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Unveiling the Multifaceted Machinery of N-terminal Protein Modifications in Plant Plastids

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Protein modifications are emerging as key regulators of numerous essential cellular processes. Virtually all proteins undergo co- and/or post-translational modifications (CTMs, PTMs). However, a comprehensive understanding of the full range of CTMs and PTMs affecting a given protein throughout its life cycle remains elusive. This is particularly true for chloroplast-localized protein modifications, including N-terminal protein modifications (NPMs), which impact the N-terminus of proteins.
The earliest NPM is the essential process of N-terminal methionine excision (NME), which involves the removal of the initial methionine (iMet) from nascent peptide chains. In plastids, NME is facilitated by methionine aminopeptidases (MetAPs), which work in conjunction with peptide deformylases (PDFs) to remove the formyl group attached to iMet. Despite the discovery of plastid NME modifiers in the early 2000s, the plastid-specific MetAPs (pMetAPs) have not been thoroughly characterized, nor have the plastid enzymes responsible for another critical NPM, N-α-acetylation (NTA).
In this study, I will present a comprehensive investigation of the plastid MetAPs and acetyltransferases families, revealing unexpected substrate flexibility and distinctive features that suggest a complex, multitasking protein modification machinery unique to plant plastids. I will also discuss how this machinery has evolved to meet the specific needs of this organelle.

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