

Conservation Genetics of the Crab *Portunus trituberculatus* in China

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Abstract

Portunus trituberculatus is the most widely fished species of crab in the world, with 98% of the catch coming off the coast of China. In order to effectively manage this important fishery it is crucial to identify the limits of populations or stocks of this species. We sampled crabs from three locations off the coast of China: Bohai Sea, Yellow Sea, and Eastern China Sea. We genetically characterized these three populations using Amplified Fragment Length Polymorphisms (AFLPs). A total of 60 individuals (20 per population) were analyzed using 10 primer combinations; and 466 loci were obtained, 360 of which were polymorphic. We conducted population genetics analyses using the software programs TFPGA, PopGene V1.31, GenAlEx6.3, and STRUCTURE V2.2, to determine genetic diversity and whether genetic population structure occurs. Our results indicate a high-level of genetic diversity within each population. High genetic differentiation is observed between the Bohai Sea population and the other two populations. A lower degree of genetic differentiation, yet significant, is observed between the Yellow Sea and Eastern China Sea populations. Our results have important implications for the management of this fishery, as they indicate each locality constitute a different stock or population.

Materials and Methods

We collected *P. trituberculatus* individuals at three localities in the Eastern coast of China (Figure 1).

We extracted DNA from 20 individuals per locality and genotyped each using Amplified Fragment Length Polymorphisms (AFLPs). We used 10 EcoRI and MseI selective primer combinations.

We estimated the percentage of polymorphic bands, within-population gene diversity (H_s), Nei's gene diversity (h), and Shannon's gene diversity index (SI) for each population.

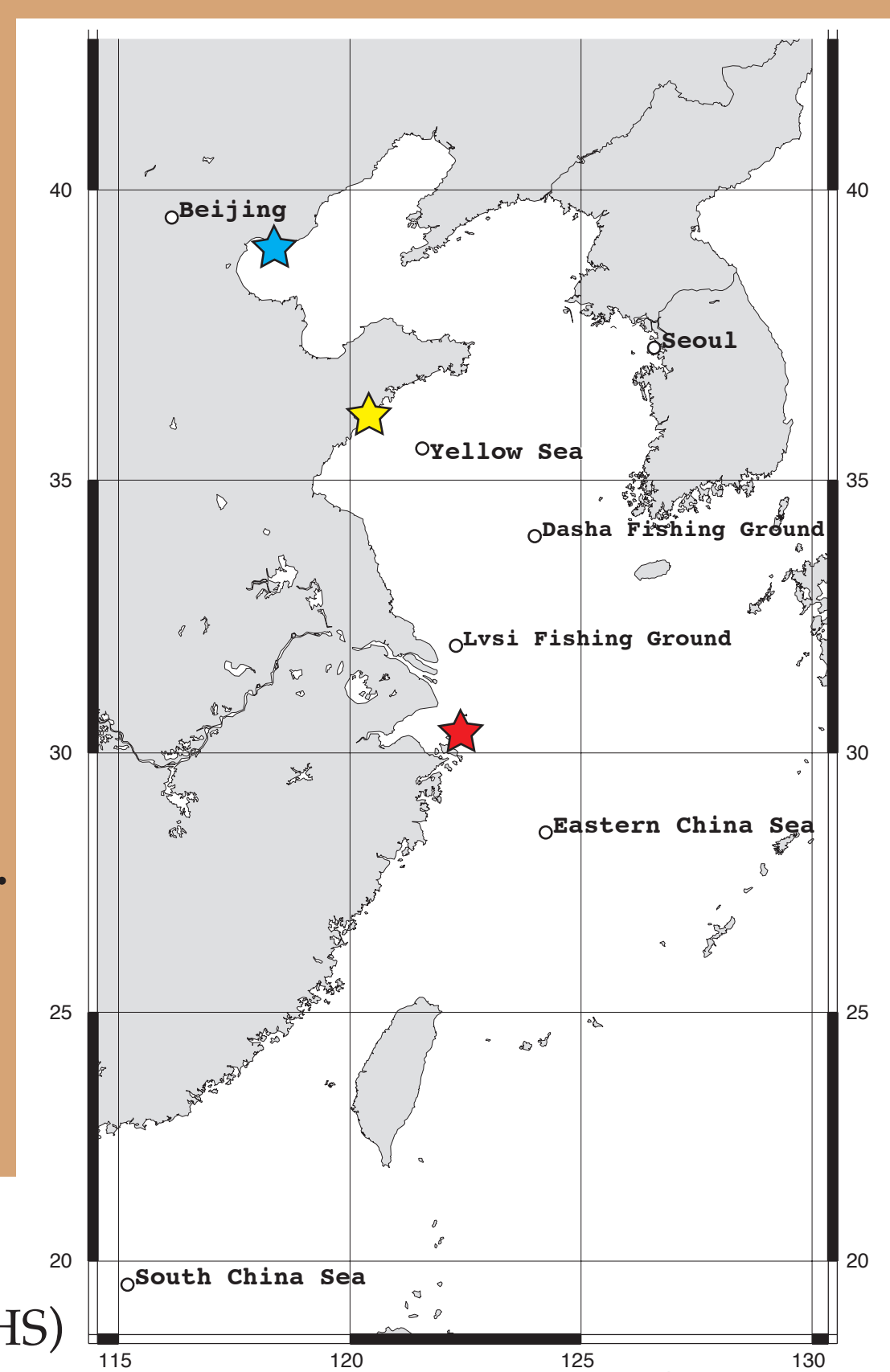
To examine genetic differentiation among populations, we calculated F_{st} , and conducted a Principal Coordinates Analysis (PCA) using the program GenAlExv.6.3 and a Bayesian population structure analyses using the program STRUCTURE. To determine K (number of clusters), we used the program STRUCTURE HAREVESTER V 0.56.4.



