Quantification of the role of orbital and millennial timescale processes on δ^{18}O and $^{17}\Delta$ signals

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The triple isotope composition of atmospheric oxygen (δ^{18}O, $^{17}\Delta$) integrates the signature of various mass dependent processes associated with hydrological cycle, biological cycle and non mass dependent photochemical reactions in the stratosphere, both on orbital and millennial timescales: changes in global seawater, hydrological cycle, relative humidity, vegetation distribution and C3/C4 plants partition. At the orbital timescale, tropospheric δ^{18}O bears a strong orbital precession signal while at the millennial timescale, d18O depicts a clear decrease in phase with Greenland InterStadial events. $^{17}\Delta$ $(\ln(\delta^{17}O+1)-\lambda^*(\ \delta^{18}O+1))$ is more directly related to variations in the global biospheric productivity with a main variability associated with the glacial – interglacial changes.

Here we make use of a global model integrating changes in climate, biosphere productivity, water isotopic composition to quantify the contribution of the different processes to δ^{18}O and $^{17}\Delta$ signals at relevant orbital periods (snapshots of pre-industrial period, Last Glacial Maximum (LGM), Heinrich event). The model accounts for the latest fractionation ratios between ^{18}O /^{16}O and ^{17}O/^{16}O associated with oxygen respiration processes and leaf transpiration, oceanic net primary production (simulated by PISCES model), the spatial and temporal variation of vegetation distribution (simulated by ORCHIDEE model), climatic conditions and isotopic composition of meteoric water and water vapor (LMDZ global circulation model)

Bacterial diversity in Baltic Sea sediments from Skagerrak and Bothnian Bay

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The biogeochemical cycling of iron is a key process in terrestrial and aquatic systems including marine environments. However, limited information exists about the diversity and metabolic pathways of microorganisms linked to the iron cycle in ocean sediments. The goal of this study was to determine the bacterial community diversity in sediment samples from Skagerrak (SK) and Bothnian Bay (BB) using pyrosequencing as a first step in characterizing microorganisms potentially involved in iron reduction at these two sites. DNA was extracted from various depths from sediments collected in SK and BB. Porewater profiles of relevant electron acceptors showed that sulfate was ~28 mM and ~ 2 mM in in SK and BB sediments, respectively. H_2S was below detection in both sediments, and Fe^{2+} and Mn^{2+} levels reached ~ 140-150 μM in SK sediments between 6-7 cm depth and ~300 μM within the first 2 cm in BB sediments. V1-V3 regions of the 16S rRNA gene were used for 454 titanium pyrosequencing and sequences were analyzed using QIIME (1). Proteobacteria dominated these sediments and potential iron- and manganese-reducing bacteria included *Desulfurmonadales*, *Alteromonadales*, *Geobacteraceae*, *Pelobacteraceae*, *Shewanellaceae*, *Myxcoccocales*, *Oceanospirillales,* and *Campylobacterales*. Additionally, *Actinobacteria,* and *Bacteroidetes* were also dominant. These results imply that marine systems are likely to harbor more metabolically diverse iron and manganese reducing microorganisms than the traditional *Shewanella* and *Geobacter* model systems.

[1] Caporaso *et al.* (2010). Nature Methods, **75**: 335-336

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