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ITS Phylogeny and Molecular Dating of some Gundelia (Asteraceae) of Anatolia

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ABSTRACT: Gundelia L. is known to be a monotypic genus according to the flora books. Gundelia tournefortii L. was the only species of the genus Gundelia L. In our research we used the recently introduced species: Gundelia aragatsi Vitek, Fayvush, Tamanyan & Gemeinholzer, Gundelia dersim Vitek, Yüce & Ergin, Gundelia munzuriensis Vitek, Yüce & Ergin, Gundelia vitekii Armağan, Gundelia komagenensis Fırat, Gundelia colemerikensis Fırat, Gundelia cilicica Fırat and Gundelia anatolica Firat, in order to reconstruct a phylogeny inference and molecular dating by using ITS region. The mentioned species were collected from Turkey and beside our collections, the ITS sequences belonging to G. tournefortii accessions of former studies were used in our research. According to the phylogeny inference, G. anatolica was different from all Gundelia accessions. Some G. tournefortii accessions belonging to former studies grouped with G. cilicica, G. dersim and G. colemerikensis, G. munzurensis clustered with G. vitekii. Gundelia komagenensis and G. aragatsi accessions were grouped as close relatives. According to the molecular dating the distinction of the genus Gundelia from the relative genera was around 14.1 million years ago (mya).

Keywords: Asteraceae, Gundelia, ITS, molecular dating, phylogeny.

Anadolu'da Yetişen Gundelia (Asteraceae) Taksonlarının ITS Filogenisi ve Moleküler Tarihlendirilmesi

ÖZ: Flora kitaplarına göre Gundelia L. monofiletik bir cins olarak bilinmektedir. Gundelia tournefortii L. cinsin tek türü olarak bilinmektedir. Çalışmamızda ITS bölgesine dayalı filogenetik analiz ve moleküler tarihleme yapmak için yeni tanımlanan türleri de kullandık. Bunlar: Gundelia aragatsi Vitek, Fayvush, Tamanyan & Gemeinholzer, Gundelia dersim Vitek, Yüce & Ergin, Gundelia munzuriensis Vitek, Yüce & Ergin, Gundelia vitekii Armağan, Gundelia komagenensis Fırat, Gundelia colemerikensis Fırat, Gundelia cilicica Fırat ve Gundelia anatolica Fırat. Adı geçen yeni türler Yürkiye'den arazi çalışmaları yaparak toplanmış ve bizim toplamalarımızın yanısıra G. tournefortii türüne ait daha önceki çalışmalarda ortaya çıkmış ITS dizileri de kullanılmıştır. Filogenetik ağaca göre, G. anatolica tüm Gundelia örneklerinden farklıdır. Daha önceki çalışmalarda toplanmış bazı G. tournefortii örnekleri G. cilicica, G. dersim ve G. colemerikensis ile birlikte kümelenmiştir. G. munzurensis G. vitekii ile grup oluşturmuştur. Gundelia komagenensis ve G. aragatsi örnekleri birbirine en yakın gruplanmışlardır. Moleküler tarihlendirmeye göre Gundelia cinsinin ayrılma zamanı 14.1 milyon yıl öncesine tarihlenmektedir.

Anahtar Sözcükler: Asteraceae, Gundelia, ITS, moleküler tarihleme, filogeni.

INTRODUCTION

Gundelia L. belongs to the tribe Lactuceae according to the chloroplast ndhF gene (Karis et al., 2001). In the flora books (Nikitin, 1960; Vasilchenko, 1961; Sofieva, 1961; Kupicha, 1975; Feinbrun-Dothan, 1978; Rechinger, 1989: Avetisian, 1995) Gundelia tournefortii L. is the only species of the genus Gundelia, and all other names were recorded as synonyms. Recently, several new species have been described, i.e. G. aragatsi Vitek, Fayvush, Tamanyan& Gemeinholzer, G. armeniaca Nersesian from Armenia, and G. dersim Vitek, Yüce&Ergin, G. munzuriensis Vitek, Yüce&Ergin, G. vitekii Armağan, G. komagenensis Fırat, G. colemerikensis Firat, G. cilicica Firat, G. anatolica and G. mesopotamica Firat from Turkey and G. tehranica Vitek & Noroozi from Iran (Firat, 2016; Firat 2017a; Firat, 2017b).

For the taxonomic evaluation. molecular systematic approach was implemented to the genus Gundelia by Vitek et al. (2010). The researchers used ITS marker to investigate the infraspecific relations of the genus. In the phylogram they have constructed, Gundelia was clearly monomorphic and the infraspecific relations were supported with low posterior probability values. However, it was still probable to distinguish the new proposed taxa as different from others, with the help of the phylogeny tree. In our study we have used the ITS sequence data to reveal the phylogeny and molecular dating of the known Gundelia taxa.

