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Investigating the role of Arabidopsis HISTONE DEACETYLASE 14 in chloroplasts

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Lysine acetylation is an important post-translational protein modification that plays a vital role in plant development and in responses to different environmental stimuli. Histone deacetylases (HDACs) are responsible for removing lysine acetylation on various proteins. While most work has focussed on the role of Arabidopsis HDACs on histone acetylation, their role in the deacetylation of non-histone proteins is much less known, although proteins of many different organelles have been found to be lysine-acetylated. From the 18 HDACs found in Arabidopsis, only HDA14 has been found to be dual-localized in plastids and mitochondria. Here we performed a quantitative mass spectrometry-based approach, using isobaric TMT labelling, to profile the lysine acetylome of an Arabidopsis *hda14* mutant compared to WT. We identified 1509 acetylation sites on 881 Arabidopsis protein groups, of which 56 sites were de-regulated in the *hda14* mutant. Most of these sites were derived from chloroplast proteins. In addition, we used different co-immunoprecipitation approaches to identify possible interaction partners of HDA14 and to identify its function in the regulation of organellar metabolism.

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