

# Allozyme variation patterns and multiple hybridization origins: clonal variation among four sibling parthenogenetic Caucasian rock lizards

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## Abstract

Allozyme electrophoresis of four sibling parthenogenetic Caucasian rock lizards *Darevskia unisexualis*, *D. uzzelli*, *D. sapphirina*, and *D. bendimahiensis* found seven clones and five variable loci. The data supported the hypothesis that *D. raddei* and *D. valentini* are the parental species of all four parthenogens. Variation patterns in *Darevskia* were summarized. Species that originated from a single F1 typically consisted of one widespread clone with a few rare clones. Species with multiple origins displayed variation only slightly higher than species with a single origin. This is contrary to other genera of parthenogenetic lizards, in which cases massive clonal variations were observed.

# Molecular phylogenetics, tRNA evolution, and historical biogeography in anguid lizards and related taxonomic families

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## Abstract

Phylogenetic relationships among lizards of the families Anguidae, Anniellidae, Xenosauridae, and Shinisauridae are investigated using 2001 aligned bases of mitochondrial DNA sequence from the genes encoding ND1 (subunit one of NADH dehydrogenase), tRNA(Ile), tRNA(Gln), tRNA(Met), ND2, tRNA(Trp), tRNA(Ala), tRNA(Asn), tRNA(Cys), tRNA(Tyr), and COI (subunit I of cytochrome c oxidase), plus the origin for light-strand replication (O(L)) between the tRNA(Asn) and the tRNA(Cys) genes. The aligned sequences contain 1013 phylogenetically informative characters. A well-resolved phylogenetic hypothesis is obtained. Because monophyly of the family Xenosauridae (*Shinisaurus* and *Xenosaurus*) is statistically rejected, we recommend placing *Shinisaurus* in a separate family, the Shinisauridae. The family Anniellidae and the anguid subfamilies Gerrhonotinae and Anguinae each form monophyletic groups

receiving statistical support. The Diploglossinae\*, which appears monophyletic, is retained as a metataxon (denoted with an asterisk) because its monophyly is statistically neither supported nor rejected. The family Anguinae appears monophyletic in analyses of the DNA sequence data, and statistical support for its monophyly is provided by reanalysis of previously published allozymic data. Anguid lizards appear to have had a northern origin in Laurasia. Taxa currently located on Gondwanan plates arrived there by dispersal from the north in two separate events, one from the West Indies to South America and another from a Laurasian plate to Morocco. Because basal anguine lineages are located in western Eurasia and Morocco, formation of the Atlantic Ocean (late Eocene) is implicated in the separation of the Anguinae from its North American sister taxon, the Gerrhonotinae. Subsequent dispersal of anguine lizards to East Asia and North America appears to have followed the Oligocene drying of the Turgai Sea. The alternative hypothesis, that anguine lizards originated in North America and dispersed to Asia via the Bering land bridge with subsequent colonization of Europe and Morocco, requires a phylogenetic tree seven steps longer than the most parsimonious hypothesis. North African, European, and West Asian anguines were isolated from others by the rapid uplift of Tibet in the late Oligocene to Miocene. Phylogenetic analysis of evolutionary changes in the gene encoding tRNA(Cys) suggests gradual reduction of dihydrouridine (D) stems by successive deletion of bases in some lineages. This evolutionary pattern contrasts with the one observed for parallel elimination of the D-stem in mitochondrial tRNAs of eight other reptile groups, in which replication slippage produces direct repeats. An unusual, enlarged TpsiC (T) stem is inferred for tRNA(Cys) in most