Genetic Distance and Variation in Tiger Crab (Orithyia sinica) and Fiddler Crab (Gelasimus arcuatus)

Jong-Man Yoon*, Su-Young Park and Yong-Ho Kim1

*Department of Aquatic Life Medicine, and 1Department of Marine Aquaculture and Biotechnology Kunsan National University, Kunsan City, Jeollabuk-do, 573-701, Korea

Introduction

We have investigated two species of crabs; one is tiger crab, and the other fiddler crab. Tiger crab (O. sinica) is one of environmentally important species, belonging to the family Calappidae, and the order Decapoda. The crab is also indigenous to some parts of the southern regions of the West Sea. In recent years the feasibility of commercial culture investigated in a recently begun project at a few of aquaculture centers and national fisheries experimental stations. Accordingly, researches need to have been made for the promotion of higher productivity in this crab. The other species of fiddler crab (G. arcuatus) is an environmentally and economically important species, belonging to the family Ocypodidae, and the order Decapoda. Fiddler crab is widely distributed in the entirety of estuary flat, brackish-water habitats, a field of reeds and seawater areas of the West Sea and South Sea in Korean Peninsula. The crabs inhabit in the estuary flats consisting of a lot of mud, sand and slime in the coastal tidal wetland where the freshwater is flowed temporarily. Many molecular and/or genetic researches have used this technique, because RAPD-PCR is an easy, reliable and relatively quick method for the investigation of numerous genomic DNAs with respect to genetic diversity in a population (Welsh and McClelland 1990; Orozco-Castillo et al., 1994). As the crab culture industry increases, the understanding of the genetics of thiscrab species becomes more necessary to evaluate the potential genetic effects induced by crabproduction operations. Our study attempt is to elucidate the genetic distances and differences within and between tiger crab (O. sinica) and fiddler crab (G. arcuatus) from Buan.

Materials and methods

Two species of tiger crab (O. sinica) and fiddler crab (G. arcuatus) were obtained from Buan in close vicinity to the West Sea in Korea. Two species of crab's muscle was collected in sterile tubes, placed on ice immediately, and stored under refrigeration until needed. Amplification products were generated via electrophoresis on 1.4% agarose (VentechBio, Korea) gel containing TBE. The electrophoresed agarose gels were stained by ethidium bromide solution, illuminated by ultraviolet rays, and photographed using a Photoman direct copy system (PECA products, USA). The 100 bp Ladder marker (Bioneer Co., Korea) was used as a DNA molecular weight marker. Using similarity

matrices to generate a dendrogram, facilitated by the PC-package program Systat version 10 (SPSS Inc., USA), a hierarchical clustering tree was constructed. Genetic differences and Euclidean genetic distances within and between populations were also calculated using the Systat hierarchical dendrogram program version 10.

Results and summary

Out of various decamer primers, the five arbitrarily selected primers OPA-09, OPA-13, OPB-15, OPB-17 and OPD-18 generated the common, specific, and polymorphic fragments. The similarity matrix ranged from 0.425 to 0.967 in the tiger crab species, and from 0.483 to 0.953 in the fiddler crab species. The average bandsharing value between the two crab species 0.619 0.010, ranged from 0.291 to 0.847. 183 fragments were identified in the tiger crab species from Buan, and 146 in the fiddler crab species from Buan: 58 polymorphic fragments (31.7%) in the tiger crab and 45 (30.8%) in the fiddler crab species. 33 common fragments(18.0%), with an average of 6.6 per primer, were observed in the tiger crab species. 55 fragments (37.7%), with an average of 11.0 per primer, were identified in the fiddler crab species. The numbers of polymorphic fragments in tiger crab species and fiddler crab were 7 (3.8%) and 7 (4.8%), respectively. The dendrogram obtained by the five primers indicates three genetic clusters. Ultimately, the longest genetic distance displaying significant molecular differences was found to exist among individuals in the two crab species, between individual TIGERCRAB no. 02 and TIGERCRAB no. 07 (0.511).

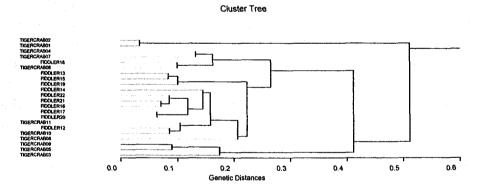


Fig. 1. The relatedness between different individuals in the tiger crab (O. sinica) and fiddler crab (G. arcuatus) from Buan was generated according to the bandsharing values and similarity matrix.

References

Orozco-Castillo, C., K. J. Chalmers, R. Waugh and W. Powell. 1994. Detection of genetic diversity and selectivegene introgression in coffee using RAPD markers. Theoretical and Applied Genetics. 87: 934-940.

Welsh, J. and M. McClelland. 1990. Fingerprinting genomes using PCR with arbitrary primers. Nucleic Acids Research 18: 7213-7218.