

Comparative Analysis of the Complete Genomes of Three *Ficus* L. (Moraceae) Species and Its Implication

Tae-Hee Kim, Joonhyung Jung and Joo-Hwan Kim*

Department of Life Science, Gachon University, Seongnam 13120, Korea

The genus *Ficus* L., containing approximately 850 species, is by far the largest genus in the Moraceae. They are mainly distributed worldwide, mainly in tropical countries. In South Korea, there are three native *Ficus* (including *F. erecta* Thunb, *F. sarmentosa* var. *nipponica* (Franch. & Sav.) Corner, and *F. thunbergii* Maxim.). Among them, *F. erecta* is effectively natural resources for the improvement of senile cognitive impairment. However, the chloroplast (cp) genome sequences and information of *F. erecta* have not been addressed. Therefore, in this study, we provide the complete cp genome of *F. erecta* and its allied species using next-generation sequencing technology. The chloroplast of *Ficus* species has typical structure which includes large and small single copy regions and a pair of inverted repeats (IRs). The sizes of cp genomes range from 160,276 bp to 160,603 bp. To determine the phylogenetic positions of these species, we conducted a maximum likelihood analysis using common protein-coding genes in chloroplast sequences. Also, we describe a newly developed single nucleotide polymorphism (SNP) markers using multiplex PCR to identify *F. erecta* based on amplification-refractory mutation system (ARMS) technique. We analyzed *matK*, *atpB* of the chloroplast genes and ITS from *F. erecta* and three related taxa, *F. carica*, *F. sarmentosa* var. *nipponica* and *F. thunbergii*. It provides useful information for molecular identification between *F. erecta* and related Korean native species.

*(Corresponding author) E-mail: kimjh2009@gachon.ac.kr, Tel: +82-31-750-8827