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Genetic variation of *Mytilus coruscus* Gould (Bivalvia: Mytilidae) populations in the East China Sea inferred from mtDNA COI gene Sequence

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ABSTRACT

In order to characterize the genetic relationship of six populations of *Mytilus coruscus* Gould in the East China Sea, a 681 bp region of mtDNA COI gene was sequenced and analyzed. Eighty four individuals in total were collected from three cultured populations and three wild populations from three localities of the coast of East China Sea. The sequences from these different populations identified 62 polymorphic sites, which included 41 singleton variable sites and 21 parsimony informative sites that defined 45 distinct haplotypes. Phylogenetic analysis showed that most haplotypes were highly interconnected with each other. Thirty seven of the 45 haplotypes were only found in their own populations, seven were found at two-four localities and only haplotype NO.2 was found in all six populations, indicating that most haplotypes were locally restricted. All haplotypes had shaped two similar branches, each including individuals from all six strains. The results of F_{ST} values indicated that the genetic distances between populations are not closely associated with their geographic distances.

1. Introduction

Mussels include many ecologically and economically important species that are found among the dominant macrofauna in littoral and shallow sub-littoral systems (Distel, 2000). The hard shelled mussel, *Mytilus coruscus* Gould 1861, is an economically important species which is widely distributed from coasts of China, Japan, and Korea (Wang, 1997). In China, it is distributed along the coast of the Bohai Sea, the Yellow Sea and the Southeast China Sea (Li et al., 2012).

M. coruscus has only been cultivated in a few regions of China and the first hatchery stock was developed in Zhejiang province and about 50,000 tons of *M. coruscus* are currently harvested in Zhejiang per year (Ye, 2012). In recent years, due to overexploitation, the proportion of naturally-born larvae has decreased and the germplasm resources of mussel aquaculture are shrinking and degenerating because of lacking genetic variability of germplasm resources and inbreeding (Zhou, 2009). Proper management and breeding programs must be implemented to preserve genetic variability and prevent inbreeding depression. However, for such programs to be successful, the information on the genetic relationships among cultured and wild populations is needed. Understanding the genetic aspects of geographic variation and population structure of

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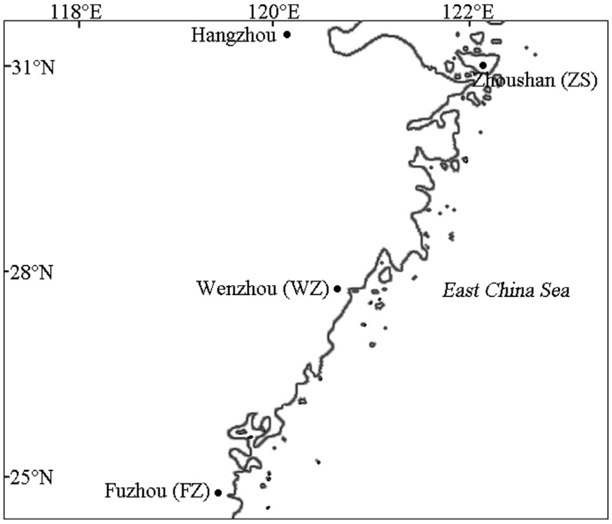

Fig. 1. Map illustrating the locations of six *M. coruscus* populations in three geographical positions studied. ZS: Zhoushan wild population (ZSw) and cultured population (ZSc) (Zhejiang Prov.), WZ: WZw and WZc (Zhejiang Prov.), and FZ: FZw and FZc (Fujian Prov.).

M. coruscus can provide important biological information for avoiding reduction of genetic diversity due to genetic drift and inbreeding in farmed strains of small population size (Allendorf, 1986; McGinnity et al., 2003).

Genetic markers, in particular the sequences of mitochondrial DNA (mtDNA), have proven to be very informative in the genetic structure and gene flow (Lakra et al., 2010; Gonzalez et al., 2012; Han et al., 2012; Liu et al., 2012; Xu et al., 2012). Because of maternal inheritance, absence of intermolecular genetic recombination, a fast evolutionary rate relative to nuclear DNA, the availability of efficient PCR primers, and a wealth of comparative data (Barrette et al., 1994), mtDNA has been extensively used for studying population structure, phylogeography and phylogenetic relationship at various taxonomic levels (Xu et al., 2009). Sequences encoding mitochondrial cytochrome oxidase subunit I (COI) are shown to be appropriate for intraspecific analysis due to the high degree of polymorphism observed (Árnason et al., 1993; Hu et al., 2008).

In this report, partial sequences of mtDNA-COI gene of 84 individuals of *M. coruscus* collected from six localities were sequenced. The sequence data were used to determine the levels of genetic variation within and between wild and cultured *M. coruscus* populations in the East China Sea.

2. Materials and methods

2.1. Sample collection and DNA extraction

A total number of 84 samples were collected from Zhoushan (Zhejiang Prov., ZS), Wenzhou (Zhejiang Prov., WZ) and Fuzhou (Fujian Prov., FZ), as shown in Fig. 1. Those individuals of *M. coruscus* are distributed in six different populations in three geographic locations. There are a farmed strain and a wild source population in each locality.

Genomic DNA was isolated from adductor using the standard proteinase K digestion and phenol/chloroform extraction procedures described by Ye et al. (2012a). DNA quality was assessed by running samples on 1% agarose gels, and DNA

Table 1
Collection sites, number of individuals per sampling site (*n*) and summary statistics of genetic variability for *M. coruscus*.

Populations	Code	No.	Haplotypes																									
			H1	H2	H3	H4	H5	H6	H7	H8	H9	H10	H11	H12	H13	H14	H15	H16	H17	H18	H19	H20	H21	H22	H23	H24	H25	H26
Zhoushan cultured strain	ZSc	11	1	5	1	1	1	1	1																			
Zhoushan wild strain	ZSw	10		3					1	1	1	1	1	1	1													
Wenzhou cultured strain	WZc	16		6				2								2	1	1	1	1	1	1						
Wenzhou wild strain	WZw	18		3	3						2	1				1							1	1	1	1	1	1
Fuzhou cultured strain	FZc	14		3												1												
Fuzhou wild strain	FZw	15		3							1					1												