## ID# 372

Title: Plant DNA in sediments: to which degree do they represent the flora? Presenting Author: Alsos, Inger Greve <u>inger.g.alsos@uit.no</u> Affiliation: UiT - The Arctic University of Norway Address: Tromsø Museum Country: Norway Authors:

Inger Greve Alsos, UiT - The Arctic University of Norway, Tromsø, Norway Eric Coissac, University Grenoble Alpes, LECA Grenoble, France Mary Edwards, University of Southampton, Southampton, UK Marie Kristine Føreid, UiT - The Arctic University of Norway, Tromsø, Norway Ludovic Gielly, University Grenoble Alpes, LECA Grenoble, France Per Sjögren, UiT - The Arctic University of Norway, Tromsø, Norway Pierre Taberlet, University Grenoble Alpes, LECA Grenoble, France Nigel Yoccoz, UiT - The Arctic University of Norway, Tromsø, Norway Abstract:

Background: Environmental DNA (eDNA) extracted from sediments has promise as a new proxy in studies of modern biodiversity and palaeobiological reconstruction. However, little is known about how well this method represents the flora. We used the g and h universal plant primers for the short and variable P6 loop region of the chloroplast trnL (UAA) intron to amplify DNA in lake sediment samples of different ages (modern, 100-200 years, and Holocene), as well as modern soil samples. We compare this with modern vegetation and other proxies (pollen and macrofossils) to evaluate the representation of different taxonomical groups, the geographical area likely to be represented, and the taphonomy of DNA.

Results: Analyses of soil samples from the Arctic showed that all species represented in the soil DNA grew within 3 m from the sampling point, most of them within 0.5 m. Lake sediments represent the flora of the catchment area, but a lower proportion of the flora were represented in the DNA record compared to soil samples. DNA and pollen of 100-200 year old lake sediments from regions where forest was planted in the mid-twentieth century showed that both proxies discern major vegetation change at the time of plantation, with similar quantitative changes. In a lake core from the Arctic dated to 8500-1200 cal. BP, all except two genera identified as macrofossils were also identified with DNA. Furthermore, DNA identified six additional taxa and more species per sample. With one DNA extraction and one PCR per sample, we detect most common species independent of sample type or age. Increasing the number of extractions or PCR repeats increased the chances of detecting rare species. Some taxonomic groups (e.g., Cyperaceae) were consistently underestimated whereas other (e.g., water plants) were overrepresented compared to the other proxies.

Significance: The local flora was well represented in the DNA of the sediments, and the method may have a higher and/or complementary taxonomic resolution than analyses of pollen or macrofossils.