Archaeal activity and diversity in Late Pleistocene permafrost sediments of the river Lena Delta, Siberia, Russia

German Jurgens[1], Uwe Münster[2], Mikhail Grigoriev[3] and Dirk Wagner[4]

1.Department of Applied Chemistry and Microbiology, P.O.Box 56, Biocenter 1A, Viikinkaari 9, FIN-00014 HELSINKI UNIVERSITY, Finland
2.Institute of Environmental Engineering and Biotechnology, Tampere University of Technology, P.O.Box 541, Korkeankoulunkatu 8, FIN-33101 Finland
3.Permafrost Institute Yakutsk, RAS, 677018 Yakutsk, Yakutia, Russia
4.Alfred Wegener Institute for Polar and Marine Research, Research Department Potsdam, 14473 Potsdam, Germany

INTRODUCTION

Permafrost soils of high-latitude wetlands are a major source of atmospheric methane, which strongly contributes to the enhanced greenhouse effect. Global climate changes are more pronounced in the Arctic than in any other region of the world. More than 14 % of the world's soil carbon is preserved in the permafrost. Therefore, predictions of the methane emission rates from northern ecosystems are important for global climate change forecasts. Methane emission rates are determined by balances of methane sources and sinks. The main source of methane is the biological methane formation - called “methanogenesis” - which is a results of the decomposition and reduction of organic material by methanogenic Archaea. Methanogenesis is highly influenced by temperature and it can be expected that methane production increases with the rising of global temperatures at high latitudes. Microbial life in these habitats, which are completely frozen most time of the year, is influenced by the extreme environmental conditions.

RESEARCH GOAL

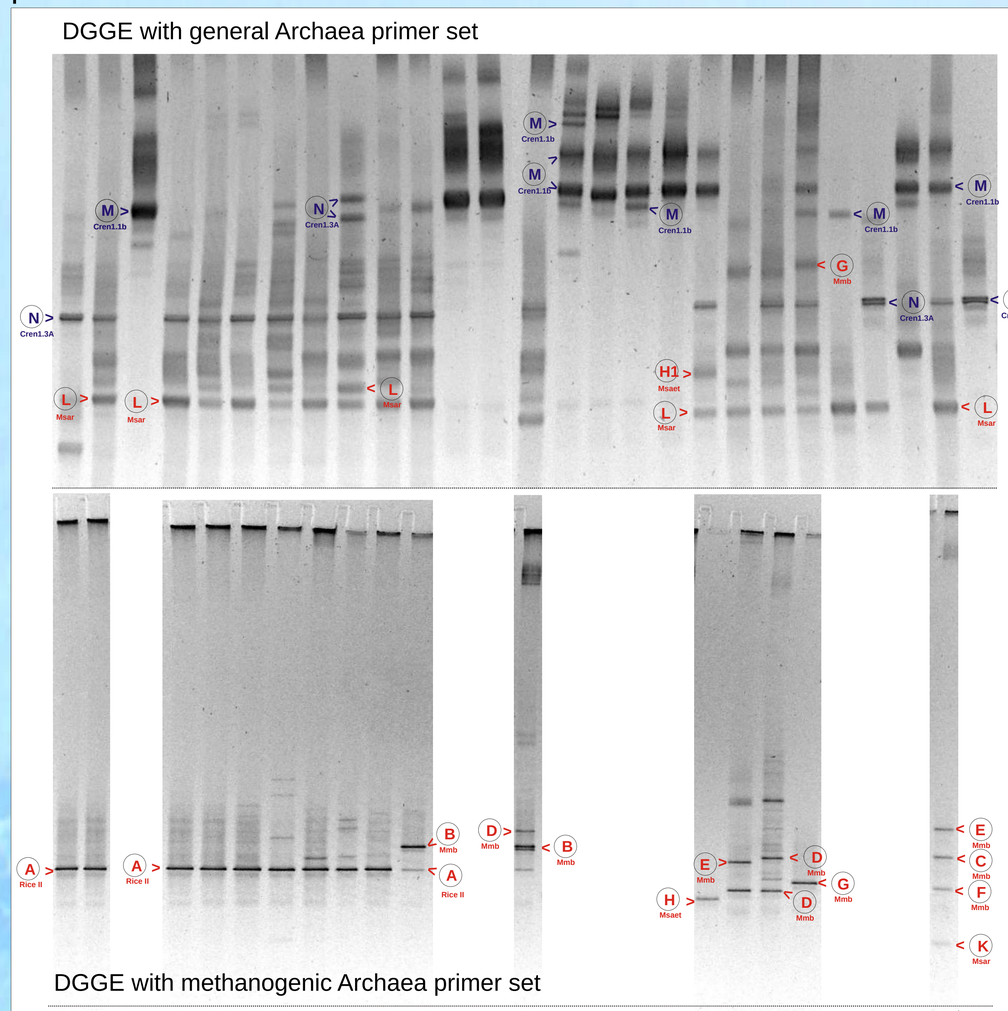
In order to improve our understanding of the function and diversity of microbes living in permafrost environments as well as the fundamental process of methane production we studied permafrost core samples taken in the river Lena Delta.

