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

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INTRODUCTION

Catfish (S. asotus) and bullhead (P. fulvidraco), 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 (S. asotus) from Yesan and bullhead (P. fulvidraco) from Dangjin neighboring Yesan and also to identify suitable RAPD markers peculiar to these species.

MATERIALS AND METHODS

Sources of genomic DNA, primer, marker and amplification conditions

Blood samples were obtained from Korean catfish (S. asotus) from Yesan and bullhead (P. fulvidraco) from Dangjin adjacent to Yesan, respectively. RAPD-PCR analysis was performed on DNA samples from a total of 22 individuals using six of decamer primers of two decades of different random primers. Purity and final concentration of DNA was estimated by calculating the ratios of the absorbance measured at 260 nm with a spectrophotometer (Shimadzu, Australia).

Analytical method

An average of whin-population similarity is calculated across all pairwise comparisons between individuals within a population. Single linkage cluster analysis was performed on the similarity matrices in order to generate a dendrogram using pc-package program Systat version 10 (SPSS Inc., USA). Genetic distances within and between populations were calculated with dendrograms produced with Systat version 10. BS values were

scored by the presence or absence of an amplified product at specific positions in the same gel from the RAPD profiles.

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 bp. In this study, six primers generated 199 polymorphic fragments (33.1 % of a total of 602 fragment) in catfish and 47 (24 % of 195 fragments) in bullhead, respectively, as summarized in table 2. Overall, these results indicate a large number of polymorphic fragments detected per primer and suggest high genetic variation in catfish from Yesan and bullhead population from Dangjin. 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). The similarity index of catfish population was higher than that of bullhead population. The potential of RAPDs to identify diagnostic markers for strain, breed, species and population identification in in fish (Partis and Wells, 1996; Hamm and Burton, 2000) has also been demonstrated.
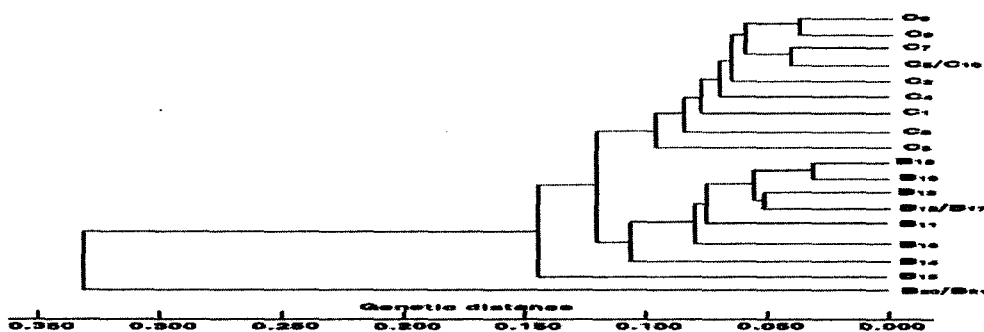

Fig. 1. Dendrogram of genetic distances showing the relatedness among different individuals of catfish (C1~C10) and bullhead (B11~B21) generated according to the bandsharing values and genetic differences matrix.

REFERENCES

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