Int J Pharm Bio Sci 2012 Oct; 3(4): (B) 927 - 934

Research Article Bio Chemistry

International Journal of Pharma and Bio Sciences ISSN 0975-6299

SPATIAL GENETIC VARIATION IN HOUSE FLY POPULATIONS, MUSCA DOMESTICA (DIPTERA : MUSCIDAE)

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ABSTRACT

Spatial genetic variation was assessed in the common house fly *Musca domestica*. Allozymes at three gene enzyme system unraveled ten loci which revealed seventeen alleles in house fly populations. F statistics revealed that except ACPH-1 and EST-3 all the other loci show inbreeding ($F_{is}>F_{st}$). Persistent heterozygosity was observed in ACPH-1(F_{is}= -0.140) which indicate random mating for this locus.

KEY WORDS: ***Musca domestica,*** **allozymes, spatial variation, genetic variability, genetic identity, genetic distance.**

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INTRODUCTION

Enzymatic markers are helpful tools for estimating genetic variation (1). The level of genetic variation among populations has received considerable attention, as it is indicative of overall species vitality and the potential for evolutionary responses to environmental changes (2).

Correlation between spatial or temporal environmental parameters and allele frequencies in natural populations give evidence of selection (3-6). The environmental heterogeneity in space or time is known to maintain genetic polymorphisms (7-13).

The spatial genetic variations in house fly populations have been analyzed only in the new world populations from USA, UK and Africa (14-20). Spatial genetic variation in house fly, *M. domestica*, populations from Allahabad, India has been analyzed in the present study.

MATERIALS AND METHODS

Sample collection

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)(Fig.1).

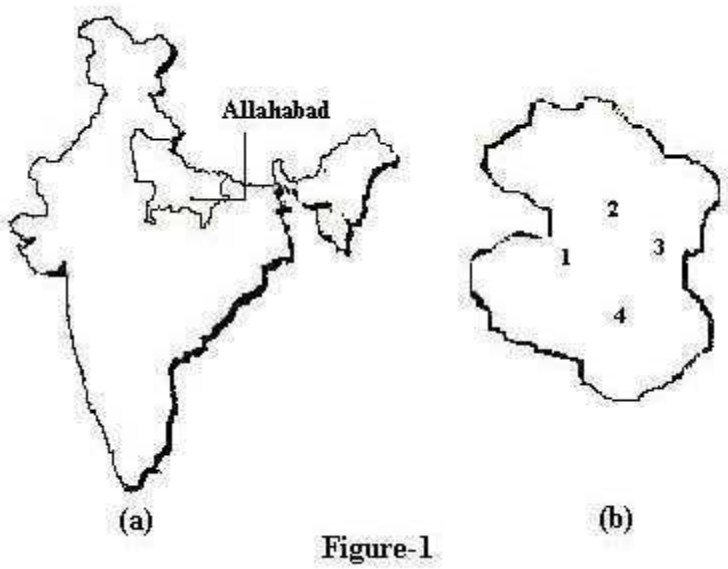

Figure 1.
(a) Map of India showing city Allahabad in Uttar Pradesh State.
(b) Map of city Allahabad showing locations of the four collection sites of Musca domestica based on qualitative difference in the food resources:
1. Meat shop (MS), 2. Vegetable market (VM)
3. Dairy farm (DF), 4. Solid food waste (SW)

Electrophoretic studies

Sample preparation and electrophoretic procedures were according to the method of Kaul *et al* (21). Fifty individuals were assayed for enzyme activity at three gene enzyme systems viz., acid phosphatase (ACPH), esterase (EST) and glucose-6-phosphate dehydrogenase (G6PD) for each sample. The staining protocols of Ayala et al (22) and Tsukamoto (23) were followed for the analysis of enzyme activity.

