

Using paleogenomics from Arctic lake sediment to track microbial methane cycling under Holocene: a window into past climate change

*A. ROUILLARD^{1,2}, M.W. PEDERSEN³, Y. WANG², M.-L. SIGGAARD-ANDERSEN², I.G. ALSOS⁴, A.A. BJØRK⁵, T.A. DAVIDSON⁶, W. FARNSWORTH⁷, S.V. FUNDER⁸, L.M. HÅKANSSON⁹, K.K. KJELDSEN⁶, N.K. LARSEN¹⁰, A.H. RUTER¹¹, M. VAN HARDENBROEK¹², S. WOODROFFE¹³, J.P. SMOL¹⁴, E. WILLERSLEV¹⁵, AND K.H. KJÆR¹⁶ & A. SCHOMACKER¹⁷

¹Dept of Geosciences, UiT The Arctic University of Norway, Tromsø, Norway; alexandra.rouillard@snm.ku.dk

²Centre for GeoGenetics, Dept of Biology, University of Copenhagen, Copenhagen, Denmark

³Arctic University Museum of Norway, UiT, Norway

⁴Aarhus University, Aarhus, Denmark

⁵Arctic Geology, UNIS, Svalbard

⁶GEUS, Copenhagen, Denmark

⁷Newcastle University, Newcastle-upon-Tyne, UK

⁸Dept of Geography, Durham University, Durham, UK

⁹Dept of Biology, Queen's University, Kingston, Canada

Arctic landmasses and lakes release significant amounts of methane (CH₄), a greenhouse gas with an atmospheric warming potential 25 times higher than CO₂ that contributes heavily to global climate change. Yet the effect of rapid warming in the Arctic on the long-term fate of natural CH₄ emissions from lakes is poorly understood. Lake sediment provide a vertically structured window into past interactions between microorganisms and their environments, and in cold climates provide some of the best preservation conditions for ancient DNA. Here we use paleogenomic techniques on lake sediment to track the establishment and dynamics of microbial communities in Arctic landscapes, with a particular focus on the sensitivity of CH₄-processing microorganisms and competitors to climate change over the Holocene period (last 11,700 years). Interactions between CH₄-microbial dynamics and elemental carbon reservoirs in the lakes, watersheds and their aquatic networks are also investigated using targeted geochemical analyses (specific compounds stable isotopes and visible near infrared spectroscopy). For the first time, ancient microbial metagenomic profiles are extracted from multiple sites across the Arctic to determine the effect of centennial to millennial climate change on this potentially important yet understudied greenhouse-related biogeochemical process.