Fig. 2. The Japanese Speckled Crab *P. trituberculatus*.

- ★ Bohai Sea (BHS)
- ★ Yellow Sea (YS)
- ★ Eastern China Sea (EHS)

Fig. 1. Sampling locations of *P. trituberculatus*. A total of 60 individuals were collected at three locations in the Eastern coast of China, 20 in each: Bohai Sea (BHS), Yellow Sea (YS), and Eastern China Sea (EHS)



Results and Discussion

Table 1. Genetic diversity. Total number of bands (N), number of polymorphic bands (N_{Pol}), and percentage of polymorphic bands ($\%N_{Pol}$) for each population. Gene diversity in each population is reported as gene diversity within population (H_s), Nei's diversity (h), and the Shannon's gene diversity index value (SI). Overall, populations show a high degree of genetic diversity across all measures.

	N	N_{Pol}	$\%N_{Pol}$	H_s	h	SI
BHS	363	277	59.83	0.2504	0.2510	0.3678
YS	457	329	71.99	0.2598	0.2598	0.3822
ECS	459	290	63.18	0.2483	0.2483	0.3688

Table 2. Pairwise F_{st} comparisons.

	YS	ECS
BHS	0.134	0.133
YS		0.091

Fig 3. Bayesian population structure analysis using STRUCTURE. $K=3$ has the highest likelihood.

