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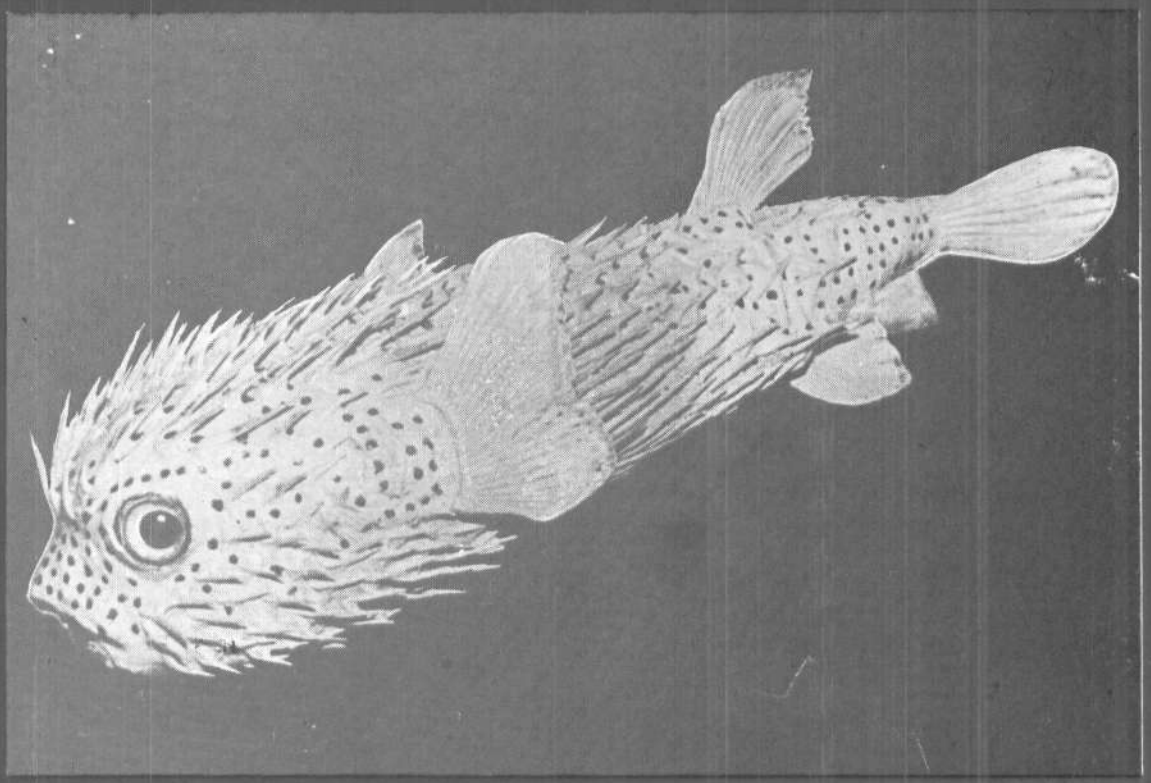

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BIOCHEMICAL GENETIC PROFILE OF THE INDIAN MACKEREL, *RASTRELLIGER KANAGURTA* OF MUD BANK AND POST MUD BANK PERIOD

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Significant increase in the fishery of economically important species of fishes and prawns occur during *chakara* season or mud bank formation. Day to day variation in the fish distribution has been noticed during monsoon season in the mud bank area. The reason attributed to such variation is the shoaling behaviour of fishes which move from deeper waters to inshore areas probably due to the process of upwelling. The catches landed at the mud bank area are from these shoals which are on the move. Each of these catches may be dominated by a particular species. It will be of interest to investigate whether the fish populations of a particular species exploited during or after the phenomenon of *Chakara* belong to homogenous or heterogenous stocks of fishes. In this respect, genetic identification and comparison of individuals of each population of relevant periods is essential. With this objective an attempt was made to study the genetic profile of the Indian mackerel *Rastrelliger kanagurta*, an economically important fish species of India. The genetic profile of the mackerel caught during the mud bank period was compared to that of the post mud bank period.

