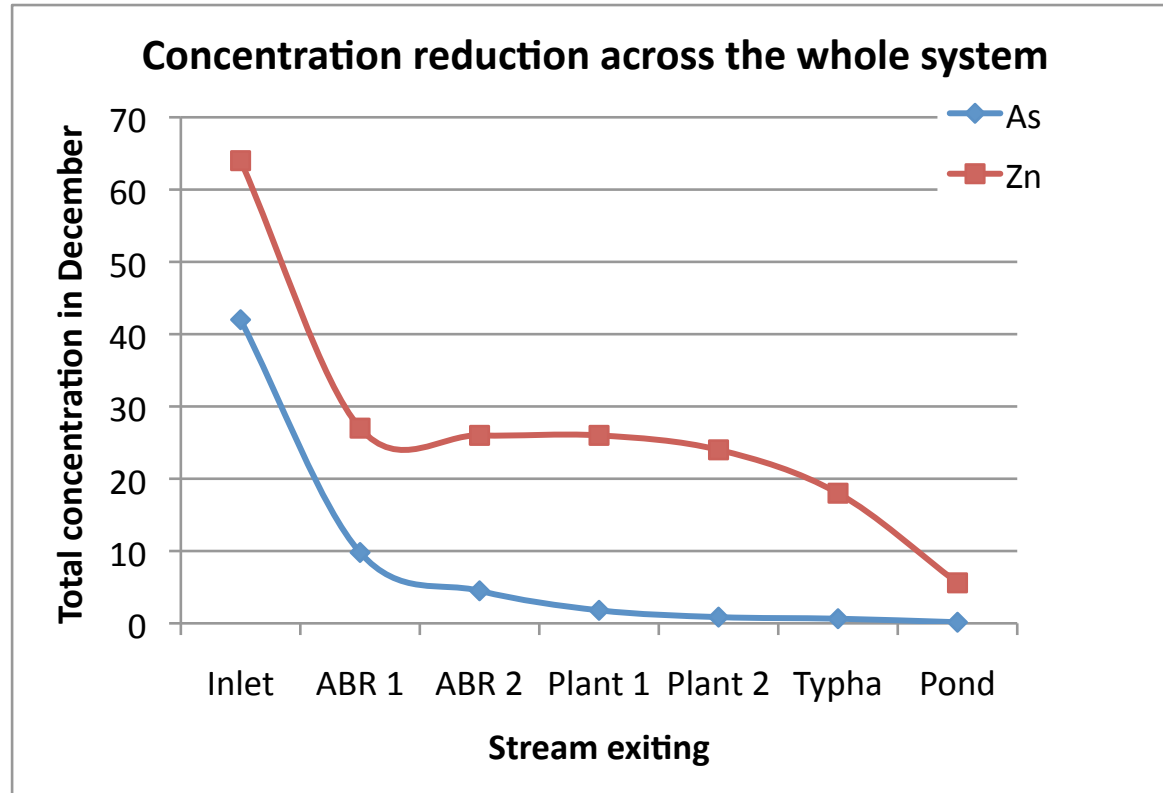
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# Trail anaerobic bioreactor: ABR1