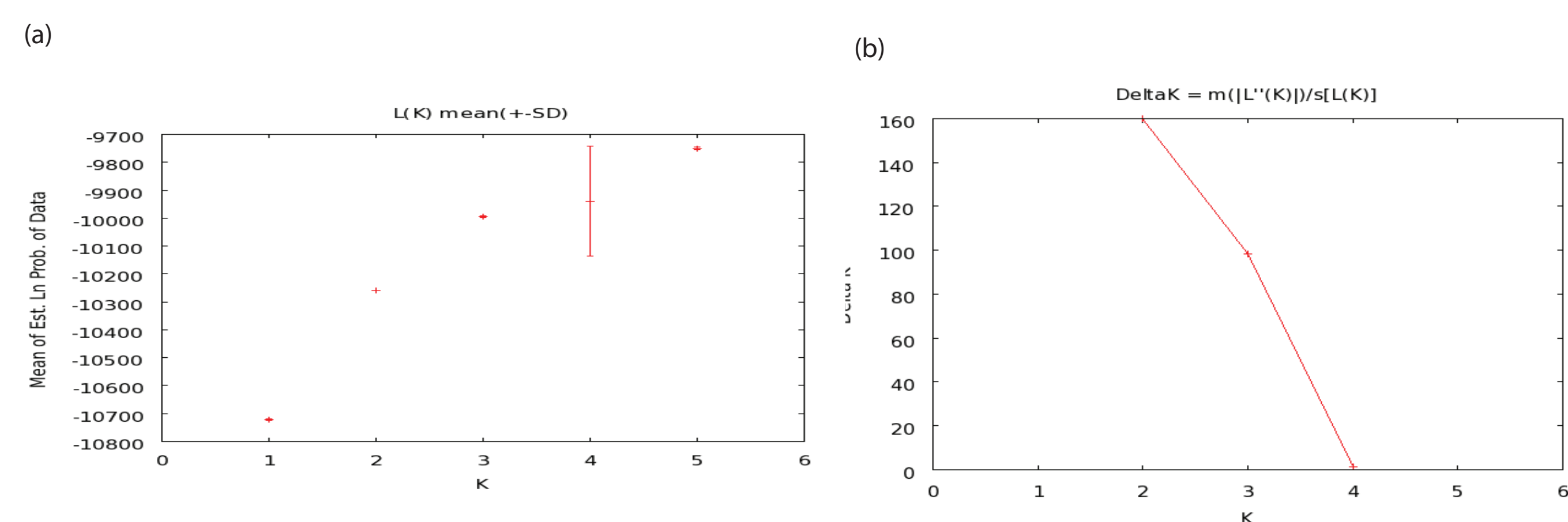
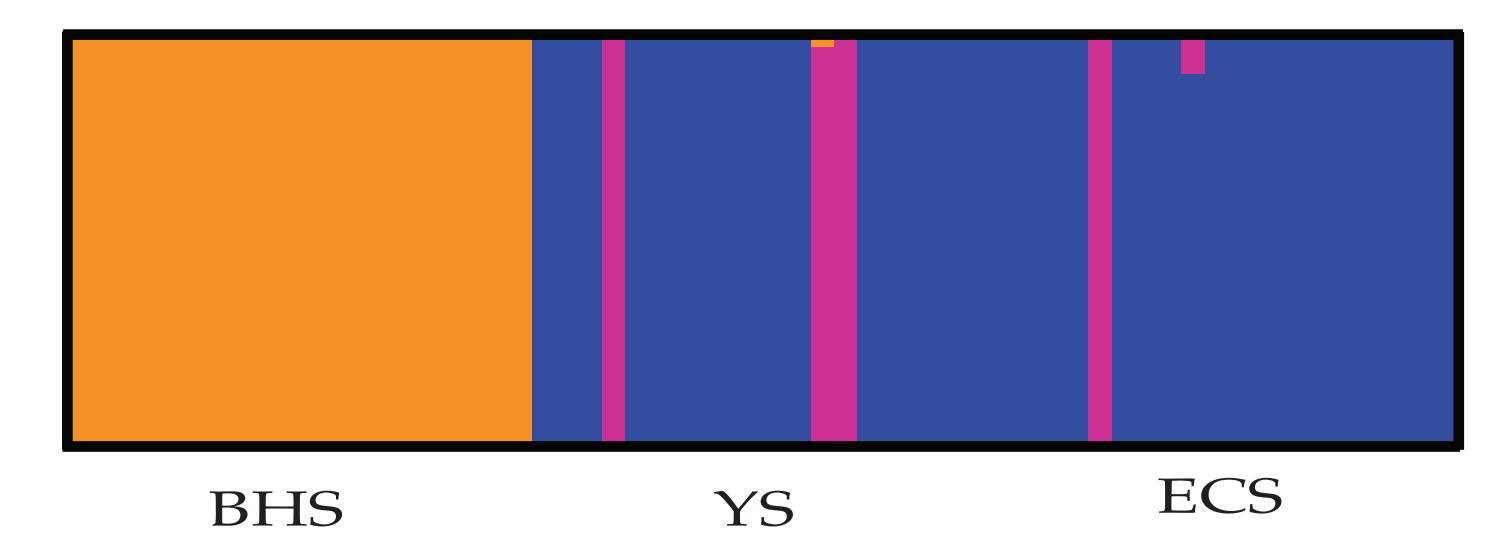
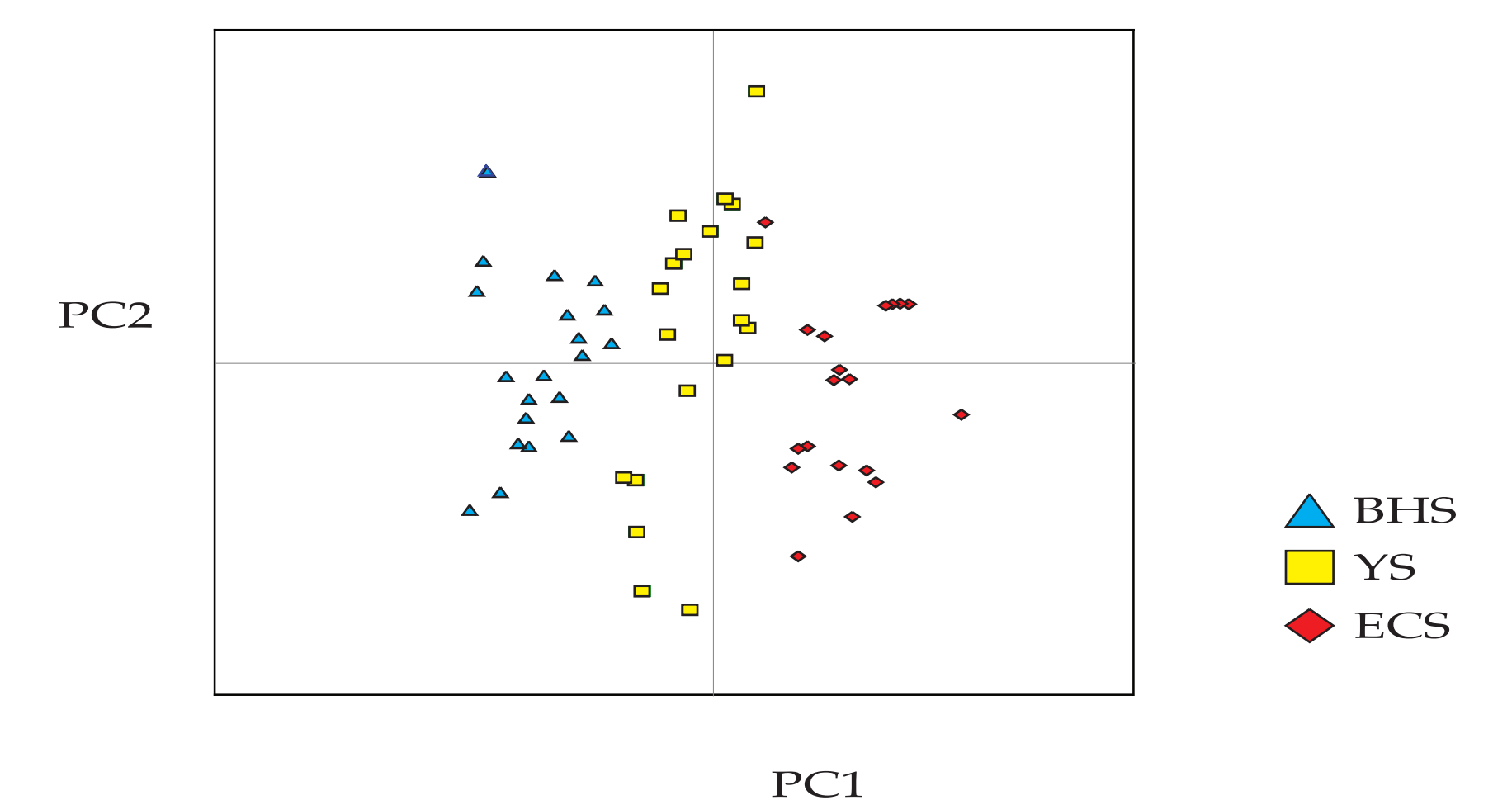


Fig 4. STRUCTURE HARVESTER analysis for K . (a) After $K=3$ the increase in the ln-likelihood plateaus and increases slightly. (b) Delta K shows that $K=3$ is the breakpoint of the curve.

Fig 5. PCA Results. Three clusters are defined along the PC2 axis, with overlap almost non-existent for the exception of one ECS individual that seems similar to YS.



Our results indicate a high-level of genetic diversity within each population. We observed high values for H_s , h , and SI , and a large number and proportion of polymorphic bands.

Significant genetic differentiation is observed between the Bohai Sea population and the other two localities; while a lower F_{st} value, yet significant, is observed between the Yellow Sea and Eastern China Sea populations. STRUCTURE analyses suggest also the Bohai Sea constitutes a different population, but show no differentiation between the Yellow Sea and the Eastern China Sea populations. However, PCA identifies a separate cluster for each population.

Our results suggest that each locality represent a different genetic stock, thus, we recommend they should be managed independently.

Acknowledgments

This work is part of National Marine Environment Investigation in China (908). Thanks to the Lab mates in Tianjin Fisheries Research Institute and special thanks to Carlos A. Santamaria for assistance in the study.