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Genetic Differences between Cultured and Wild Penaeid Shrimp (*Penaeus chinensis*) Populations Analysed by RAPD-PCR

Jong-Man Yoon[1*], Ee-Yung Chung[2] and Gye-Woong Kim[3]

[1]Department of Marine Biomedical Science, College of Ocean Science and Technology, Kunsan National University, Kunsan City, 573-701, Korea
[2]Department of Marine Aquaculture and Biotechnology, College of Ocean Science and Technology, Kunsan National University, Kunsan City, 573-701, Korea
[3]Department of Animal Resources Science, College of Industry Science, Kongju National University, Yesan-kun, 340-802, Korea

INTRODUCTION

Penaeid shrimp (*Penaeus chinensis*), economically important aquacultural species, belonging to family Penaeidae including genus Fenneropenaeus, widely inhabit the West Sea and South Sea in the Korean Peninsula and the Gulf of Pohai in China under the natural ecosystem. Consequent of the rapid increase in seed production, there is a need to understand the genetic traits and composition of this fish species in order to evaluate exactly the patent genetic effects induced by seed production operations. Thus, the applications of RAPD to aquaculture had been to identify genetic similarity and difference among a few of fish species and/or invertebrates apart from geographic sites (Callejas and Ochando, 1998; Mamuris et al., 1999). This research was made by RAPD-PCR and also by hierarchial clustering analysis based on the RAPD data in order to elucidate genetic differences between cultured and wild penaeid shrimp populations from Kunsan.

MATERIALS AND METHODS

Muscle collection, sources of genomic DNA, decamer primers and molecular markers

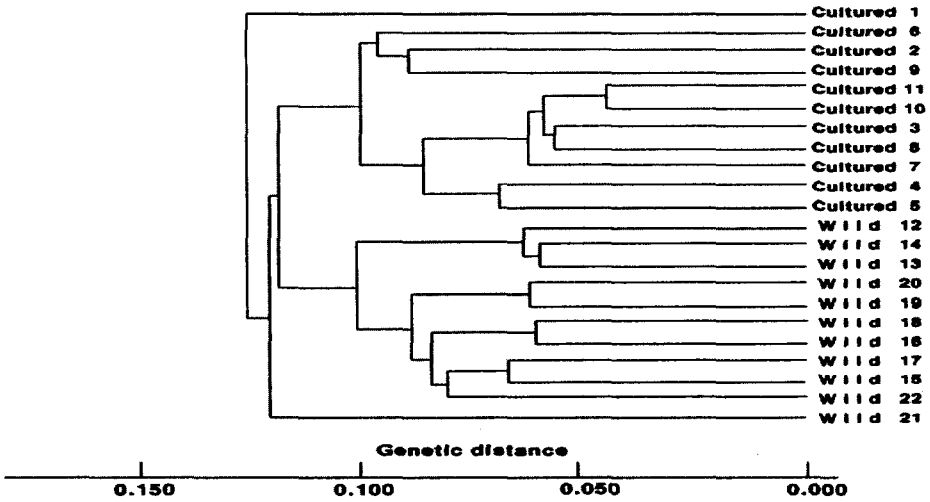
Muscle tissues were collected separately from penaeid shrimp (*Penaeus chinensis*) from Kunsan. RAPD-PCR analysis was performed on DNA samples extracted from a total of 23 individuals using seven of decamer primers of two decades of different random primers. First of all, in order to obtain reliable and reproducible results, DNA extraction should be carried out according to the separation and extraction methods (Yoon and Park, 2001).

Amplification conditions and analytical methods

Two decades of decamer primers (5′ to 3′) obtained from Operon Technologies, USA. Of the 20 arbitrary primers, seven decamer primers showing reproducible and clearly scorable, polymorphic and specific fragments, were used to identify genetic similarity and difference. RAPD-PCR was performed using a DNA Thermal Cycler (Perkin Elmer Cetus, USA) according to protocol. Hierarchial clustering was analysed on the similarity matrices in order to generate a dendrogram using pc-package program Systat version 10 (SPSS Inc., USA). Genetic distances (Euclidean distances) within- and between-population were calculated with dendrograms produced with Systat version 10.

RESULTS AND DISCUSSION

In the present study, seven primers generated 102 polymorphic fragments (32.2% of a total of 317 fragment) in cultured population and 148 (38.4% of 385 fragments) in wild population, respectively. Overall, these results illustrated a large number of polymorphic fragments detected per primer and suggested high genetic variation in penaeid shrimp population from Kunsan. The shortest genetic distance (0.046) displaying significant molecular differences was between Cultured No. 11 and No. 10. The shortest genetic distance (0.059) displaying significant molecular differences was also between Wild No. 14 and No. 13.



<Fig. 1> Hierarchial dendrogram of genetic distances showing the relatedness among different individuals of cultured penaeid shrimp population (Cultured 1 ~ Cultured 11) and wild (Wild 12 ~ Wild 22) generated according to the similarity matrix.

The single linkage dendrogram resulted from reliable four primers, indicating five genetic groupings composed of group 1 (Cultured No. 1), group 2 (Cultured No. 6, 2 and 9), group 3 (Cultured No. 11, 10, 3, 8, 7, 4 and 5), group 4 (Wild No. 12, 14, 13,

20, 19, 18, 16, 17, 15 and 22) and group 5 (Wild No. 21). RAPD data analysis, including genetic distance and clustering analysis, were applicable for the study of genetic relationships among a few of species of the genus.

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