ORGANIZATION AND VARIATION OF rDNA IN PINUS SYLVESTRIS

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We examine the chromosomal organization, structure and variation of ribosomal RNA genes (rDNA) in Scots pine (*Pinus sylvestris*). In a conifer genome, rRNA genes are present in thousands of copies, which are tandemly arranged at several loci. rRNA-loci are also called nucleolus organizers (NORs) because of their ability to form nucleoli in interphase cells. NOR-specific silver staining was used to reveal the number and location of rDNA-containing sites in Scots pine chromosomes. There are at least 8-10 NORs in the haploid Scots pine genome (n=12), distributed on most chromosomes.

The structure and variation of rDNA repeats were studied by Southern hybridizations using nonradioactive digoxigenin labeling and detection techniques. The size of the rDNA repeat unit proved to be about 27 kb. This corresponds to the size of the rDNA unit in *Pinus radiata* (Cullis et al.). A restriction map of the coding region has been constructed.

rDNA variation was studied with 11 restriction endonucleases in Scots pine populations from southern (61°N) and northern (67.5°N) Finland. A heterologous probe (the complete rDNA repeat unit from flax) was useful in detecting restriction site variation both within and between populations. However, no rDNA repeat length heterogeneity was detected in this study. Some of the rDNA variants detected with Hind III seem to be present only in the northern Scots pine population, but only small samples have been studied by now. In order to characterize the structure and variation of rDNA more thoroughly, cloning of the rDNA repeat unit of Scots pine has been undertaken. This will facilitate the detection of variability in the intergenic spacer (IGS) region of rDNA.