

Mitochondrial phylogeny of Anura (Amphibia): a case study of congruent phylogenetic reconstruction using amino acid and nucleotide characters

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Motivation

We explore whether phylogenetic analyses of the same sequence data set at the amino acid and nucleotide level are able to recover congruent topologies, as well as the advantages and limitations of both alternative approaches. As a case study, mitochondrial protein-coding genes were used to discern among competing hypotheses on the phylogenetic relationships of major anuran amphibian lineages.

Methods

To properly address this phylogenetic question, the complete nucleotide sequences of the mitochondrial genomes of two archaeobatrachian species, *Ascaphus truei* and *Pelobates cultripes*, were determined anew. Bayesian and maximum likelihood phylogenetic inferences of the same sequence data set were performed based on both amino acid and nucleotide characters, with the latter analysed either as codons or as a reduced data set of first+second (P12) codon positions. In addition, likelihood-based ratio tests were performed to evaluate the support of alternative topologies.

Results

The different data sets arrived at congruent and highly supported topologies, suggesting a similar phylogenetic resolving power of the two character types provided that correctly selected sites and appropriate evolutionary models are used. The reconstructed anuran mitochondrial phylogeny supports the paraphyly of Archaeobatrachia, with *Ascaphus* as sister group to all the remaining anurans, and *Pelobates* as sister group of Neobatrachia. However, the employed tree reconstruction methods and likelihood-based ratio tests seemed to be negatively affected by the fast evolving sequences of neobatrachians, suggesting that the phylogeny of Anura here presented is not definitive, and needs further investigation using extended taxon sampling.

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Supplementary informations

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