

The impact of post-translational modifications on the activity of ARGONAUTE1 in *Arabidopsis thaliana*

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ABSTRACT

Arginine methylation (R-methylation) is a post-translational modification classified into three different types: the mono-methylation (MMA), the symmetric (sDMA) and asymmetric dimethylations (aDMA) (Ahmad and Cao, 2012). Each type of R-methylation is deposited by different members of the same protein family: the PRMTs (Protein Arginine Methyltransferases) (Ahmad and Cao, 2012). Many of their substrate are involved in the regulation of various gene expression steps, such as transcription, mRNA splicing and mRNA fate (Blanc and Richard, 2017). Among their targets, the Argonaute/PIWI proteins, key effectors of RNA silencing, have been shown to be R-symmetrically di-methylated in animals, but also in plants as recently demonstrated for AGO2 protein (Kirino *et al.*, 2009; Nishida *et al.*, 2009; Hu *et al.*, 2019). This modification impacts their activity, acting on protein stability and/or AGO sRNA loading (Kirino *et al.*, 2009; Nishida *et al.*, 2009; Hu *et al.*, 2019). In animals, Aub and AGO3 R-methylation impacts the regulation of transposons in germline cells, while in plants, AGO2 R-methylation regulates the plant resistance against bacteria (Kirino *et al.*, 2009; Nishida *et al.*, 2009; Hu *et al.*, 2019). In our study, we focus on AGO1, one of the major actors of post-translational gene silencing in plants. We show that AGO1 is symmetrically dimethylated on arginines by PRMT5 in *A.thaliana*. However, AtAGO1 exhibits atypical signatures compared to its animal and other identified plants counterparts. We are now trying to decipher the impacts of R-methylation on AGO1 activity in *A.thaliana*.

References

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