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Phylogeography of *Lacerta agilis* Based on the Mitochondrial Cytochrome *b* Gene Sequences: First Results

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The phylogeny and phylogeography of *Lacerta agilis* was inferred from the nucleotide sequences of mitochondrial cytochrome *b* gene. 49 specimens of *Lacerta agilis* originating throughout its distribution range including several localities from Eastern Kazakhstan, *Lacerta praticola* and *Lacerta media* as outgroups were used for the analysis. Phylogenetic reconstruction was carried out from 857 base pairs of cytochrome *b* using Neighbor Joining, Maximum Parsimony and Maximum Likelihood algorithms.

The monophyly of the *Lacerta agilis* is supported by 100% bootstrap value. The results indicate that within *Lacerta agilis* species three genetically distinct groups were identified. One of these groups comprises specimens from the large part of European Russia, Caucasus and Kazakhstan, which are morphologically treated as *L. a. exigua*, *L. a. brevicaudata* and *L. a. altaica* subspecies. According to our molecular data this group shows a high genetic similarity and should be considered as *L. a. exigua*. Second group includes two subgroups of *L. a. agilis*, *L. a. argus* specimens from Denmark, Germany, Czech Republic and *L. a. chersonensis* from Northwest Russia respectively. Specimens of *L. a. boemica* from Northern Caucasus form the last group, which appears to be genetically very distinct from other groups of *Lacerta agilis*.

Keywords Molecular phylogeography; cytochrome *b* gene; *Lacerta agilis*