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Molecular Phylogeny of Some Euphorbia Species (Euphorbiaceae) Implied from nrDNA and cpDNA Markers from Turkey

Aysun Patterson, Hande Morgil, Orhan Kücüker, Gül Cevahir Öz
Istanbul University
İstanbul, Turkey
aysunpatterson@gmail.com; hande.morgil@istanbul.edu.tr; kucuker@istanbul.edu.tr;
cevahirg@istanbul.edu.tr

Extended Abstract

Euphorbia is a genus of plants in the Euphorbiaceae family. It contains at least 2,100 species and is one of the most diverse groups of flowering plants on earth.They all produce a mostly white latex which they exude when cut, and this sap is often toxic. There are 109 taxa of *Euphorbia* L. in Turkey. The intrageneric classification of *Euphorbia* is extremely difficult due to the species richness accompanied by a subcosmopolitan distribution, the extreme morphological plasticity among certain species (often relating to the habitat) and the convergent evolution of certain morphological characters. Despite considerable efforts to classify and understand the striking morphological diversity in *Euphorbia*, little is known about interspecific relationships within the taxon. Recent molecular phylogenetic studies using several chloroplast DNA (cpDNA) markers and nuclear (nrDNA) internal transcribed spacer (ITS) sequences provided new insights into the delimitation of subgeneric taxa in *Euphorbia* (Horn et al., 2009).

In our study we aimed that using molecular analyses in 20 taxon from Trakya region. To delimitate this disjoint taxa, we carried out phylogenetic analyses of the internal transcribed spacer (nrITS) using a broad sampling, with emphasis differences between other *Euphorbia* species from litterateur. Subsequently, we carried out phylogenetic analyses focused on this clade using nuclear (ITS) and chloroplast (trnL-trnF) markers, with the aim of comparing the phylogenetic relationships within the taxa and reconstructing its biogeographic history (Allan et al., 2004).

Total genomic DNA, from fresh or silica gel-dried leaf tissues, taken from field collections or herbarium specimens (in the herbaria ISTF), was extracted using the Plant/Fungi Plant extraction kit (Norgen, Sweden) modified by adding 5 µl of proteinase K at 20 mg/ml (Pereira, pers. comm.) in order to avoid the interference of secondary compounds that occur in Euphorbia. Two nrDNA regions—the internal transcribed spacer (ITS1, 5.8S, ITS2) and cpDNA regions (the trnL-trnF non-coding region, including the trnL intron and the trnL-trnF intergenic spacer were amplified using the universal primers which were designed from NBCI Nucleotide GeneBank (Thiv et al., 2010).

Polymerase chain reactions (PCR) were performed. We tried many primers (Barres et al., 2011) but we could not get any positive result therefore we designed four new primers from NCBI (ITS-F1 TTGCGGCCTACTAACCAAAC ITS-R1 TTGCGTTCAAAGACTCGATG; ITS-F2 GTTTGCGGCCTACTAACCAA ITS-R2 TTGCGTTCAAAGACTCGATG; trnL-F1 TTCCAAATTGAAGAAAGGATTGA trnL-R1 TTTGCTCAAAGATGGGCATT trnL-F2 TCAATATCGACAACAAGGCAAT trnL-R2 GCTCAAAGATGGGCATTTGTA). The alignments and the phylogenetic analyses are still in process.

Allan, G.J., Francisco-Ortega, J., Santos-Guerra, A., Boerner, E., & Zimmer, E.A. (2004). Molecular Phylogenetic Evidence For The Geographic Origin And Classification Of Canary Island Lotus (Fabaceae:Loteae). *Molec. Phylog. Evol.*, 32, 123–138.

Barres, L., Vilatersana, S., Molero, J., Susanna, A., & Casals, M. (2011). Molecular Phylogeny Of Euphorbia Subg. Esula Sect. *Aphyllis (Euphorbiaceae) İnferred From Nrdna And Cpdna Markers With Biogeographic İnsights.*

Horn, J.W., Van Ee, B., Morawetz, J.J., Riina, R., Berry, P.E., Steinmann, V.W., & Wurdack, K. (2009). Phylogeny And Evolution Of Growth Forms İn The Giant Genus Euphorbia (Euphorbiaceae). *Botany and Micology Conference*, Snowbird, Utah.

Thiv, M., Thulin, M., Hjertson, M., Kropf, M., & Linder, H.P. (2010). Evidence for a Vicariant Origin of Macaronesian-Eritreo/Arabian Disjunctions in Campylanthus Roth (Plantaginaceae). *Molec. Phylog. Evol.*, 54, 607–616.