

Cave ice microbiom along a Chronosequence in Svarthamar Ice Cave, North Norway

The Norwegian partner of CAVEICE, an ERANET project on cave ice microbiology and isotope stratigraphy

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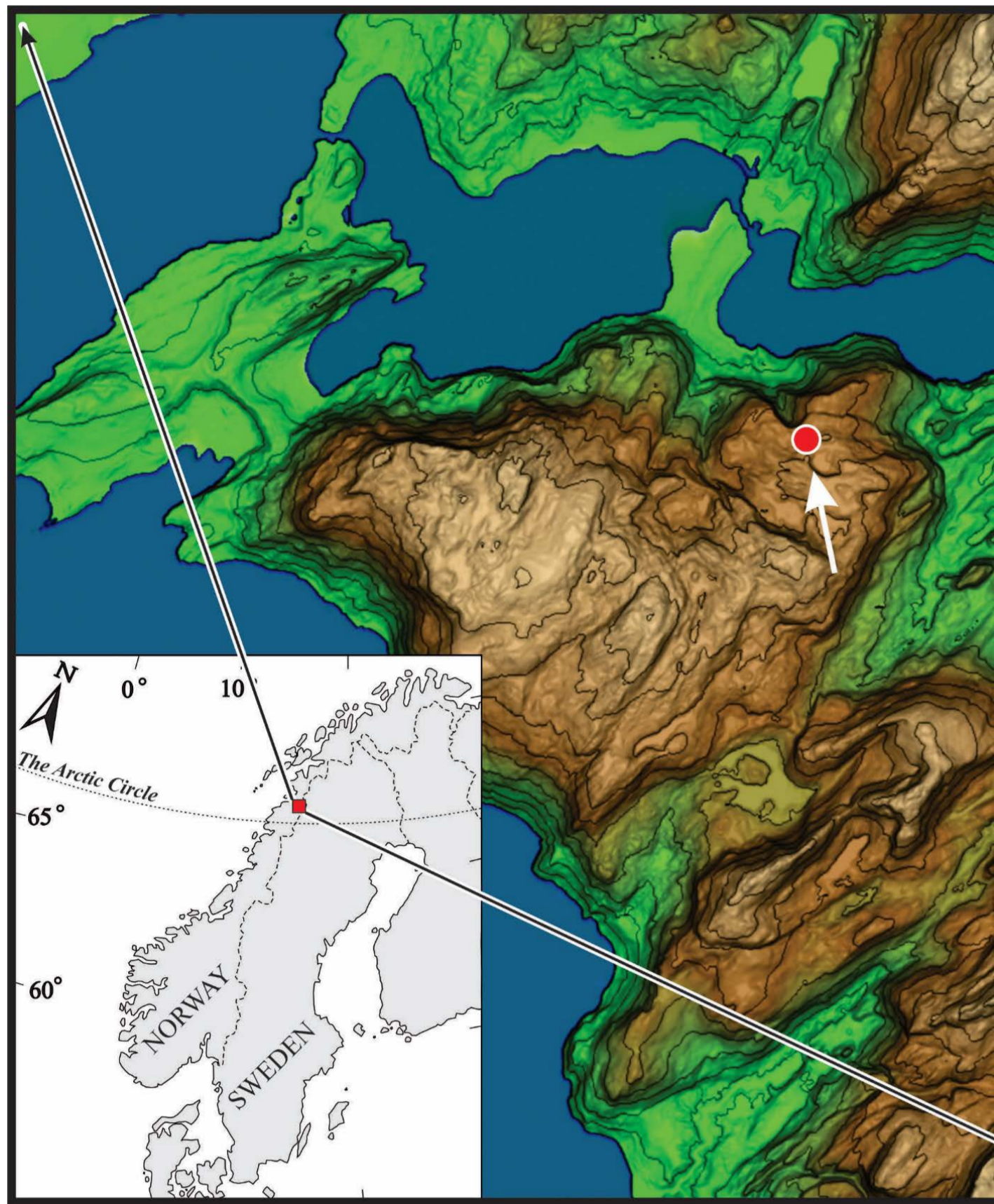


