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Allozyme variation in house fly populations, *Musca domestica* from Allahabad, India

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Abstract

Allozyme variation was assessed in the four populations of the common house fly Musca domestica. Allozymes at three gene enzyme system unraveled four loci which revealed nine alleles. F statistics revealed that except XDH all the other loci show inbreeding (F_{is}>F_{st}). Very little genetic differences have been found among the populations of M.domestica.

Keywords: *Musca domestica*, allozyme variation, inbreeding, genetic identity, genetic distance.

Introduction

Enzyme polymorphism in natural population are useful tool for estimating genetic variation[1]. The level of genetic variation within populations of a species indicate species vitality and potential for evolutionary responses to environmental changes[2].

Musca domestica Linaeus, common house fly with cosmopolitan distribution is of great medical and sanitary importance as these are vectors of many diseases causing organism[3-11].

Genetic variations among house flies population have been analyzed using allozyme in different parts of the world[12-19]. However such studies have been sporadically carried out in Indian subcontinent[20-22]. In the present study allozyme variation in house fly, *M. domestica* from four different localities of Allahabad (U.P.) India has been analyzed to determine population diversity.

Material and Methods

The house flies *Musca domestica L.* were collected using sweep nets from four different locations with qualitative difference in the food resources i.e., Meat shop (MS), Vegetable market (VM), Dairy farm (DF) and Solid food waste (SW).

Fifty individuals were assayed for enzyme activity at three gene enzyme systems viz., malic enzyme (ME), aldehyde oxidase (AO) and xanthine dehydrogenase (XDH). Sample preparation and electrophoretic procedures were according to the method of Tripathi et al 2010[20]. The enzyme systems studied, staining solutions, gel and electrode buffer are given in table-1. Genotype information, genetic identity and genetic distance were calculated as described earlier[21].

Results and Discussion

The three gene enzyme systems analyzed in present study viz., malic enzyme (ME), aldehyde oxidase (AO) and xanthine dehydrogenase (XDH) resolved four loci among the four populations. The activity of ME and XDH were confined to single locus figure-1 and 3 while the activity of AO was confined to two loci figure-2. All the four loci analyzed were polymorphic, which revealed nine alleles. Allele frequencies and Chi-square values are presented in table-2. Three loci viz., ME, AO-1 and AO-2 showed significant departure from Hardy-Weinberg equilibrium.

Flies from meat shop (MS) and dairy farm (DF) shared all the alleles while flies from vegetable market (VM) shared alleles at two locus i.e., ME and XDH with these two populations. The flies from solid food waste (SW) revealed fixed differences at ME and XDH, where it is monomorphic, however these flies shared VM at locus AO-1 and MS and DF at locus AO-2 table-2.

Table-1
Summary of electrophoresis and staining protocols followed in the present study

Enzyme	Gel/ electrode Buffer	Staining buffer	Substrate/Coenzyme	Dyes	Reference
ME (E.C.1.1.1.40)	0.1M Tris-HCl (pH 8.5)	0.1M Tris-HCl (pH 7.4)	Malic acid / NADP	NBT PMS	Tsukamoto (1989) [23]
AO (E.C.1.2.3.1)	0.1M Tris-HCl (pH 8.5)	0.1M Tris-HCl (pH 7.4)	Benzaldehyde	NBT PMS	Tsukamoto (1989) [23]
XDH (E.C.1.2.1.37)	0.1M Tris-HCl (pH 8.5)	0.1M Tris-HCl (pH 7.4)	Hypoxanthine / NADP	NBT PMS	Tsukamoto (1989) [23]

Table-2
Allele frequencies and Chi-square values in different collections of *M. domestica*

Locus	Allele	MS	VM	DF	SW
ME (n=50)	a	0.60	0.43	0.39	1.00
	b	0.40	0.57	0.61	-
	χ^2	8.17*	6.72*	3.26	-
AO-1 (n=50)	a	-	0.60	-	0.55
	b	-	0.40	-	0.45
	χ^2	-	8.17*	-	7.76*
AO-2 (n=50)	a	0.44	-	0.35	0.48
	b	0.56	-	0.65	0.52
	χ^2	7.45*	-	0.79	6.40*
XDH (n=50)	a	0.20	0.40	0.29	1.00
	b	0.42	0.60	0.45	-
	c	0.38	-	0.26	-
	χ^2	0.62	1.61	2.62	-

