rDNA INTERGENIC SPACER OF *HAPLOPAPPUS GRACILIS*: SEQUENCE ANALYSIS AND CYTOLOGICAL LOCALISATION

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The rDNA Intergenic Spacer (IGS) plays an important role in cellular processes as rDNA transcription regulatory sequences and pre-rRNA processing signals are located in (Hemleben & Zentgraf, 1994; Fernandez *et al.*, 2000 and references therein). As a consequence, studies on the molecular organisation of the IGS are important; furthermore comparative analyses in different species give information on the evolutionary changes of conserved and variable sequences.

We present and analyze here the nucleotide sequence of the rDNA IGS of *Haplopappus gracilis* (Nutt.) Gray (Asteraceae), one of the six angiosperms showing the lowest chromosome number. *Haplopappus gracilis* is one of the best explored (Cremonini, 2005 and references therein). This species has a DNA content of 2C = 4.10 pg (Bennett, 1972) and the chromosome complement is composed of a pair of V-shaped chromosomes (I) and a pair of J-shaped chromosomes (II), i.e the nucleolar chromosomes (Jackson, 1957), so representing an interesting model for studying genome organisation.

The IGS sequence analysis reveals the presence of two kinds of IGS (indicated as short and long IGS) of different length and features. The long IGS is characterized by the presence of four blocks of repeated sequences and of multiple putative promoter sequences. The short IGS is lacking of the most of the repeated elements and of the entire putative promoter regions, but it shows high homology with the long IGS in the conserved regions. As a consequence, the short IGS represents, in our opinion, a putatively non functional gene or pseudogene. Experiments of fluorescent *in situ* hybridisation of digoxigenin-labelled probes suggest a different distribution of the two kinds of IGS in the nucleolar chromosomes of *H. gracilis*; besides differences in the signal intensity between homologous chromosomes were observed.

Fig. 1. *Haplopappus gracilis* flower-heads

Hemleben V., Zentgraf U., 1994. Structural organization and regulation of transcription by RNA polymerase I of plant nuclear ribosomal RNA genes. In: Nover L. (Ed.) Results and problem in cell differentiation: 20. Plant promoters and transcription factors. Springer, Berlin Heidelberg New York: 3-24.

Fernandez M., Polanco C., Ruiz M.L., Perez de la Vega M., 2000. A comparative study of the structure of the rDNA intergenic spacer of *Lens culinaris* Medik. and other legume species. Genome 43: 597-603.

Cremonini R., 2005. Low chromosome number angiosperms. Caryologia 58: 403-409.

Bennett M.D., 1972. Nuclear DNA content and minimum generation time in herbaceous plants. Proc. R. Soc. Lond. B Biol. Sci. 181: 109-135.

Jackson R.C.,1957. New low chromosome number in plants. Science 126: 1115-1116.

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