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Mitochondrial DNA relationships among North Palaearctic *Eptesicus* (Vespertilionidae, Chiroptera) and past hybridization between Common Serotine and Northern Bat

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Abstract

Interspecific hybridization was proposed as one of the explanations for the lack of differentiation between mtDNA of the morphologically divergent bats *Eptesicus serotinus* and *E. nilssonii*. However, only West European populations of these species were examined so far. The cytochrome *b* mitochondrial gene sequences of *E. serotinus* originating from Russia were compared with those of other North Palaearctic *Eptesicus*. Common serotines from the Caucasus, Central and South Russia constitute a separate monophyletic group, distinct from western *E. serotinus* populations, *E. nilssonii*, and also from *E. isabellinus*. Only a common serotine from Kaliningrad region proved to be a member of the West European clade. According to these results one may suppose that most of Russian population of *E. serotinus* escaped the hybridization event that led to fixation of alien mitochondrial genome in the West European populations. Given that (i) preliminary nuclear data support the distinction between *E. serotinus* and *E. nilssonii* and (ii) *E. serotinus* appears morphologically homogeneous throughout the European part of its range, we consider that this past mtDNA introgression has no direct taxonomic implications. For the first time included in a molecular phylogenetic analysis, *E. gobiensis* was shown to be a full species, related to *E. nilssonii*. From our mtDNA phylogenetic tree, the taxonomic validity of the subgenus *Amblyotus* appears doubtful.

Key words: *Eptesicus serotinus*, mtDNA introgression, cytochrome *b*, molecular taxonomy

Introduction

In the last decades the application of molecular methods in bat taxonomy initiated significant changes in our understanding of phylogenetic relationships among extant species (Hoofer & van den Bussche, 2003; Mayer, *et al.*, 2007; Ruedi & Mayer, 2001; Spitzenberger, *et al.*, 2006). Among the most surprising findings of molecular studies on European chiropterans is the pattern of mitochondrial DNA (mtDNA) diversity found within the genus *Eptesicus* (Ibanez, *et al.*, 2006). An unexpected result was the recovering of high similarity of mtDNA between the northern bat (*E. nilssonii*) and the common serotine (*E. serotinus*) in Western Europe (Mayer & Helversen, 2001)—a surprising outcome given that *E. nilssonii* was never previously treated as a close relative to common serotine. The two species are readily distinguishable on the basis of many diagnostic morphological traits (e.g. Bobrinskiy, *et al.*, 1965), including body size (*E. serotinus* is significantly larger). Moreover, *E. nilssonii* is often placed in a separate subgenus or even genus *Amblyotus* (Tiunov, 1997; Horacek, *et al.*, 2000), characterized, among other things, by its relatively primitive dentition. *E. nilssonii* and *E. serotinus* are noticeably different also, in their ecological affinities and patterns of distribution (Fig. 1). Whereas the northern bat inhabits mostly boreal and temperate woodlands of Northern Palaearctic; the common serotine is found in various habitats in temperate and subtropical regions from South-Western

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