MS= Meat shop, VM = Vegetable market, DF= Dairy farm, SW= Solid food waste (in all the tables); n= number of individuals in each sample; *=Populations not in Hardy Weinberg equilibrium

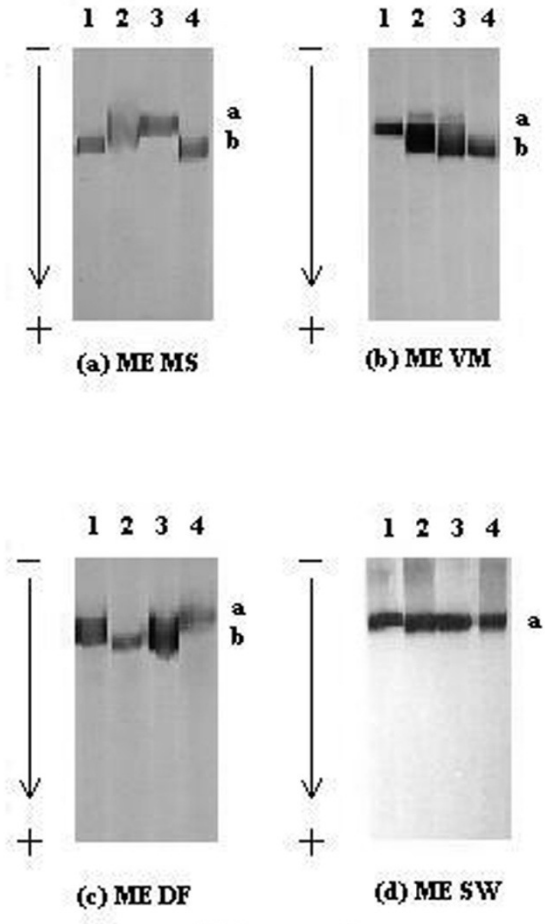

Figure-1
Electrophoretic phenotypes of Malic Enzyme (a) ME MS (b) ME VM (c) ME DF (d) ME SW in *Musca domestica.* The regions of electromorphs are indicated on the right

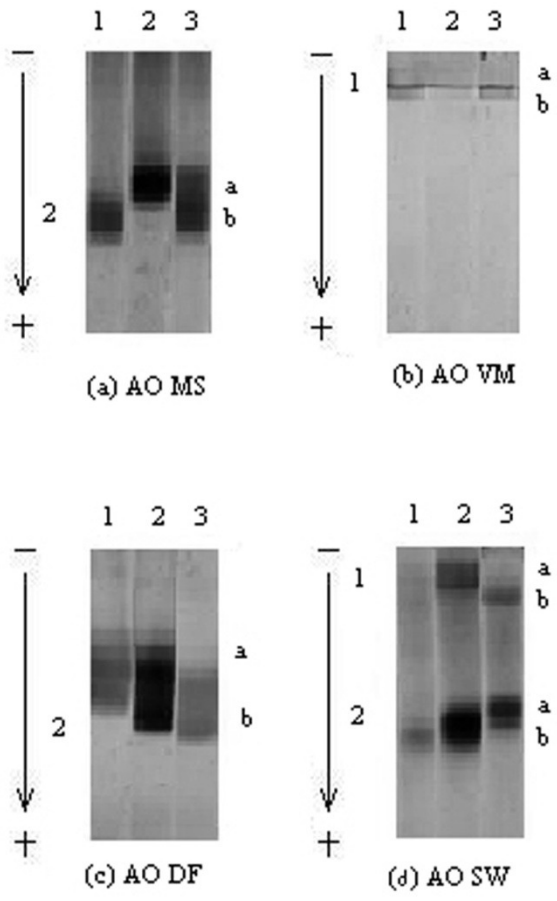

Figure-2
Electrophoretic phenotypes of Aldehyde oxidase (a) AO MS (b) AO VM (c) AO DF (d) AO SW in *Musca domestica.* The regions of activity are indicated on the left and electromorphs are indicated on the right

