

Abstract

The Middle East is occupied by three species of family Emballonuridae which are morphologically divided into several subspecies. Those could be defined only poorly and intraspecific diversity of these species is resolved unsatisfactorily. This is the reason why the molecular genetic analysis, which can revise the diversity on the new unused level, were used in this thesis. Based on data from sequencing of both mitochondrial and nuclear markers the phylogenetic analysis was performed. That analysis adds new information about interspecific and intraspecific relationships among populations of this family in this area.

Bats (Chiroptera) of the family Emballonuridae are characterised by tail perforating the uropatagial membrane on its dorsal side in the half of its length and by reduction of the phalangi which makes long and narrow wing. The family is widespread circumtropically and is divided into two subfamilies. The subfamily Emballonurinae could be sometimes divided into two tribes, new-world Diclidurini and old-world Emballonurini. The representatives of the subfamily Taphozoinae occur only in the Old World. Middle East is occupied by three species of this family. *Coleura afra* inhabits only southern Arabic peninsula and the populations from this area are ranked in subspecies *C. a. gallarum*. *Taphozous nudiventris* should occur Middle East in three subspecies. Two of them belong to smaller morphotype, *T. n. nudiventris* a *T. n. zayidi*, and the third one belongs to larger morphotype *T. n. magnus*. *Taphozous perforatus* in this area is ranked mostly as two subspecies, *T. p. perforatus* a *T. p. haedinus*.

In the molecular analysis there were used three mitochondrial markers (Cyt-*b*, D-loop, 16S) and five nuclear markers (Rag2 and introns ACOX, COPS, STAT a BGN). Afterwards in the phylogenetic analysis methods were used of Bayesian analysis and Maximum likelihood analysis for creating of phylogenetic trees. Also the haplotype network were computed and the molecular dating of representatives of whole family was performed as well.

The results show, that sequences of *C. afra* are very uniform and indicate the representatives from Arabic peninsula are very related each other and they belong into one subspecies. Sequences of *T. nudiventris* are divided into two lineages, which could be partly correspond with two size morphotypes. In smaller morphotype the individuals are very related each other. That would indicate presence of subspecies *T. n. nudiventris*, while *T. n. zayidi* would be apparently just synonym. The larger morphotype is so much distinguished from smaller morphotype, especially by mitochondrial markers, that *T. n. magnus* could be guaranteed to be declared as a subspecies and perhaps even as a separate species. But part of sequences of

larger morphotype is more related to sequences of smaller morphotype. The issue is not properly solved and it requires a following study. Species *T. perforatus* is not intraspecifically so divided as previous species. That could indicate *T. p. haedinus* does not occur Middle East.

Other results could confirm presence of two tribes in the subfamily Emballonurinae, on the other side it does not support the subgenus *Liponycteris* in the genus *Taphozous*. It is because subgenus *Taphozous* in current concept would be parafyletic taxon, respectively subgenus *Liponycteris* would lie on an inner branch of subgenus *Taphozous*.