



Phylogenetic relationships of *Pseudohynobius* (Urodela, Hynobiidae) inferred from DNA barcoding analysis

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ABSTRACT. As a proven tool, DNA barcoding can identify species rapidly and unambiguously. In this study, we used mtDNA cyt b, COI, and 16s rRNA sequences of six species of *Pseudohynobius*, *Protrohynobius puxiongensis*, *Liua shihi*, *Ranodon sibiricus*, and *Pachyhynobius shangchengensis*, to reconstruct the phylogenetic relationships using Bayesian inference and maximum likelihood methods. Approximate lineage divergence times were also estimated, the divergence between them was calculated to have taken place mainly in Miocene. Our results showed that: 1) *Ps. guizhouensis* is an independent and valid species that is a sister species to *Ps. kuankuoshuiensis*; 2) five *Pseudohynobius* species formed a monophyletic group; 3) *Ps. tsinpaensis* is different from *L. shihi*, and should be classified as belonging to the *Liua* genus; and 4) *Pr. puxiongensis* is the sister lineage to all *Pseudohynobius*

species, and should therefore be named *Pseudohynobius puxiongensis*.

Key words: *Pseudohynobius*; *Protohynobius puxiongensis*; mtDNA COI; mtDNA cyt b; mtDNA 16s rRNA