

The Phylogenetic Survey on Turkish *Salix* L. inferred from cpDNA and nrDNA data setPelin ACAR¹, Funda Ö.DEĞİRMENCİ¹, Zeki KAYA¹,¹Dep. of Biological Sciences/Graduate School of Natural and Applied Sciences, METU,
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Aims of the study: The genus *Salix* L. is represented by more than 500 species in the world. Naturally, about 27 *Salix* sp. are found in Turkey. This genus has been commonly used as biomass production for energy, phytoremediation and pharmacological products. The traditional methods for identifying the species based on morphology are insufficient to classify them. The objective of this study is to reveal the phylogenetic relationships of native willow species in Turkey by using chloroplast and nuclear DNA regions.

Material and Methods: The sequence data are obtained from non-coding chloroplast (trnT-F), encoded chloroplast (*matK* and *rbcl*) and nuclear (*ITS* and *ETS*) regions of *Salix* species (25 taxa). The molecular diversity and phylogenetic analyses were performed by the MEGA software.

Results: Sequence data of both cpDNA (4552bp) and nrDNA (999bp) regions had high number of variable sites and most of them were parsimony informative sites. The resulting cpDNA and nrDNA phylogeny revealed that Turkish willow species tree for all studied regions are mostly monophyletic with having two well supported clades as subgenus *Salix* and subgenus *Vetrix*. Such a combined markers enabled reliable subgenus-level classification (subg. *Salix* and *Vetrix*). The phylogenetic tree constructed with cpDNA sequence data differs from the nrDNA tree in regard to the taxa positions which can be explained by the intensive hybridization and introgression gene transfer events among *Salix* species. The phylogenetic analyses with molecular data have produced results showed the complex relationships among Turkish willows. This study provides detailed information about molecular phylogenetic relations with a large number of Turkish *Salix* species for the first time.

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