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Mitochondrial DNA variation and population genetic structure in the small yellow croaker at the coast of Yellow Sea and East China Sea

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ABSTRACT

Small yellow croaker is one of the most important fishery species in China. The mass–scale artificial propagation of this fish species was initially developed in 2015 with the aim of facilitating the fish production stock enhancement and aquaculture programs in the future. In the present study, the wild broodfish and its corresponding progeny along with three other wild populations were sampled and subjected to sequence analysis of the mitochondrial cytochrome *c* oxidase subunit I gene. The genetic diversity and population genetic structure were evaluated with a total sample size of 141 individuals representing the populations of the Yellow Sea (Qingdao and Lvsi populations) and the East China Sea (Xiangshan and Ningde populations). The wild populations were characterized by high haplotype diversity (0.925–0.976) and low nucleotide diversity (0.376%–0.560%). The hierarchical analysis of molecular variance (AMOVA) analysis and the values of pairwise Φ-statistics (Φ_{ST}) indicated non-significant genetic differentiation among the four wild populations. The hatchery stock XSH exhibited lower indices of genetic diversity compared with the wild populations that could be attributed to the small effective population size. The findings of the present study have valuable insight to the sustainable management and utilization of this resource.

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1. Introduction

The small yellow croaker *Larimichthys polyacis*, is considered one of the most widely marketed fishery species that is mainly distributed along the coastal waters of the China Sea including the Bohai Sea, the Yellow Sea and the East China Sea (FishBase, 2014). *Larimichthys polyacis* has a high annual consumption due to its delicate flavor and rich nutritional value. The production of this fish is in short supply in local fish markets despite of an annual capture production of more than 300,000 tons (FAO, 2014). Furthermore, the ocean pollution and the extended fishing in the past decade have led to a dramatic decrease in the population of wild fish types of China. Certain conservation strategies, such as the Summer Fishing Moratorium have been

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adopted in an effort to preserve the population of *Larimichthys polyacis* (Cheng et al., 2004). In addition, stocking cultured organisms is another strategy for replenishing depleted marine fish stocks. Domesticated broodstock would ensure a consistent production of seed for stock enhancement programs. However, the small yellow croaker is particularly sensitive to various environmental stresses, such as hypoxia and air exposure that cause certain difficulties in the process of hatchery breeding. During the period 2014 to 2015, a broodstock of the small yellow croaker that was captured from the coastal waters of Xiangshan was set up (Fig. 1). The artificial propagation of this fish was developed and 50,000 juveniles were produced in 2015 (Zhan et al., 2016). The success of the artificial breeding of the small yellow croaker will immensely facilitate the enhancement of the fish production stock and aquaculture in the future to ease the fishing pressure and fulfill the requirements of the domestic markets.

The sustainable exploitation and proper resource management of fish species can be considerably enhanced by understanding the genetic diversity and population structure of the fish species. Genetic markers can be used effectively for the estimation of the genetic variation and the population structure in fish species. The aforementioned parameters provide a basis for the adequate management of fish populations and the production of sustainable fisheries (Fromentin et al., 2009). Several genetic studies have investigated the genetic variation of the small yellow croaker using molecular markers such as microsatellites (Li et al., 2013), mitochondrial DNA (mtDNA) (Xiao et al., 2009) and single−nucleotide polymorphism (SNP) (Zhang et al., 2015). The studies that were based on mitochondrial (mtDNA) and microsatellite markers demonstrated no significant differentiation, suggesting a panmictic population of the small yellow croaker (Xiao et al., 2009; Li et al., 2013). In contrast to the aforementioned observations, Wang et al. (2013) revealed low levels of genetic differentiation between geographically distant populations of the small yellow croaker using a limited number of microsatellites. The latter study identified two loci that were found to be under diversifying selection. These studies that aimed notably at fish production stock identification, yielded certain discrepancies and/or conflicting results. In addition, the basic genetic variation in the hatchery stocks of the small yellow croaker was not investigated in the aforementioned studies. A comprehensive understanding of the genetic diversity in the wild and hatchery stocks of the small yellow croaker is crucial to the management of fish production and the aquaculture development programs.

The samples from the wild broodfish were collected from the coast water of Xiangshan (XSW) and their F1 offspring (XSH). The remaining three wild populations (Qingdao (QD), Lvsi (LS) and Ningde (ND)) were further collected for genetic analysis (Fig. 1). The samples in the present study could cover most parts of the natural distribution of this species in China. The aim of the study was to obtain baseline information regarding the genetic diversity and population structure of the small yellow croaker and to compare the genetic diversity between the wild type fish and the hatchery stock fish. The baseline information collected is critical for resource conversation and utilization of this species.

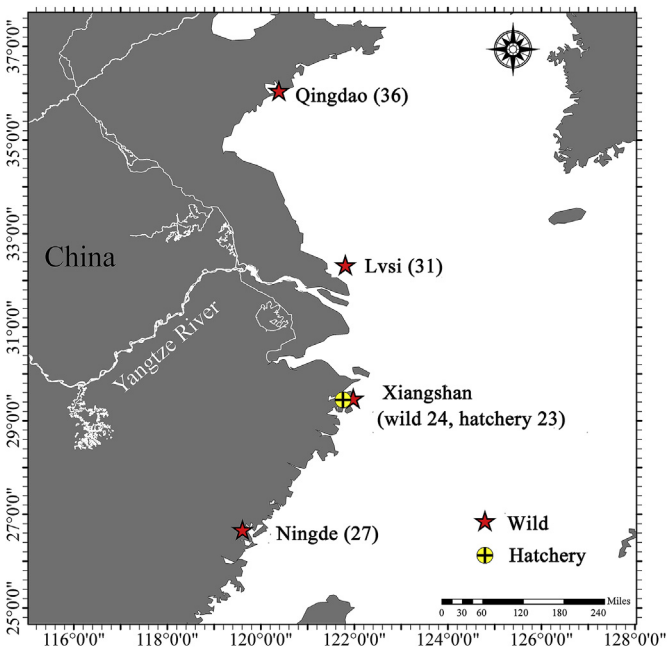

Fig. 1. Map of the small yellow croaker sampling locations. The four sampling sites were Qingdao (QD), Lvsi (Lvsi), Xiangshan (XS) and Ningde (ND), respectively. Numbers in the parentheses indicate the sample size.

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