

Variation in Mitochondrial DNA and Phylogenetic Relationships of Fishes of the Subfamily Sparinae (Perciformes: Sparidae) in the Coastal Waters of Taiwan

Chuen-Tan Jean¹, Cho-Fat Hui^{2,*}, Sin-Che Lee² and Che-Tsung Chen³

¹Department of Fishery Biology, Taiwan Fisheries Research Institute, Keelung, Taiwan 202, R.O.C.

²Institute of Zoology, Academia Sinica, Taipei, Taiwan 115, R.O.C.

³Department of Fishery Science, College of Fisheries, National Taiwan Ocean University, Keelung, Taiwan 202, R.O.C.

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Chuen-Tan Jean, Cho-Fat Hui, Sin-Che Lee and Che-Tsung Chen (1995) Variation in mitochondrial DNA and phylogenetic relationships of fishes of the subfamily Sparinae (Perciformes: Sparidae) in the coastal waters of Taiwan. *Zoological Studies* 34(4): 270-280. Mitochondrial DNA (mtDNA) sequences that included the non-coding D-loop region, the tRNA^{Phe} gene, and a part of the 12S rRNA gene from 60 individuals belonging to 5 Sparinae species were sequenced to document the mtDNA sequence variations as well as to elucidate the phylogenetic relationships of these species. The intraspecific and interspecific comparisons of aligned sequences demonstrate that the tRNA^{Phe} gene and the 12S rRNA gene are highly conserved. The left and right domains of the D-loop region contain a higher A content and a lower G content, and are highly variable in both sequences and lengths. The central domain of the D-loop region contains a lower A content and a higher G content, and is more conserved than the other two domains. The conserved sequence elements TAS, CSB-2, and CSB-3, which have been reported previously from other vertebrates, are maintained in Sparinid fishes. The intraspecific pairwise sequence distances using the Tamura-Nei model ranged between 0.0021-0.0130 in *Acanthopagrus australis*, 0.0000-0.0115 in *A. berda*, 0.0014-0.0209 in *A. latus*, 0.0014-0.0093 in *A. schlegeli*, and 0.0000-0.0056 in *Sparus sarba*. The interspecific pairwise sequence distances using the Tamura-Nei model, ranged from 0.1498 to 0.1914 between species of *Acanthopagrus*, and from 0.2386 to 0.2708 between species of the genera *Acanthopagrus* and *Sparus*. The phylogenetic tree constructed by UPGMA based on the mtDNA sequence data shows the same topology as that based on allozyme electrophoresis data, but it is different from that based on morphometric data.

Key words: mtDNA, Sequence variation, Interspecific relationships, Sparinae.

Fishes of the subfamily Sparinae, commonly known as porgies, are important commercial species for food consumption and recreational fisheries in estuarine and coastal waters of Taiwan. They also have become pond-cultivated species after the proven success of artificial mass propagation of fingerlings (Lin and Yen 1980, Lin et al. 1988, Leu et al. 1991).

In Taiwan, the subfamily Sparinae contains two genera and five species. The genus *Acanthopagrus* includes four nominal species, namely *Acanthopagrus schlegeli*, *A. latus*, *A. berda*, and *A. australis*. The genus *Sparus* includes only

one species, *Sparus sarba* (Lee 1983, Jean and Lee 1992). Among these five species, *A. berda* and *S. sarba* are the most widely distributed species, extending from southern Japan, Southeast Asia, Australia, the Indian Ocean, and the Red Sea to southeastern Africa. *A. latus* occurs in southern Japan, Southeast Asia, Australia, the Indian Ocean, and the Red Sea to northeastern Africa. *A. schlegeli* is found around Japan, South Korea, China, with its southernmost extension to Taiwan. The distribution of *A. australis* ranges from northern Australia to southern Japan (Okinawa) (Hayashi 1993).

*To whom all correspondence and reprint requests should be addressed.