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BIOCHEMICAL GENETIC POLYMORPHISM IN THE INDIAN MACKEREL *RASTRELLIGER KANAGURTA* FROM MANGALORE REGION

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The Indian mackerel, *Rastrelliger kanagurta* is a commercially important pelagic marine fish. An all India average landing of 66,584 tonnes of mackerel has been reported during 1950-1983 by James *et al.*, (*Mar. Fish. Infor. Serv., T & E Ser.*, No. 114 : 1991). The possible existence of mackerel spawning grounds in several areas has been indicated by Rao (*Proc. Symp. Scomb. Fish., Mar. Biol. Ass. India*, **2**, 574-585 : 1962). A detailed knowledge about genetic structure of the stocks evolving from the different spawning grounds is a prerequisite for the scientific exploitation and management of the mackerel fishery. Keeping this in view a study on the identification of genetic stocks in Indian mackerel has been taken up by Central Marine Fisheries Research Institute. Mangalore being an important area of mackerel fishery, genetic nature of a population sample from this area was tested recently.

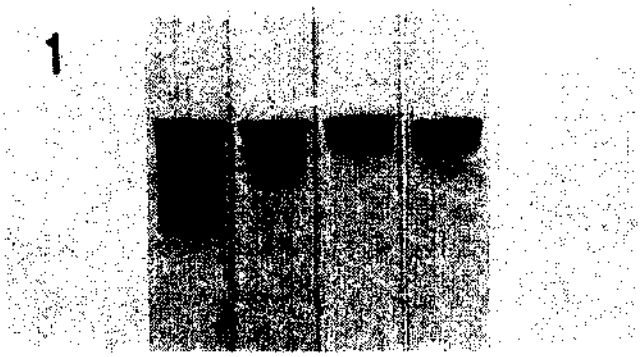
Electrophoresis is the modern and most popular technique used for studying the genetic variability within and among the populations of plants and animals. Genetically controlled tissue enzymes are the most suitable parameters for genetic variability studies. In the present study Polyacrylamide Gel Electrophoresis was used to study the genetic variability in Indian mackerel. This report describes the genetic variability at the enzyme loci controlling Glucose 6-Phosphate dehydrogenase (G6-PD), Xanthine dehydrogenase (XDH), Alcohol dehydrogenase (ADH), Peroxidase (PO), Aldehyde oxidase (AO), Isocitric dehydrogenase (IDH), Lactate dehydrogenase (LDH) and Sorbitol dehydrogenase (SDH) in the

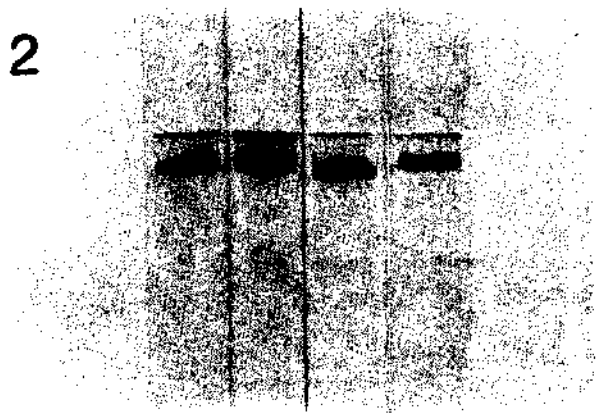
samples collected from Mangalore region. The optimum conditions in terms of buffer, pH, tissue etc. standardised and selected for screening the population, are given in Table 1. The band pattern of each enzyme obtained after electrophoresis, was recorded and analysed further, to determine the number of loci and genotypes. The frequency of alleles at each locus were calculated for each enzyme. The Chi-square goodness of fit was also tested. The degree of genetic variability was estimated by the proportion of polymorphic loci and heterozygosity.

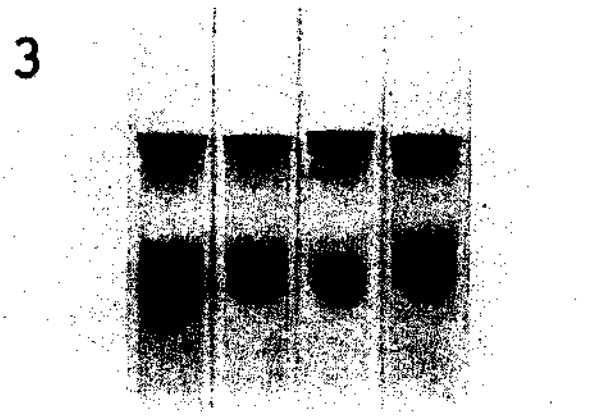
R. kanagurta specimens collected from Mangalore region were in the size range of 20.8 to 23.3 cm with mean 21.2 ± 3.19 cm. The electrophoretic pattern obtained for G6-Pd, XDH, ADH, PO, and AO are shown in Fig. 1-5. The gene

