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## 1986 Redux: New genera of anoles (Squamata: Dactyloidae) are unwarranted

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### Introduction

The year 1986 gave us Madonna's *True Blue*, Geraldo Rivera opening Al Capone's vaults, and a new taxonomy of anoles (Guyer and Savage, 1986). Each of these greatly anticipated events began with considerable promise but ended up adding nothing of depth to the culture of the time. Madonna's best work was behind her, Capone's vaults were a letdown, and the proposed anole taxonomy was unsupported and poorly executed (Cannatella and de Queiroz, 1989; Williams, 1989), but was mostly done in by the paucity of data available at the time. In the ensuing years, Madonna showed some staying power and Geraldo reinvented himself, but the erection of a handful of nonmonophyletic genera was not enough to achieve the apparent goal of preserving Savage's (1973) genus *Norops* as a valid name for anole lizards with transverse processes on their posterior caudal vertebrae (Etheridge, 1959). The genera *Dactyloa*, *Ctenonotus*, *et al.* lived on in Savage's (2002) excellent Costa Rica guide but were mostly ignored by those not working in Costa Rica.

In 2012 we have Lady Gaga continuing Madonna's tramp-diva legacy, TMZ filling Geraldo's gossip-news niche, and an ostensibly new taxonomy of anoles from Nicholson *et al.* (2012). But just as Lady Gaga recycles Madonna and TMZ unnecessarily claims Geraldo's old job, the anole taxonomy of 2012 doesn't offer much that is new, and doesn't improve much on something that was misguided and unfortunate in 1986. Below I argue why it would be scientifically irresponsible to adopt the Nicholson *et al.* (2012) taxonomy for anoles. Nicholson *et al.* (2012) selectively adopted results of their own flawed, unstable, and conflicting analyses, selectively incorporated pertinent published data and results, and changed names for over 100 species that have never been included in a phylogenetic analysis. The proposed taxonomy is unnecessary and unwarranted according to standard taxonomic practice. It should not be adopted by the scientific or nonacademic communities.

Below I focus on taxonomic issues. Other problems with Nicholson *et al.* (2012) will be addressed elsewhere. I use 'Nicholson *et al.*' to refer to the 2012 paper, and list species names without generic designations.

### Some of the proposed genera are not monophyletic

Although debates over Linnaean versus phylogenetic taxonomy continue, pretty much every working systematist today agrees that genera, if they are to be recognized, must be monophyletic. Remarkably for a published taxonomic paper, most of the genera proposed by Nicholson *et al.* do not meet this minimum requirement. This fact is a major problem with their taxonomy--the proposed genera are demonstrably not valid according to nearly universally accepted standards of animal taxonomy. Table 1 summarizes this conclusion with reference to the two trees evaluated by Nicholson *et al.* and an additional tree published a year earlier (Alfoldi *et al.*, 2011) that included much more character data than Nicholson *et al.* The analysis that includes the most characters (Alfoldi *et al.*, 2011) recovers two of the proposed genera as nonmonophyletic, and the analysis that includes the most taxa—Nicholson *et al.*'s Fig. 5—recovers five of the proposed genera as nonmonophyletic. The species groups continue the theme of taxonomic assignment that only partially follows their phylogenetic results. Of the 23 species groups of Nicholson *et al.* that are not monotypic, six are not monophyletic in their most densely sampled tree.

Even if one were to ignore 'problematic' taxa in order to preserve the monophyly of the proposed genera (which I do not advocate doing), the remaining genera are extremely poorly supported. For example, suppose we exclude *occultus*, *darlingtoni*, *argenteolous*, *lucius*, *bonairensis*, *chloris*, *peraccae*, *apollinaris*, *christophei*, and *barbouri* in order to render the proposed genera monophyletic in the tree of Nicholson *et al.* that includes the most taxa and data (Nicholson *et al.*: Fig. 5). In this case, seven of eight genera are supported at bootstrap values of less than 50%.