Population samples

Rastrelliger kanagurta specimens for the present study were collected from Ambalapuzha region during the mud bank (June '94) and post mud bank (December '94) periods. The fish samples were kept frozen at —20°C prior to analysis.

Genetic analysis

The genetic analysis of individual samples was carried out by disc gel electrophoresis of tissue enzymes like Glucose-6 phosphate dehydrogenase (G6PD), Xanthine dehydrogenase (XDH), Alcohol dehydrogenase (ADH), Peroxidase (PO), Aldehyde oxidase (AO) and Sorbitol dehydrogenase (SDH). Optimum conditions in terms of buffer, pH and tissue used for the screening of animals are given in Table 1. The band pattern obtained after staining the gel was recorded and analysed further to determine allelic frequencies and number of loci controlling each enzyme. Gel photographs showing banding pattern for the enzymes are shown in Figure 1. The Chi-square values (X^2) and heterozygotic deficiency were calculated to study whether the population is in Hardy Weinberg equilibrium. Genetic variation was estimated from the proportion of polymorphic loci and the average heterozygosities. Allelic frequencies, X^2 values, observed heterozygosities and heterozygotic deficiency for the different enzyme loci are given in Table 2.

TABLE 1. *Optimum electrophoretic conditions for different enzymes*

Enzyme	Buffer	pH		Tissue
		Tank	Gel	
Glucose-6-phosphate dehydrogenase	0.5 M Tris versin borate	8.0	8.0	Liver
Xanthine dehydrogenase	0.5 M Tris versin borate	8.0	8.0	Liver
Alcohol dehydrogenase	0.5 M Tris versin borate	8.0	8.0	Liver
Peroxidase	0.3 M Borate	8.0	8.5	Muscle
Aldehyde oxidase	0.5 M Tris	8.0	8.0	Muscle
Sorbitol dehydrogenase	0.5 M Tris versin borase	8.0	8.0	Eye lens

Genetic profile

A total of 12 polymorphic loci encoding for 6 enzyme systems were scored from the banding pattern. While XDH appeared to be controlled by a single diallelic locus G6PD, ADH, PO, and AO were controlled by two polymorphic loci in both groups. SDH appeared to have a multi locus control of which three exhibited the allozymic polymorphism. All the animals in both the groups showed consistent banding pattern for most of the enzymes.

A comparison of estimated allele frequencies at the 12 identified loci was made between mud bank and post mud bank periods. The estimated differences in the values of allele frequencies between the two populations did not vary significantly except at ADH2 and SDH3. Chi-square values indicated that population was in Hardy-Weinberg equilibrium for most of the loci.

TABLE 2. *Allelic frequencies X2, heterozygosities (Ht) and heterozygotic deficiencies (Hd) of polymorphic loci in Indian mackerel, Rastrelliger kanourta collected during mud bank and post mud bank period*

Enzyme/ Pritein	Locus	Mud bank				Post mud bank			
		P	X^2	Ht.	Hd.	P	X^2	Ht.	Hd.
Glucose-6-phosphate hydrogenase	G6PD 1	0.74	0.72	0.17	-0.54	0.86	0.33	0.26	0.008
	G6PD 2	0.33	0.20	0.34	-0.22	0.45	0.15	0.30	-0.38
Xanthine dehydrogenase	XDH	0.40	11.28*	0.75	0.56	0.40	1.85	0.63	0.32
Alcohol dehydrogenase	ADH 1	0.61	1.78	0.36	-0.23	0.69	0.08	0.46	0.09
	ADH 2	0.54	0.01	0.50	0.06	0.32	0.26	0.37	-0.14
Peroxidase	PO 1	0.48	0.14	0.53	0.06	0.63	0.40	0.50	0.09
	PO 2	0.46	5.09	0.28	-0.42	0.47	3.54	0.27	-0.44
Aldehyde oxidase	AO 1	0.85	1.39	0.29	0.16	0.77	0.03	0.33	-0.05
	AO 2	0.35	8.59*	0.21	-0.53	0.32	0.26	0.37	-0.14
Sorbitol dehydrogenase	SDH 1	0.90	0.11	0.11	0.00	0.83	0.70	0.33	0.17
	SDH 2	0.76	0.12	0.39	0.08	0.83	0.70	0.33	0.17
	SDH 3	0.63	0.76	0.56	0.22	0.88	0.28	0.23	0.09