CORE CHARACTERIZATION

Characterization of this core includes **geochemical** methods such as sedimentology, geochemistry, radiocarbon dating and gas analyzing as well as **microbiological** methods such as isolation of microorganisms**,** studies of their activity and molecular ecology work.

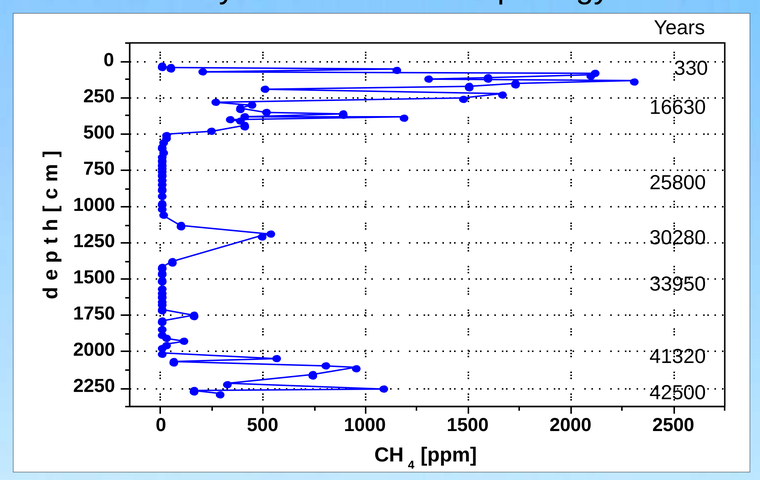
MOLECULAR ANALYSIS - DGGE WITH TWO SETS OF ARCHAEAL 16S rRNA GENE PRIMERS

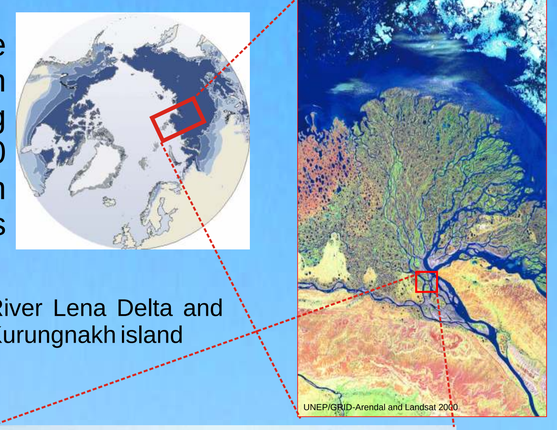
Environmental DNA was extracted from 30 core samples, chosen according to methane concentration. Both low and high methane concentration samples were used. In order to get a community profile of each sample DGGE analysis was performed. Two sets of Archaeal 16S rRNA gene primers were used - one was designed for amplification of all Archaea and other set was specific for methanogens. DGGE analysis shows the presence of diverse Archaeal communities in tested samples of different depths. Bands (indicated on DGGE gel pictures and phylogenetic trees) were excised from the DGGE gel and sequenced, showing similarity with environmental sequences of methanogenic Archaea (Methanomicrobiales and Methanosarcinales) and Crenarcheota (Group I.1b and GroupI.3A). Several samples show presence only Crenarchaeotal sequences and had no amplification with methanogenic primers.



STUDY SITE

The field investigations were carried out on the Kurungnakh Island (N 72°20, E 126°17), located in the Lena Delta, Siberia, Russia. A 25-meter long permafrost core from Late Pleistocene (about 42500 years old) was taken during the joint Russian-German expedition in the summer 2002 and divided in 72 parts based on the cryostructure and morphology of the core.





METHANE CONCENTRATION MEASURMENTS

Analysis of the methane concentration in a long permafrost core was performed for the first time. Significant methane concentrations were observed in samples from the surface down to 3-5 m and also in samples from deep parts of the core (around 22 m, 42500 years old). This indicates a possible activity of methanogenic Archaea under extreme sub-zero temperatures. Important questions are: (1) where does this methane come from and (2) why do some core layers have high concentration of methane while in others no methane was detected.

AUTHORS CONTRIBUTION

Dirk Wagner (AWI) and Mikhail Grigoriev (PIY) were the leaders of joint Russian-German expedition LENA 2002 and were responsible for the permafrost drilling. Dirk Wagner performed the core preparation, methane and microbiological analysis. German Jurgens and Uwe Münster have done molecular analysis.

Note: Sequences marked in bold font were recently retrived (using same methanogenis primerset) from permafrost affected soils the closely situated region of Siberian Arctic (see article in press: **FEMS Microbiology Ecology**, 2006,Ganzert,L.,Jurgens,G.,Münster,U., Wagner, D. **Methanogenic communities in permafrost affected soils of the Laptev Sea coast, Siberian Arctic characterized by 16S rDNA fingerprints**

CONCLUSION AND FUTURE PLANS

The results indicated the existence of a permafrost microbiota, which was well adapted to the extreme environmental conditions of the permafrost. The knowledge of the activity, physiology and ecology of the microbial community is fundamental for understanding trace gas fluxes in the Arctic. In perspective, these approaches provide the basis for future environmental studies that deal with the fate of microorganisms and carbon stored in permafrost in the course of climate changes and the search of extraterrestrial life.

Contacts:
german.jurgens@helsinki.fi
dwagner@awi-potsdam.de
uwe.munster@tut.fi