



## Systematics of the Common Kingsnake (*Lampropeltis getula*; Serpentes: Colubridae) and the burden of heritage in taxonomy

R. ALEXANDER PYRON<sup>1,3</sup> & FRANK T. BURBRINK<sup>2</sup>

<sup>1</sup>Dept. Of Biology, The Graduate School and University Center, The City University of New York, 365 5<sup>th</sup> Ave. NY, NY 10016.

E-mail: rpyron@gc.cuny.edu

<sup>2</sup>Dept. Of Biology, 6S-143, The College of Staten Island, 2800 Victory Blvd. Staten Island, NY 10314.

E-mail: burbrink@mail.csi.cuny.edu

<sup>3</sup>Corresponding author

### Abstract

We present a systematic revision of the *Lampropeltis getula* group, based on a recent range-wide phylogeographic analysis. We define our theoretical and operational concepts of species delimitation, and provide diagnoses based on mitochondrial DNA evidence, ecological niche modeling, morphology, and historical precedence. We find support for the recognition of five distinct species, which bear the name of the nominate subspecies found primarily within the range of each phylogeographic lineage: the Eastern lineage (*Lampropeltis getula*, Eastern Kingsnake), the Mississippi lineage (*L. nigra*, Black Kingsnake), the Central lineage (*L. holbrooki*, Speckled Kingsnake), the Desert lineage (*L. splendida*, Desert Kingsnake), and the Western lineage (*L. californiae*, California Kingsnake). Interestingly, all of these taxa had originally been described as distinct species and recognized as such for up to 101 years (in the case of *L. californiae*) before being demoted to subspecies. We discuss the impact that increasingly detailed genetic information from phylogeographic analyses may have on traditional taxonomy.

**Key words:** classification, *Lampropeltis getula*, North America, phylogeography, subspecies, taxonomy

### Introduction

The delimitation of species is a primary goal of systematic biology (Sites & Marshall 2004; Wiens 2007), and species identification is a major application of molecular phylogenetics (Avice 2000; Wiens & Penkrot 2002; Lemmon *et al.* 2007; Mulcahy 2008). Recently, traditional taxonomy has been in upheaval, as the uncovering of cryptic phylogeographic lineage diversity has resulted in the discovery of many species which are morphologically similar, para- or peri-patric, and represent portions of wide-ranging species complexes that had long been perceived as single species (Wake 1997; Avice 2000; Burbrink *et al.* 2000; Wiens & Penkrot 2002; Sinclair *et al.* 2004). Additionally, historical inertia may promote the continued recognition of hazily defined species or subspecies whose phylogeny may be imprecisely known, resulting in a taxonomic ‘burden of heritage’ for systematists. We speculate that this is a combination of two factors. First is the necessity of continuing to recognize current taxonomic arrangements under the principle of priority of the International Code of Zoological Nomenclature, based on their historical primacy. Second is the tendency for the more obvious, but potentially less evolutionarily significant and phylogenetically less informative attributes such as color pattern variation to dominate the attention of investigators.

This may occasionally result in a tendency both to ascribe differences to visually distinct but genetically homogeneous populations, and to group as conspecific visually similar populations (see, in part, Burbrink *et al.* 2000; Baird *et al.* 2006). While such patterns may reveal intriguing sources of information regarding local adaptations and population interactions, their utility as a source of evolutionary or phylogenetic information is