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Evolutionary Genetics of African Toads (Anura: Bufonidae: Amietophrynus)

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African "true" toads (frog genus *Amietophrynus*) include 39 morphologically conserved species that live in a panoply of habitats from the fringes of the Sahara to the mountains of South Africa. We examined the evolutionary relationships of these African bufonids by sequencing a 550 bp fragment of the 16S mitochondrial gene, and based on these results, collected a further 4 kb of combined mitochondrial (12S–16S) and nuclear (CXCR4, POMC, and RAG1) sequence data from sixty-two divergent samples of the genus *Amietophrynus*, and several bufonid outgroups. DNA sequences were analyzed with maximum parsimony, maximum-likelihood and Bayesian inference with the programs PAUP, RAxML and MrBayes v.3.1, respectively, after appropriate models of nucleotide substitution were identified in the program jModelTest. Our phylogeny agrees in most respects with the results of the most comprehensive, previously published hypothesis investigating the relationships of African bufonids (e.g., the monophyly of African *Amietophrynus* is well supported). However, our improved taxonomic sampling and resulting phylogeny supports several novel relationships, elucidates chromosome evolution in the group, demonstrates the importance of the Congo Basin as a center of endemism, and notes widespread cryptic speciation, suggesting that current diversity of *Amietophrynus* is vastly underestimated.