

## Article



## A reassessment of *Cuora cyclornata* Blanck, McCord and Le, 2006 (Testudines, Geoemydidae) and a plea for taxonomic stability

PHILLIP Q. SPINKS<sup>1</sup>, ROBERT C. THOMSON<sup>2</sup> & H. BRADLEY SHAFFER<sup>3</sup>

2320 Storer Hall, University of California, Davis, CA 95616. E-mail: ¹pqspinks@ucdavis.edu; ²rcthomson@ucdavis.edu; ³hbshaffer@ucdavis.edu

## **Abstract**

We analyze the phylogenetic variation present in the *Cuora trifasciata* species complex using mitochondrial and nuclear DNA sequence data. We use this information to evaluate the recent description of *Cuora cyclornata* Blanck, McCord, and Le (2006), and reinterpret this proposed species in light of likely mitochondrial introgression. Our results indicate that the pattern of variation within the *Cuora trifasciata* species complex is better explained by mitochondrial introgression coupled with hybridization and/or clinal variation, than it is by the presence of a previously unrecognized species. We also use our phylogeny as a framework for discussion of additional proposed changes to generic level taxonomy in this critically imperiled clade. Our results highlight the importance of appropriate data sampling in taxonomic revisions and suggest that *Cuora cyclornata* be treated as a junior synonym of *Cuora trifasciata*.

## Introduction

The Asian box turtles (genus *Cuora*) could be the "poster children" of chelonian conservation biology. Seventy-five percent of the contained species (9/12) are in peril; seven species are critically endangered including *C. yunnanensis* Boulenger (which was declared extinct, but has since been found in the wild [Zhou and Zhao, 2004]), one is endangered, and one is vulnerable (IUCN, 2008). A sound, defensible taxonomy for these turtles is absolutely essential, as species-level taxonomy is key to understanding and protecting biodiversity (Turtle Taxonomy Working Group, 2007a). However, delimiting species for *Cuora* is complex because we know very little about patterns of intraspecific variation in the wild, some named taxa are very similar genetically, and there is widespread interspecific and intergeneric hybridization involving numerous *Cuora* species and related geoemydid genera (Parham *et al.*, 2001; Spinks & Shaffer, 2007; Spinks *et al.*, 2004; Stuart & Parham, 2004; Stuart & Parham, 2007; Wink *et al.*, 2000).

The greatest threat facing these turtles is over-exploitation for the Asian turtle trade. *Cuora* spp. are intensively collected to satisfy the increasing demands of the pet trade and food markets of China (Parham *et al.*, 2001; Stuart & Parham, 2004; van Dijk *et al.*, 2000). As a consequence, many species are extremely rare in the wild, thereby making population genetic or phylogeographic analyses all but impossible. For example, *C. pani* Song, and *C. aurocapitata* Luo and Zong are two recently described, Critically Endangered species (IUCN, 2008) for which almost no field-verified specimens are available (Luo & Zong, 1988, cited in Parham & Li, 1999). Since we have virtually no understanding of intraspecific patterns of genetic or phenotypic variation in nature, the differences among *C. aurocapitata* and *C. pani* could be attributed to clinal variation within a single taxon (McCord & Iverson, 1991; Parham & Li, 1999). Combined with the widespread movement of, and breeding among, species of *Cuora* for the Asian turtle market and the heavy past reliance on market-purchased specimens for taxonomic work, sorting out species boundaries and interspecific