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# Deciphering the role of miR845 in the epigenetic regulation of transposable elements in Brassicaceae

Corinne Mhiri\*<sup>1</sup>, Armand Garcia<sup>1</sup>, Florian Maumus<sup>2</sup>, Nathalie Choisne<sup>2</sup>, Marie-Angèle Grandbastien<sup>1</sup>, and Filipe Borges<sup>1</sup>

<sup>1</sup>Institut Jean-Pierre Bourgin – AgroParisTech, Université Paris-Saclay, Institut National de Recherche pour l’Agriculture, l’Alimentation et l’Environnement – INRAE Centre de Versailles, Route de St-Cyr (RD10), 78026 Versailles Cedex, France

<sup>2</sup>Unité de Recherche Génomique Info – Institut National de Recherche pour l’Agriculture, l’Alimentation et l’Environnement – INRAE, Centre de recherche de Versailles, bat.18 Route de Saint Cyr 78000 Versailles, France

## Abstract

In plants, transposable elements (TEs) are predicted targets of endogenous microRNAs (miRNAs), suggesting that miRNA-TE interactions could represent an ancient evolutionary force driving epigenetic regulation and genome expansion. This includes the highly conserved miR845 family that targets specifically retrotransposons in *Arabidopsis* pollen, in a mechanism that has been implicated in the regulation of parental genome dosage in triploid seeds (1). However, the role of miR845 in epigenome reprogramming and TE evolution remains poorly understood. Interestingly, natural variation in miR845 activity was observed in *Arabidopsis thaliana*, where the loss of miR845 correlates with increased TE expression in pollen and low triploid seed abortion (1). In addition, within the Brassicaceae family, we have recently confirmed the absence of functional *MIR845* genes in *Arabis alpina*, where a massive genome expansion resulted from increased activity of predicted miR845 targets (2). In order to investigate the role of miR845 in these species, we have generated *MIR845* complementation lines of *A. thaliana* Ler-0 and *A. alpina*, which were able to restore strong miR845 expression in pollen. I will present our preliminary small RNA and transcriptome analysis of these lines, where we expect to find important mechanistic insight on the role of miR845 in the epigenetic control of TEs during reproduction and seed development. Ultimately, we expect that this work will allow to elucidate the impact of miR845 in the evolution and expansion of retrotransposons in plant genomes.

## References:

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- 2 Willing, E.-M. et al. Genome expansion of *Arabis alpina* linked with retrotransposition and reduced symmetric DNA methylation. *Nat Plants.* 2015, 1, 14023. <https://doi.org/10.1038/nplants.2014.23>

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\*Speaker