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Occupancy of lysine acetylation in Arabidopsis proteome via chemical labelling and mass spectrometry measurements

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In course of the day, the environmental conditions are changing, so that the plants have different needs of proteins and their functions. As a result, the proteome needs to change constantly and in a dynamic way. Post-translational modifications (PTM´s) change the properties of present proteins and have a massive impact on their functions, structures and activities. Such a modified protein has a changing mass, that is detectible by mass spectrometry. We are looking at the acetylation of lysine residues over the whole proteome of Arabidopsis (e.g. adult leafs). Using a method for chemical labelling of lysine with heavy (D6-)acetic anhydride (Baeza et al. 2020), we want to define the occupancy from lysine residues, that were naturally acetylated in Arabidopsis, through to different stages of the day/night. Therefore, we use various proteases to generate lots of peptides, with different cleaving sites, measure them by mass spectrometry and determine the occupancy of lysine acetylation. For a better understanding which impact the site-specific acetylation of lysine has in plants and how big the changes are during different stages and environmental conditions.

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