



Population genetic structure of mantis shrimps *Oratosquilla oratoria*: Testing the barrier effect of the Yangtze River outflow



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ABSTRACT

In order to ascertain impact of freshwater outflow from the Yangtze River on the gene flow of coastal species, the population genetic structure of mantis shrimps *Oratosquilla oratoria* in the East China Sea and Yellow Sea was analyzed by the partial mitochondrial DNA 16S rRNA gene. A total of 124 individuals from seven localities in the East China Sea and Yellow Sea were collected and 31 haplotypes were detected, giving an overall haplotype diversity of 0.8193 ± 0.0272 and nucleotide diversity of 0.0036 ± 0.0022 . Two genetically divergent lineages were revealed, which displayed strong differences in the geographical distribution. Significant genetic differentiation between the East China Sea and Yellow Sea were also revealed by the results of AMOVA and pair-wise F_{ST} . The present result supported our hypothesis that barrier effect of the Yangtze River outflow on gene flow of coastal species depend on differentiation salinity tolerance of species. It demonstrated that genetic pattern of *O. oratoria* in the East China Sea and Yellow Sea may be attributable to the interplay between salinity and the species' life history traits.

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1. Introduction

In the Northwestern Pacific, the separation of the sea basins during the Pleistocene glaciers was recognized as important environment barrier to dramatically influence the current genetic structure of various marine species (Liu et al., 2007; Ni et al., 2014). However, besides historical events, recent studies revealed that contemporary environment factors also played an important role in shaping population genetic structure of marine species (Ni et al., 2012). As the third largest river in the world, Yangtze River pours into the East China Sea with an average annual discharge of 924 billion m^3 (Su and Yuan, 2005). The front area of the freshwater plume in summer can reach about 100 km away from the river mouth, with salinities between 25 and 30 (Zhou et al., 2008). Freshwater outflow from the Yangtze River has been assumed as a major barrier for the genetic connectivity of some coastal species (Beardsley et al., 1985; Dong et al., 2012; Han et al., 2015a). However, Ni et al. (2012) pointed out that the barrier effect of the Yangtze River outflow was not validated for some bivalve species with broad salinity tolerance, which had the abilities to maintain gene exchange between populations of both estuary sides.

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Thereby, the barrier effect of the Yangtze River outflow on gene flow of coastal species might depend on differentiation salinity tolerance in species. The marine species with the biological character of sensitivity to low salinity might be influenced by the Yangtze River outflow.

To test this hypothesis, mantis shrimp *Oratosquilla oratoria* widely distributed in the East China Sea and Yellow Sea, was served as a model species to ascertain the barrier effect of the Yangtze River outflow in shaping the genetic structures of marine species. Two biological characteristic may influence the population structure of *O. oratoria*, resulting in different genetic patterns. Larvae of *O. oratoria* have a long planktonic stage of between 36 and 59 days (Hamano and Matsuura, 1987). Considering the long planktonic stage, the degree of genetic differentiation among populations of *O. oratoria* is expected to be low. On the other hand, *O. oratoria* is a euryhaline species, but it is sensitive to low salinity. It can tolerate the salinity ranging from 20 to 40 and larvae of *O. oratoria* almost stopped feeding at a salinity of lower than 15 (Liu et al., 2006, 2012). The biological characteristic for sensitive to low salinity might indicate that low salinity caused by influx of river will be physical barrier for the dispersal of larvae and induce genetic differentiation. Previous genetic study of *O. oratoria* in Hong Kong has given some evidence, revealing genetic heterogeneity among populations over a small spatial scale (Lui et al., 2010). The genetic heterogeneity between western and eastern waters of Hong Kong could be attributed to low salinities (average salinity: 10 to 20) due to the summer discharge of freshwater from the Pearl River. Moreover, *O. oratoria* is an important economic resource, confirmation of whether or not different genetic stocks occur in the East China Sea and Yellow Sea would represent a great contribution to conservation policies and population management.

In order to test the barrier effect of the Yangtze River depending salinity tolerance of species, we surveyed the phylogeographical structure of *O. oratoria* in the East China and Yellow Sea by analysis of mitochondrial DNA 16S rRNA gene. By addressing these issues, we expect to gain better understanding of the genetic distribution as well as evolutionary mechanisms for marine coastal species in the Northwestern Pacific.

2. Materials and methods

2.1. Sample collection

From 2011 to 2015, one hundred and twenty four individuals of *O. oratoria* were collected from seven geographic locations from the East China Sea and Yellow Sea (Fig. 1 and Table 1). Muscle samples were obtained and preserved in 95% ethanol or frozen for subsequent DNA extraction. Two individuals of *Erugosquilla woodmasoni* were collected from Zhanjiang, Guangdong Province, China to serve as an out group for phylogenetic analyses.

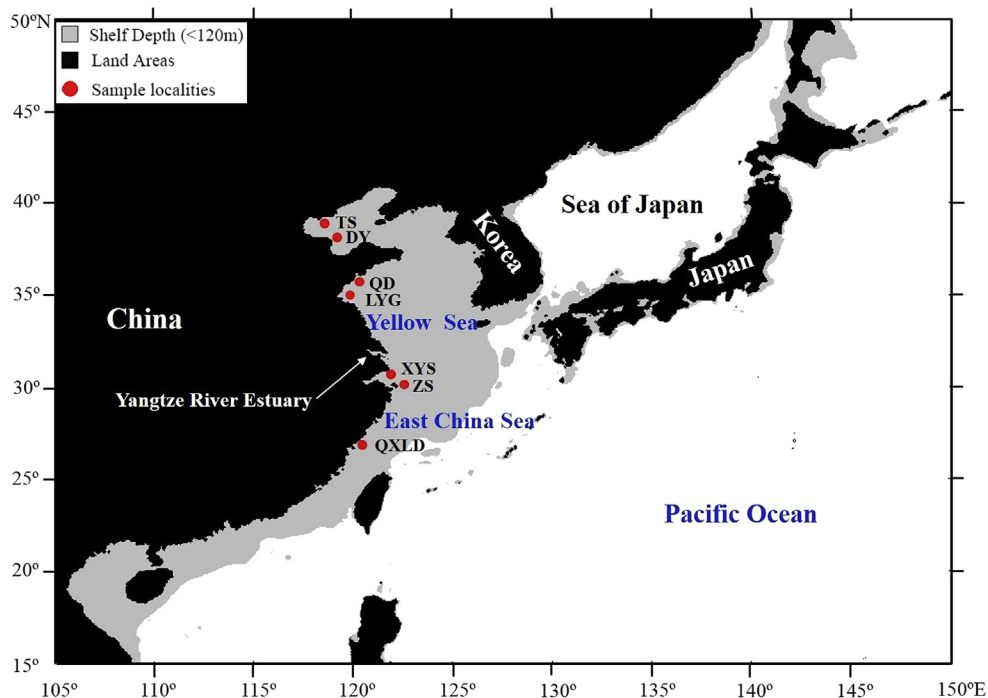


Fig. 1. Map showing sample locations of *Oratosquilla oratoria*, samples are marked by abbreviations that correspond to Table 1. Shaded sea areas are continental shelves that would have been exposed to the air during periods of low sea level.

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