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Genetic variability assessed by microsatellites in cultured populations of the Pacific oyster (*Crassostrea gigas*) in China

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Abstract

Five cultured populations of Pacific oyster, *Crassostrea gigas*, were examined at seven polymorphic microsatellite loci to assess the levels of allelic diversity and heterozygosity within and differentiation among the populations. The genetic variability of the seven loci was high for all the populations. The average numbers of alleles per locus ranged from 19.1 to 26.0, while the average observed and expected heterozygosity ranged from 0.474 to 0.616, and from 0.916 to 0.949, respectively. F_{st} and R_{st} values showed significant genetic differentiation among the five cultured populations. Genetic differences between the populations were also detected by pairwise comparison based on allelic distribution. The Neighbor-joining tree topology constructed on the basis of genetic distances between populations showed a clear separation of the northern three populations and southern two populations, suggesting that geographically separated cultured populations of *C. gigas* could be genetically differentiated unless seeds are transplanted among them. The useful information on the genetic variation and differentiation in cultured populations obtained in this study can be applied for future genetic improvement by selective breeding, and to design suitable management guidelines for the Pacific oyster.

Keywords: Genetic variation; Cultured populations; Microsatellites; *Crassostrea gigas*

1. Introduction

Oysters are the largest molluscan group cultured in China. The production of oyster reached 3.62×10^6 metric tons in 2002 in China, accounting for 37.6% of total marine molluscan yield (DOF, 2003). Although about twenty species of oysters are naturally distributed along the coast of China (Zhang and Lou, 1956), most of the output comes from the three species of the Pacific oyster (*Crassostrea gigas*), zhe oyster (*C. plicatula*) and jinjiang oyster (*C. rivularis*). Official statistics do not distinguish individual oyster species, but experts estimate the Pacific oyster may account for about 10–20% of the national total (Guo et al., 1999).

Pacific oysters being cultured in China were originally introduced from Japan. In 1979, the Pacific oysters were first transplanted to Zhejiang province from Japan, and then moved to most parts of the Chinese coast including Liaoning and Shandong provinces in the north, and Fujian and Guangdong provinces in the south through the activities of oyster farmers (Wang et al., 2004). The Pacific oyster grows faster than the native zhe oyster and Suminoe oyster, reaching 8 to 10 cm after the first growing season, so it has been preferentially adopted for farming, and rapidly become the dominant farmed oyster in China.

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Pacific oyster seeds are produced exclusively in hatcheries, where larvae are cultured in large concrete tanks ranging from 10 to 100 m^3. To improve the increasing valuable Pacific oyster industry, growers are considering selective breeding programs. Because of the high fecundity of oyster species, relatively few parents are required to generate the numbers of offspring needed. So, there were concerns that genetic variability might have been lost during the more than 20 years of artificial cultivation. However, no information is currently available for the genetic variation in cultured populations of the Pacific oyster. Understanding of genetic diversity and differentiation among populations is essential for the sustainable management, selective improvement and to avoid genetic erosion in the oyster.

Among the molecular markers available in population genetics, microsatellites emerged as those with finest resolution for labeling of populations and individuals, due to their high variability, abundance, neutrality, co-dominance and unambiguously scoring of alleles (Weber and May, 1989; Tautz, 1989). Microsatellite genotyping has proved to be a powerful tool for accurate genetic assessment of population differentiation and pedigree tracing of hatchery populations from various fishery animals (Neff, 2001; Norris et al., 2000; Yu and Guo, 2005; Sugaya et al., 2002; Li et al., 2003a). Several studies have been published documenting their occurrence in the Pacific oyster genome (Magoulas et al., 1998; Huvet et al., 2000; McGoldrick et al., 2000; Li et al., 2003b; Sekino et al., 2003). They have been applied to the genetic study of the oyster in various aspects, such as hybridization, reproductive success, genetic load, identification of larvae, and construction of genetic map (Huvet et al., 2004; Boudry et al., 2002; Launey and Hedgecock, 2001; Morgan and Rogers, 2001; Hubert and Hedgecock, 2004). However, there are few reports available for microsatellite analysis of population structure in the Pacific oyster.

In the present study, we used seven microsatellite markers to estimate the level of genetic diversity within five hatchery populations of Pacific oyster, and to compare the degree of genetic differentiation between them.

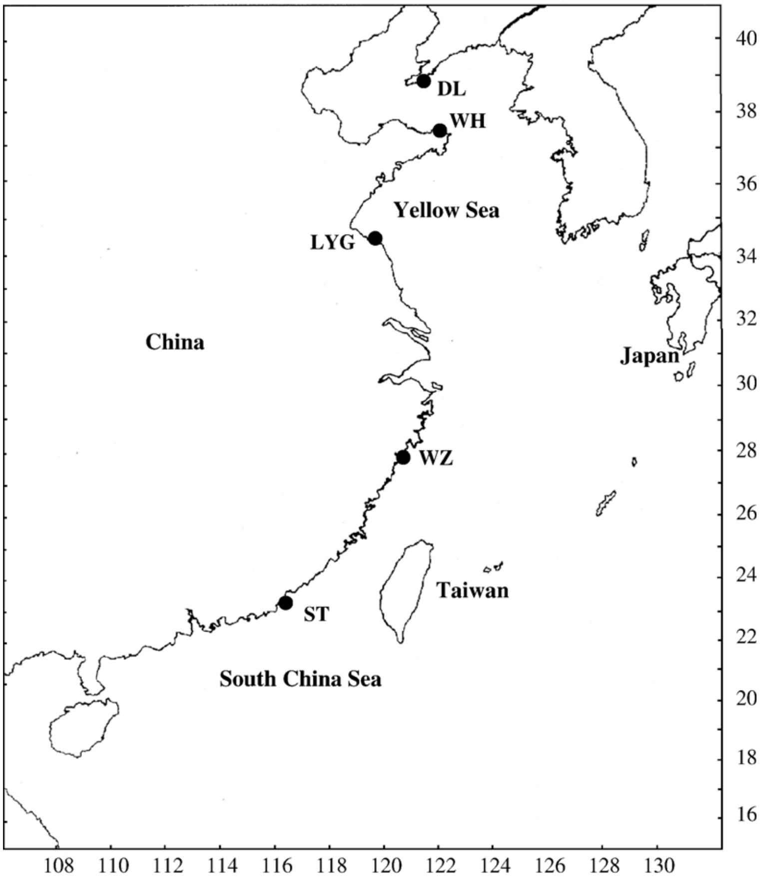

Fig. 1. Map showing locations and abbreviated names for five cultured Pacific oyster samples (●) in China.