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Population relationships of *Oomyzus scaposus* (Hymenoptera: Eulophidae)

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Abstract

Comparison of COI DNA barcodes from Iranian and other populations of *Oomyzus scaposus* and other species of *Oomyzus*.

Population relationships of *Oomyzus scaposus* (Thomson) (Hymenoptera: Eulophidae)

- 1 *We extracted DNA from the wasps using Tissue DNA genomic DNA extraction mini kit (Favorgen) according to the manufacturer's instructions.*
- 2 *Partial sequences of the mitochondrial gene Cytochrome Oxidase I (COI) were amplified using the primers HCO and LCO (Folmer et al., 1994). PCR cycling conditions consisted of an initial denaturation of 3 min at 94°C followed by 35 cycles, each of 30 s at 94°C, 40 s at 52°C and 30 s at 72°C, and a final extension of 72°C for 10 minutes. After a check through electrophoresis, all the PCR products were sequenced by Bioneer Corporation (Korea).*
- 3 *Forward and reverse sequences were assembled using Geneious, version 2019.*
- 4 *Sequence similarities were checked using the BLAST program of the GenBank database.*
- 5 *The sequences were submitted to GenBank under accession numbers OP784016 and OP784017. All specimens used for sequencing are represented by voucher specimens belonging to the same populations and collected at the same time from the same host and are deposited in the private collection of the first author (AB). For phylogenetic analysis, 15 COI sequences of *Oomyzus* species available in the GenBank database (NCBI) were retrieved (see accession numbers in Fig. 3). A parasitoid wasp, *Baryscapus*, from another genus of the same subfamily (Tetrastichinae) was included as an outgroup for phylogenetic analysis.*
- 6 *Phylogenetic relationships were reconstructed using MEGAX with the Kimura 2-parameter (K2) distance model, and the Maximum Likelihood (ML) method. One thousand bootstrap replicates were performed to assess branch support in the given tree.*
- 7 *Pairwise Kimura-2-parameter (K2P) distance was measured to understand the evolutionary divergence rate among the species based on the COI gene – estimating the pairwise intra- and inter-species K2P distances among the sequences.*