

Genetic Differences within and between Populations of Korean Catfish (*S. asotus*) and Bullhead (*P. fulvidraco*) Analysed by RAPD-PCR

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ABSTRACT

Of the 20 arbitrarily chosen primers, six oligonucleotides decamer primers were used on the basis of the number of the polymorphisms generated in catfish (*Silurus asotus*) from Yesan and bullhead (*Pseudobagrus fulvidraco*) from Dangjin in Korea. Six primers were used generating a total of 602 scorable bands in catfish and 195 in bullhead population, respectively, ranging in size of DNA fragments from less than approximately 100 to larger than 2,000 base pairs (bp). Six primers yielded 199 polymorphic fragments (33.1 %) in catfish and 47 (24 %) in bullhead, respectively. In the present study, a total of 328 common fragments (an average of 54.7 per primer) were observed in catfish population, whereas 84 (an average of 14.0 per primer) in bullhead. The total number of specific fragments in catfish and bullhead population were 76 and 64, respectively.

INTRODUCTION

Korean catfish and bullhead, economically important aquacultural species, belonging to order Siluriformes including two family Siluridae and Bagridae, respectively, are considered to be closely related to each other by various authors. Two fish species widely inhabit the slow river and stream that flows to the West Sea and South Sea in the Korean Peninsula. This research was made by RAPD-PCR using two decades of random primers and also by single linkage cluster analysis in order to elucidate genetic differences within and between populations in Korean catfish from Yesan and bullhead from Dangjin neighboring Yesan and also to identify suitable RAPD markers peculiar to these species.

MATERIALS AND METHODS

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

Muscle samples collected from catfish (*Silurus asotus*) from Yesan and bullhead (*Pseudobagrus fulvidraco*) from Dangjin were refrigerated at -70°C until use. Samples of sliced muscle were placed into 10 ml test tubes, to which an 4 volumes of lysis buffer I was added. Purity was estimated by calculating the ratios of the absorbance measured at 260~280 nm. The final concentration was estimated

by agarose electrophoresis and EtBr staining. The values were calculated according to Nei and Li (1979) and Jeffreys and Morton (1987). Comparing two lanes, the BS was calculated as follows: $BS = 2(Nab) / (Na+Nb)$. Nab: the number of bands shared by the samples b and a. Na: the total number of bands in a. Nb: the total number of bands in the sample b.

RESULTS AND DISCUSSION

In the present study, six primers were used generating a total of 602 scorable bands in catfish and 195 in bullhead population, respectively, ranging in size of DNA fragments from less than approximately 100 to larger than 2,000 b. The bandsharing values approach based on the presence or absence of amplified DNA bands was used to estimate similarity indices. In the present study, the average similarity index between catfish No. 5 and No. 9 showed the highest level within catfish population (0.945), whereas the similarity index between catfish No. 1 and No. 2 showed the lowest level (0.575). Also, the similarity index between bullhead No. 20 and No. 21 showed the highest level within catfish population (1.000), whereas the similarity index between bullhead No. 8 and No. 21 showed the lowest level (0.063). Overall, the similarity index between two populations was lower than that within population. In the concrete, the similarity index of catfish population was higher than that of bullhead population. All catfish individuals also revealed close genetic affinities, as compared with bullhead individuals, as summarized in figure 1. It appears from the RAPD-PCR data that this large genetic difference in bullhead population may be genetic polymorphism.

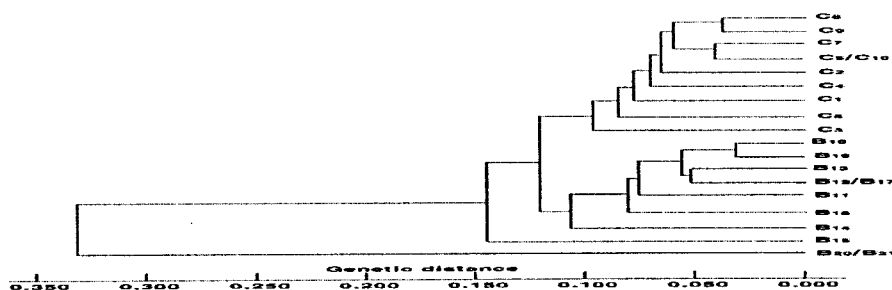


Fig. 1. Dendrogram of genetic distances showing the relatedness among different individuals of catfish (C1~C10) and bullhead (B11~B21) generated according to the bandsharing values and genetic differences matrix in Table 3.

REFERENCES

- Jeffreys, A.J. and D.B. Morton. 1987. DNA fingerprints of dogs and cats. *Anim. Genet.*, 18: 1-15.
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