OP101
A Case Study on the Pollinator Bee Diversity: Barcoding the Members of the Genus *Halictus* s. str. Latreille (Halictidae: Apoidea: Hymenoptera) of Turkey

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Aim of the study: Bees (Apoidea: Hymenoptera) are the most important group of pollinators and regarded as a keystone group in the ecosystem. There are about 20,000 identified bee species living in the World. Due to the global decline in feral honeybees, many researches have been focused on investigating the current status of wild bees. Among these *Halictus* s. str. Latreille is one of the mostly distributed taxa all around West Palaearctic Region and Turkey. In this study, we aimed to integrate both classical taxonomy with the DNA-based analytical approaches (barcoding) to evaluate the diversity of this group in Turkey.

Material and Methods: Study was carried on 153 specimens from 25 species which had been identified by classical taxonomy, previously. Partial *COI* sequences were used for three DNA-based analytical methods (Statistical Parsimony Networks-TCS, Automatic Barcode Gap Discovery-ABGD, General Mixed Yule Coalescent-GMYC). Intra- and inter-specific pairwise distances were calculated using a Kimura 2 parameter (K2P) in the MEGA v6 and visualized using the "sppDist" function in SPIDER package in R. The proportion of correctly identified specimens based on morphology was estimated using the Best Match (BM), Best Close Match (BCM) and All Species Barcodes criteria in the program SpeciesIdentifier tool of TaxonDNA.

Results: The study has compared classical taxonomy and three DNA-based analytical methods for the performance on delimiting the species boundaries. DNA based species identifications resulted in 32 OTUs. Classical taxonomy confirmed 19 species clearly. The rest of the species which are especially belonging to *Monilapis* group was found problematic in both DNA based tools and morphological examinations. The use of different analytical methods and parameters indicates that the true number of *Halictus* species may be higher than the estimated species based on morphology. Species delimitation methods detect misidentified specimens via morphological characters and these specimens seem to be morphologically similar and share similar morphological characteristics. Sequences that are delimited with a variety of quantitative methods are candidate species to examine for future studies. Overall, our study suggests that different types of methodologies should be considered together in obtaining true richness of pollinator bee species for the countries.