



Phylogeography and systematic revision of the Egyptian cobra (Serpentes: Elapidae: *Naja haje*) species complex, with the description of a new species from West Africa

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Abstract

We use a combination of phylogenetic analysis of mtDNA sequences and multivariate morphometrics to investigate the phylogeography and systematics of the Egyptian cobra (*Naja haje*) species complex. Phylogenetic analysis of mitochondrial haplotypes reveals a highly distinct clade of haplotypes from the Sudano–Sahelian savanna belt of West Africa, and that the haplotypes of *Naja haje arabica* form the sister group of North and East African *N. h. haje*. Multivariate morphometrics confirm the distinctness of the Arabian populations, which are consequently recognised as a full species, *Naja arabica* Scortecci. The Sudano-Sahelian populations are also found to represent a morphologically distinct taxon, and thus a separate species, which we describe as *Naja senegalensis* sp. nov. The new species differs from all other members of the *N. haje* complex by a combination of colour pattern and scalation characteristics (especially higher numbers of scale rows around the neck), and the possession of a unique clade of mtDNA haplotypes. The distribution of the new species includes savanna areas of West Africa, from Senegal to western Niger and Nigeria.

Key words: mitochondrial mtDNA, *Naja senegalensis* sp. nov., *Naja haje*, *Naja anchietae*, *Naja annulifera*, *Naja arabica*, phylogeny, snakes, West Africa

Introduction

Recent decades have seen a tremendous surge in the use of molecular markers both for inferring phylogenetic interrelationships of groups of organisms and for taxonomic revisions. Mitochondrial DNA (mtDNA) sequences have dominated this field (Avice, 2000). Phylogeographic studies, relating evolutionary relationships among haplotypes to their geographic distribution, have allowed the reconstruction of the biogeographical history of species complexes, and, especially when performed across multiple co-distributed species, the reconstruction of the history of entire biotas (e.g., Rull, 2008).

In systematics, important applications of mtDNA have included phylogenetic reconstruction in general, but particularly species delimitation (Wiens & Penkrot, 2002). However, for the latter, mtDNA sequences do not represent an adequate source of evidence unless supported by additional markers. Multiple distinct haplotype clades can co-exist in a single gene pool, and phylogeographic patterns can remain in place despite extensive continued gene flow across mitochondrial haplotype distribution boundaries (Thorpe & Richard, 2001; Ogden & Thorpe, 2002). Consequently, the presence of multiple haplotype clades need not indicate the presence of more than one species (Puorto *et al.*, 2001). Additional evidence is therefore required to test whether mitochondrial haplotype clades represent independently evolving organismal lineages (= species), or