MATERIALS AND METHODS

Plant material

A total of 10 herbarium specimens for each species were collected from the field and deposited in the herbaria ANK, E and VANF [acronyms according to Thiers (2016)], and in the personal herbarium of the author (Herb. Fırat). The ITS sequences were gathered from NCBI GeneBank are as follows: *Scorzonera purpurea* AJ633477, *Tragopogon*

KF050360. albinervis Warionia saharae AY190608, Scolymus maculatus AJ633469, Catananche caerulea AJ633465 were used as outgroups and Gundelia aragatsi ssp. steineri 1 FN582290, G. aragatsi ssp. steineri 2 FN582289, G. aragatsi FN582288, G. aragatsi FN582283, Gundelia sp. FN582287, G. tournefortii FN582281, G. tournefortii FN582284, G. tournefortii FN582277, *G*. tournefortii FN582285, G. tournefortii FN582278, G. tournefortii AY504691, tournefortii FN582282, G. G. tournefortii FN582279. *G*. tournefortii FN582280, G. tournefortii FN582286 were used with our own collections to construct the phylogeny tree.

DNA extraction, amplification, and sequencing

Total DNA was isolated with the DNAeasy Plant Mini Kit following the manufacturer's protocols (Qiagen, Germany). The amplification of ITS region, including 5.8S ribosomal RNA gene, was performed using primers ITS1 and ITS4 (White *et al.*, 1990). The PCR amplification of ITS followed Warwick *et al.* (2004). Purification and sequencing were performed by Bioeksen (İstanbul).

Data Analysis

Sequences were aligned manually by using BioEdit (Hall, 1999). The aligned ITS sequences were analyzed using Bayesian approaches following BEAST1.8.0 (Drummond et al., 2012). For the Bayesian analyses, GTR + Gamma model was chosen as best model according to Akaike Information Criterion (AIC). Two independent Marcov Chain Monte Carlo (MCMC) runs were conducted with 10 million generations and sampled every 1,000 generations. Each run was checked in Tracer v1.5 (Rambaut and Drummond, 2007). Among the trees obtained 25% (5,000) were discarded as burn-in. Treeannotater v.1.7.5 programme was used to obtain the maximum clade credibility tree.

We used an external calibration point introduced by Tremetsberger *et al.* (2013). The age of Scolymus hispanicus L. and Catananche caerulea L. was set to 13.6 Ma (million years ago) with ± 0.42 Ma standard deviation. Divergence time estimation was performed under the lognormal clock model. GTR with four gamma categories were used as a substitution model and Yule process of speciation was used as a tree prior. MCMC runs was conducted with 100 million generations and sampled every 10,000 generations. Each run was checked using Tracer v1.5 (Rambaut and Drummond, 2007) and then combined in Logcombiner v1.7.5. Treeannotater v.1.7.5 program was used to obtain a single posterior probability and maximum clade credibility tree was visualized using Figtree v1.3.1 (Anonymous, 2016).

RESULTS AND DISCUSSION

According to the phylogeny reconstruction, *G. anatolica* derived from all other *Gundelias* (Fig.

1). The rest of the species grouped under two major clades. First group consisted G. colemerikensis, G. dersim, G. munzuriensis, G. tournefortii, G. vitekii, G. komagenensis and G. aragatsi. Gundelia colemerekensis clearly derived from G. dersim (posterior probability 1.0) in the first subclade. The species with ca.3 flowered cephaloid compound (G. munzuriensis, G. vitekii, G. aragatsi) grouped together in the second subclade. All other investigated taxa have ca. 6-flowered cephaloid compound. Second group comprised G. tournefortii accessions of Vitek et al. (2010) and G. cilicica. As described in the introduction part of this paper, formerly Gundelia was considered as a monotypic genus. The squences gathered from the genebank were identified according to the flora books, therefore Gundelia accessions were named all as G. tournefortii. These G. tournefortii samples



Figure 1. The phylogeny tree of the *Gundelia* species; numbers on branches indicate clade credibility, x bar shows the time scale (mya).

Şekil 1. *Gundelia* türlerinin filogenetik ağacı; dalların üzerindeki sayılar clade credibility değerleridir, x ekseni zaman aralığını göstermektedir (milyon yıl önce).

could be identified with comparing the newly described species and our phylogeny tree could give an idea for naming the species. For example, FN582284, FN582277, FN582285, FN582278, AY504691, FN582282, FN582279, FN582280, FN582286 could be *G. cilicica* or could be some other species close to *G. cilicica*. FN582287 could be *G. aragatsi*. FN582281 could be either

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G. munzurensis or *G. vitekii*. According to the molecular dating, the distinction of the genus *Gundelia* from the relative genera was around 14.1 mya mid-Miocene. The distinction of the ca.3 flowered cephaloid compound species group from the ca. 6-flowered cephaloid compound species group was around 7.3 mya late Miocene of the Cenozoic.

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