# Overall removal:

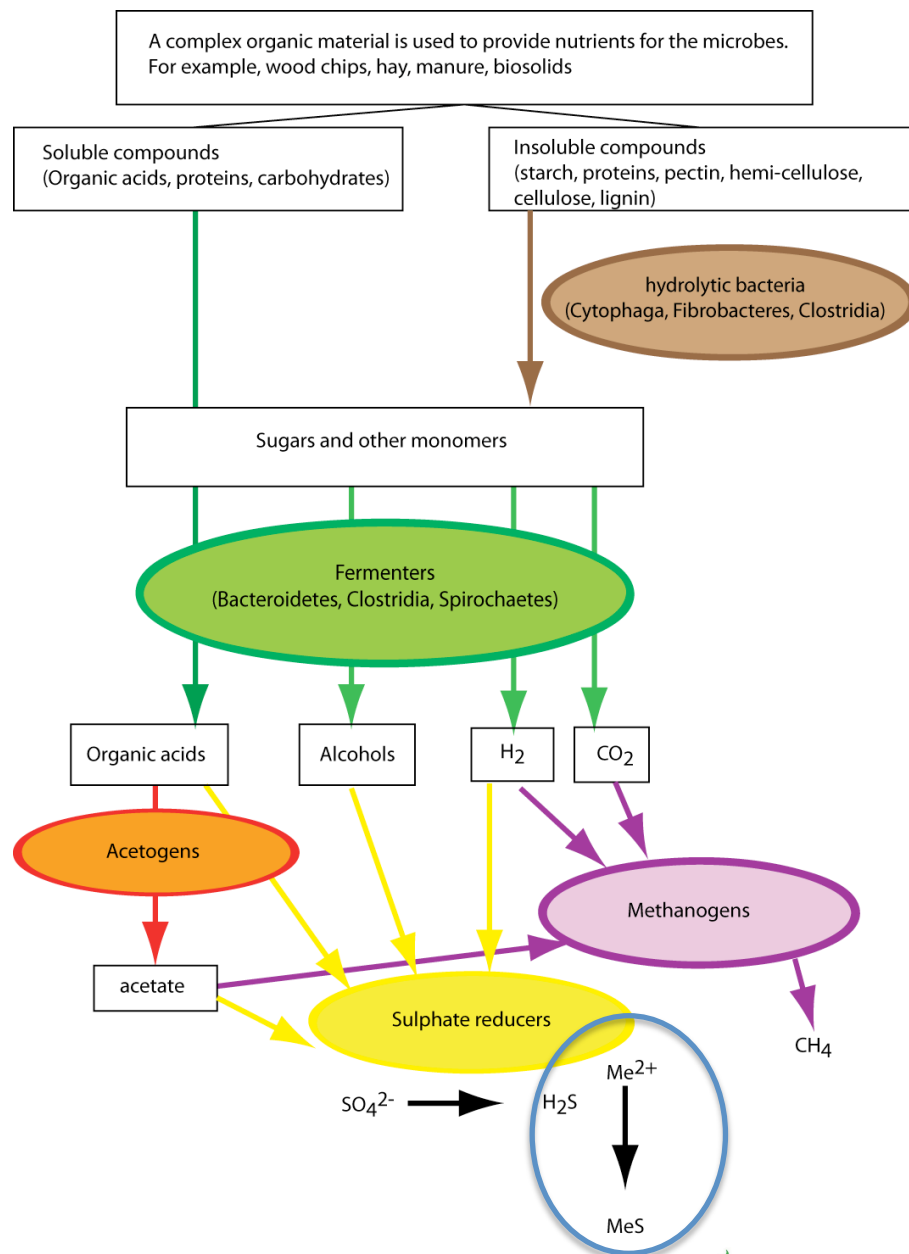


# The Mount Polley Mine pilot-scale treatment pond.

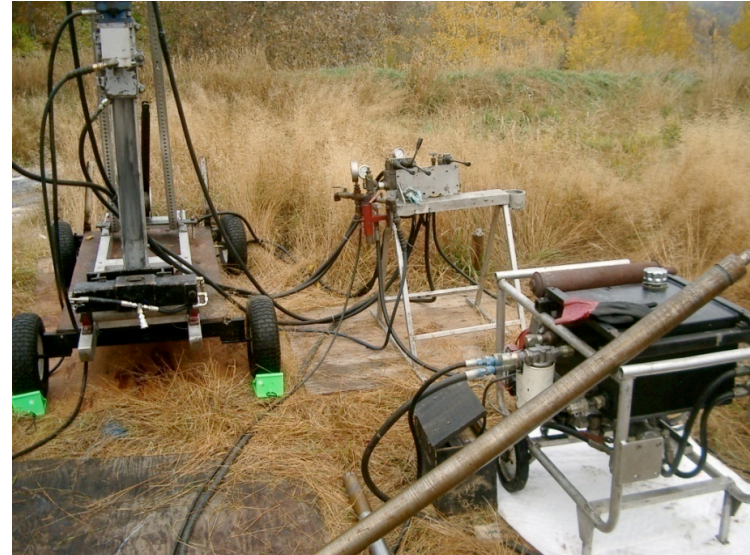


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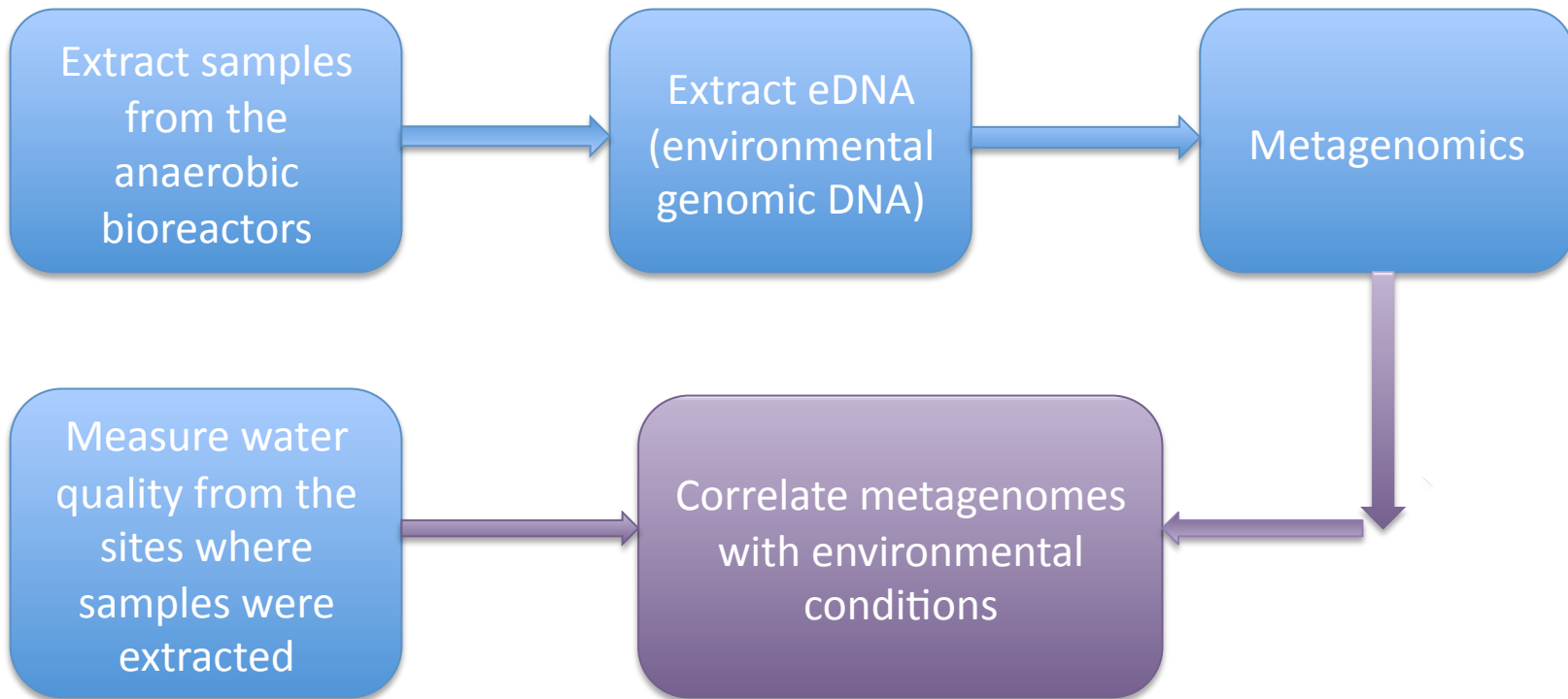
# Samples are taken from the treatment system



