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ANALYSIS OF LTR RETROTRANSPOSONS IN THE GENUS *POPULUS*

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Retrotransposons are a ubiquitous component of plant genomes. They are especially abundant in species with large genomes. *Populus* species have relatively small genomes for which large genomic resources are available, however studies focused on poplar retrotransposons dynamics are rare. With the aim to study the retrotransposon component of the poplar genome, we have scanned the complete *P. trichocarpa* genome sequence in search of full-length LTR retrotransposons, i.e., retrotransposons characterised by two long terminal repeats at the 5' and 3' ends.

A computational approach based on detection of conserved structural features, on building multiple alignments, and on similarity searches allowed to obtain a database of 1,479 putative full-length LTR-retrotransposons. Ty1-*copia* elements were more numerous than Ty3-*gypsy*. However, many LTR-retroelements were not assigned to any superfamily because lacking of diagnostic features and non-autonomous. LTR-retrotransposon remnants were by far more numerous than full-length elements, indicating that during the evolution of poplar, large amplification of these elements was followed by DNA loss. Within superfamilies, Ty3-*gypsy* families are made of more members than Ty1-*copia* ones. Retrotransposition occurred with increasing frequency following the separation of *Populus* sections, with different waves of retrotransposition activity between Ty3-*gypsy* and Ty1-*copia* elements. Recently inserted elements appear more frequently expressed than older ones. Finally, different levels of activity of retrotransposons were observed according to their position and their density in the linkage groups.

To analyse the occurrence of diversity in the retrotransposon pool of different poplar species, a Illumina DNAseq experiment was performed in *Populus deltoides* and *P. nigra*. Using CLC Bio Workbench 5.0, 10x Illumina reads of *P. deltoides* or *P. nigra* were assembled into contigs. All *P. deltoides* and *P. nigra* contigs were masked with the *P. trichocarpa* retrotransposon database. The pairwise comparisons indicated that the majority of *P. trichocarpa* retrotransposons occurred also in *P. deltoides* and *P. nigra*.

On the whole, the results support the view of retrotransposons as a community of different organisms in the genome, whose activity (both retrotransposition and DNA loss) has heavily impacted and probably continues to impact poplar genome structure and size.