

Molecular authentication of Korean *Artemisia* Herbs by *trnL-F* and *trnT-L* regions in Chloroplast DNA

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엽록체 DNA의 *trnL-F* and *trnT-L* 지역을 활용한

한국산 쑥속 식물에 대한 분자생물학적 연구

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Objectives

Forty-one *Artemisia* species are distributed throughout Korea. Of these, *A. annua*, *A. apiacea*, *A. princeps*, *A. argyi*, *A. capillaries*, *A. gmelinii*, *A. japonica*, *A. keiskeana*, and *A. selenensis* are used primarily in medicinal materials in traditional oriental medicine. Medicinal *Artemisia* species are also known by their medicinal names: *A. annua*, *A. apiacea*, *A. capillaris*, *A. gmelinii*, *A. japonica*, *A. keiskeana*, and *A. selengensis* are called 'Hwanghwaho', 'Cheongho', 'Injinho', 'Haninjin', 'Moho', 'Amryeo' and 'Yugino', respectively, and *A. princeps* and *A. argyi* are called, 'Aeyup'. However, morphological identification of *Artemisia* herbs is very confusing due to similarities in the shapes of young leaves. Therefore, we performed phylogenetic analysis and PCR-RFLP for *trnL-F* and *trnT-L* region to identify *Artemisia* plants at the DNA level.

Materials and Methods

1. PCR primers for *trnL-F* and *trnT-L* regions (Taberlet et al. 1991)

trnL-F: Forward 5' - CGAAATCGGTAGACGCTACG-3'

Reverse 5' - ATTTGAACTGGTGACACGAG-3'

trnT-L Forward 5' - CATTACAAATGCGATGCTCT-3'

Reverse 5' - TCTACCGATTTCGCCATATC-3'

2. PCR-RFLP

PCR products of *trnL-F* and *trnT-L* region were digested with six restriction enzymes; *AluI*, *HaeIII*, *HinfI*, *RsaI*, *TaqI* and *Tsp509I*.

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Results

- From the phylogenetic tree based on the *trnL-F* region, three clades were generated (Fig. 1). *A. argyi*, *A. feddei*, *A. indica* var. *orientalis*, *A. lavandulaefolia*, *A. rubripes*, *A. selengensis*, *A. stolonifera*, *A. sylvatica*, *A. sp. 1*, *A. sp. 2* formed clade I. However, *A. selengensis* was represented to be relatively heterogeneous from other taxon in clade I. *A. capillaris* and *A. japonica* formed clade II.
- Some specific banding patterns will be useful as a DNA marker for distinguishing Korean *Artemisia* species (Fig. 2).

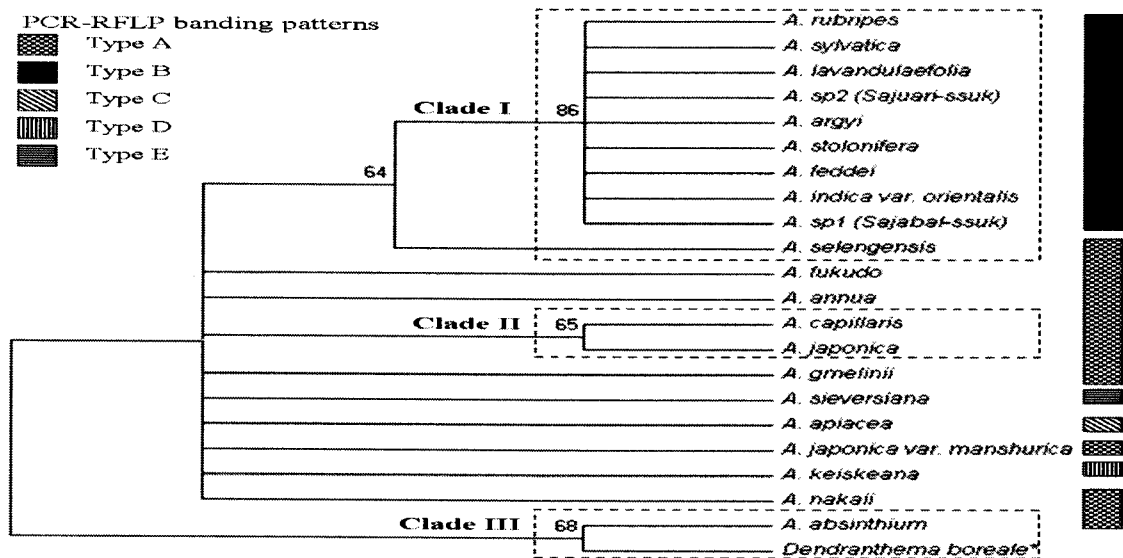


Figure 1. Phylogenetic tree based on the *trnL-F* sequence.

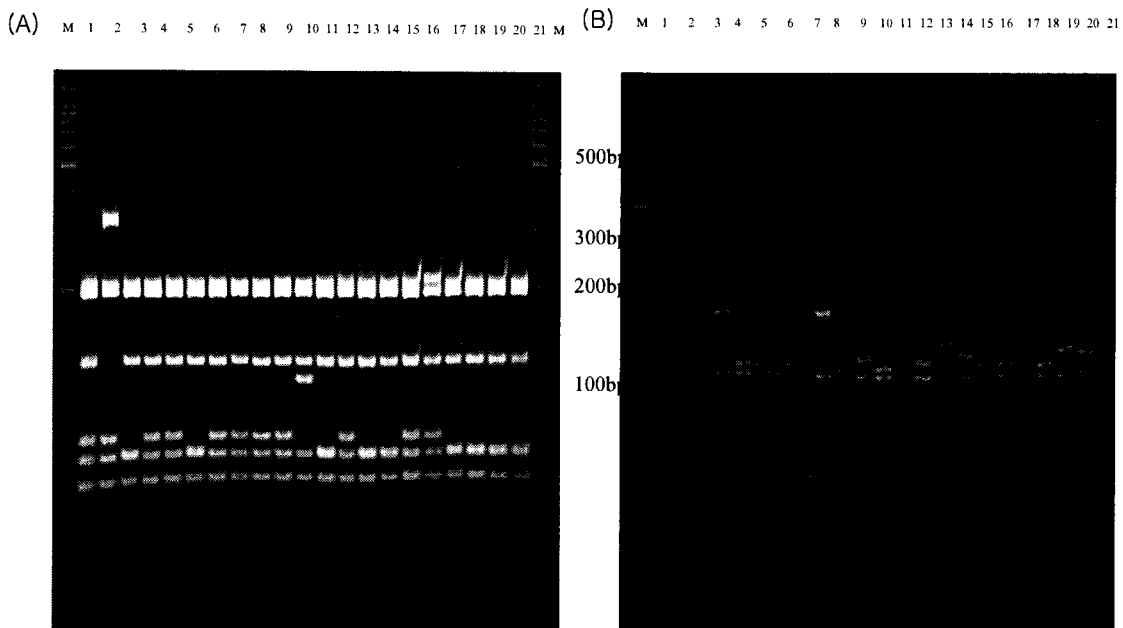


Figure 2. PCR-RFLP patterns of *trnL-F* and *trnT-L* region.