Nitrogen isotope fractionation patterns of chlorophyll track taxonomic shifts in a natural phytoplankton community

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Chlorophyll is produced by all photosynthetic organisms, and is therefore an ideal target for compound-specific ^{15}N analysis to study the dynamics between changes in the N cycle and primary production. In laboratory cultures, the difference between the N isotope ratio ($\delta^{15}N$) of chlorophyll and the $\delta^{15}N$ of biomass, known as ε_{por}, varies taxonomically. These taxonomic patterns have potential applications for studying productivity in both modern and ancient environments, but have not yet been demonstrated robustly in nature. Here we take advantage of the annual cyanobacterial bloom occurring in Lake Erie, USA, which results in a transition from a eukaryote-dominated to cyanobacteria-dominated phytoplankton community. The resulting time-series shows that environmental observations agree with laboratory observations: ε_{por} endmember values are ~5‰ and ~ -15‰, for eukaryotic algae and freshwater cyanobacteria, respectively. Because the range and sensitivity of ε_{por} is the same in nature as in the laboratory, the Lake Erie data advocate for ε_{por} as a reliable tracer of the relative contributions of cyanobacteria and eukaryotic algae to primary production in aquatic environments. Furthermore, the agreement between culture studies and the environment suggests that there is likely to be a fundamental biosynthetic or physiological explanation for why chlorophyll N isotopes are fractionated differently among major algal groups, independent of growth condition or original N source. Because chlorophyll biosynthesis is closely linked to cellular N assimilation and allocation, we hypothesize that differences in fractionation between major algal groups may be explained by differences in intracellular N partitioning.