PE-11

Genetic Similarity and Diversity in Crucian Carp (*Carassius carassius*) Populations by Polymerase Chain Reaction-Random Amplified Polymorphic DNAs

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ABSTRACT

Genomic DNA was extracted from the blood of the freshwater crucian carp(*Carassius carassius*) from Kunsan in Korea, representing genetic similarity by polymerase chain reaction amplification of DNA as twelve of arbitrary primers. The electrophoretic analysis of polymerase chain reaction-random amplified polymorphic DNAs (PCR-RAPD) products showed the high levels of similarity between different individuals in crucian carp. Out of 12 primers, 6 generated 266 highly reproducible RAPD markers, producing approximately 2.1 polymorphic bands per primer. The degree of similarity varied from 0.18 to 0.76 as calculated by bandsharing analysis. The RAPD outlines obtained with DNA of different two crucian carp populations from Kunsan were more or less different(0.47 and 0.70). This result implies the genetic similarity due to raising in the same environmental conditions or inbreeding within the crucian carp.

INTRODUCTION

There were so far used various molecular biological methods including restriction fragment length polymorphism (RFLP)(Hallerman and Bekmann, 1988), random amplified polymorphic DNAs (RAPD)(Welsh and McClelland, 1990) based on the polymerase chain reaction (PCR) in a variety of organisms. Especially, applications of RAPD to most fisheries had been at the levels of a few of fish species and crustacean apart from geographic sites(Tassanakajon et al., 1998). In this study, DNAs isolated from the blood were analyzed by 12 random primers in order to identify genetic diversity and similarity and develop the specific genetic markers in a few of crucian carp(*Carassius carassius*) populations from Kunsan at the genetic and molecular level.

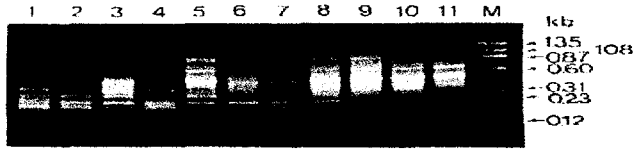
MATERIALS AND METHODS

Crucian carp(*Carassius carassius*) DNA samples were obtained from a few of lakes and aquaculture facilities in the periphery of Kunsan in Korea. RAPD analysis was performed on genetic DNA samples from a total of 50 crucian carp using 12 different random primers. Amplification was performed in a DNA Thermal Cycler with highest quality reagents to achieve reproducible results. Amplification products were separated by electrophoresis in 1.4% agarose gels with TBE and detected by staining with ethidium bromide.

The gels were illuminated with UV light and taken photographs by photoman direct system. Bandsharing calculation of DNA sequences was somewhat modified 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 on.

RESULTS AND DISCUSSION

Of the 12 arbitrarily selected primers, six random primers were used on the basis of the number and frequency of the polymorphisms producted. The bands in the molecular weight range from 0.07 to 1.35 kilobase pairs generated by random primer OPA-2 were observed(Fig. 1). In six primers of the 12 RAPD primers used, the number of bands produced per primer varied from 1 to 15 with an average of 8.3. A total of 549 amplification products were produced of which 266 were polymorphic(48.5%). About 8.6% of total polymorphic bands were either specific to crucian carp. Especially, primer OPA-2 generated the highest number of fragments among the primers used with the average of 6.0. The degree of similarity varied from 0.18 to 0.76 as calculated by bandsharing analysis. Also, the average level of bandsharing was 0.51 ± 0.08 within the crucian carp populations. In addition, the RAPD outlines obtained with DNA of different crucian carp populations from Kunsan in Korea were more or less different. Especially, the RAPD outlines obtained with DNA of crucian carp population of a site(lanes 1-11) were much more varied than those of the other(lanes 12-22).



<Fig. 1>.Amplification products were electrophoresed on a 1.4% agarose gel with TBE and detected by staining with ethidium bromide. Individual specific RAPD patterns of crucian carp amplified by arbitrary OPA-2(TGCCGAGCTG). Each lane shows different individual DNA samples. M: Marker.

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