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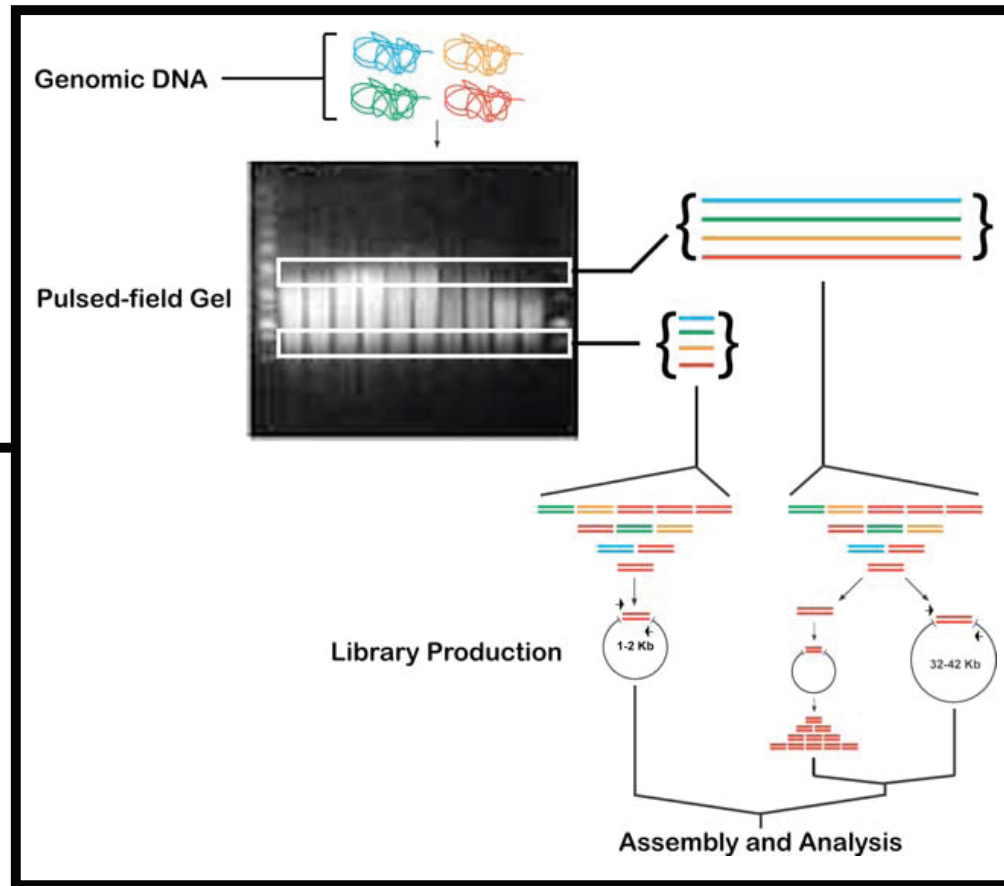
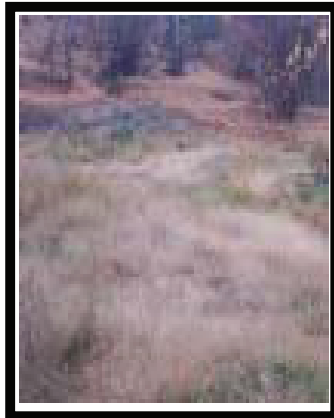


