

Phylogeography of the *Mauremys mutica* complex and the implications for conservation management.

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Abstract

For more than three decades, the Asian turtle crisis has resulted in the decline of every native species in China. For some species, such as the yellow pond turtle (*Mauremys mutica*), wild populations have dwindled to near functional extinction. Previous studies show there is deep genetic divergence of *M. mutica* sensu lato between populations north and south of the Pearl River Drainage but no data to show if phylogeographic structure occurs within these two main types. In this study, we found clear phylogeographic structure. In northern types, we found two main clades, corresponding to mainland China and island clades (Taiwan and Yaeyema Islands) with uncorrected p values of 0.00-2.0% divergence in our 2353 bp concatenated mtDNA data set. For the southern types, we found three main clades corresponding to Hainan, Mainland (Vietnam/Guangxi) and the Annam pond turtle (*Mauremys annamensis*) with divergence ranging from 1.0-1.8% among these three groups. Moreover, the identification of northern and southern types by phenotype was roughly 98% accurate, which, coupling with the deep genetic divergence in mtDNA (5.5-6.7%) and in the 6056 bp nuDNA data set (0.16-0.37%) provide sufficient evidence for northern *M. mutica* to be an independent species, and individuals from the southern clade should be regarded as subspecies of *M. annamensis*. Finally, we provide the most comprehensive database to date which can be used to determine the region of origin for captive stock. Making the large captive populations of *M. mutica*, under the right conditions, potentially valuable for restocking or augmentation of wild populations.

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