

BOOK OF ABSTRACTS



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**GENETIC DIVERSITY OF BAT-FLIES AND MITES
IN TWO CAVE-DWELLING BAT SPECIES IN SERBIA**

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Bats (Chiroptera) can differ widely in their social organisation, from living in small groups to large colonies counting several thousands of individuals. Such ecological differences can lead to drastic discrepancies in the population dynamics of parasites they carry. European bat species are infected by a wide range of specialized ectoparasites. Bat flies (Diptera: *Hippoboscoidea* – fam. *Nycteribiidae*) and wing-mites (Acari: *Mesostigmata* - fam. *Spinturnicidae*) differ strongly in their phenology and life-histories. The objective of this study was to characterize the species assemblage, genetic diversity and host specificity of bat flies and mites collected from two cavernicolous bat species commonly found in Serbia, which have different migration potentials, and can be found both separate and in shared roosts. A total of 219 flies and 205 mite specimens were collected from the common bentwing bat (*Miniopterus schreibersii*) and greater horseshoe bat (*Rhinolophus ferrumequinum*) at eight localities in Serbia and one in Bosnia and Herzegovina. Flies were morphologically identified and all samples were sequenced for a single mitochondrial gene (16S in mites and COI in flies), allowing for a comparison of within and between-colony genetic diversity among the dominant ectoparasite species in the sample (*Nycteribia schmidlii*, *Phthiridium biarticulatum*, *Spinturnix psi* and *Eyndhovenia euryalis*). Notably, all ectoparasite species showed marked specificity towards their primary hosts, even in roosts that were shared by both bat host-species. Additionally, this data constitutes some of the first reference sequences for commonly used barcoding sequence fragments for several of the investigated species.

NYCTERIBIIDAE, SPINTURNICIDAE, mtDNA, CHIROPTERA