



Comparison of complete mitochondrial DNA control regions among five Asian freshwater turtle species and their phylogenetic relationships

Y. Jiang, L.W. Nie, Z.F. Huang, W.X. Jing, L. Wang, L. Liu and X.T. Dai

School of Life Sciences, Anhui Normal University,
Provincial Key Lab of the Conservation and Exploitation Research of
Biological Resources in Anhui, Wuhu, China

Corresponding author: L.W. Nie
E-mail: lwnie@mail.ahnu.edu.cn

Genet. Mol. Res. 10 (3): 1545-1557 (2011)
Received December 10, 2010
Accepted May 2, 2011
Published August 1, 2011
DOI 10.4238/vol10-3gmr1205

ABSTRACT. The complete mitochondrial DNA (mtDNA) control regions (CR), cytochrome b (Cyt b), NADH dehydrogenase subunit 4 (ND4) and cytochrome oxidase subunit I (CO I) genes of four Asian freshwater turtles, *Mauremys japonica*, *Ocadia sinensis*, *M. mutica*, and *Annamemys annamensis*, were sequenced using universal PCR and long-PCR techniques. Combined with CR sequences of *Chinemys reevesii*, the composition and structure of CR of the five species were compared and analyzed. Three functional domains (TAS, CD and CSB) in CR and their conserved sequences (TAS, CSB-F, CSB-1, CSB-2, and CSB-3) were identified based on sequence similarity to those of other turtles. At the 3' end of CSB, six type motifs of variable number of tandem repeats (VNTRs) of five species were recognized, in which the TTATATTA motif may be the VNTR motif of the ancestral species of these five turtles. Comparison of nucleotide divergences among Cyt b, ND4, CO I, and CR of 11 turtle species using transitions + transversions and transversions-only methods supported the conclusion that CR evolved 2.6- to 5.7-fold faster than the other mtDNA genes.

After excluding VNTRs of CR, molecular phylogenetic trees were constructed with maximum parsimony, maximum likelihood and Bayesian inference methods. The results supported an expanded clade of *Mauremys*, which included species formerly in *Ocadia*, *Chinemys*, *Mauremys*, and *Annamemys*; this was also reflected in the results of VNTR analysis.

Key words: *Mauremys*; Mitochondrial DNA; Control region; Variable numbers of tandem repeats; Evolution rate; Phylogenetic