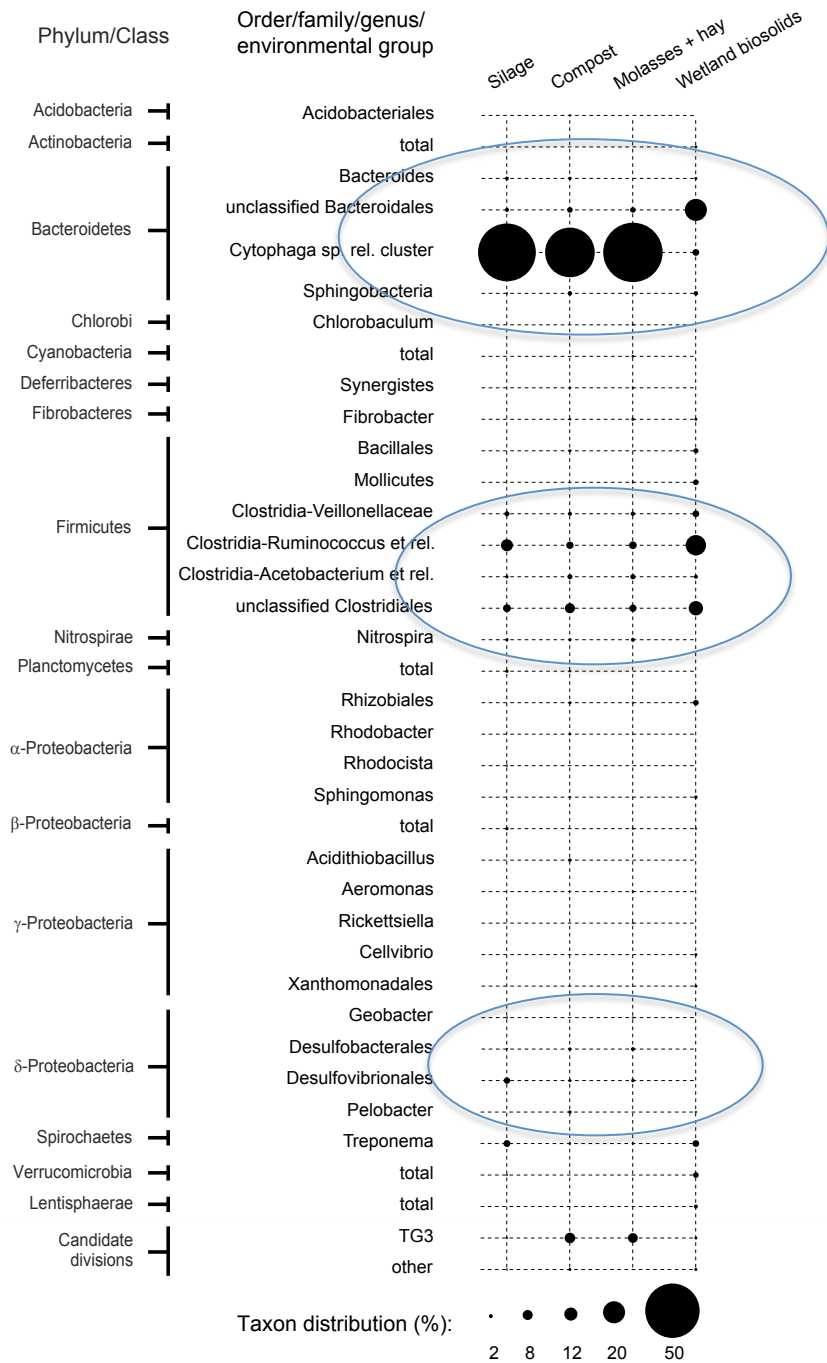
# Methodology:





