

## Publication

Accumulation of transposable elements in selfing populations of *Arabidopsis lyrata* supports the ectopic recombination model of transposon evolution

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Transposable elements (TE) can constitute a large fraction of plant genomes, yet our understanding of their evolution and fitness effect is still limited. Here we tested several models of evolution that make specific predictions about differences in TE abundance between selfing and outcrossing taxa, and between small and large populations. We estimated TE abundance in multiple populations of North American *Arabidopsis lyrata* differing in mating system and long-term size, using transposon insertion display on several TE families. Selfing populations had higher TE copy numbers per individual and higher TE allele frequencies, supporting models which assume that selection against TEs acts predominantly against heterozygotes via the process of ectopic recombination. In outcrossing populations differing in long-term size, the data supported neither a model of density-regulated transposition nor a model of direct deleterious effect. Instead, the population structure of TEs revealed that outcrossing populations tended to split into western and eastern groups - as previously detected using microsatellite markers - whereas selfing populations from west and east were less differentiated. This, too, agrees with the model of ectopic recombination. Overall, our results suggest that TE elements are nearly neutral except for their deleterious potential to disturb meiosis in the heterozygous state.

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