

Phylogenetic Position of *Eptatretus chinensis* (Myxinidae: Myxiniformes) Inferred by 16S rRNA Gene Sequence and Morphology

Ya-Wen Chen¹, Hsueh-Wen Chang², and Hin-Kiu Mok^{1,*}

¹Institute of Marine Biology, National Sun Yat-sen University, Kaohsiung, Taiwan 804, R.O.C.

²Institute of Biological Sciences, National Sun Yat-sen University, Kaohsiung, Taiwan 804, R.O.C.

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Ya-Wen Chen, Hsueh-Wen Chang, and Hin-Kiu Mok (2005) Phylogenetic position of *Eptatretus chinensis* (Myxinidae: Myxiniformes) inferred by 16S rRNA gene sequence and morphology. *Zoological Studies* 44(1): 111-118. Analysis of the present dataset indicated variations in external and internal taxonomic morphological characters of *Eptatretus chinensis* occurring in the South China Sea. Molecular evidence from its 16S rRNA gene sequence indicated a close relation of *E. chinensis* with *Paramyxine sheni* and other species of *Paramyxine* with crowded gill apertures. This species is similar to *E. burgeri* and *P. sheni* in the lack of some slime pores in the branchial region. On the other hand, it shares branching of the ventral aorta close to the heart (a derived character state for the Eptatretinae) with some other congeners (but not *E. burgeri*) and *P. sheni*. <http://www.sinica.edu.tw/zool/zoolstud/44.1/111.pdf>

Key words: Myxinidae, *Eptatretus chinensis*, Morphology, 16S rRNA, Phylogeny.

Eptatretus chinensis (Fig. 1) was first described in 1994 based on 5 type specimens collected from the South China Sea (113° 14'E, 19° 37'N) at a depth of 600 m (Kuo and Mok 1994). It is a 6-gilled hagfish species with a 3-cusp multicuspoid in each tooth row and slime pores next to most of the gill apertures. Due to the small number of specimens then available, detailed variations in the morphometric measurements and meristic counts could not be determined in the original description.

A hypothesis of the phylogenetic interrelationships for 11 myxinid species was constructed by Kuo et al. (2003) based on mitochondrial 16S rRNA gene sequence. This study included the following species: 3 *Eptatretus* species (i.e., *E. burgeri*, *E. cirrhatus*, and *E. stoutii*), 2 *Paramyxine* species (*P. cheni* and *P. sheni*), 3 *Quadratus* [*Paramyxine*] species (*Q. nelsoni*, *Q. taiwanae*, and *Q. yangi*), 3 *Myxine* species (*M. circifrons*, *M. formosana*, and *M. glutinosa*), and 3 undescribed *Myxine* species from Taiwanese waters (*Myxine*

sp. 1, sp. 2, and sp. 3). The resulting molecular phylogenetic tree (Fig. 2) shows that (1) both the Myxininae and Eptatretinae are monophyletic subfamilies; (2) *P. cheni* is the plesiomorphic sister species for the remaining 7 eptatretine species which form a closely related group; (3) the genus *Paramyxine* is diphyletic (i.e., not monophyletic);



Fig. 1. *Eptatretus chinensis*. Total length, 354 mm.

* To whom all correspondence and reprint requests should be addressed. E-mail: hinkiu@mail.nsysu.edu.tw