

N-terminal Protein Acetylation Regulates Defined Stress Responses in Arabidopsis

N^α-terminal protein acetylation (NTA) affects up to 90 % of cytosolic proteins in human and Arabidopsis, where it influences localisation, activity, association and stability of target proteins. In eukaryotes NTA is catalysed by three major N^α-terminal acetyltransferases, NatA, NatB and NatC. All three complexes differ in their subunit composition as well as in their substrate specificity. NatA and NatB consist of the GNAT-type catalytic subunits NAA10 and NAA20 as well as the ribosome binding subunits NAA15 and NAA25, respectively.

Both complexes appear to be conserved from yeast to Arabidopsis regarding substrate specificity and subunit composition. Although in plants the biological relevance of NTA is still enigmatic, its importance is illustrated by corresponding loss-of-function mutants: While the loss of NatB results in retarded growth, the lack of NatA is lethal already in the globular stage of embryo development. The significance of NTA under non-stressed conditions in combination with the high number of substrates indicates that NTA participates in plant developmental processes and may contribute to stress responses in plants. Indeed we found, that *Atnaa20* loss-of-function mutants are hypersensitive to osmotic stress as well as to DTT-induced ER stress. In contrast, the response to drought was not affected by the loss of NatB activity. On the contrary, NatA depleted plants are more tolerant to drought stress, but behave like wild type under ER- and osmotic stress. These data not only identifies NTA as an important determinant during Arabidopsis stress responses, but also indicates a so far unexpected specificity of different Nat complexes towards specific kinds of stresses.