B96 Establishing the rDNA IGS Structure of *Cannabis Sativa*

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The educational objective of this presentation is to establish the rDNA IGS structure of *Cannabis sativa* as a means of both classification and identification.

The rDNA IGS structure was established for the use of classification and identification of *Cannabis sativa* in this study. DNA fragments of rDNA IGS were amplified by PCR from four Cannabis samples and two fragments, 1kb and 1.5kb, were obtained. After cloning and sequencing analysis, 2 regions dispersed and 6 different repeat units were found in 1.5kb DNA fragment. There are 3 repeat units with 2 copies of each in the first region, the first half of IGS sequences. The sequences of repeat units are CTCTTTCCCTTTGGGACTTGATATG, CCAAAGTGTTGGTCGGGTTCAACAAAAGACTTA and CCGAA-AAATAATTTTTTTCTGTGGTGTTG. The second region is composed of another 3 different repeat units but with different copies of each. The sequences of repeat units are CTAAGAGTGGGTGCACA, GCCCTTGTTGTGCCTTGGTGCA and CTGCACCCACACGTGAGGT- TAACTGAC. In the repeat sequences there are point polymorphisms observed in this study. In the sequence comparison of 1 and 1.5kb fragments, the sequences of 1kb fragment were found highly consistent with the 5' end sequence of 1.5kb DNA fragment including the first repetitive DNA region. There are, however, one 9bp insertion/deletion and 14 point polymorphisms observed in the relevant position. The DNA sequences of this 1.5kb were compared with all the plant sequences registered in GenBank by Fasta program of GCG software. The result showed that this DNA fragment was significantly different from any other DNA sequence so far recorded. These specific and complex variations of IGS may be related to the species and geographic distributions.

***Cannabis sativa*, rDNA IGS, Species Identification**

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