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Invalidity of *Hynobius yunanicus* and molecular phylogeny of *Hynobius* salamander from continental China (Urodela, Hynobiidae)

KANTO NISHIKAWA, JIAN-PING JIANG, MASAFUMI MATSUI, YUN-MING MO, XIAO-HONG CHEN, JONG-BUM KIM, ATSUSHI TOMINAGA & NATSUHIKO YOSHIKAWA

[1]*Graduate School of Human and Environmental Studies, Kyoto University, Kyoto 606-8501, Japan*
[2]*Chengdu Institute of Biology, the Chinese Academy of Sciences, Chengdu 610041, China*
[3]*Natural History Museum of Guangxi, Nanning 530012, China*
[4]*College of Life Sciences, Henan Normal University, Xinxiang 453007, China*
[5]*College of Natural Sciences, Inha University, Incheon 402-751, South Korea*
[6]*National Institute for Environmental Studies, 16-2 Onogawa, Tsukuba 305-8506, Japan.*
[7]*Corresponding author. E-mail: hynobius@zoo.zool.kyoto-u.ac.jp*

Based on morphological and molecular analyses, Xiong *et al*. (2007) synonymized *Hynobius yunanicus* Chen *et al*. with *Pachyhynobius shangchengensis* Fei *et al*., both from continental China. Their study, however, was not substantial enough in that morphology of types of neither species was compared, only a partial mitochondrial cytochrome b (cyt b) sequence was employed, and data for *H. chinensis* was lacking. In order to reassess their conclusion, we morphologically examined type specimens of both species, and compared their complete cyt b (1141 bp) sequences, together with all the six recognized continental *Hynobius* species and some congeners from Japan and South Korea.

We examined morphology of the holotype and paratypes of *H. yunanicus* (College of Life Sciences, Henan Normal University=HENNU 99082403, 0504III013, 0504III015, 0205II062), a "*H. yunanicus*-like" subadult (Sample 13= Chengdu Institute of Biology, Chinese Academy of Sciences=CIB HN2007012002, see Table 1), and a paratype of *P. shangchengensis* (CIB 00223), all of which were collected from Huangbaishan, Shangcheng County, Henan Province (type locality of the two species). The subadult specimen could be identified as *H. yunanicus*, because it had numerous white spots on dorsum (vs. no spot in *P. shangchengensis*), and unconnected maxilla and pterygoid (vs. connected in *P. shangchengensis*). Additional *P. shangchengensis*, three juveniles and five adults of from Jinzhai County, Anhui Province (CIB 72887-72894) and an adult from unknown locality in Mt. Dabie (Sample 16= Graduate School of Human and Environmental Studies, Kyoto University=KUHE 38563) were also examined. From diagnostic skull characteristics (Fei *et al*. 1985; Chen *et al*. 2001), all of the specimens examined could be treated as intraspecific variation in one species.

We then compared complete sequences of cyt b among our own 11 samples, together with six species from GenBank data (Table 1). Tree topologies of maximum likelihood and Bayesian (Fig. 1) analyses were identical and samples of *Hynobius* were monophyletic with respect to the outgroup. The "*H. yunanicus*-like" subadult (Sample 13) had a sequence identical with that of one larval *P. shangchengensis* (Sample 14) and formed a monophyletic group with other larval and adult *P. shangchengensis* (Samples 14-16) with a small uncorrected p-distance of 2.2%. Other *Hynobius* species from continental China were monophyletic and separated into two lineages (Lineages I and II, see Fig. 1), with *H. chinensis* being closest to *H. maoershanensis* in the Lineage I.

Our new sequences of Samples 13-16 are identical to or very slightly different (0-3.2% in corresponding region) from those of *H. yunanicus* and *P. shangchengensis* available from GenBank (AY593138, EF433581-EF433586, DQ333812, and DQ335747: Zeng *et al.* 2006; Zhang *et al.* 2006; Xiong *et al.* 2007).

Our survey on skull morphology and mitochondrial DNA sequence failed to detect any definite difference between *H. yunanicus* and *P. shangchengensis*. We thus conclude the former doubtlessly a subadult of the latter.

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