* Significant at 1% ($p < 0.01$)

The average number of alleles per locus was 1.79 and the proportion of polymorphic loci was 0.75. The average observed heterozygosities in the animals of the two groups were 0.30 and 0.32 respectively and did not differ significantly. The results suggested that the mackerel samples collected from mud bank and post mud bank periods have closely comparable genetic profile.

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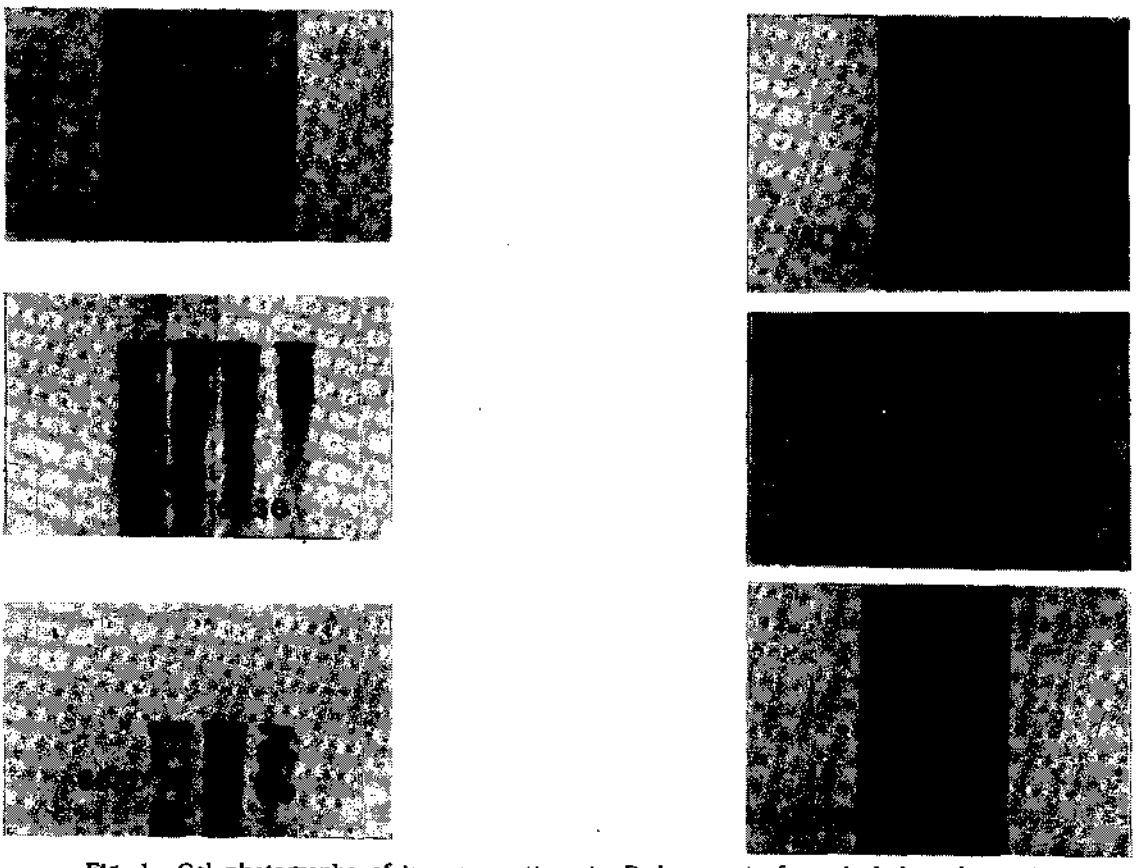

Fig. 1. Gel photographs of isozyme pattern in *R. kanagurta* from Ambalapuzha region.