



A phylogenetic reassessment of African fossorial skinks in the subfamily Acontinae (Squamata: Scincidae): evidence for parallelism and polyphyly

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Abstract

The Acontinae is a well-supported clade of limbless skinks from sub-Saharan Africa for which three fossorial genera—*Acontias*, *Acontophiops*, and *Typhlosaurus*—have been traditionally recognized. However, recent phylogenetic analyses demonstrate conflicting support for the monophyly of *Acontias* and *Typhlosaurus*, despite limited taxon sampling for the latter genus. We re-investigate acontine evolutionary relationships, including all currently recognized species of *Typhlosaurus*, in phylogenetic analyses of mitochondrial (*Cytb*, *Co1*, *16s*) and nuclear (*Rag1*) gene sequences. Our results show that *Typhlosaurus* is polyphyletic and represented in three distinct clades, one of which constitutes the sister lineage to other acontines. The remaining typhlosaurs form strongly-supported clades with either *Acontophiops* or the recently-described genus *Microacontias* (formerly *Acontias lineatus* and *A. litoralis*). We use this new phylogenetic framework to revise acontine taxonomy. *Typhlosaurus* is restricted to five species from southwestern Africa, all characterized by an attenuate body form. *Acontias* is expanded to include the former *T. aurantiacus*, *T. cregoi*, and *T. lineatus* groups as well as *Acontophiops* and *Microacontias*. Species transfer between acontine genera created two secondary homonyms; thus the affected taxa are assigned replacement names.

Key words: molecular phylogenetics, convergence, taxonomy, *Acontias*, *Typhlosaurus*

Introduction

The convergent evolution of limb reduction is a common theme among squamate reptiles and is particularly prevalent in scincid lizards, where it has evolved independently at least ten times (Wiens *et al.* 2006; Brandley *et al.* 2005). Most limbless skinks are fossorial (Wiens *et al.* 2006), and as with other fossorial squamates, recurring adaptations to burrowing (i.e., fusion of cranial elements, fusion of head scales, attenuate body form) make phylogenetic inference intractable from a morphological perspective (e.g., Kearney & Stuart 2004; Köhler *et al.* 2010; Mott & Vieites 2009). Analyses of DNA sequence data have helped clarify higher-level scincid relationships (Whiting *et al.* 2003; Brandley *et al.* 2005) and have confirmed high levels of convergence suspected among its numerous fossorial taxa (Reeder 2003; Schmitz *et al.* 2005; Skinner *et al.* 2008; Crottini *et al.* 2009; Köhler *et al.* 2010).

The subfamily Acontinae is a clade of limbless, burrowing skinks that inhabit sub-Saharan Africa (Greer 1970). Although acontine monophyly is well supported (Whiting *et al.* 2003; Brandley *et al.* 2005), the validity and taxonomic composition of its three genera have been recently challenged (Daniels *et al.* 2006). In a molecular phylogenetic survey of the nominate genus, *Acontias*, Daniels *et al.* (2006) called into question a long-held hypothesis that generic-level relationships are reflected in a transformation sequence of eyelid character states (Broadley 1968; Broadley & Greer 1969). Broadley (1968) perceived this sequence as follows: 1) movable eyelids (as observed in *Acontias*) constitute the “primitive” character state; 2) immovable, semi-transparent eyelids (in the monotypic *Acontophiops*) represent an “intermediate” state relative to the 3) “derived” lidless condition (in *Typhlosaurus*). However, Daniels *et al.*’s (2006) phylogeny