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Exploring the role of histone modifications in response to nitrate variation for cytokinin biosynthesis

In soil, nitrate concentration fluctuates and is often a limiting factor of crop growth and development. Cytokinin (CK), a class of hormone promoting cell division, is necessary for the long-distance nitrate signaling, especially an intermediate form of *trans*-zeatin (tZ): the tZ-riboside (tZR). Interestingly, genes encoding for the enzymes permitting the production of this tZR, IPT3 and *CYP735A2* are strongly induced by nitrate and repressed by a starvation. However, the underlying mechanisms of these regulations remain poorly understood. Our research aims to understand how variation in nitrate availability impacts the transcriptional regulation of CK biosynthesis genes through chromatin modification. By the analysis of post-translational modifications of the histone H3, and expression profile during a kinetic of nitrate variation (nitrate-starvation-nitrate resupply), we observed that the chromatin profiles at CK biosynthesis genes change dynamically during nitrate variation in correlation with the transcripts profile. To better understand the role of this chromatin dynamic and effectors involved, we are now analyzing mutants impaired for different chromatin regulators (deposition or removal of histone marks). Our recent results suggest that the chromatin dynamic constitutes a new regulatory mechanism in response to nitrate availability for CK biosynthesis genes regulation. I will illustrate these results by presenting the characterization of *IPT3* chromatin profiles during the nitrate variation.