The metabolic sensitivity of hydrogen isotope fractionation differs between plant compounds

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Hydrogen stable isotope analyses (δ2H) of plant derived organic compounds are a useful tool for ecological, environmental, and palaeoclimatological research. However, during organic compound synthesis, variable biosynthetic 2H-fractionation has been suggested to occur as a result of changes in plant carbon fluxes. So far, inference has been based on examining the δ2H patterns of plant compounds along environmental gradients, among plant species, and between plant organs. In an alternative approach, we used four plant species with four different types of mutations that cause impaired starch synthesis to assess whether variability in carbon metabolism affects the biosynthetic 2H-fractionation during cellulose, phytol, and acetogenic lipid synthesis. We found that mutants with impaired starch synthesis always had higher cellulose and phytol δ2H values compared to the wild type. By contrast, 2H-fractionation during acetogenic lipid biosynthesis generally did not show strong metabolic sensitivity. We rationalise these differences by considering the biosynthetic pathway of each compound and the likely source of the variable isotope fractionation. In different organic compounds, the sensitivity of variable biosynthetic 2H-fractionation to changes in C-metabolism depends on incorporation of specific H atoms from precursor molecules. As such, we determined that the similar increase in cellulose and phytol δ2H values as an effect of impaired starch synthesis most likely originates in triose-phosphates.
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