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Geographic Variation in Gizzard-shad (*Konosirus punctatus*) Populations

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Introduction

Gizzard-shad (Konosirus punctatus) live in Korea, Japan, the South China Sea, and the Gulf of Pohai and throughout the world. Korean seawater fish gizzard-shad is one species of an ecologically important fish species, belonging to the family Clupeidae, and the order Clupeiformes. Particularly in autumn, the gizzard shad gain fat and attain an excellent chewy texture. The Gizzard Shad Festival is aimed to introduce the superior specialties of our region and distribute the fresh seafood directly to the consumers at low prices, in order to contribute to the profitability of the local dwellers and the long-term development of the region. the potential of RAPD to identify diagnostic markers for breed, stock, species and population identification in teleosts (Partis and Wells 1996; Yoon and Kim 2004; Siti Azizah et al., 2005), and in shellfish (Klinbunga et al. 2000b; Kim et al. 2004) has been demonstrated. Our study attempts to elucidate the genetic distances and differences within and among gizzard-shad geographical populations. We performed clustering analyses of three populations of gizzard-shad (K. punctatus) in the in Seocheon, Busan and Gochang regions of Korea.

Materials and methods

Three geographical populations of gizzard-shad (K. punctatus) were obtained from three different regions in Korea: Seocheon, Busan and Gochang in three coastal areas of Korea. Gizzard-shad muscle wascollected in sterile tubes and stored at -40? until needed. RAPD analysis was performed on the muscle extract of 30 individuals using eight arbitrarily selected primers. Optimal DNA concentrations for amplification were determined by testing several dilutions, one of which was taken as the standard for every subsequent amplification. The electrophoresed agarose

gels were illuminated by ultraviolet rays, and photographed using a Photoman direct copy system (PECA Products, Beloit, WI, USA). Using similarity matrices to generate a dendrogram, facilitated by the PC-package program Systat version 10 (SPSS Inc., USA), produced the hierarchical clustering tree. Euclidean genetic distances within- and between-populations were also calculated using the hierarchical dendrogram program Systat version 10.

Results and summary

Genomic DNA samples isolated from three geographical gizzard-shad (Konosirus punctatus) populations in Seocheon (Seocheon SC), Busan (Busan BS) and Gochang (Gochang; GC) collected in the West Sea, off the Korean Peninsula, were PCR-amplified repeatedly. Eight decamer and 20-mer primers generated a total of 713 fragments in the SC population, 791 in the BS population, and 732 in the GC population, with a DNA fragment size ranging from 100 to 2,800 bp. We identified 50 unique fragments for the SC population, 70 unique fragments for the BS population and 130 for the GC population: 120 shared fragments for the three populations. There were 108 specific fragments (15.1%) for the SC population, 74 (9.4%) for the BS population, and 67 (9.2%) for the GC population. Eight primers also generated 48 polymorphic fragments (6.7%) for the SC population, 26 (3.3%) for the BS population, and 16 (2.2%) for the GC population. The similarity matrix ranged from 0.756 to 0.936 for the SC population, from 0.800 to 0.938 for the BS population, and from 0.731 to 0.959 for the GC population. Using various decamer and 20-mer primers, RAPD-PCR may be applied to identify specific/polymorphic markers that are particular to a species and geographic population, and to define genetic diversity, polymorphisms, and similarities among geographical gizzard-shad populations.

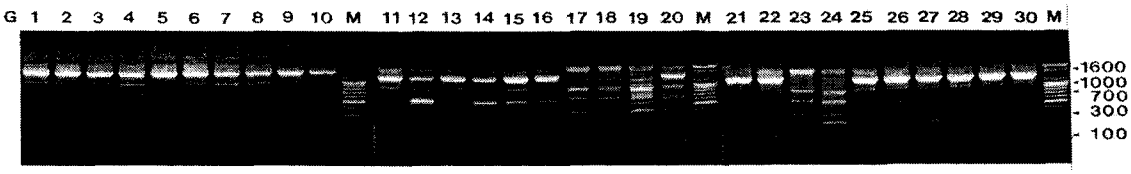

Figure 1. RAPD-PCR-generated electrophoretic profiles of individual gizzard-shad (K. punctatus) of three geographic populations. DNA isolated from Seocheon (lane 1 ~ 10), Busan (lane 11 ~ 20) and Gochang (lane 21 ~ 30) were amplified by random primers BION-01 (A), BION-03 (B), BION-06

(C), BION-11(D), BION-13 (E) BION-14 (F) BION-19(G) and URP-01(H).

References

Kim, J. Y., C. Y. Park, and J. M. Yoon. 2004. Genetic differences and DNA polymorphism in oyster (Crassostrea spp.) analysed by RAPD-PCR. Korean Journal of Genetics 26: 123-134.

Klinbunga, S., A. Boonyapakdee, and B. Pratoomchat. 2000b. Genetic diversity and species-diagnostic markers of mud crabs (*Genus Scylla*) in Eastern Thailand determined by RAPD analysis. Marine Biotechnology 2: 180-187.

Partis, L. and R. J. Wells. 1996. Identification of fish species using random amplified polymorphic DNAMolecular and Cellular Probes 10: 435-441.

Yoon, J. M. and J. Y. Kim. 2004.Genetic differences within and between populations of Korean catfish (*S. asotus*) and bullhead (*P. fulvidraco*) analysed by RAPD-PCR. Asian-Australasian Journal of Animal Sciences 17: 1053-1061.

Siti Azizah, M. N., A. Ruzainah and I. Patimah. 2005. Development of RAPD markers in the eel-loach (*Pangio* spp.) for genetic discrimination and monitoring of wild and cultured populations. World Aquaculture 36 (1): 37-43.