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Analysis of central metabolism in developing oilseeds of Brassica napus

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Seeds develop by absorbing nutrients from their mother plant, and using these to synthesize a combination of starch, protein and lipid. The size and number of seeds which finally develop determines the crop's yield, while their composition determines the end-use quality of the crop. A combination of metabolomics, enzyme activity profiling, 13^C-based metabolic flux analysis (MFA) and computational analysis is made as part of an attempt to understand regulation of central metabolism of the developing plant seed. Targeted metabolite profiling using LC-MS/MS succeeded in identifying ~100 intermediates within the central metabolism, including sugars, amino acids, nucleotides and their sugars, signaling molecules and intermediates of glycolysis and citric acid cycle. Some of these metabolites differed quantitatively between the accessions and displayed a significant shift corresponding to flux. With increasing flux through glycolysis and lipid synthesis across the genotype accessions, levels of several glycolytic intermediates decrease significantly. Our data indicate that mechanisms of allosteric control are of major importance in controlling the flux partitioning between starch and lipid, specifically the feedback inhibition of phosphofructokinase and ADP-glucose pyrophosphorylase by phosphoenolpyruvate and phosphoglycerate, respectively. In addition, other compounds like cyclic AMP and sucrose-6-phosphate were identified to be potentially involved in so far unknown mechanisms of metabolic control.

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