

**PB-05 Bacterial community structure of an alpine cryoconite sample,
as revealed by pyrosequencing analyses**

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Variable domains, V1 and V2, of bacterial 16S rRNA gene were amplified with universal primers 27F and 338R from environmental DNA of a glacier cryoconite sample collected in the Ötztaler Alps in Austria (Rettenbachferner, altitude 2760 m above sea level). PCR products were directly sequenced by pyrosequencing method and a total of 31,427 sequences were obtained by the forward primer. 1,467 OTUs were recovered by 97% similarity cutoff and the highest OTU diversity was recovered from *Bacteroidetes* (371), and followed by *Betaproteobacteria* (247), *Alphaproteobacteria* (142), *Actinobacteria* (117), *Deltaproteobacteria* (76), *Gammaproteobacteria* (59), *Cyanobacteria* (50), and several minor divisions.

**PB-06 Arctic marine sediments host thermophilic microbial
communities capable of complex organic matter mineralization
via hydrolysis, fermentation and sulfate reduction**

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Degradation of complex organic matter in marine sediments involves the combined activities of different groups of microorganisms. Under anaerobic conditions hydrolytic enzyme-secreting microbes initially convert benthic biomass-derived macromolecules into simpler organic compounds (sugars, amino acids, long chain fatty acids, nucleic acids), which are then fermented to produce VFA (volatile fatty acids; e.g. acetate, propionate and butyrate) that are oxidized by terminal respiratory processes such as sulfate reduction. These processes are widespread in sediments from a range of locations, including the permanently cold sediments of Svalbard fjords in the high arctic (79° north) where year-round temperatures are close to 0°C. Despite this cold *in situ* temperature, thermophilic sulfate-reducing bacteria (SRB) have been detected in the Svalbard sediments following pre-pasteurization of sediment slurries for 20 minutes at 80°C. Subsequent incubation of pasteurized sediments at 50°C stimulated sulfate reduction rates that increased until SRB substrates (VFA) were depleted. In addition, VFA levels themselves increased dramatically (relative to killed abiotic controls) to much higher-than-*in situ* concentrations prior to being consumed during sulfate reduction, indicating that arctic sediments also host fermentative thermophiles. Addition of algal biomass (*Spirulina*) to these incubations enhanced fermentation and sulfate reduction rates, suggesting a coupling between these processes and hydrolysis of macromolecules by thermophiles that secrete thermostable (at 50°C) enzymes. High temperature hydrolysis was confirmed using fluorescently-labelled high molecular weight polysaccharides, demonstrating that enzymatic hydrolysis of pullulan and arabinogalactan, but not chondroitin or fucoidan, was catalyzed by thermophiles from the arctic sediments. Arctic marine sediments thus host distinct thermophilic microbial populations with capacities that mirror, yet are independent from, *in situ* organic matter degradation pathways via hydrolysis, fermentation and sulfate reduction.