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Challenging the role of plastid co-translational N-terminal modifications upon stress responses

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Co-translational N-terminal modifications of plastid genome-encoded proteins also belong to key mechanisms for the stability and function of these proteins. Previous studies have already shown that the plastid-localized methionine aminopeptidase isoforms MetAP1B, MetAP1C and MetAP1D remove the N-terminal methionine of several nascent peptides, while particular the role of MetAP1C is crucial for the N-terminal processing of RbcL. The plastid proline aminopeptidase 2 (APP2) is proposed to be responsible for the cleavage of the second N-terminal amino acid residue serine in RbcL, which is positioned before a proline, while isoforms of GCN5-N-terminal acetyltransferases (GNAT) specifically acetylates different dedicated enzymes for the modification of either the N-termini of proteins or internal lysine residues. We are interested in investigating the specific role of these enzymes for the maturation of plastid-localised proteins, with particular emphasis on RuBisCO, and have used single and double mutants for MetAP1C, APP2 and GNAT7 (map1c, gnat7, app2-4, map1c x gnat7, map1c x app2-4, gnat7 x app2-4) to analyse the physiological and biochemical effects of the missing proteins for the N-terminal processing of plastid-encoded proteins under standard and stress conditions. In particular, single and double map1c mutants showed phenotypic changes in response to cold treatment, such as pale green leaves and slow growth compared to the WT plants. Altered photosynthetic capacities were detected due to reduced protein content of various proteins in the chloroplasts involved in photosynthesis and carbon assimilation.

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