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Molecular and cytological analyses of the major centromere and pericentromere repeats of *Brassica rapa* and their distribution in the related *Brassica* species

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Objectives

Inspection and comparison of the distribution of each repeat in the genome of three basic Brassica species, *B. rapa*, *B. nigra*, and *B. oleracea* and their allopolyploids revealed the composition and the evolutionary process of the fast evolving (peri)centromere structure in the genus *Brassica*.

Materials and Methods

1. Material

Plant - *B. rapa*, *B. nigra*, *B. oleracea*, *B. juncea*, *B. carinata*, *B. napus*

2. Methods:

Chromosome karyotype analysis and FISH

Results and Discussion

We have identified the major centromeric and pericentromeric retrotransposons of *Brassica rapa* by sequence characterization of 10204 BAC end sequences, two (peri)centromeric BAC clones and FISH analyses. Three copies of the centromere-specific retrotransposon of Brassica (CRB) are identified as the nest insertions in an array of 176 bp centromeric tandem repeats (CentBr) in BAC clone 01P13. In BAC clone 15B20, various pericentromere-specific retrotransposons (PCRBr) are intermingled with the CentBr array and a large block of a degenerate tandem repeat (TR238) flanking 5S-25S rDNA. FISH revealed that the CRB is located at the confined centromere region of all chromosomes in three basic Brassica species and their resynthesized amphidiploid species. We find that the 176 bp CentBr repeats are found at the centromere region in *B. rapa* and *B. oleracea* but not in *B. nigra*. The PCRBr elements are major components in large pericentromeric blocks of four chromosomes of *B. rapa* but not in *B. oleracea* and *B. nigra*. In most cases, allopolyploid species possessed each repeat element as the additive number of FISH signals as detected in *B. rapa* (A), *B. nigra* (B) and *B. oleracea* (C), respectively. FISH results demonstrated that the newly identified CRB, TR805, PCRBr, and TR238 elements compose major centromeric and pericentromeric repeats along with the known CentBr and rDNA elements. In *B. rapa*, these repeats are present in constitutive heterochromatin regions representing almost 45% of the genome.

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