



Get an eyeful of this: a new species of giant spitting cobra from eastern and north-eastern Africa (Squamata: Serpentes: Elapidae: *Naja*)

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Abstract

We describe a new species of giant spitting cobra, *Naja ashei* sp. nov., from eastern and north-eastern Africa. The species was previously regarded as a colour phase of the black-necked spitting cobra, *N. nigricollis*. However, mtDNA sequence data show it to be more closely related to *N. mossambica* than *N. nigricollis*. The new species is diagnosable from all other African spitting cobras by the possession of a unique clade of mtDNA haplotypes and a combination of colour pattern and scalation characteristics. Its distribution includes the dry lowlands of northern and eastern Kenya, north-eastern Uganda, southern Ethiopia and southern Somalia.

Key words: *Naja ashei* sp. nov., *Naja nigricollis*, *Naja mossambica*, Serpentes, Elapidae, Africa, mitochondrial DNA, phylogeny, multivariate morphometrics

Introduction

Among venomous snakes, cobras are among those that have the highest public awareness profile. Nevertheless, our understanding of the taxonomy of the group has until recently remained woefully inadequate, particularly in terms of understanding the species limits within different well differentiated species groups. Within the genus *Naja*, the most extensively revised taxa are the Asian representatives of the genus, where successive revisions have raised the number of recognised species from one to eleven (Wüster & Thorpe, 1991; Wüster *et al.*, 1995; Wüster, 1996; Slowinski & Wüster, 2000) and the African spitting cobras, in which the number of recognised species has risen from one to five (Broadley, 1968, 1974; Roman, 1968, 1969; Wüster & Broadley, 2003). Although conventional morphological approaches have contributed considerably to the resolution of the systematics of these complexes (e.g., Broadley, 1968, 1974), more advanced approaches such as multivariate morphometrics (e.g., Wüster & Thorpe, 1989, 1992) and their combined use with mtDNA sequences (e.g., Wüster *et al.*, 1995, 1997; Slowinski & Wüster, 2000; Wüster & Broadley, 2003; Broadley & Wüster, 2004) have been especially valuable in unravelling the systematics of groups with more subtle patterns of morphological variation.

The combined use of morphological data and mtDNA adds considerable additional rigour to any attempt to diagnose and understand species limits, compared to using either marker system in isolation. Morphological differences between populations may be due either to natural selection, independent of phylogenetic affinities, or to phylogenesis (Thorpe *et al.*, 1994, 1995), and the pattern of variation alone cannot differentiate between these two hypotheses. On the other hand, the presence of multiple mtDNA haplotype clades does not necessarily indicate the presence of multiple species (e.g., Puerto *et al.*, 2001), and may even mask patterns of