Exploring phylogenetic relationships within the family Lacertidae

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Lacertidae family is one of the most diverse and widespread families throughout Eurasia and Africa. Several studies so far have attempted to unravel the phylogeny of Lacertidae using DNA sequence data, while in some of them those datasets were also compared to alternative sources of evidence, primarily morphology. However, the intrafamily relationships remain unclear. During the last few years constructing DNA phylogenies has become highly popular, leading to the accumulation of a large number of available sequences in genetic databases. In an effort to explore the relationships within the family of Lacertidae, we retrieved from GenBank all published sequences (cmos, 16S rRNA, 12S rRNA, cyt b, ND1, ND2, and COI), forming a concatenated dataset, in which each genus is represented by one chimeric sequence. Phylogenetic inference analyses were conducted using Maximum Likelihood (ML) and Bayesian inference (BI).



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