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W219 : Evolution of Genome Size

Chromosomal Distribution Of Pine Repetitive DNA Sequences

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The genomes of higher eukaryotes are composed of euchromatin and heterochromatin. In plants, about 75% of the genome is heterochromatic DNA. The genomes of the pines (*Pinus* spp.; $2n = 2x = 24$) are enormous with 1C contents ranging from 20 to 30 Gb, and the fraction of their repetitive DNA being even higher than for most plant species. Recently we isolated and sequenced 33 repetitive genomic DNA clones from loblolly pine (genotype 7-56) and used these as FISH probes on pine metaphase chromosome spreads. The intensities of the FISH signals were quantified against intensities of a well characterized 18S-28S rDNA probe. All but a few clones showed fairly dispersed genome-wide distribution patterns. However, one of the random genomic, small insert (~2 Kb) clones, PT-7G-2H13, a putative gypsy-like retrotransposon, produced a single pair of discrete signals distal to a major 18S-28S rDNA site. Based on the loblolly pine reference karyotype (Genome 50:241-251, 2007) this repetitive DNA locus can be tentatively assigned to Bin 32 and thus appears to unambiguously identify Chromosome 7 in loblolly pine. Additional FISH research is being conducted to allow loblolly pine linkage groups to be correlated with their cytologically-defined chromosomes.

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