The influence of light on soil community structure and consequences for soil CO\textsubscript{2}, CO\textsuperscript{18}O and COS exchange

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The stable oxygen isotope composition of atmospheric CO\textsubscript{2} and the mixing ratio of carbonyl sulphide (COS) are potential tracers of biospheric CO\textsubscript{2} fluxes at large scales. However, the use of these tracers hinges on our ability to understand and better predict the activity of the enzyme carbonic anhydrase (CA) in different soil microbial groups, including phototrophs. Because different classes of the CA family (α, β and γ) may have different affinities to CO\textsubscript{2} and COS and their expression should also vary between different microbial groups, differences in the community structure could impact the 'community-integrated' CA activity differently for CO\textsubscript{2} and COS. Four soils of different pH were incubated in the dark or with a diurnal cycle for forty days to vary the abundance of native phototrophs. Fluxes of CO\textsubscript{2}, CO\textsuperscript{18}O and COS were measured to estimate CA activity alongside the abundance of bacteria, fungi and phototroph genes. The abundance of soil phototrophs increased most at higher soil pH. In the light, the strength of the soil CO\textsubscript{2} sink and the CA-driven CO\textsubscript{2}-H\textsubscript{2}O isotopic exchange rates correlated with phototroph abundance. COS uptake rates were attributed to fungi whose abundance was positively enhanced in alkaline soils but only in the presence of increased phototrophs. In addition we developed a metabarcoding approach to reveal the interactions of specific taxonomic groups including photosynthetic eukaryotic algae and cyanobacteria when exposed to light and their impact on flux rates. Our findings demonstrate that soil-atmosphere CO\textsubscript{2}, COS and CO\textsuperscript{18}O fluxes are strongly regulated by the microbial community structure in response to changes in soil pH and light availability and support the idea that different members of the microbial community express different classes of CA, with different affinities to CO\textsubscript{2} and COS.