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The high-level classification of skinks (Reptilia, Squamata, Scincomorpha)

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Abstract

Skinks are usually grouped in a single family, Scincidae (1,579 species) representing one-quarter of all lizard species. Other large lizard families, such as Gekkonidae (s.l.) and Iguanidae (s.l.), have been partitioned into multiple families in recent years, based mainly on evidence from molecular phylogenies. Subfamilies and informal suprageneric groups have been used for skinks, defined by morphological traits and supported increasingly by molecular phylogenies. Recently, a seven-family classification for skinks was proposed to replace that largely informal classification, create more manageable taxa, and facilitate systematic research on skinks. Those families are Acontidae (26 sp.), Egerniidae (58 sp.), Eugongylidae (418 sp.), Lygosomidae (52 sp.), Mabuyidae (190 sp.), Sphenomorphidae (546 sp.), and Scincidae (273 sp.). Representatives of 125 (84%) of the 154 genera of skinks are available in the public sequence databases and have been placed in molecular phylogenies that support the recognition of these families. However, two other molecular clades with species that have long been considered distinctive morphologically belong to two new families described here, Ristellidae **fam. nov.** (14 sp.) and Ateuchosauridae **fam. nov.** (2 sp.). Morphological diagnoses and species content for all nine families of skinks (Scincomorpha) are presented.

Key words: reptile, lizard, evolution, systematics, taxonomy, classification

One of every four species of lizard is a skink (Infraorder Scincomorpha) making them a significant component of reptile diversity. However, skinks are usually placed in a single family, Scincidae Oppel (1811). Recently, a seven-family taxonomic scheme was proposed to replace formal and informal group names for skinks that have become widely used over the years (Hedges & Conn 2012). The impetus for the proposed change was (1) the increasing support in molecular phylogenies for the monophyly of the informal groups, and (2) the need to make more taxonomic room in a family that had become excessively large (1,579 species)—the largest family of lizards. Partitioning large taxa is beneficial for systematic work because it creates manageable taxa for study. For example, it reduces the number of comparisons needed when a new taxon is described. Examples of other large families of lizards that have been broken into multiple families for the same reason, recently, are the geckos, Gekkonidae s.l. (e.g., Gamble *et al.* 2008) and iguanids, Iguanidae s.l. (e.g., Townsend *et al.* 2011). The aim here is to review the evidence for these family-level clades, provide morphological diagnoses, describe two additional families, and list species content for each of the nine families.

Most skink genera have been included in molecular phylogenetic studies and those studies have largely corroborated the morphologically-defined suprageneric groups in the past (Austin & Arnold 2006; Brandley *et al.* 2005; Crottini *et al.* 2009; Dolman & Hugall 2008; Gardner *et al.* 2008; Grismer *et al.* 2011; Hedges & Conn 2012; Hutchinson *et al.* 1990; Linkem *et al.* 2011; Mausfeld *et al.* 2002; Pyron *et al.* 2013; Reeder 2003; Schmitz *et al.* 2005; Schmitz *et al.* 2004; Siler *et al.* 2011; Skinner *et al.* 2011; Smith *et al.* 2007; Whiting *et al.* 2004). For the remainder of the genera with no molecular evidence, it has been possible to allocate them to higher taxa based on morphology alone (Broadley 2006; Chan-ard *et al.* 2011; Couper *et al.* 1996; Darevsky & Orlov 1994; Das *et al.* 1998; Fuhn 1969; Greer 1967; Greer 1970; Greer 1974; Greer 1991; Greer *et al.* 1985; Greer & Nussbaum 2000; Hedges & Conn 2012; Ineich *et al.* 2004; Sadlier *et al.* 2006; Sakata & Hikida 2003; Wagner *et al.* 2009). A comprehensive morphological revision of all skinks is needed because the foundational work was done mostly decades ago (e.g., Camp 1923; Mittleman 1952; Greer 1970; 1974; 1977; 1979; 1986; Welch 1982; Mausfeld & Vrcibradic 2002; Bauer 2003).

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