

ITS2 Secondary Structure and CBC Species Concept: A Case Study on the Genus *Noccaea* Moench (Brassicaceae)

Kurtuluş ÖZGİŞİ¹, Burcu DAŞER ÖZGİŞİ², Atila OCAK¹, Burcu TARIKAHYA HACIOĞLU³,
Barış ÖZÜDOĞRU^{2,4}

¹ Department of Biology, Eskişehir Osmangazi University, Turkey

²Department of Biology, Hacettepe University, Turkey

³Republic of Turkey Ministry of Food, Agriculture, and Livestock, Central Research Institute for Field Crops, Biotechnology Research Center, Ankara, Turkey

⁴Biogeography Research Laboratory, Hacettepe University, Turkey
kurtulusozgisi@gmail.com

Aim of the study: The main aim of the current study is to contribute infrageneric classification of taxonomically problematic crucifer genus *Noccaea* s.sl. using secondary structure of internal transcribed spacer 2 (ITS2) region.

Material and Methods: Genomic DNA of 83 specimens from 35 different *Noccaea* taxa were extracted and ITS region amplified. For structural analysis, 5.8S-ITS2-28S regions were annotated using the HMMs-based annotation tool present at the ITS2 database V. Delimited ITS2 sequences were submitted to the RNA folding program Mfold Server and RNAstructure, Version 5.8. The structures and sequences were aligned by 4SALE. Visualization of the secondary structures was drawn using VARNA 3.9. By using ITS2 sequence-structural alignment dataset, phylogenetic tree was constructed using phangorn in the statistical framework R.

Results: In almost all *Noccaea* specimens, which were investigated, has 188 bp long ITS2 sequence. But two taxa have different length (187, 191 bp.). The analysis of ITS2 folding pattern of all specimens produced mostly similar secondary structures with four different hairpin structures. But the length and content of helix are different. The longest one is Helix III and the lowest ones is Helix IV. Although taxa can be identified with distinct fruit character, they can not be separated only using the methods based on compensatory base changes (CBC) species concept. Also the taxa, which grouped together, can have hemi-CBCs, which suggested being useful at population and species level studies. As a result of the study, ITS2 secondary structure analyses and CBC species concept were discussed in detail for the taxonomically difficult genus *Noccaea*.

Acknowledgements: This study was supported by Eskişehir Osmangazi University Scientific Research Projects Coordination Unit (Projects no. 2015/681)

Keywords: *Noccaea*, ITS2, Secondary Structure, rRNA.