



# Development of polymorphic microsatellite markers and the population genetic structure of the half-fin anchovy, *Setipinna taty*

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**ABSTRACT.** Microsatellite markers for the half-fin anchovy *Setipinna taty* were developed from the enriched (CA)<sub>15</sub> genomic library, and they were used for the population genetic studies of the half-fin anchovy from Chinese coastal areas. Samples were collected from five localities of the East China Sea and the Yellow Sea. Eleven simple sequence repeat markers were used to assess genetic differentiation in 30 individuals at each locality. As a result, 59 alleles were recorded over all loci with an average of 5.36 alleles per locus. Observed and expected heterozygosities ranged from 0.27 to 0.73 and 0.50 to 0.89, respectively. Analysis of molecular variation indicated that the variation within individuals was high (70.68%), while variations of individuals within and among populations were low (22.47 and 6.85%). The phylogenetic tree showed that these populations could be divided into two clusters: populations of the East China Sea, which came from Ninghai, Xiangshan and Zhoushan, and populations of the Yellow Sea, which were from Yantai and Weihai. It revealed that significant geographic structure existed in this species. All of the results indicated that high genetic diversity existed in the half-fin anchovy from different

geographic populations. This conclusion was consistent with the classification based on morphological and physiological characteristics.

**Key words:** Population genetic structure; Genetic diversity; Microsatellite markers; *Setipinna taty*