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# Tracing the allocation of recently assimilated C into key metabolites in Norway spruce (Picea abies) shortly after bud break

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Plants allocate carbon (C) to sink tissues depending on phenological, physiological or environmental factors. We still have little knowledge on C partitioning into various cellular compounds and metabolic pathways, especially during tree growth after bud break. Here we investigated C partitioning of freshly assimilated C in Norway spruce by in-situ 13C short-term pulse labeling 15 days after bud break. We quantified 13C incorporation into tree compartments (needles, branches, stem) and into water soluble organic carbon (WSOC) by elemental analyzer-isotope ratio mass spectrometry (EA-IRMS). In addition, we determined 13C allocation into key metabolites of amino acids, hemicellulose sugars, fatty acids and alkanes by compound-specific 13C analysis via gas chromatography-combustion-isotope ratio mass spectrometry (GC-C-IRMS).
The 13C allocation within the trees reflected the needles as major C sink accounting for 86% of the freshly assimilated C. After 6 h 13C was distributed over a broad spectrum of plant metabolites but not homogenously. Highest allocation was observed into structurally relevant compound classes of hemicellulose-derived sugars and proteinogenic amino acids (0.6% and 10% of needle 13C, respectively). However, needle growth also caused high C allocation into pathways not involved in formation of structural compounds like pathways in secondary metabolism, C-1 metabolism or amino acid synthesis from photorespiratory acitivity. C allocation into such pathways could be identified due to the high enrichment of key metabolites within the amino acids. In addition, high 13C allocation was found into the n-alkyl lipid biosynthesis (0.2 % of needle 13C) with 1) higher allocation into intracellular than cuticular fatty acids, presumably for thylakoide membrane formation and 2) decreasing 13C allocation along the lipid transformation and translocation pathways (precursor fatty acids (C16 & C18) > elongated long chain fatty acids > decarbonylated n-alkanes).
Consequently, the combination of 13C pulse labeling with compound-specific 13C analysis of key metabolites enabled identification of relevant C allocation pathways during needle growth after bud break. Besides primary metabolism, synthesizing structural cell compounds, a complex network of various pathways consumed the freshly assimilated 13C and kept the majority of the assimilated C in the growing needles.