# Build libraries:

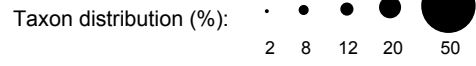




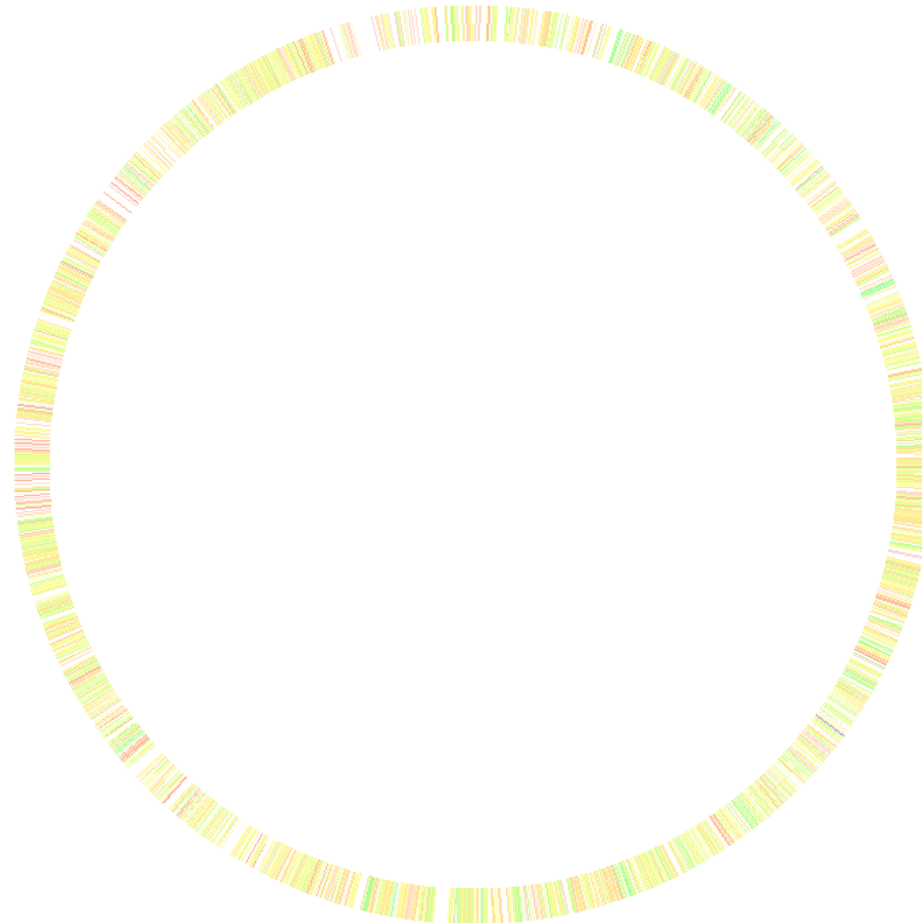
Bacteria that degrade cellulose materials

Fermentative and acetogenic bacteria

Sulphate-reducing bacteria

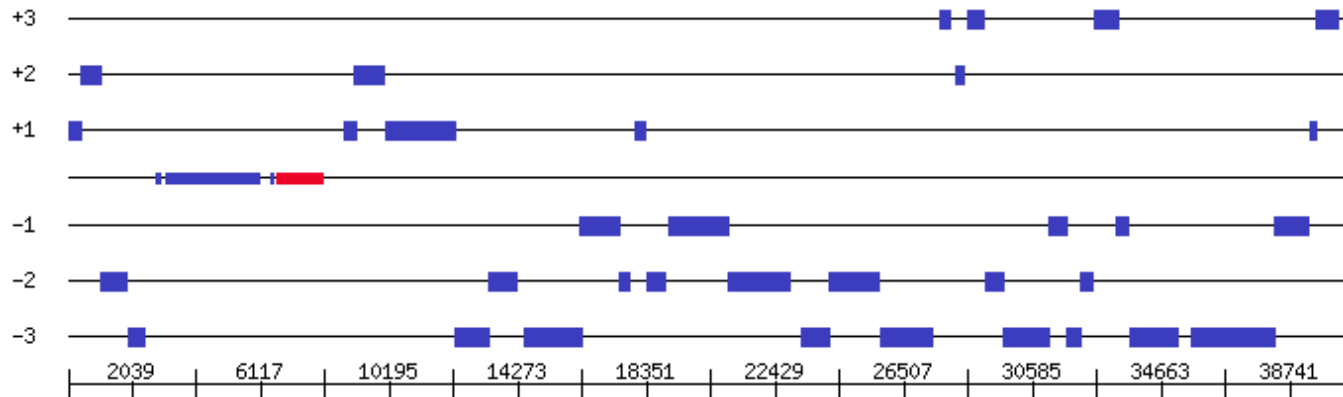


The comparison organism (assembled contigs from wetland fosmid library; minimum contig length: 2000 bp) were aligned to the reference genome (*Methanocorpusculum labreanum* Z). The result list the genes of the reference organism in chromosomal order and display hits on the comparison organisms accordingly.