Figure 1. Key map, Svarthamar cave



Fig 2. Close-up of ice stratigraphy

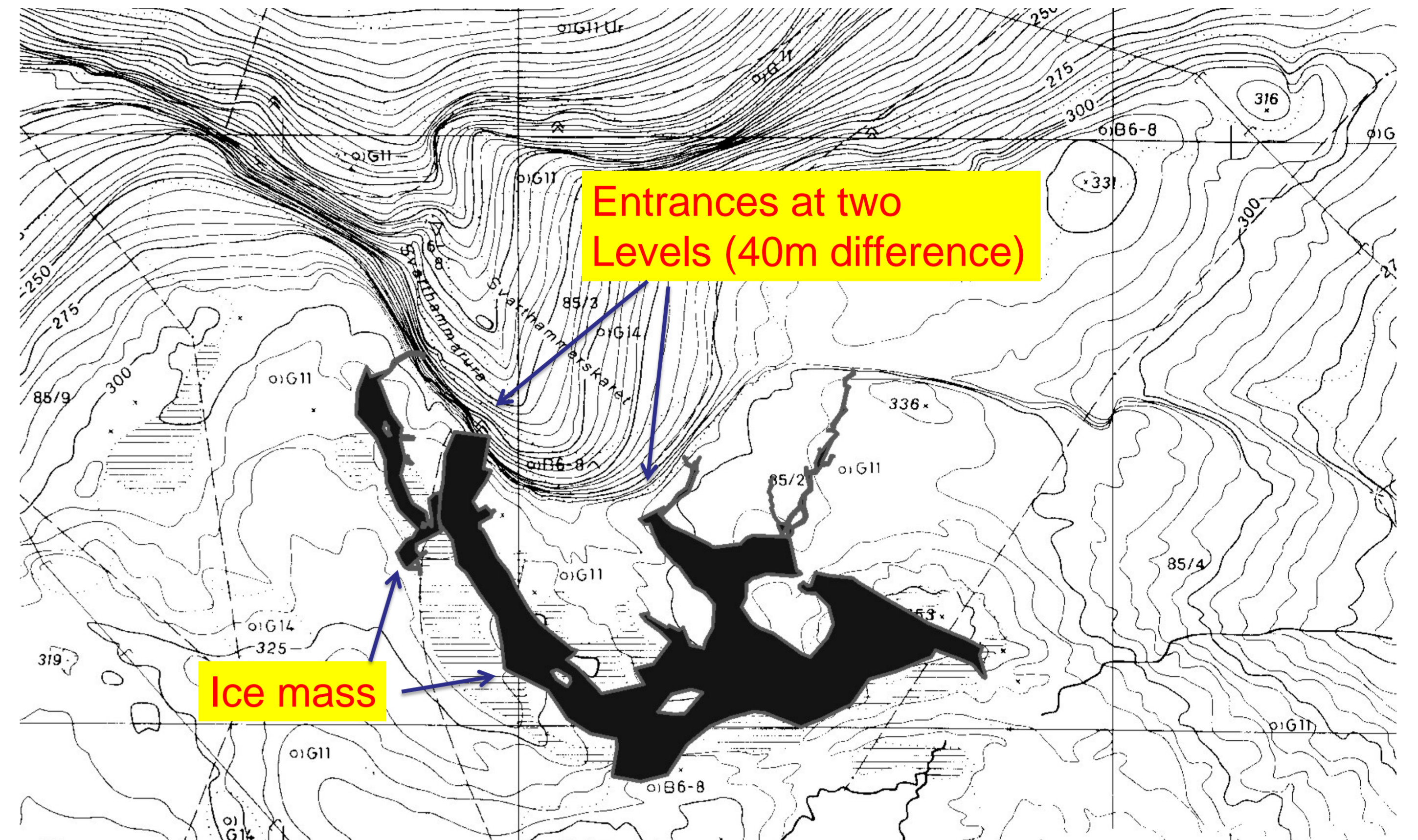


Fig. 3. Outline of Svarthamar cave. Ice mass indicated

Background and project description

Ice caves represent highly preserved and relatively unexposed ice environments constituting a unique archive for studying the impact of climate and anthropogenic pollution on the microorganisms living there. Still there is only scarce information about the indigenous ice-microbiota, and their vulnerability to climate change. In this project we will study the total and active microbial communities from ice caves of different climate and pollution exposures in order to understand the microbial diversity and metabolisms along a Chrono sequence model reflecting the impact of both climate and environmental pollution on cave ice microbioms. In our part of this project we will focus on the Svarthamar Ice cave in Norway, (Figs 1& 3) which is a perennial ice mass hosted within a karst cave. The Svarthamar cave is a two-entrance, dynamic ice cave, possessing the largest cave room in Scandinavia and is one of the lowest altitude ice caves in Europe. Radiocarbon dating of plant debris at the base of The 20m thick ice mass indicates

that ice accumulation commenced after AD 1200 (Lauritzen 1996 & et al. 2005), Fig. 5. As the entire Chrono sequence is exposed inside the cave (Figs. 2 & 4) ice cores will be drilled and samples covering the entire time span. The ice core will be melted slowly and the ice water will be filtered onto 0.2 µM filter to collect the microbial biomass, which will be used for RNA and DNA extraction. The functional variability of total and active-embedded microbiome will be determined by direct sequencing using illumina sequencing technology of metagenomes and metatranscriptome from the ice and be compared with other ice and glacier caves processed within the project. Further analyses in order to gain insight into the microbial community structure and metabolism will be achieved through the reconstruction of the microbial transcriptome and genome resources of the entire microbial community. These data will be important to reveal the first identities and functions of the key players in these unique and vulnerable ecosystems due to climate change.