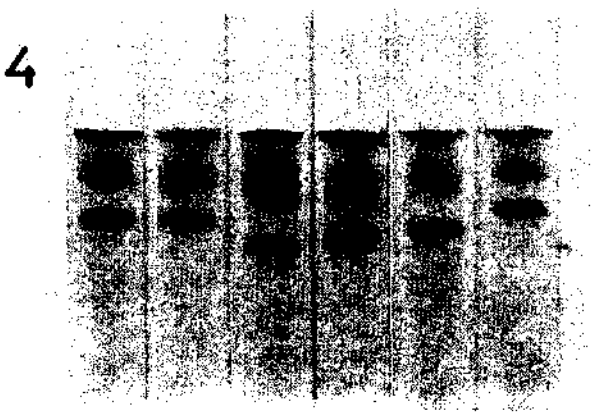
TABLE 1. *Buffer systems and tissues used for different enzyme*

Enzyme	Buffer	pH		Tissue
		Tank	Gel	
Glucose 6-phosphate dehydrogenase	0.5 M Tris Versene borate	8.0	8.0	Liver
Xanthine dehydrogenase	0.5 M Tris Versene borate	8.0	8.0	Liver
Alcohol dehydrogenase	0.5 M Tris Versene borate	8.0	8.0	Liver
Peroxidase	0.3 M Borate	8.0	8.5	Muscle
Aldehyde oxidase	Tris citric	8.26	8.31	Muscle
Lactate dehydrogenase	0.55 M Tris 0.043 M citric acid	7.0	7.0	Liver
Isocitric dehydrogenase	0.155 M Tris 0.043 M citric acid	7.0	7.0	Liver
Sorbitol	0.214 M K_2HPO_4 0.027 M citric acid	7.0	7.0	Eye lens









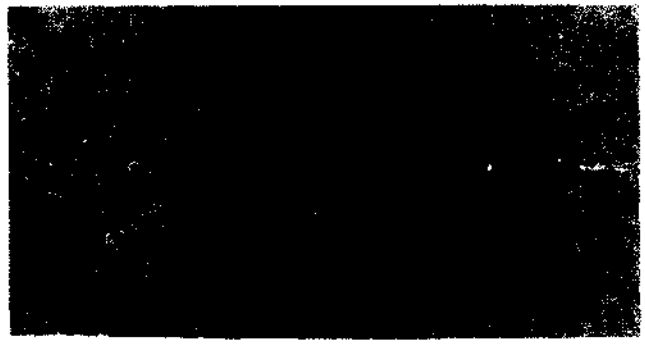


Fig. 1-5. Gel photographs showing electrophoretic band pattern of enzymes. (1) G6-PD, (2) XDH, (3) ADH, (4) PO and (5) AO in Indian mackerel.

TABLE 2. *Allelic frequencies of enzymatic loci in Mangalore population*

Enzyme	Locus	N	Allelic frequency	Heterozygosities
Alcohol dehydrogenase	ADH_1	34	0.82**	0.058
	ADH_2	34	0.56**	0.76
Xanthine dehydrogenase	XDH	34	0.32	0.29
Peroxidase	PO_1	28	0.57	0.36
	PO_2		0.62	0.32
Glucose 6 — Phosphate dehydrogenase	$G6PD_1$	34	0.90	0.15
	$G6PD_2$	34	0.50	0.35
Aldehyde oxidase	AO_1	44	0.48*	0.31
	AO_2	44	0.56	0.47
Lactate dehydrogenase	LDH	30	1.0**	—
Sorbitol dehydrogenase	SDH	30	1.0**	—
Isocitric dehydrogenase	IDH	27	1.0	—

* = $P < 0.05$ ** = $P < 0.01$

frequencies and Chi-square values for the difference between observed and expected phenotypes for each polymorphic enzyme are given in Table 2. The comparative analysis of the zymogram pattern indicated that ADH, XDH, PO, G6-PD and AO are controlled by polymorphic loci. The XDH appeared to be controlled by a single diallelic locus whereas others were under the control of two different diallelic loci. The population was observed to be in Hardy Weinberg equilibrium at all loci except ADH and AO_1 loci. Significant departures were observed at ADH_1 and ADH_2 loci ($P<0.01$) and AO_1 locus ($P<0.05$). The deviation at ADH locus was because of deficiency of heterozygotes. The average number of alleles per locus and average heterozygosity were 1.75 and 0.255 respectively. Some phenotypic variations in the total number of eye lens and serum proteins in mackerel from Mangalore were known earlier. The allelic frequencies of the loci controlling the enzymes ADH, XDH, PO, G6-PD and AO indicated the genetic polymorphism at these loci. IDH locus appeared to be nonpolymorphic as single band pattern was observed at the same position in all individuals. On the other hand LDH and SDH showed a multiband pattern in all the specimens tested. Hence these two enzymes were also considered as nonpolymorphic since no homozygous phenotype was observed for LDH and SDH enzymes. A detailed biochemical genetic study of different regional populations may give a real genetic composition of Indian mackerel. The work in this direction is in progress.