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SYSTEMATICS

Comparative analysis of mitochondrions in European water frogs of the genus *Pelophylax*

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Abstract

The moderate evolutionary rate of vertebrate mitogenomes renders their genes suitable for constructing models in phylogenetic studies. The comprehensive coverage of the entire mitochondrion allows for a more detailed reconstruction of phylogenetic relationships within taxonomic groups. The molecular phylogeny of water frogs of the genus *Pelophylax* closely related to the widespread invasion of the marsh frog, which represents a series of cryptic species with unresolved taxonomic status, as well as the molecular mechanisms induced genome elimination in hemiclinal species. Currently, there are nearly 50 complete mitochondrial genomes in genetic databases for Western Palaearctic water frogs. In the recent study, we are adding data on 30 mitochondrial genomes of water frogs from the Caucasus, the Volga drainage region, Saint Petersburg, and Moscow, obtained through next-generation sequencing.

The total length of mitochondrions in water frogs averages 17,900 bp. An analysis of 47 mitochondrions from western Palaearctic green frogs of the genus *Pelophylax* revealed 4,190 mutations, 3,684 polymorphic sites, and 1,474 singleton mutations. 36 haplotypes were identified. The highest levels of nucleotide and haplotype diversity were observed in genes encoding NADH dehydrogenase, cytochrome c oxidase, and cytochrome b. The ribosomal RNA genes exhibited the high variability in the pool frog, *P. lessonae*. The overall topology of Maximum Likelihood and Bayesian phylogenetic trees is consistent, with some exceptions at specific positions within clades. The largest uncorrected genetic distance was noted between *P. cretensis* and *P. shqipericus* (0.129), while the smallest was observed between *P. ridibundus* from the Volga region and Europe (0.001). The Central European clade of the marsh frog is characterized by the lowest levels of genetic variability, whereas the highest levels were recorded for Anatolian *P. cf. bedriagae* that includes several undescribed cryptic species.