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SÉMINAIRE

Transposable element sequences and their epigenetic control: tunable engines of rapid adaptation in plants?

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Eukaryotic genomes are to a great extent shaped by the transposable element (TE) sequences they contain, most of which have long lost any ability to transpose. Nonetheless, we showed using the model plant *Arabidopsis thaliana* that the few mobile TE copies present in extant genomes are a major, if not the main, generators of large effect, mostly deleterious, mutations in nature. In addition, we found that natural genetic variation in RNA-directed DNA methylation (RdDM) activity, an epigenetic pathway that controls the environmental sensitivity of TEs, modulates their mobilization. Specifically, weaker RdDM activity is associated with higher levels of transposition rates in nature and appears to be positively selected at the edge of the species' ecological niche. These results indicate that transposition is a potent engine of allelic exploration that is genetically and environmentally-tunable, which may facilitate as a consequence the rapid adaptive response of species to abrupt changes in the environment. In addition, because TE sequences, whether mobile or not, are targeted by DNA methylation which is not extensively reset at every generation in plants, they can also provide a multiplicity of substrates for natural epiallelic exploration. Indeed, out of ~7000 TE sequences present in the reference strain Col-0 for which we could experimentally induce a severe loss of DNA methylation, we found that ~1000 are present in the unmethylated form in at least one of the 720 natural strains for which methylome data are available. Furthermore, consistent with the inheritance properties of TE hypomethylation that we defined experimentally, strength of RdDM trans-targeting of TE sequences is also the major genetic determinant of their epivariation in nature. Moreover, natural TE epivariants are enriched near genes, a pattern further reinforced in strains overexpressing a component of the polymerase-associated factor 1 (Paf1) complex. Remarkably, when located near stress response genes, natural TE epivariation is often associated with environmental and phenotypic variation, which is suggestive of an adaptive role in nature despite their relatively short-term persistence. Altogether, our findings indicate that thanks to their capacity to epimutate, TE sequences that are retained in the genome may still contribute to phenotypic variation and adaptation long after they have lost their ability to transpose.