PE-3

Genetic Similarity and Difference of Marsh Clam (*Corbicula leana*) Obtained by RAPD-PCR

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ABSTRACT

Genomic DNA from the muscle of marsh clam (*Corbicula leana*) from Gochang was extracted in order to identify genetic differences and similarity by randomly amplified polymorphic DNAs-polymerase chain reaction. 3.28 of the 23.0 polymorphic bands per lane were found to be polymorphic in marsh clam. Also, about 4.34% of total polymorphic bands were either specific to marsh clam. The major common bands of 0.28 kb generated by primer OPB-15 (GGAGGGTGTT) were present in every individuals, respectively, which were polymorphic. This common bands which present in every individuals should be diagnostic of specific strains, species and/or their relatedness. Primer OPB-19 (ACCCCCGAAG) produced the highest number of specific bands, which was 12. The specific minor band of 0.07 kb was present in lane 22, which were polymorphic. Especially, only a specific band (1.35 kb) identifying individuals was observed in lane 22.

INTRODUCTION

Marsh clam (*Corbicula leana*) is a commercially important mollusks species, which is distributed all over the Yellow Sea. This clam have been used as food materials of the broth to chase a hangover in Korea. By the way, as in other bivalve species, the wild marsh clam, population/density of this mollusks is decreased significantly owing mainly to imprudent tidal land reclamation project and reckless development during the last four decades. In spite of its economic and scientific importance, little information is available on the genetic relationships among a few of wild marsh clam populations in Korea. This research was made by RAPD-PCR using two decades of random primers and also by bandsharing analysis in order to identify genetic similarity and differences within populations in wild marsh clam (*Corbicula leana*) from Gochang.

MATERIALS AND METHODS

Muscle collection, Sources of genomic DNA, primer, amplification and data analysis

Muscle samples marsh clam (*Corbicula leana*) were obtained from a brackish water site in the periphery of Gochang in Korea. Samples of sliced muscle were placed into 10 ㎖ test tubes, to which an 4 volumes of lysis buffer I was added. In order to achieve good results,

DNA extraction should be performed according to the general separation and extraction procedures. The final concentration was estimated by agarose electrophoresis and EtBr staining. Bandsharing values of DNA products was quantified using the formula of Jeffreys and Morton (1987): If the comparison between the three lanes, the formula would be: BS = 3(Nabc)/ (Na+Nb+Nc) and so forth.

RESULTS AND DISCUSSION

The major common bands which present in every individuals should be diagnostic of specific strains, species and/or their relatedness. Primer OPB-19 (ACCCCCGAAG) produced the highest number of specific bands, which was 12. Also, the specific major band in the molecular weight in approximately 0.60 kb was observed in lane 2, 11 and 18 and also in lane 10, 13 and 20 (molecular weight, 1.08 kb). Especially, only a specific band (1.35 kb) identifying individuals was observed in lane 22. The Intra-population variation was revealed in the band patterns identified by this primer. This specific primer was also found to be useful in the individual identification of crucian carp, resulting from the different DNA polymorphism among individuals (Liu et al., 1998). The bandsharing values (BS) within marsh clam population from Gochang altered from 0.40 to 0.76 as calculated by bandsharing analysis, showing an average level of 0.58±0.04. Also, BS value generated by primer OPA-15 (GGAGGGTGTT) was higher than any other primers in marsh clam population, which was 0.76. Bandsharing values were calculated as an expression of similarity of RAPD polymorphic bands of animals from either the same or different breeds (Mohd-Azmi et al., 2000).

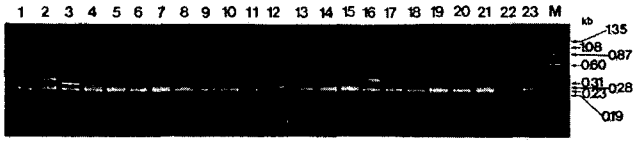

Fig. 1. Individual specific RAPD patterns (23 lanes) in marsh clam (*C. leana*) from Gochang amplified by primer OPB-15 (GGAGGGTGTT). M: Molecular size marker (ΦX174 DNA marker digested with *Hae*III).

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