

## Chromosome rearrangements and evolutionary diversification of duplicated genomes

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Chromosome rearrangements (CRs) are known to promote the reduction of genome size and chromosome numbers (i.e. diploidization) in plants undergoing recurrent whole-genome duplications. Such phenomenon appears decisive for the evolutionary diversification of plants, however the genomic basis of chromosomal restructuring remains underexplored.

In our study, we combine cutting-edge sequencing technologies (Oxford Nanopore, PacBio Iso-Seq and Hi-C) to build, annotate, and compare chromosome-scale genome assemblies of closely related *Biscutella* species. These plant species diversified independently following a whole genome duplication event and colonized different environmental niches, making the *Biscutella* genus a unique system for understanding the impact of diploidization on plant adaptation in natural populations.

The availability of chromosome-scale genome assemblies is crucial for investigating structural variation. Although the complexity of large and repetitive plant genomes often hinders such analyses, we provide guidelines for the assembly and annotation of high-quality genomes and shed light on the molecular mechanisms underlying CRs (with a special focus on transposable elements). Through comparative genomics, we quantify the impact of different restructuring events on genome divergence and assess molecular processes that alter genome size and content, determining to what extent different types of restructuring events affect the gene space vs the repetitive fraction during diploidization and species diversification.