**First data of molecular phylogeny in *Poecilimon affinis* complex from Balkan Peninsula**

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Phylogeny is derived from the traditional classification of organisms, the Linnaeus taxonomy, which is based on the principle of "general similarity of features". Initially, only morphological features were used in phylogenetic analyzes. Organisms were sometimes classified based on the few structures that led to incorrect conclusions. There are organisms in the world that have, among others, strongly morphological differentiation due to sexual dimorphism or depending on environmental factors. Modern systematics try to classify organisms in terms of kinship, both on the basis of morphological and molecular data. The project aims at revising the systematics of highly variable groups of bush-cricket taxa, the *Poecilimon affinis* complex, through revealing the genetic structure and phylogenetic relationships of its populations in the central and western Balkans.. Why did I choose these organisms? Why should we research them? Systematics of the *Poecilimon ornatus* group, which include taxa closely related to the studied complex, is generally agreed on. However, this does not concern to the species included in its composition, among which there are many subspecies and synonyms. They were described only on the basis of morphological features, as well as singing diversity. We applied a multilocus approach testing one mitochondrial gene fragments: mitochondrially encoded NADH dehydrogenase 2 (ND2), and two nuclear introns: internal transcribed spacer 1 (ITS1) and 2 (ITS2) on 15 specimens belonging to 6 species, collected from 7 populations from Balkans region.

Phylogenetic trees show significant differences between specimens from different populations but belong to the same species. It may be a result of (multiple) isolation and reconnection of population underlied by climatic oscillatons during the Quaternary. The obtained result is an introduction to future research on population genetics and phylogeography of this complex from the Palearctic area and explanation of the systematic position of taxa.