

(05-1-7)

## Complete sequence and organization of the cucumber (*Cucumis sativus* L. cv. Baekmibaekdadagi) chloroplast genome

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### Objectives

Cucumber is one of the most widely used plants for research into photosynthesis and greening physiology. In this study, we conducted to know the complete sequence and organization of the cucumber chloroplast genome.

### Materials and Methods

#### 1. Material

Cucumber (*C. sativus* cv. Baekmibaekdadagi, Dongbu Hannong Chemical Co. Ltd. Seeds Division, Seoul, Korea) seeds were planted in a pot containing a synthetic soil. They were grown to the 8-leaf stage in a greenhouse.

#### 2. Methods

The complete sequence and organization of the chloroplast genome was identified through a series of processes: isolation of chloroplast DNA from intact chloroplasts, cloning of several large size pieces of genome into fosmid vectors, construction of a shotgun library, mass sequencing, gene annotation, and comparative genome analysis.

### Results and Discussion

The nucleotide sequence of the cucumber chloroplast genome was completed (DQ119058). The circular double-stranded DNA, consisting of 155,527 bp, contained a pair of inverted repeat regions (IRa and IRb) of 25,187 bp each, which were separated by small and large single copy regions of 86,879 bp and 18,274 bp, respectively. The presence and relative positions of 113 genes (76 peptide-encoding genes, 30 tRNA genes, 4 rRNA genes, and 3 conserved open reading frames) were identified. The major portion (55.76%) of the *C. sativus* chloroplast genome consists of gene-coding regions (49.13% protein coding and 6.63% RNA regions; 27.81% LSC, 9.46% SSC and 18.49% IR regions), while intergenic spacers (including 20 introns) make up 44.24%. The overall G-C content of *C. sativus* chloroplast genome was 36.95%. Sixteen genes contained one intron, while two genes had two introns. The expansion/contraction manner of IR at IRb/LSC and IR/SSC border in *Cucumis* was similar to that of *Lotus* and *Arabidopsis*, and the manner at IRa/LSC was similar to *Lotus* and *Nicotiana*. In total, 56 simple sequence repeats were identified in the *C. sativus* chloroplast genome. There were 28 multiple As (10-17 bases), 27 multiple Ts (10-17 bases), and 1 multiple C (11 bases), but no multiple Gs in the *C. sativus* chloroplast genome.