Fig. 4. Part of the exposed ice mass (1990)

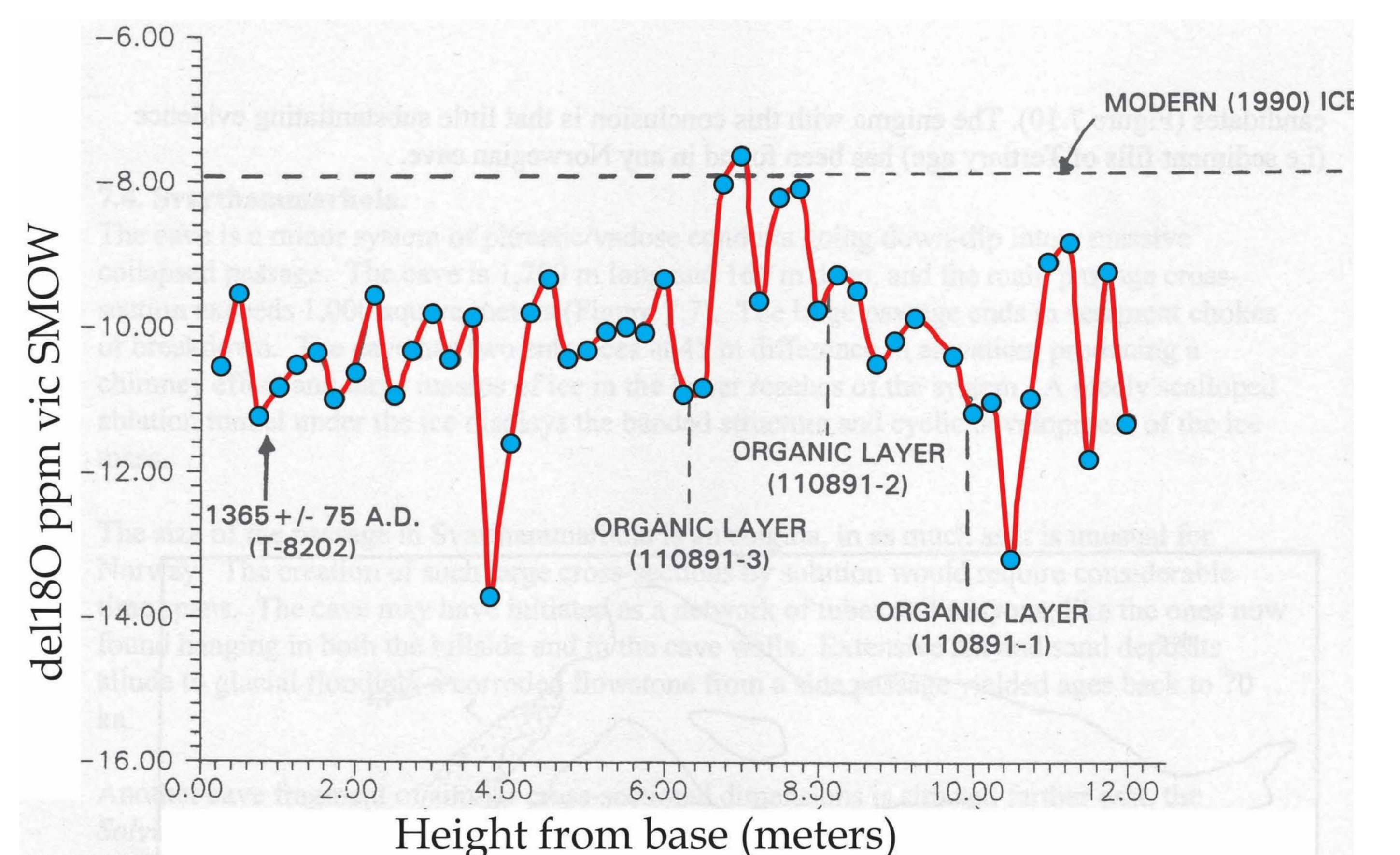


Fig. 5. Oxygen isotope stratigraphy of the lowermost 12 m of the ice mass, (Lauritzen 1996)

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