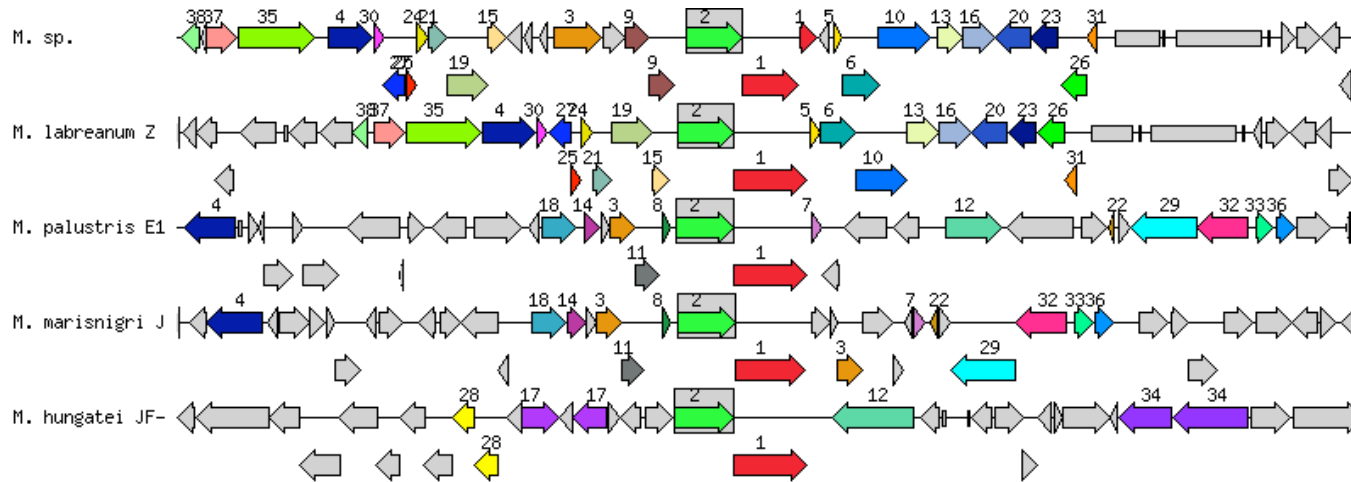


	Percent protein sequence identity															
Bidirectional best hit	100	99.9	99.8	99.5	99	98	95	90	80	70	60	50	40	30	20	10
Unidirectional best hit	100	99.9	99.8	99.5	99	98	95	90	80	70	60	50	40	30	20	10

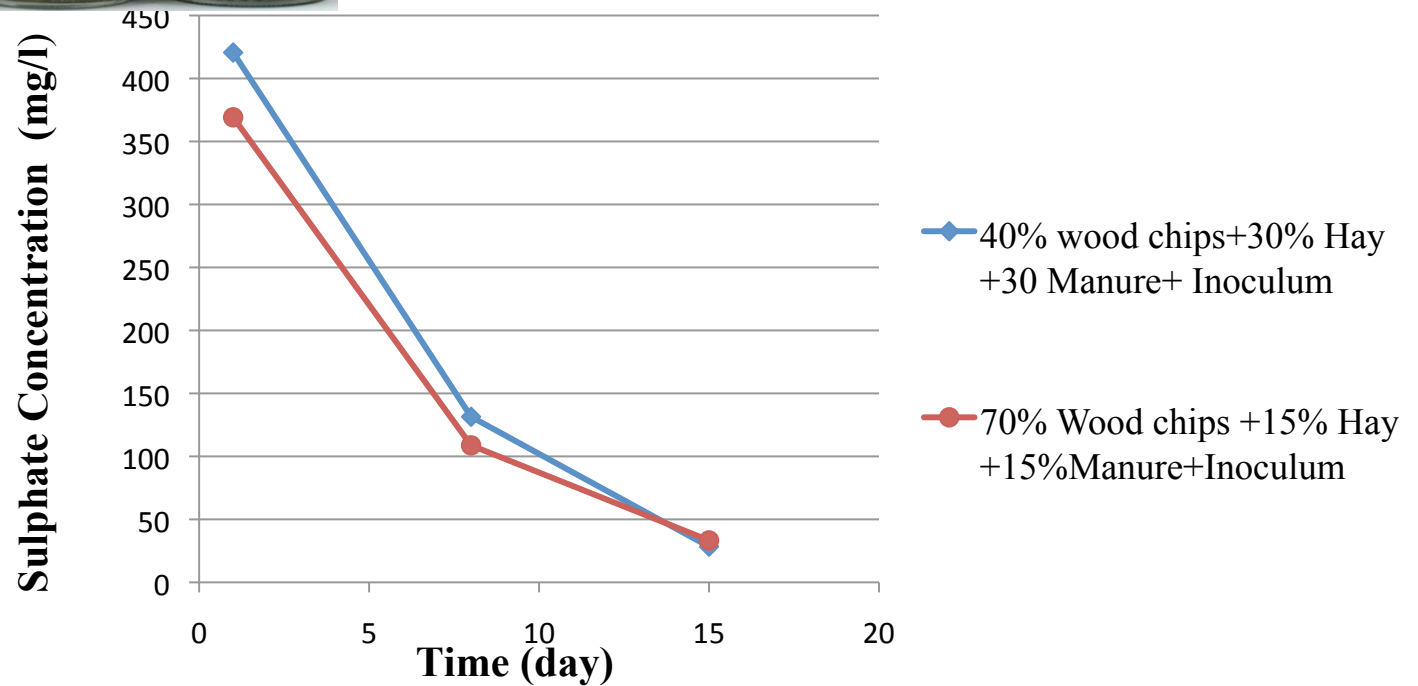




assembled contig 1382 annotation: 40,789 bp length (marked red in upper window: 16S rDNA); lower window: gene organization comparison with four different methanogenic reference genomes



