



Diversity of Archaea in submarine permafrost sediments of the Laptev Sea, Siberian Arctic

K. Koch (1), C. Knoblauch (2), D. Wagner (1)

(1) Alfred Wegener Institute for Polar and Marine Research, Research Department Potsdam, Telegrafenberg A43, 14473 Potsdam, Germany, (2) Institute of Soil Science, University of Hamburg, Allende-Platz 2, 20146 Hamburg, Germany, kkoch@awi-potsdam.de

Atmospheric methane is the second most important greenhouse gas after carbon dioxide. Carbon-rich permafrost sediments are an important source of methane. Due to the Holocene rise of the artic sea level, large areas of formerly coastal permafrost were buried under the sea, creating a submarine permafrost. In order to better understand the methane cycle in submarine permafrost, geochemical and molecular ecological studies on archaeal diversity have been carried out which particularly examine the role of methanogens. In this study frozen sediments were extracted from a 77 meter deep core in the Laptev Sea shelf, North Eastern Siberia, which have been dated to approximately 111,000 years BP.

In these sediments the total organic carbon (TOC) content varied between 0.03 and 8.70 % with highest values between 53m - 62m depth below the sea floor. Methane concentrations varied along the core between 0 - 284 nmol CH₄ g⁻¹. Highest values were found in the layer with the highest amount of TOC. Extremely low δ¹³ CH₄ values (-75 per mille) indicated active methanogenesis in this zone.

A nested polymerase chain reaction (PCR) amplification for denaturing gradient gel electrophoresis (DGGE) was applied to the samples with low and high amount of methane in order to analyze the archaeal diversity in submarine permafrost sediments based on 16S rDNA. For the nested PCR, the archaeal primers Ar4F-Ar958R were used, followed by GC_PARCH340F-Ar958R, GC_357F-0619R and GC_340F-519R as second primer combinations. DNA fragments from DGGE gels were sequenced and phylogenetically analysed.

Further clone library analyses are planned for a detailed study on the microbial com-

munity composition and their function in the submarine ecosystem.