



DENDROGRAM RELATIONSHIP OF CYPRINIFORM FISHES IN SOUTHERN WESTERN GHATS, INDIA

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Abstract

The phylogenetic analysis of dendrogram revealed *D. aequippinatus* in Manimuthar and Karaiyar showed similar range with Ramanathi followed by Kalikesam and Kallar showed distinct relationship. The phylogenetic analysis showed 50-100% similarity range from selected species among the populations of *D. aequippinatus*. Subsequently, the populations of *G. mullya* showed similar data between the study site Karaiyar and Kallar but the site Kalikesam showed highly distinct relationship.

Key words : *D. aequippinatus*, *G. mullya*, *Dawkinsia filamentosa*, phylogenetic, dendrogram.

Introduction

Biological diversity has undergone restrictions due to direct and indirect anthropogenic activities. The reduction in the site of natural population faces the environmental changes due to loss of genetic diversity (Artoni *et al.*, 2009). Most of the fishes used for human consumption are obtained from wild areas such as rivers and major lentic water bodies (Agostinho *et al.*, 2008). The application of genetics in the conservation of species has received increasing attention in last few decades. In the conservation biology, knowledge of the relatedness between populations is particularly important in absorbed breeding programs that attempt to reduce incestuous mating in order to minimize inbreeding and loss of genetic variations (Frankham *et al.*, 2002). It is well known that, a decline in genetic variation reduces the ability of a population to adapt to environmental changes, therefore, decreases its long term survival (Arif and Khan, 2009). Hence, loss of genetic diversity results in lower individual fitness and poor adaptability level of biodiversity advances in molecular biology techniques have provided the basis for bringing out virtually unlimited numbers of DNA markers. The clarification of taxonomic designations often needs to be addressed before appropriate conservation programs can be successfully implemented (Veronica *et al.*, 2011).

Materials and Methods

A total of 15 samples were collected in five different study sites represent three genus of *Devario aequippinatus*, *Garra mullya* and *Dawkinsia filamentosa*. From each specimen, approximately 1×1 cm of caudal fin tissue was excised and stored in to absolute ethanol for DNA isolation. DNA extraction and purification were performed according to the standard procedure (Hills *et al.*, 1996).

Data Analysis

Inter Simple Sequence Repeats polymorphic DNA patterns were analyzed and reported. Genetic distance between populations was calculated using the software SPSS and Biodiversity. Genetic distance values would be utilized to construct a dendrogram through clustering analysis and Analysis of variance (ANOVA) to determine the relationship between the five populations of three cyprinids individual species.

Statistical Analysis of Genetic Variation

Genetic variance of the selected cyprinids fish's was statically performed between populations and within populations of overall five different sites of Southern Western Ghats indicates that the variation existed within a population of P=0.014 and 4% variation among the population of *D. aequippinatus*. Moreover the variation

among the population of 4% was noticed in *G. mullya* and *D. filamentosa*. P values of significance level were performed in *G. mullya* (0.001) and *D. filamentosa* of 0.141 variations within a population. The statistical analysis of Shannon’s index results indicates that the variation within a population of five different sites of *D. aequippinatus* (I=0.52) and (I=0.47) was observed both in *G. mullya* and *D. filamentosa* (Table 1).

Result and Discussion

The ISSR DNA markers noticeably described within the populations between five sites of *D. aequippinatus* showed that the genetic variations in five different sites of 74-90% from their high values were in Manimuthar of 90% similarity matrix and low values were in Ramanathi of 74% similarity matrix. The *D. aequippinatus* genotypes in their respective clusters based on their genetic divergence. However the highest similarity between five sites was detected in Kalikesam of 90%

levels and lowest was detected in Ramanathi sites of 67% similarity showed in *G. mullya* genetic divergence. Subsequently, the *D. filamentosa* genetic divergence represented Karaiyar of 92% high similarity distinct between other sites and the lowest similarity between the populations was detected in Kalikesam of 69%. As the cluster based analysis demonstrated their genotypes variation. The overall total primers of genetic divergence were obtained in the genotypes of three Cypriniformes fishes.

Inter Simple Sequence Repeats DNA markers noticeably depicted in three cyprinids fish genotypes into their respective clusters based on their genetic divergence (Fig. 1). The ISSR polymorphism rate of 46.48% is obviously lower than that reported by Li *et al.*, (2008, 2009). Similarly the dendrogram relationship of *D. filamentosa* population in Kalikesam was highly distinct to other. Among them the Ramanathi and Manimuthar are resemblance but Kallar and Karaiyar moreover

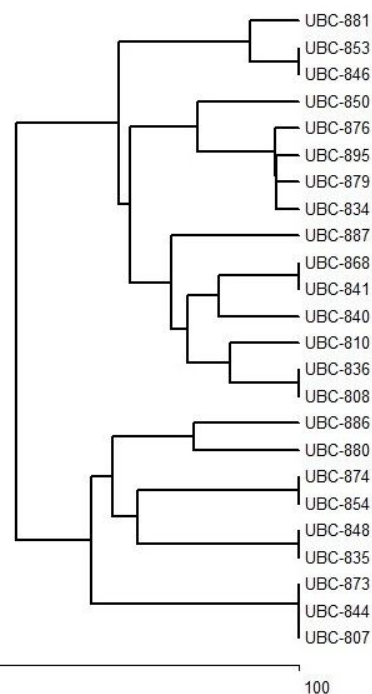


Fig. 1: Dendrogram relationship of ISSR Primers

Table 1: Analysis of variance (ANOVA) within/among populations using ISSR markers

	<i>D. aequippinatus</i>			<i>G. mullya</i>			<i>D. filamentosa</i>		
	Between Group	Within Group	Total	Between Group	Within Group	Total	Between Group	Within Group	Total
Degrees of Freedom(df)	4	490	494	4	495	90.15	4	470	474
Sum of Square	2.32	89.62	91.93	3.33	86.82	90.15	1.32	89.35	90.67
Fixed	-	-	0.716	-	-	0.727	-	-	0.704
Variance	-	-	0.004	-	-	0.007	-	-	0.002
p-value	0.014	-	-	0.001	-	-	0.141	-	-
Shannon’s Index	0.52	-	-	0.47	-	-	0.47	-	-

similar. To ascertain a minimum genetic variety, strong populations with high heterozygosity or genetic variation are preferable (Fevolden *et al.*, 1994). Lee (1999) has explored the phylogenetic and physiological relationships among populations of a euryhaline copepod and found evidence for several repeated invasions across the range of the species.

Conclusion

The assessment of the present study reveals the disturbances on removal of river bank natural vegetation, channel modification, mining and pilgrim activities altered and disturbed the habitats have less species diversity and high genetic differentiation encountered in Kallar and Kalikesam site concluded the conservation and management plans must be done for restoration and maintenance process to block the ecological changes in ecosystem.

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