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Population genetic structure of the ark shell *Scapharca broughtonii* Schrenck from Korea, China, and Russia based on COI gene sequences

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1. Introduction

Recently, the use of mitochondrial DNA (mtDNA) has a high resolution of molecular phylogenesis, population genetics, and conservation, in which detection of polymorphism for natural populations is necessary. The cytochrome c oxidase subunit I (COI) gene of mtDNA is conservative, and is one of the most conserved protein-encoding genes in the mitochondrial genome (Brown, 1985). The population genetic structure of shellfish using the mtDNA COI gene has been studied (An et al., 2000; Arnaud et al., 2000; Kim et al., 2000; Lee and Kim, 2003; Matsumoto, 2003), while the genetic understanding between strains and geographic areas for the ark shell has been limited. Our objectives were as follows: (1) to analyze genetic population structure, (2) to estimate levels of gene flow in the ark shell at geographically separate regional populations, and (3) to characterize the genetic diversity within local populations. A test of genetic population structure allows us to determine which ark shells have formed a large genetic group or not. We can also attempt to answer the following questions: Are the ark shell belonged to a single phylogenetic group? What is the extent and nature of genetic variation among geographical populations?

2. Materials and Methods

Phylogenetic analysis was performed by parsimony method incorporated in PHYLIP (Phylogeny Inference Package) ver. 3.5c (Felsenstein., 1993) as a subprogram NEIGHBOR. To obtain the genetic tree, the data set was iterated 1,000 times using a subprogram SEQBOOT. Individual trees from each iterated data set were obtained using the subprogram DNAMLK with the option of Kimura's 2-parameter method (Kimura, 1980), which attempts to correct observed dissimilarities for multiple substitutions in

sequences evolving with a transition bias. A consensus tree representing reliability at each branch in the tree was obtained using the subprogram CONSENSE. To investigate the magnitude and pattern of genetic diversity within localities, genetic diversity and mean number of pairwise differences among haplotypes, gene diversity, and nucleotide diversity were calculated using Arlequin ver 1.1 (Schneider et al., 1996). Mean number of differences between all pairs of haplotypes in the sample was obtained by considering the number of mutations having occurred since the divergence of any two haployptes, and the frequency of the ones involved in the calculation. Nucleotide diversity was calculated by estimating the probability that two randomly chosen homologous sequences will be different (Nei, 1987).

4. Results and Discussion

The hierarchical relationship among the populations analyzed by the Holsinger and Mason- Gamer (HM-G) method (1996) was shown in Fig. 1. The six Korean localities were grouped together with neighboring ones: Jinhae (locality 6) differentiated from localities 1, 4, 3, and 2 (genetic distance d=0.325). On the basis of the deeper node, d in some nodes [Gamak (locality 1), Dukyang (locality 4), Taean (locality 3) and Namhae (locality 2)] was negative, suggesting that the ark shell found in those waters appears to form one large and close genetic group regardless of their geographic barriers. Although Korean localities were separated with Russian and Chinese localities based on genetic distance (d=0.275 and d=0.349, respectively), statistically significant structuring was not found (p=0.022 and p=0.013, respectively).
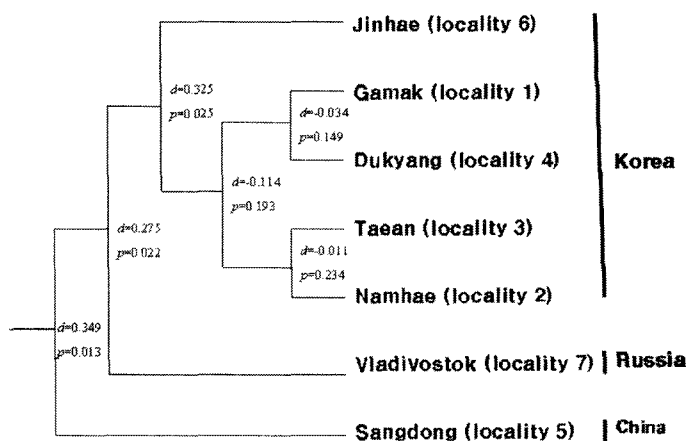

Fig. 1. Hierarchical genetic relationships among localities analyzed using Holsinger and Mason-Gamer method (1996). The value at each node is the genetic distance (d) between its two daughter nodes and the pvalue is the significance of differentiation based on 10,000 random re-sampling.

5. Conclusion

The analysis of mitochondrial COI gene sequences of the ark shell to understand population genetic structure of the ark shells showed that the ark shell populations in Korea were formed of individuals randomly dispersed over geographic areas and that the gene flows between populations were relatively high. However, we found that Jinhae (locality 6) was a genetically distinct population that was different based on the estimation of geographical distance, population structure, and variance analysis. Yet, statistically significant differences could be not given. We also detected considerable genetic differences between the Korean, Chinese and Russian populations, suggesting the continued existence of heterogeneity between groups across geographically distant regions. This kind of study will be used as a source for the broad understanding of invading marine species and their effect on the ecology of native species.

References

An, H. S., Jee, Y. U., Park, D. W., Ryu, H. Y. and Min, K. S., 2000. Genetic variation in populations of the pacific oyster (*Crassostrea gigas*), based on the mitochondrial COI gene sequence, Korean J. Genetics, 22, 249-255.

Aranishi, F. and Okimoto, T., 2005, Sequence polymorphism in a novel non-coding region of Pacific oyster mitochondrial DNA, J. Appl. Genet., 46, 201-206.

Arnaud-Haond, S., Bonhomme, F. and Blanc, F., 2003, Large discrepancies in differentiation of allozymes, nuclear and mitochondrial DNA loci in recently funded pacific populations of the pearl oyster *Pinctada margaritifera*, J. Evol. Biol., 16, 388-39.