The Society of Chromosome Research

1. *De novo* initiation of telomere sequences at the healed break points of wheat deletion chromosomes: Hisashi TSUJIMOTO, N. USAMI, K. HASEGAWA, T. YAMADA, K. NAGAKI and T. SASAKUMA (Kihara Inst. Biol. Res., Yokohama City Univ.)

When chromosomes are broken, the break points become highly unstable and acquire a property to fuse with other broken ends. The break points are, however, eventually stabilized, and, therefore, the broken chromosomes are transmitted to the daughter cells without further morphological change. This phenomenon known as 'healing of break points' is realized by addition of telomere repetitive sequences at the break points by telomerase that primarily synthesizes of the telomere sequence at normal chromosome terminals. In many higher organisms, however, this property has not been well investigated. In this study, we examined the telomere sequences in wheat deletion lines on chromosome 1B. Lines that showed break points around the nucleolar organizer region were first cytologically selected, and then their precise break points were determined by a fragment of rDNA and RFLP markers. In three lines in addition to one previously reported, the DNA fragments including the break points were amplified by PCR using primers of rDNA and telomere. The DNA sequences revealed the property of the telomerase activity at the break points. The telomere sequences initiated from two to four nucleotides of the original ribosomal DNA sequence that were also the components of the unit of telomere repetitive sequence. No specific sequences or structures were observed at or around the break points. Newly synthesized telomere sequences at all of the four break points contained considerable numbers of atypical telomere sequence units, especially, TTAGGG that is the common unit of mammalian telomere sequences. Based on these results, we discuss the property of plant telomerase to initiate *de novo* telomere sequences at break points.

2. Repetitive DNA in lettuce chromosomes in reference to C_0t-analysis and *copia*-like retrotransposon: Hideyuki MATOBA, Hiroshi UCHIYAMA and Tetsuo KOYAMA (Dept. Appl. Bio. Sci., Coll. Bioresource Sci., Nihon Univ.)

Highly repetitive DNA was isolated from the lettuce genomic DNA by the C_0t-analysis based on S1 nuclease. The C_0t -1 and C_0t -0.1 DNA amounted to 38.2% and 19.0% of the genomic DNA, respectively. FISH revealed the uniform distribution of the C_0t -1 DNA in all regions of all chromosomes. On the other hand, C_0t -0.1 DNA probes were hybridized with satellites and centromeres, and weak signals were detected at the interstitial regions of some chromosomes.
The *copia*-like retrotransposon was detected by means of PCR, with lettuce genomic DNA or cDNA from lettuce callus as templates. The amplified DNA were cloned, and six and three clones from the genomic DNA and cDNA, respectively,were sequenced. These sequences were found to have 73.3 - 75.8% homology with the sequence of the sunflower's *copia*-like retrotransposon and classified in two groups by their sequence homology. The *copia*-like elements from the cDNA were grouped in one cluster. Southern hybridization analysis showed that the C_0t -1 and C_0t -0.1 DNA contained the *copia*-like elements. The *copia*-like elements could exist as middle or highly dispersal repeated DNA sequences in the genome of lettuce.

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