POPULATION GENETIC STRUCTURE OF THE LARGE YELLOW CROAKER ALONG THE CHINESE COAST

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The large yellow croaker (*Pseudosciaena crocea*) is a commercially important fishery species with a wide distribution along the Chinese coast. Recently, stock enhancement has been implemented to replenish the wild populations depleted by over-fishing and habitat degradation. Unfortunately, the population differentiation of the large yellow croaker, which is necessary for the development of a long-term strategy for fishery management and stock enhancement, has not been elucidated. Based on morphological features and reproductive seasonality, three geographical stocks, including Daiqu, Minyuedong and Naozhou, have been previously proposed. In the present study, genetic variations in wild large yellow croaker from eight locations along the Chinese coast from southern Yellow Sea to Beibu Bay (Gulf of Tonkin) were analyzed using five microsatellite loci and mitochondrial DNA (mtDNA) control region (859 bp) sequences. The aim was to identify genetic stock management units in relation to stock enhancement.

Control region sequence analysis showed that inter-population genetic distances (0.0131 to 0.0154) were small and overlapped with values within populations (0.0115 to 0.0162). Pairwise F-statistics analyses revealed limited genetic differentiation between samples from different geographical regions. Neighbor-joining tree and minimum-spanning network analysis of control region haplotypes showed that samples from the three proposed stocks were mixed randomly.

Analyses of pairwise F_{ST} values using five microsatellite loci with relatively higher polymorphism revealed no significant genetic differentiation ($F_{ST} < 0.01$) among samples collected from southern Yellow Sea to the South China Sea at the east of Hainan Island. The only exception involved samples from Guanjinyang (GJ) in Fujian province which were differentiated from the other samples. The level of genetic variability in these samples was close to that in cultured populations from the same area, suggesting that wild samples from GJ may have been mixed with cultured fish escaped from cages or those from stock enhancement. In general, our results suggested high level of gene flow among most populations along the Chinese coast. Yet pairwise F_{ST} estimates were > 0.05 between samples from Beibu Bay or Qiongzhou Strait and those from the other locations, suggesting the occurrence of a genetically discrete population in Beibu Bay to the west of Hainan Island. To conclude, results from both mtDNA and microsatellite analysis do not support the separation of the three proposed and generally accepted geographical stocks. Our data are relevant to issues concerning fishery management, and stock enhancement of this fish species should take into consideration the occurrence of the two geographical stocks defined in this study.