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Revision of the West Palaearctic *Cimex* species. Preliminary report

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Abstract

A modern interpretation of the phylogeny, relationships, host specificity and coevolution with hosts of the West Palaearctic *Cimex* species (Heteroptera Cimicomorpha Cimicidae) represents a topic of the project. A definitive resolution of the taxonomic confusion in the *Cimex pipistrelli* (Jenyns) species group is the underlying issue. Just preliminary results are shown in the species presence; the processing of available samples is not finished.

Key words: *Cimex*, parasite–host relations, taxonomy, cytochrome oxydase subunit I.

Introduction

Cimicidae (Heteroptera Cimicomorpha) is a worldwide spread family containing more than one hundred species. All are obligatory parasites of birds and mammals, including man. Bats are generally considered as the original hosts.

Besides the two semisynanthropic and cosmopolitan species - *Cimex lectularius* L. and *Cimex hemipterus* (F.), which are also infestants of bats, the genus *Cimex* comprises of two groups: the *Cimex pipistrelli* (Jenyns) group (on bats in the Palaearctic region) and the *Cimex pilloselus* (Horváth) group (on bats in the Neartic region).

Besides *C. pipistrelli*, two more species of this group were described from Europe: *Cimex dissimilis* (Horváth) and *Cimex stadleri* Horváth. Some authors accept all the species valid (e.g., Usinger, 1966), some only one (e.g., Povolný, 1957), however, most recent authors follow Péricart (1972; 1996) in acceptance of two valid species, *C. pipistrelli* (after Péricart, 1996 distributed in British Isles, Netherlands and Germany) and *C. dissimilis* (spread in most European countries).

The current project concentrates particularly on a definitive resolution of the taxonomic confusion in the *C. pipistrelli* species group. However, a contribution to the reconstruction of the phylogeny of all West Palaearctic *Cimex* species, their host specificity and coevolution with hosts will be provided after finishing processing samples.

Results

A total of 77 individuals of 43 population samples belonging to *C. pipistrelli* group were processed. Maximum parsimony analysis of 710bp long sequences of cytochrome oxydase subunit I showed two distinct haplotype groups, designated as types A and B.

Type A was detected in 16 samples. Sequences showed polymorphism in 2% bases among samples, relationships among samples of haplotype A were not resolved.

Type B was detected in 26 samples. Samples from the Czech and Slovak Republics are 100% homogenous, sample from Switzerland differs in one base. This would suggest a recent expansion of the haplotype to the central Europe.

Distribution of the haplotypes weekly reflects relations among bat populations. It is believed that *Nyctalus noctula* (Schreber) contributes highly to the dispersal of the batbugs. In contrast to other bat species 1) it travel long distances between winter and summer roosts, 2) males rather create groups that often change shelters during summer, 3) findings on the body of the bat are numerous (in contrast to no such record from other bat species).

Canonical discriminant analysis performed using 28 morphological characters showed slight morphological divergence between the haplotype groups A and B. Main contribution to the divergence were the ratios of length to width of all femora and tibiae. Morphological characters used to discriminate the three described species are not useful to discriminate the two haplotypes. In the sense of the three described species just one species is recognized.

Discussion and conclusions

Length of pronotal bristles, which is used to discriminate *C. dissimilis* and *C. stadleri* from *C. pipistrelli*, is consistent among processed samples from continental Europe. It is significantly higher in samples from the United Kingdom, which have been only measured. Present results of the study seem to confirm the presence of two species of *C. pipistrelli* group according to Péricart, 1972.

Samples of *C. pipistrelli* group from British Isles and other countries along with samples of *C. lectularius*, *C. hemipterus* and *Cimex emarginatus* (Simov) will be processed soon.

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