## Abstract

The dissertation thesis presents contributions solving several faunistic, biogeographical, taxonomic, and phylogenetic problems of selected groups of bat parasites together with surveys of potential pathogens in some representatives of these parasitic groups linked to the bats of the Old World. In the first part of the thesis, the taxonomy of prostigmata mites – chiggers (Trombiculidae) – coming from Eurasia and Africa is elaborated. Results of a detailed morphological and morphometric study are the descriptions of five new taxa belonging to four genera: *Chiroptella*, *Grandjeana*, *Rudnicula*, and *Trombicula*. At the same time, the results revise the differentiation within the group *Trombicula* sensu stricto, summarize the findings of species of individual genera and correct the inclusions of the originally described species within individual genera, with the final output of creating identification keys to the genera. The first sketch of the results of the study of the relations between chiggers and bats is included in this section, representing the description of the specific links among individual segments of both groups. In addition, there are studies presenting new findings and morphometric examinations of velvet mite nymphs collected from bats in Indonesia, as well as morphometric data and morphological comparisons of mesostigmatic mites (Spinturnicidae) with the descriptions of nymphal stages of the *Spinturnix myoti* group in eastern and south-eastern Europe. The second part of the thesis corrects some of the previously published data and presents new findings of soft ticks of the family Argasidae – *Secretargas transgariepinus* and *Reticulinasus salahi* from the Middle East, which resulted in a newly defined range of distribution of the parasitic species and also revision of the lists of their hosts. At the same time, the presence of MHV-68 virus and the *Bartonella* bacteria in two monoxenous parasites (*Eucampsipoda aegyptia* and *Reticulinasus salahi*) of the Egyptian fruit bat (*Rousettus aegyptiacus*) from the Palaearctic part of its distribution range was surveyed using the PCR method. The presence of both potential pathogens has been confirmed in most of this geographic distribution of this host bat. In addition, the presence of other microorganisms was also addressed, which confirmed the presence of *Borrelia burgdorferi* sensu lato in *S. transgariepinus* from Jordan and *R. salahi* from Oman, bacterium *Rickettsia* sp. closely related to *Rickettsia slovaca* in *S. transgariepinus* from Jordan and *Candidatus* Ehrlichia shimanensis in *R. salahi* from Oman.