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Phylogenetic relationships of the *Dactyloa* clade, based on molecular and morphological data

The understanding of phylogenetic relationships within *Anolis* has seen great advances in the past ten years due to a significant number of phylogenetic studies based primarily on molecular data. Despite this large effort, there is still a large void of information regarding mainland species. According to recent phylogenies (Poe, 2004; Nicholson et al., 2005) mainland species belong to two non-nested clades: an unnamed clade (designated the M2 clade by Pinto et al. [2008]), which includes the deeply nested Central and South American species derived from Greater Antillean ancestors and *Dactyloa* (same as the *latifrons* series of Etheridge [1959] and the M1 clade of Pinto et al. [2008]), which represents one of the early branches in *Anolis* and includes species from Central and South America and the Lesser Antilles.

The *Dactyloa* clade is composed of 76 currently recognized species distributed from Costa Rica to Peru, including the Amazon region and the southern Lesser Antilles. Species are distributed from sea level to 3000 m of elevation, with most of them found in well-preserved forested habitats. Within *Dactyloa*, six different subgroups (ranked as species groups by Williams [1976*a*] and series by Savage and Guyer [1989]) have been described based on morphological characters (Williams, 1976*b*): *aequatorialis*, *laevis*, *latifrons*, *punctatus*, *roquet*, and *tigrinus*. More recently, based on phylogenetic studies (e.g., Jackman et al. 1999; Poe 1998, 2004), the species previously placed in the genus *Phenacosaurus* are considered part of *Dactyloa* as well.

To reconstruct the phylogeny of *Dactyloa,* we analyzed new nucleotide sequence data from one nuclear (RAG-1, ~2900b) and two mitochondrial (ND2, ~1500b; COI, ~700b) gene regions. We included molecular data from 42 *Dactyloa* species from Panama, Colombia, Ecuador, Venezuela and the southern Lesser Antilles, as well as 10 outgroup species (3 non-*Anolis* Polychrotinae and 7 non-*Dactyloa Anolis*).

Likelihood and Bayesian (under different data partitions) analyses of each gene region separately, both mitochondrial regions combined, and all three regions combined strongly support *Dactyloa* as a monophyletic group; topology tests (Approximately Unbiased Test and

Bayesian hypothesis tests) further support its monophyly. In addition, data provide strong support–with further support from topology tests–for the monophyly of the *roquet* series of the southern Lesser Antilles. In contrast, the *punctatus*, *latifrons* and *aequatorialis* series, previously circumscribed based on morphological characters, were not inferred in the optimal trees and their monophyly was rejected by topology tests as well. *Phenacosaurus* species were not inferred as a monophyletic group, though a group composed of all *Phenacosaurus* species except *A. neblininus* was inferred as a clade; topology tests failed to reject the hypothesis of monophyly of this group.

Molecular data were combined with morphological data from 60 species of *Dactyloa* and 6 outgroups species (including non-*Anolis* Polychrotinae and non-*Dactyloa Anolis*). Sixty-six characters: 33 of external morphology and 33 of osteology were analyzed using parsimony and Bayesian methods. For the parsimony analysis, continuous characters were coded using Torres-Carvajal's (2007) modified step-matrix gap weighting method and polymorphic characters were coded using the frequency parsimony method of Berlocher and Swofford (1997). For the Bayesian analysis, continuous characters were coded using Thiele's (1993) gap weighting method and polymorphic characters were coded using the modal condition. Parsimony and Bayesian analyses of the combined dataset inferred *Dactyloa* to be monophyletic, though nodal support was low (bootstrap = 46%, Bayesian posterior probability = 0.80). In agreement with the analysis of the molecular data alone, the *roquet* series was the only subgroup (from those previously described based on morphological characters) inferred with the combined dataset; topology tests further support its monophyly. In addition, topology tests rejected the monophyly of *aequatorialis*, *latifrons* and *punctatus* series, though it failed to reject the monophyly of the *tigrinus* series and the *Phenacosaurus* subgroup.

In addition to the *roquet* series, four other major clades with distinct and coherent geographic ranges were consistently inferred across analyses of the molecular data alone and in combination with morphology: first, a western clade that includes 10 species distributed in the western and central cordilleras of Colombia, the western slope of the Ecuadorian Andes and the Pacific lowlands of Colombia and Ecuador; second, a clade of 13 species for which all males reach a snout to vent length larger than 100 mm, mostly distributed below 1000m of elevation in the pacific lowlands from Costa Rica to Ecuador, Malpelo island and the inter-Andean valleys of Colombia; third, an eastern clade including 12 species distributed in the Amazon region, the northern portion of the eastern cordillera of Colombia, the Sierra Nevada de Santa Marta (Colombia) and the Venezuelan Andes; finally, a clade containing 6 species previously placed in the genus *Phenacosaurus* distributed in high elevations (between 1300-3000m) of the Andes of Colombia, Venezuela and Ecuador.

These five major clades were inferred with strong support with the molecular data alone, and with strong to weak support with the combined dataset. However, the relationships among them remain uncertain as different analyses and/or gene regions inferred different patterns with a wide range of nodal support values.

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