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Structure, evolution and expression of ribosomal RNA genes in plant genomes: new approaches to old questions

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Abstract

Analysing the composition, organisation and evolutionary dynamics of repetitive DNAs such as ribosomal RNA genes (rDNA) can contribute valuable information on the evolution of plant genomes. We are especially interested in species with unusual rRNA genes since our discovery of linked rDNA in genus *Artemisia*. Most plants present 5S and 18S-5.8S-26S (35S) rDNA *loci* tandemly arranged and physically separated (S-type arrangement). However, *Artemisia*'s rDNAs are linked in the same operon with the 5S gene in the opposite strand (L-type arrangement). A similar organisation had only been found in one moss and one liverwort and it was almost the same as the one described for yeast. Later, it was discovered that about 25% of species of family Asteraceae could have a similar organisation. We also managed to demonstrate the expression and epigenetic modification of 5S genes in L-type Asteraceae. The quest for alternative rDNA organisations was further moved to gymnosperms, in which previous fluorescent *in situ* hybridisation (FISH) studies suggested this possibility. By studying all gymnosperm divisions (in species such as *Cryptomeria*, *Ephedra*, *Ginkgo*, *Gnetum* and *Welwitschia* among others) a fascinating range of rDNA arrangements was found. At present, research is being conducted as to determine the organisation of rDNA *loci* in chromosomes of selected gymnosperm species. Additionally, the modes of evolution in small (5S) and large (35S) rDNA cluster are being analysed in L-type and S-type taxa, including both angiosperms and gymnosperms, by amplicon sequencing of rRNA genes and combining classical and next generation sequencing (NGS) strategies.