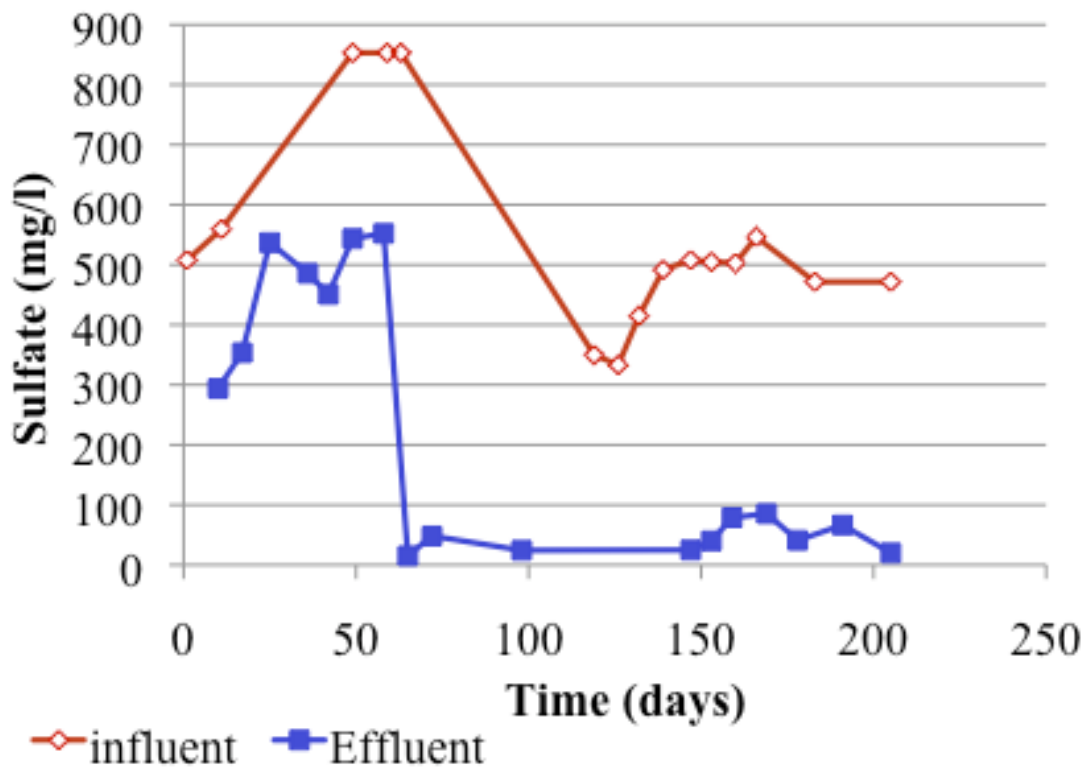
# Batch tests of organic material



# Continuous column tests



< 100 mg/l  
sulfate



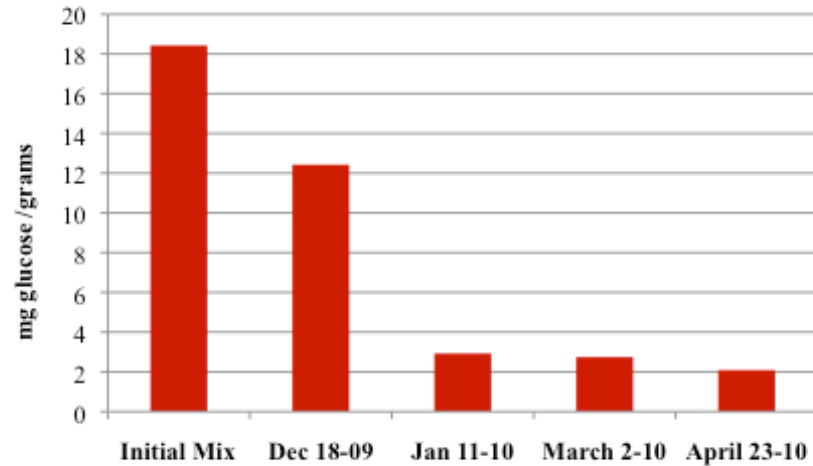
Synthetic mine drainage,  
500 mg/l sulfate



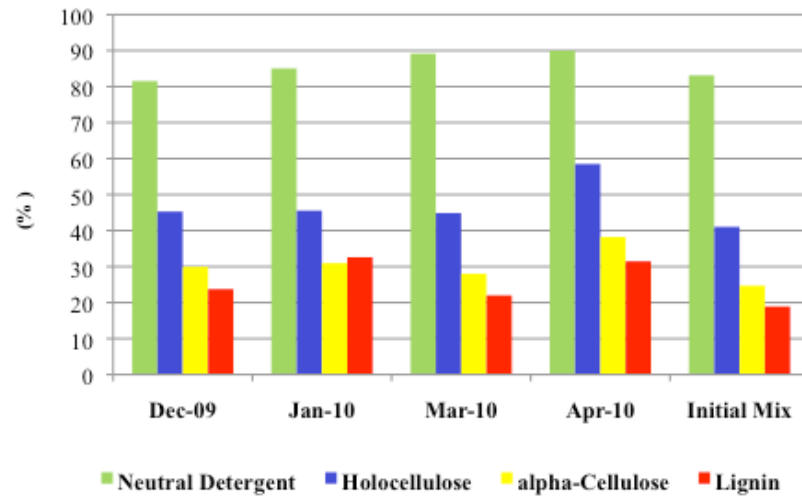
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# Changes in organic matter characterization



