

Cycling of silicic acid and nitrate in the Eastern Equatorial Pacific: Insights from stable silicon and nitrogen isotopes

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We present the first direct comparison between dissolved stable silicon ($\delta^{30}\text{Si}(\text{OH})_4$) and nitrogen ($\delta^{15}\text{NO}_3^-$) isotopes in the upwelling area off Peru to investigate the biogeochemical processes controlling nutrient cycling in one of the globally largest Oxygen Minimum Zones (OMZs). Nitrate is a generally important source of new nitrogen for phytoplankton, whereas silicic acid is a key nutrient for diatoms, which dominate the phytoplankton assemblages in upwelling areas. Silicon and nitrogen isotopes in the euphotic zone of the upwelling area are mainly controlled by biological utilization during which the lighter isotopes are preferentially incorporated into the organisms. Silicon isotopes are subject to a relatively simple cycling only influenced by utilization and subsequent dissolution of diatoms. In contrast, there are additional processes exerting control the N isotope composition of dissolved nitrate including anoxic ammonium oxidation (anammox) and/or denitrification within the OMZ. Given that the water masses feeding the coastal upwelling cells originate from the suboxic zone, the surface waters near the shelf show low $\delta^{30}\text{Si}(\text{OH})_4$ values (2‰) under strong upwelling conditions corresponding to high $\delta^{15}\text{NO}_3^-$ values (14‰). During the cruise a large mesoscale eddy was present in the study area and clearly influenced the nutrient stable isotope composition, as well as the phytoplankton community. Pronounced silicic acid limitation in the center of the eddy structure is indicated by high $\text{NO}_3^-:\text{Si}(\text{OH})_4$ ratios (~15) leading to the highest $\delta^{30}\text{Si}(\text{OH})_4$ values (3.7‰) accompanied by high $\delta^{15}\text{NO}_3^-$ values (16‰). The results show that both water mass mixing and remineralization processes influence the dissolved nitrogen and silicon isotope composition. Due to grazing of zooplankton and/or microbial remineralization a larger fraction of the nitrogen is recycled within the upper water column compared to silicic acid, which is more efficiently transferred to the deep waters. This is indicated by a smaller degree of utilization for nitrate in comparison to silicic acid in the study area. The combination of $\delta^{30}\text{Si}(\text{OH})_4$ and $\delta^{15}\text{NO}_3^-$ helps to disentangle utilization and N-loss processes and better understand paleo records and.

Determination of microbial consortia and its adaptation to environmental changes in the Neo-Archaean

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Isotopic fingerprints in Archaean sediments track metabolic processes, and are often the best evidence of biological activity. However poor and limited preservation make reconstitution of Archaean environments from rock records very challenging. Studying multiple localities around the world for one specific period helps to create a better picture of Archaean environments for this time window, but it is still a succession of snapshots, and such models can be misleading.

This work uses three cores and coexisting stromatolitic deposits from proximal but spatially different localities to reconstitute contemporary but sedimentologically varied Archaean environments. Well preserved 2.7 to 2.65 Ga sediments from the Belingwe Greenstone Belt (Zimbabwe) have been studied. The Manjeri and Cheshire Fms, laid down in a continental basin, consist of carbon- and sulphur-rich cherts and dark shales, as well as shallow-water limestones. In carbon-rich sections in cores from the Shavi and Jimmy Members, Manjeri Fm, and stromatolite surface outcrops, the overall 39‰ range for $\delta^{13}\text{C}_{\text{red}}$ and the overall 40‰ range for $\delta^{34}\text{S}$, plus $\Delta^{33}\text{S}$, molybdenum and iron isotopic information, suggest a wide spectrum of bacterial consortia, showing adaptations to environmental changes. This allows us to map out a wide sequence of microbial/sedimentary facies in coexisting microbial consortia in evolving prokaryotic communities.