

CENTROMERIC SEQUENCES IN THREE POPLAR SPECIES

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The evolution of centromere structure in plants is far to be clarified. It is mainly composed of tandem repeated sequences and retrotransposons, mainly of the *Gypsy* superfamily. Usually, centromeric repeats are species specific, hence they can be used also to study evolutionary relationships between species.

Though the genome of *Populus trichocarpa* has been entirely sequenced, the structure of centromeres has received little attention. We searched for putative centromeric satellites in the poplar genome using the TandemRepeat Finder software. We identified two types of putative centromeric repeats. The first type, whose consensus sequence is 107 bp long, should allow the identification of the centromere position in 9 over 19 chromosomes forming the haploid complement. The second, a consensus sequence 142 bp long, should identify the centromere of 6 chromosomes. No putative centromeric repeats were found in the remaining 4 chromosomes, probably because of underrepresentation of repetitive sequences in the currently available poplar genome sequence.

We overlapped a map track of putative centromeric repeats for each chromosome with the distribution of retrotransposons along poplar chromosomes. In all chromosomes in which the centromere position seemed to be identified, there was a significant overlap between the putative centromeric position and the accumulation of full-length *Gypsy* retrotransposons, suggesting the association between centromeric repeats and these retroelements. It is however to be recalled that the definition of the centromere position requires biochemical and cytological validation, for example by BAC in situ hybridization.

The presence of two different centromeric repeats in two groups of chromosomes should be related to an ancient interspecific hybridization occurred during *P. trichocarpa* evolution.

We also performed slot blot experiments in other two poplar species, *P. deltoides* and *P. nigra*, using the two *P. trichocarpa* putative centromeric repeats as probes. Such repeats occur also in these two species. Moreover the 142 bp long sequence shows high similarity to a 145 bp tandem repeat sequence isolated by Rajagopal et al. (1999) in another poplar species, *P. ciliata*, that was described as putatively centromeric.

On the whole, the results indicate that the two putative centromeric sequences can be very useful for studying the evolution of the poplar genus.