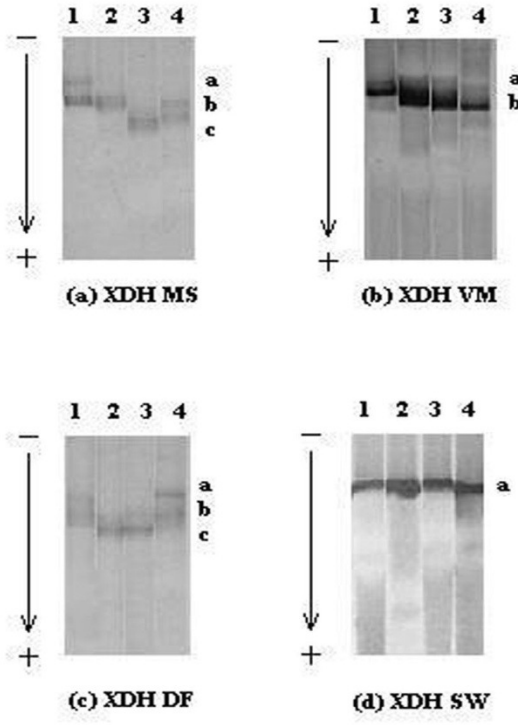

Figure-3
Electrophoretic phenotypes of Xanthine dehydrogenase (a) XDH MS (b) XDH VM (c) XDH DF (d) XDH SW in *Musca domestica.* The regions of electromorphs are indicated on the right

Number of alleles ranged from 1.85 to 2.07 with a mean of 1.97. The percentage of polymorphic loci ranged from 50.00% to 75.00% with a mean of 68.75% and the mean observed heterozygosity ranged from 0.250 to 0.447, with a mean of 0.356. The mean expected heterozygosity ranged from 0.483 to 0.534, with a mean of 0.510 table-3. Nei's genetic identity values were highest between the samples collected from MS and DF (I=0.955) and the Nei's genetic distance values were lowest between these two populations (D=0.046) table-4. As revealed by the Wright's F statistics very little genetic variation seems to have has occurred among house fly populations analyzed in the present study. Except XDH all the other loci reveal inbreeding table-5.

Conclusion

It seems that the flies collected from MS and DF are genetically very similar. This may be due to the fact that the larval food substrates from the two collection sites were more or less similar as suggested by Thomas and Barker[24]. As well as the house fly population analyzed in the present study are characterized by a high level of inbreeding. Thus the present findings support the tenet that very little genetic differentiation has accompanied the population differentiation among house flies in Allahabad region of India[22].

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Table-3
Genetic variability in different collections of house flies populations

Population	Sample Size	Number of loci	Mean Effective no. of alleles	Percentage of polymorphic loci	Mean observed heterozygosity (H_o)	Mean expected heterozygosity (H_E)
MS	50	4	1.85	75.00%	0.447	0.534
VM	50	4	2.07	75.00%	0.287	0.483
DF	50	4	1.95	75.00%	0.440	0.526
SW	50	4	2.01	50.00%	0.250	0.497
Mean	50	4	1.97	68.75%	0.356	0.510

H_O = No. of heterozygotes / Total no. of individuals, $H_E = 1- \Sigma x_i^2$ (Nei, 1972), where x_i is the frequency of ith allele at a locus

Table-4
Genetic identity (I) and genetic distance (D) among house flies in different collections

		(I)			
	Population	**MS**	**VM**	**DF**	**SW**
(D)	**MS**	-	0.558	0.955	0.636
	VM	0.584	**-**	0.607	0.621
	DF	0.046	0.499	-	0.572
	SW	0.452	0.477	0.559	-

I= Jxy/√Jx Jy, D= -In I, Where Jx y is the arithmetic mean of Jx y=$\sum x_i y_i$ over all loci, Jx is the arithmetic mean of ix =$\sum ix_i^2$ over all loci, and x_i (or y_i) is the frequency of the ith allele in the first (or second) population.

Table-5
Wright's F statistics for all the variable loci.

Loci	F_{is}	F_{st}
ME	0.474	0.243
AO-1	0.461	0.001
AO-2	0.267	0.010
XDH	0.055	0.284
Mean	0.314	0.135

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