Applications of transient isotopic labeling to assess metabolic fluxes of primary metabolism in plant tissues

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Improving plant composition and yield through metabolic engineering is an important goal to meet future food and other renewable resource demands. At the heart of plant productivity is the balance of carbon assimilation through photosynthetic activity and its partitioning including steps that respire carbon as well those that produce protein, oil, carbohydrates or other compounds. Measuring dynamic plant activity such as the fluxes through cellular metabolism requires isotopic tracers that can assess atom transitions without disturbing pathway operation. The choice of isotope substrates is constrained to those that are endogenous sources for the tissue under study which can greatly limit the experiment, for example, in autotrophic tissues CO2, is the primary source of carbon. Analogously other pathways in metabolism are either linear (e.g. some secondary metabolite pathways) or primarily use a single source of carbon for biosynthesis (e.g. acetyl-CoA for lipids).

Flux analysis in plants has been limited to central metabolism in tissues the exhibit long metabolic steady states including studies in seeds and cells. Thus the constraints of biological operation have hindered what could be accomplished by computational flux analysis however recent applications of nonstationary MFA utilize transient isotopic labeling and can therefore involve much shorter time frames that are less limited by choice of tracer. Here, plant-based labeling studies aimed at deciphering metabolic operation in multiple tissues will be described. Such studies suggest what may be possible through new modeling tools, strategies with isotopic labeling, mass spectrometry and MFA that are being developed to better elucidate biochemical network operation and plant function.