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Characterization of 18S rDNA in 10 *Polygonatum* Species

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Objectives

This study was conducted to investigate the variation in sequence, the base composition and the sequence similarity of 18S ribosomal RNA coding region(18S rDNA) in 10 *Polygonatum* species or clones.

Materials and Methods

1. Plant materials

10 *Polygonatum* species or clones including Polygonatum sibiricum DELAR.

2. Methods

18S forward(AJ242597) and reverse(AJ242598) primers were used for PCR and sequencing of the 18S rDNA. PCR fragments were cloned directly into pGEM-T vector. Sequencing reactions were carried out in the automated sequencer, and Multiple sequence alignments were constructed with the aid of the ClustalW program.

Results and Discussion

The entire 18S rDNA region of 10 *Polygonatum* species or clones ranged from 913 bp to 914 bp. Variations in 8 variable sites or 0.9% in the region were attributable to nucleotide substitution and deletion. T→C transition happened in 4 sites, and A→G transition happened in 1 site. C→A transversion happened in 1 site, and deletion happened in 2 sites. Transition rates were five times that of transversion. Base compositions of 18S rDNA were 23.09~23.33% in adenine, 23.33~23.52% in guanine, 25.60~25.85% in thymine and 27.38~27.79% in cytosine. Pyrimidines(cytosine and thymine) were more than purines(adenine and guanine). The A+T content of 18S rDNA of 10 *Polygonatum* species or clones averages 48.99%, ranging from 48.80% to 49.18%, and the G+C content averages 51.01%, ranging from 50.82% to 51.20%. Pairwise sequence comparisons indicated that 18S rDNA sequence similarity ranged from 99.7% to 100%.

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