

Variation in Mitochondrial DNA Sequences of Black Porgy, *Acanthopagrus schlegeli*, in the Coastal Waters of Taiwan

Chuen-Tan Jean¹, Sin-Che Lee^{2,*}, Che-Tsung Chen³ and Cho-Fat Hui²

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.

Tel: 886-2-27899520. Fax: 886-2-27858059. E-mail: sclee@gate.sinica.edu.tw

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

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Chuen-Tan Jean, Sin-Che Lee, Che-Tsung Chen and Cho-Fat Hui (1998) Variation in mitochondrial DNA sequences of black porgy, *Acanthopagrus schlegeli*, in the coastal waters of Taiwan. *Zoological Studies* 37(1): 22-30. Mitochondrial DNA sequences that include the 5' end of the D-loop region, the 3' end of the D-loop region, the tRNAPhe gene, and the 5' end of the 12S rRNA gene were determined from 49 specimens of *Acanthopagrus schlegeli* and 1 specimen of *A. australis* collected from 7 locations along the coastal waters of Taiwan and Matsu off the coast of mainland China, and from an aquaculture pond. Among 33 haplotypes identified from the 49 mtDNA sequences, there were 32 variable sites, most of which occurred in the 5' end of the D-loop region. Pairwise sequence distances among haplotypes, using the Tamura-Nei model, range between 0.0014 and 0.0127. The phylogenetic tree constructed by use of the unweighted pair-group method with arithmetic average shows neither significant genealogical branches nor geographic clusters. All of the bootstrap confidence levels resulting from 1000 bootstrap tests are below 50%. Furthermore, the sequence-statistics test reveals little genetic differentiation. Apparently, wild black porgies in the coastal waters of Taiwan and Matsu off the coast of mainland China, belong to a single population. There is no significant genetic differentiation between the wild and pond-cultivated populations.

Key words: *Acanthopagrus schlegeli*, mtDNA, Genetic structure.

Black porgy *Acanthopagrus schlegeli* is distributed in the West Pacific coasts from Japan and Korea to the East China Sea and Taiwan. It is an important food fish and a target species of recreational fisheries in estuarine and coastal waters of Taiwan. It is also a highly valued cultivated fish species in Taiwan. In addition to *A. schlegeli*, there are 3 other closely related species (*A. australis*, *A. berda*, and *A. latus*); altogether they comprise the so-called *A. schlegeli* species complex. In coastal waters of Taiwan, *A. schlegeli* is the most abundant species among the 4 species. Having close resemblance in external features, their easily confused species status can be discriminated by isozyme electrophoresis (Jean et al. 1995b) and mtDNA sequencing (Jean et al. 1995a). Due to the drastic decrease in wild populations, there is an

urgent need to resurrect these stocks through conservation, management, and mariculture. Defining the systematic status and population structure of a species is a basic prerequisite for making informed decisions regarding rational exploitation and management, as well as for correct interpretation of ecological investigations (Ferguson and Mason 1981).

Due to maternal inheritance and a relatively faster evolutionary rate, mitochondrial DNAs (mtDNA) have been used to provide insights into population genetic structure, gene flow, hybridization, biogeography, and phylogenetic relationships of various animals (Avice et al. 1986, Moritz et al. 1987, Bartlett and Davidson 1991, Bowers et al. 1994, Sang et al. 1994, Taylor and Dodson 1994, Jean et al. 1995a).

*To whom correspondence and reprint requests should be addressed.