

핵 내 DNA의 내부 전사 부위에 의한 26개 재배 홍화 품종의 유전적 관련성

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**The Genetic Relationships of 26 Cultivated Safflower, *Carthamus tinctorius* L.,  
by Internal Transcribed Spacers of Nuclear rDNA**

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**Objectives**

Safflower, *Carthamus tinctorius* L., is a member of the family Compositae or Asteraceae, cultivated mainly for its seed, which is used as edible oil and as birdseed. Studies to clarify the overall status of several countries of this species were not conducted. Thus, the aim of this paper was to determine the compositions of the components of *C. tinctorius* for the first time and to compare it with the composition of *C. tinctorius* from the other countries.

**Materials and Methods**

○ Materials

Cultivated seeds were collected from 149 natural populations of *C. tinctorius* of 26 countries including Korea. Randomly selected seeds were sown in to an outdoor plot with same environmental conditions and 100 seedling plants from each origin were randomly sampled.

○ Methods

Genomic DNA was extracted with the plant DNA Zol Kit (Life Technologies Inc., Grand Island, New York, USA) according to the manufacturer's protocol. Extracted DNA was quantified using a DyNA 200 fluorimeter (Amersham Pharmacia Biotech) according to the manufacturer's instructions. Primer sets of about 20 bases in length (ITS1 and ITS2) were used for PCR analysis. These primers were based on well-characteristic DNA Sequences and were designed making use of conserved regions of the 18S and 28S rRNA genes to amplify the noncoding regions between the (ITS1 and ITS2) and 5.8S rRNA gene.

**Results**

DNA sequencing of ITS1, 5.8S, and ITS2 for 26 populations of safflower were successful

within safflower varying from 703 to 704. Alignments of the safflower were great

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in all of the species. Aligned nucleotide sequences of the length of ITS1 were varied similarity among the species' sequences, the unusual ITS1 insert were shown. In addition, variations were shown in nucleotide substitutions and indels. Only the 482th sequence has Y in 12 populations instead of C. The 642th sequence had T in three populations, one was Y, and other populations were C. The 649 position had deleted in eight populations. Azerbaijan had inserted G in the 676 position.

Table 1. Results from Tajima's neutrality test for nine sequences

M	S	ps	$\Pi$	D
26	40	0.057	0.027	2.955

M = number of sites, S = Number of segregating sites, ps = S/M, and  $\pi$  = nucleotide diversity. D is the Tajima test statistic.

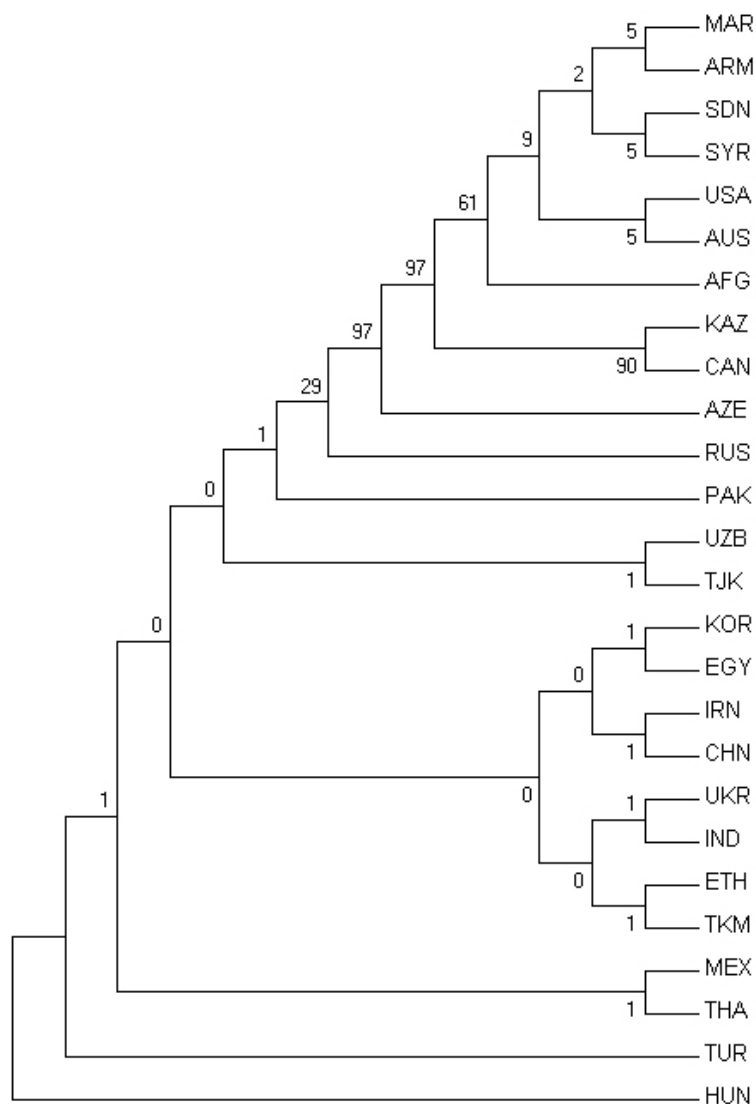


Figure 1. The NJ tree for *C. tinctorius* based on ITS analysis using MEGA 4x1.