Soluble carbohydrates



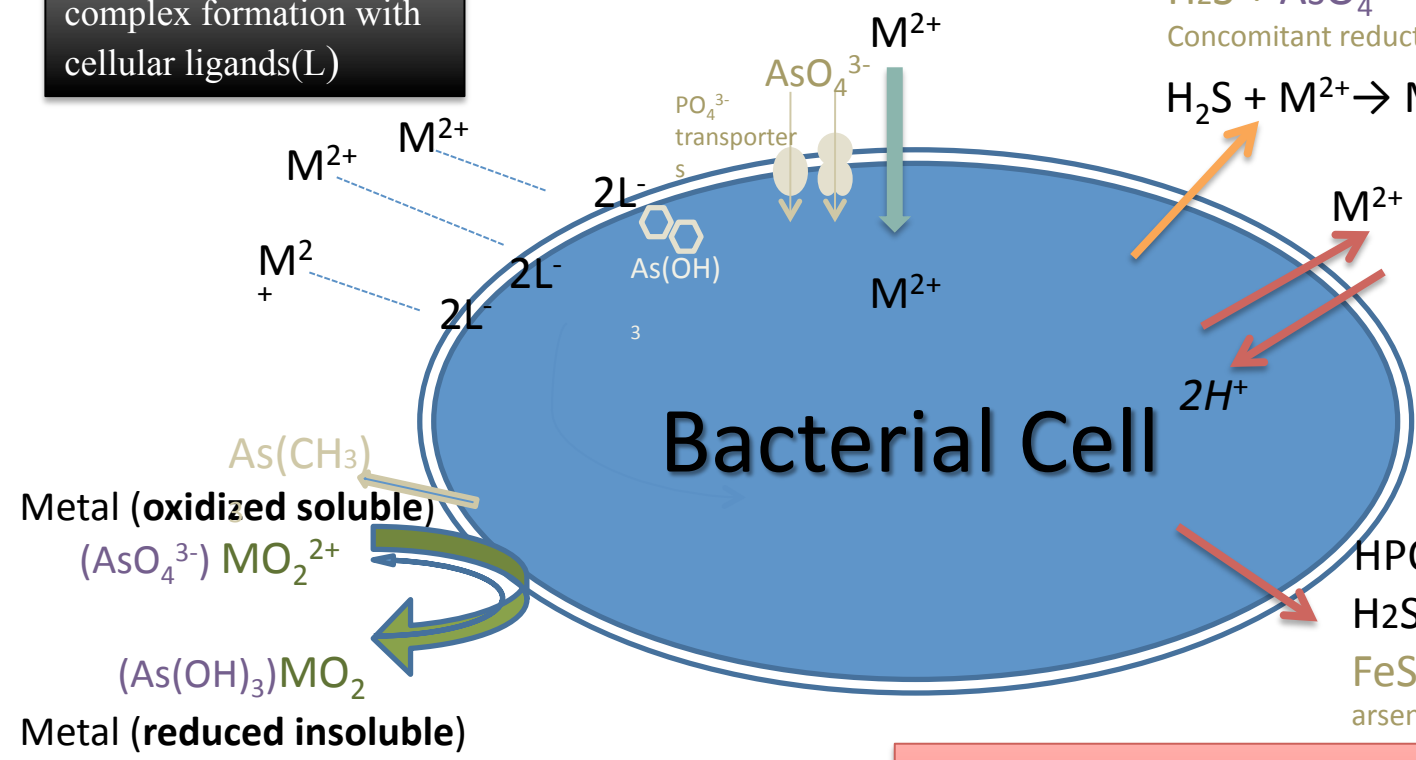
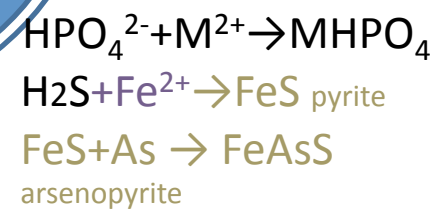
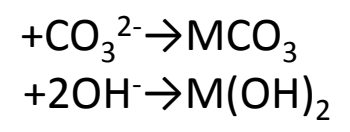
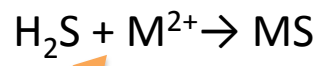
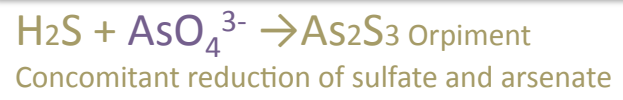
Recalcitrant components



**Biosorption**  
 Chemical sorption of metal cations via complex formation with cellular ligands(L)

**Bioaccumulation**  
 Cellular uptake of metal .

**Biomineralization**  
 Formation of insoluble metal precipitates



**Biotransformation**  
 Reduction of high valence metal to lower valence insoluble species.

**Microbially enhanced chemisorptions of metals**  
 Intercalation of metal cation into the crystal of a pre-deposited precipitate

