

Abstract:

Three species of the genus *Hypsugo* occur in the Western Palearctic. According to available sources, the species *Hypsugo arabicus* occurs only in the south of Iran (provinces of Sistan and Baluchistan) and in the northeast of Oman. The range of *Hypsugo ariel* lines the west of the Arabian Peninsula and can be also found in Egypt and Sudan. *Hypsugo savii* can be found in a wide range of areas from the Canary Islands through Western, Central and Southern Europe, the Balkans to the Middle East and Central Asia. The intraspecific and interspecific relationships of these three species have not yet been sufficiently investigated. Based on the data obtained from the sequences of mitochondrial and nuclear markers, a phylogenetic analysis was performed, which supplements the information on the intraspecific and interspecific relationships of the populations of this genus in the Western Palearctic. Two mitochondrial markers (Cyt-*b* and D-loop) and four nuclear markers (Rag2 and ACOX, COPS, STAT introns) were used for molecular analysis. Subsequently, Bayesian analysis methods and the Maximum likelihood method were used in the phylogenetic analysis to create phylogenetic trees. Furthermore, haplotype networks were created and p-distances between individual populations were calculated.

In the species *H. arabicus*, significant genetic divergence between the populations of Iran and Oman was detected based on the analysis of the mitochondrial gene for cytochrome *b*. The Iranian populations differed from the Omani ones with uncorrected p-distance values of 3.74–4.78 %, which could indicate separation of the Iranian populations at the subspecies level. In the species *H. ariel*, analysis of the mitochondrial cytochrome *b* gene revealed significant genetic diversity among populations from Egypt, which differed from other populations from Yemen, Oman, and Jordan by uncorrected p-distance values of 6.07–6.54%, which could indicate separation Egyptian individuals at the level of a separate taxon. These two hypotheses were also confirmed by the concatenated phylogenetic tree of the entire matrix within the analysis. In the species *H. savii*, three main lineages were defined by the analysis of the available samples from the Western Palearctic. The first line included Spanish populations of *H. savii*, four samples from Switzerland and one from Slovenia. The second lineage included populations from Morocco, Italy, Switzerland, Slovenia, Hungary, Austria and the Czech Republic. The third lineage included the populations of the Balkan Peninsula and Middle East. This line was subsequently divided into two sublimes, which, however, had a maximum difference of 2 % between them. The three main lines differed from each other in uncorrected p-distance values by more than 8 %. Based on the analysis, these three lineages could represent three subspecies of *H. savii*. However, to clarify this hypothesis, a more thorough study is needed, which will include bats of *H. savii* from all localities of the Western Palearctic, where *H. savii* has been recorded so far. All three examined species were clearly separated within the genus *Hypsugo*, which was confirmed by all marker analyses.

Key words: Chiroptera, *Hypsugo*, Western Palearctic, molecular genetic analysis