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Detecting climate-change responses of plants and soil organic matter using isotopomers

Jürgen Schleucher (1), Ina Ehlers (1), Javier Segura (2), Mahsa Haei (2), Angela Augusti (3), Iris Köhler (4), Pieter Zuidema (5), Mats Nilsson (2), and Mats Öquist (2)

(1) Medical Biochemistry & Biophysics, Umeå University, Umeå, Sweden (jurgen.schleucher@chem.umu.se), (2) Forest Ecology & Management, SLU, Umeå, Sweden, (3) Institute of Agro-envinronmental and Forest Biology IBAF - Ecophysiology, Porano, Italy, (4) USDA-ARS Global Change and Photosynthesis Research Unit, Urbana, IL, USA, (5) Forest Ecology and Forest Management, Wageningen University, Wageningen, Netherlands

Responses of vegetation and soils to environmental changes will strongly influence future climate, and responses on century time scales are most important for feedbacks on the carbon cycle, climate models, prediction of crop productivity, and for adaptation to climate change. That plants respond to increasing CO_2 on century time scales has been proven by changes in stomatal index, but very little is known beyond this. In soil, the complexity of soil organic matter (SOM) has hampered a sufficient understanding of the temperature sensitivity of SOM turnover. Here we present new stable isotope methodology that allows detecting shifts in metabolism on long time scales, and elucidating SOM turnover on the molecular level.

Compound-specific isotope analysis measures isotope ratios of defined metabolites, but as average of the entire molecule. Here we demonstrate how much more detailed information can be obtained from analyses of intramolecular distributions of stable isotopes, so-called isotopomer abundances. As key tool, we use nuclear magnetic resonance (NMR) spectroscopy, which allows detecting isotope abundance with intramolecular resolution and without risk for isotope fractionation during analysis.

Enzyme isotope fractionations create non-random isotopomer patterns in biochemical metabolites. At natural isotope abundance, these patterns continuously store metabolic information. We present a strategy how these patterns can be used as to extract signals on plant physiology, climate variables, and their interactions. Applied in retrospective analyses to herbarium samples and tree-ring series, we detect century-time-scale metabolic changes in response to increasing atmospheric CO_2, with no evidence for acclimatory reactions by the plants. In trees, the increase in photosynthesis expected from increasing CO_2 ("CO_2 fertilization) was diminished by increasing temperatures, which resolves the discrepancy between expected increases in photosynthesis and commonly observed lack of biomass increases. Isotopomer patterns are a rich source of metabolic information, which can be retrieved from archives of plant material covering centuries and millennia, the time scales relevant for climate change.

Boreal soils contain a huge carbon pool that may be particularly vulnerable to climate change. Biological activity persists in soils under frozen conditions, but it is largely unknown what controls it, and whether it differs from unfrozen conditions. In an incubation experiment, we traced the metabolism of 13C-labeled cellulose by soil microorganisms. NMR analysis revealed that the 13C label was converted both to respired CO_2 and to phospholipid fatty acids, indicating that the polymeric substrate cellulose entered both catabolic and anabolic pathways.

Both applications demonstrate a fundamental advantage of isotopomer analysis, namely that their abundances directly reflect biochemical processes. This allows obtaining metabolic information on millennial time scales, thus bridging between plant-physiology and paleo sciences. It may also be key to characterizing SOM with sufficient resolution to understand current biogeochemical fluxes involving SOM and to identify molecular components and organisms that are key for SOM turnover.