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Regulatory Metabolic Networks In Plant Development And Response To Stress

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Metabolism consists of a complex dynamic network of interacting cellular and biochemical pathways and gene expression mechanisms through which regulatory genes (such homeotic genes) implement their effect on plant growth, development and response to physiological and external signals. Our laboratory aims at elucidating regulatory networks associated with nitrogen and amino acid metabolism occurring in vegetative tissues and during seed development. Our approach includes transgenic plants in which we have modified the metabolism of lysine as well as the α-amino butyric acid (GABA) shunt of the TCA cycle. These plants are being analyzed by proteomics, microarrays,

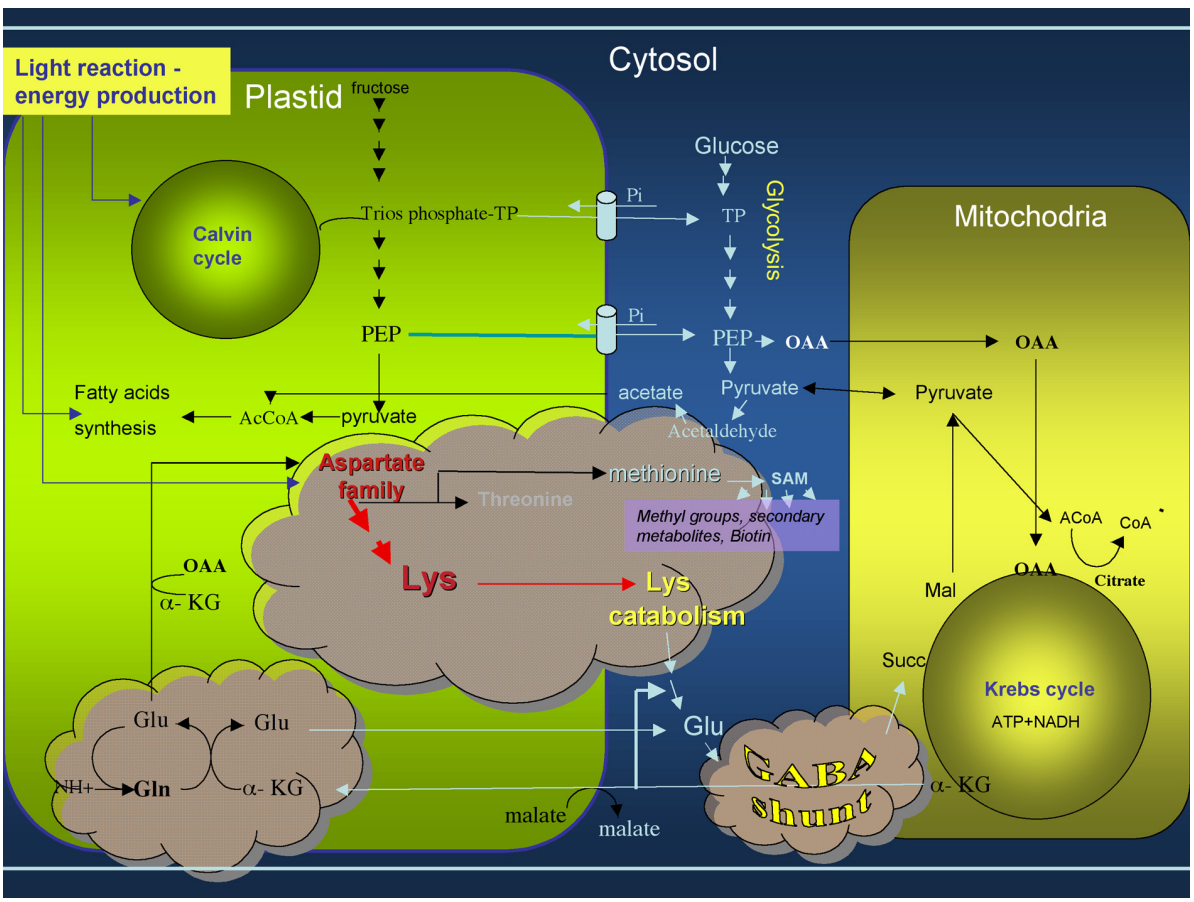

Fig. 1 *Metabolic networks regulating carbon/nitrogen metabolism in a plant cell.*
Abbreviations- Glu, glutamate; Gln, Glutamine; Lys, Lysine; Asp, Aspartate; PEP, phosphoenolpyruvate; OAA, oxalic acid; α-KG, α-ketoglutaric acid; Succ, succinic acid; GABA, γ-aminobutyric acid; SAM, s-adenosyl methionine

metabolic profiling and bioinformatics approaches to elucidate networks that are concertly regulated at the mRNA, protein and metabolite levels. Initial data is presented in this poster.

Metabolic networks also include intracellular pathways of degradation of proteins into amino acids, which are used to produce new proteins needed for new developmental programs. We are studying the function of a plant gene family (Atg8) that is homologues to a yeast protein associated with autophagy. In situ expression analysis of distinct members of this family suggests a multiple non-redundant function in plant development and response to stress. In addition, RNAi-mediated suppression of expression of one of these gene isoforms showed that it plays a major regulatory role in pollination and reproduction.

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