Comparing species delimitation methods based on single-locus data: A case study on the genus *Halictus* Latreille, 1804 (Halictidae: Apoidea: Hymenoptera)

Burcu Daşer 1, Fatih Dikmen 2, Ahmet Murat Aytekin 1

1 Division of Applied Biology, Department of Biology, Hacettepe University, Ankara, Turkey.  2 Division of Zoology, Department of Biology, Istanbul University, Istanbul, Turkey

Email: burcudsr@gmail.com

The diversity of life is the basis of all biological studies and species diagnosis is the first step in determining questions such as detection of biological diversity, ecological, biogeographical and evolutionary problems. Due to the restrictions on the morphology-based identification of species, more effective methods for species identification have become inevitable. DNA barcoding was originally developed for fast and reliable identification of species using a short DNA sequence and COI is accepted as the universal DNA barcode region for the animal kingdom. Such short sequence data would be useful for other kind of DNA-based methods to delineate operational taxonomic units (OTUs). In this study morphology-based delimitation of the species boundaries were compared with DNA-based methods (Parsimony networks, Automatic Barcode Gap Discovery-ABGD, General Mixed Yule Coalescent-GMYC) with the samples from the genus *Halictus*. The study was carried out with 25 species which were identified according to morphological characters. As a result of this comparison, ABGD initial partition method gave 25 OTUs parallel to morphology-based identification but delimitation boundaries of OTUs were not match with morphology in terms of specimens. Parsimony networks with 95% cut-off value and GMYC with single threshold model gave 32 OTUs but differ in two OTUs and these results were higher than the morphology-based species delineation. Integrating three different DNA-based results with morphology-based results suggests that parsimony network and GMYC outperformed ABGD. Overall, our study suggests that all DNA-based methods should be considered together with and these results might be integrated to morphology-based results for obtaining efficient results.

**Keywords:** DNA Barcoding, *Halictus*, integrated taxonomy, species delimitation