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Genetic Differences and DNA Polymorphism between Fleshy Prawn, *Fenneropenaeus chinensis* and Chinese Ditch Prawn, *Palaemon gravieri* Analyzed by RAPD-PCR

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Introduction

Shrimps and prawns are the most favored marine products in Korea due to its taste and nutrition, and the Korean people consume them in large quantities in the world. Among shrimps and prawns, the fleshy prawn (*Fenneropenaeus chinensis*) is one of economically important aquacultural species belonging to the family Penaeidae including genus Fenneropenaeus. Chinese ditch prawn (*Palaemon gravieri*) is widely distributed in the West Sea and South Sea in the Korean Peninsula as well as in the several areas of China under the natural ecosystem. The size and the type of the prawn varies according to their habitat such as the temperature, the depth of the water, the nutrition etc. However, in spite of their economic and scientific consequences, a little information currently exist regarding the genetics and early development of these two prawn speciesin Korea (Kim et al., 2004). Particularly, the clustering analysis of the genetic distance between various fishes and mollusks species or populations from the different geographic sites has been performed using RAPD-PCR is of little quantity (Yoon and Park, 2001). Here, to elucidate the genetic distances and the differences in prawns, we performed the clustering analysis of fleshy prawns and Chinese ditch prawns growing in the West Sea (Buan). Here, we also analyzed the genetic diversity of prawns in Korea.

Materials and methods

Fleshy prawn (*F. chinensis*) and Chinese ditch prawn (*P. gravieri*) growing in the West Sea was obtained from Buan. The muscle tissue of prawn was collected in sterile test tubes, placed the tubes in liquid nitrogen immediately, and stored until needed. RAPD-PCR was performed using two Programmable DNA Thermal Cyclers (Perkin Elmer Cetus, USA). DNA amplification was performed in a 25 l sample, containing 10 ng of template DNA, 20 l premix (Super-Bio Co., Korea), and the 1.0 unit primer. Amplification products were generated via electrophoresis on 1.4% agarose (VentechBio, Korea) gel containing TBE. The 100 bp DNA Ladder (Bioneer Co., Korea) was used as DNA molecular weight marker. The bands were detected by stainingwith ethidium bromide. The agarose gels electrophoresed were photographed by photoman direct copy system (PECA products, USA) under ultraviolet illumination. The average of within-population similarity is calculated by the pairwise comparison between individuals within a species. 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. Systat version 10 was also used to obtain other statistical results, including means, standarderrors, and t-test scores.

Results and summary

DNA isolated from fleshy prawn (*Fenneropenaeus. chinensis*) and Chinese ditch prawn (*Palaemon. gravieri*) obtained from Buan in the West were amplified at several times by PCR. The size of DNA fragments generated by seven primers varies from 50 to 1,600 bp. Here, 358 fragments were identified in the fleshy prawn species from Buan and 301 in the Chinese ditch prawn species: 18 polymorphic fragments (5.03%) in the fleshy prawn species and 12 (3.99%) in the Chinese ditch prawn species. 66 common fragments, the average 9.4 per primer, were observed in the fleshy prawn species and 44 fragments, the average 6.3 per primer, in the Chinese ditch prawn species. The number of specific fragments in the fleshy prawn species and Chinese ditch prawn species was 38 and 47, respectively. In the fleshy prawn species from Buan, the 11 identical banding patterns generated by the primer OPA-12 were observed in approximately 500 bp, which were identical (Fig. 1). The primer, OPA-12, notably produced the highest number of fragments, a total of 74, although the average was 6.7. 2 specific and 3 polymorphic major and/or minor bands generated by random primer OPB-04. The dendrogram obtained by the seven primers, indicates seven genetic clusters. The genetic distance between two prawn species ranged from 0.071 to 0.642. RAPD-PCR analysis has revealed the significant genetic distance between two prawn species pairs.

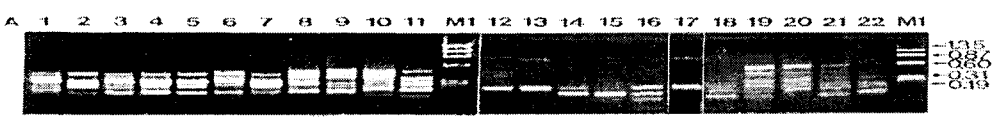

Fig. 1. RAPD-PCR-generated electrophoretic profiles of fleshy prawn (*F. chinensis*) and Chinese ditch prawn (*P. gravieri*).

References

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