Data analysis

The relative mobility of each band was calculated and expressed as R_f values (x 100) following the method of Tsukamoto and Horio (24). Electrophoretic genotypes were determined by comparison of relative mobility of the bands. Genetic interpretations were made by conventional method; single bands were considered to represent homozygotes and multiple banded phenotypes represented heterozygotes (25). At polymorphic loci, groups of similar R_f values were considered to represent a single allele. The mean value for each group was used to designate that particular allele. The genotype information at each locus was used to calculate allele frequencies (26).The genotype information, thus obtained, was used to estimate genetic variability using polymorphic loci, mean observed (H_o) and expected (H_E) heterozygosity (27). Test for conformity to Hardy-Weinberg equilibrium was carried out by Chi-square and Wright's F statistics (28). Genetic identity (I) and genetic distance (D) values were calculated according to the method of Nei (27).

RESULTS AND DISCUSSION

The three gene enzyme systems analyzed in present study viz., acid phosphatase (ACPH), esterase (EST) and glucose-6-phosphate dehydrogenase (G6PD) resolved ten loci among the four populations . In all the three gene enzyme systems the activity was present at multiple loci. In ACPH and G6PD activity was confined at two locus (ACPH-1, ACPH-2, G6PD-1 and G6PD-2). Whereas six loci were observed in esterase (EST-1, EST-2, EST-3, EST-4, EST-5, and EST-6). Enzyme activity at EST-2, EST-4, EST-5, and EST-6 loci were monomorphic while it was polymorphic at all the other loci. Among the polymorphic loci ACPH-1 was characterized by the presence of three alleles while rests of the loci were encoded by two alleles.

Seventeen putative alleles were analyzed at ten loci. Out of ten loci only six were polymorphic which revealed thirteen alleles. Allele frequencies and Chi-square values are presented in table 1. The flies from meat shop (MS) and dairy farm (DF) shared all the alleles except at the three monomorphic loci viz., EST-4, EST-5 and EST-6. The flies from vegetable market (VM) also shared all the alleles with these two populations except at G6PD-2 locus. The flies from solid food waste (SW) revealed fixed differences at ACPH-1, EST-1, EST-3 and EST-6. The populations from MS, DF and VM have six alleles, which were not present in the samples collected from SW.

Table 1.
Allele frequencies and Chi-square values in spatial collections of M.domestica.

Locus	Allele	MS	VM	DF	SW
ACPH	a	0.60	0.43	0.57	-
(n=50)	b	0.25	0.40	0.57	-
	c	0.15	0.17	0.28	-
	χ^2	22.22*	1.84	19.60*	-
ACPH-2	a	0.36	0.42	0.45	0.48
(n=50)	b	0.64	0.58	0.55	0.52
	χ^2	2.17	8.63*	1.27	5.74*
EST-1	a	1.00	1.00	1.00	0.53
(n=50)	b	-	-	-	0.47
	χ^2	-	-	-	22.85*
EST-2	a	1.00	1.00	1.00	1.00
EST-3	a	0.56	0.46	0.42	-
(n=50)	b	0.44	0.54	0.58	-
	χ^2	30.11*	18.23*	8.62*	-
EST-4	a	1.00	1.00	-	1.00
EST-5	a	1.00	1.00	-	1.00
EST-6	a	1.00	1.00	-	-
(n=50)					
G6PD-1	a	0.68	0.53	0.58	0.47
(n=50)	b	0.32	0.47	0.42	0.53
	χ^2	15.60*	5.38*	6.09*	3.69
G6PD-2	a	0.47	-	0.44	0.52
(n=50)	b	0.53	-	0.56	0.48
	χ^2	3.25	-	3.54	11.54*

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.

The extent of genetic variation among four populations, mean effective number of alleles per locus, percentage of polymorphic loci and mean heterozygosities are summarized in table 2.

Table 2.
Genetic variability in spatial collections of house flies populations.

Population	Sample Size	Number of loci	Mean effecti-ve no. of alleles	Percentage of polymo-rphic loci	Mean observed hetero-zygosity (H_o)	Mean expected hetero-zygosity (H_E)
MS	50	10	2.07	50.00%	0.452	0.488
VM	50	10	1.92	40.00%	0.430	0.527
DF	50	10	1.98	50.00%	0.320	0.507
SW	50	10	2.00	40.00%	0.335	0.499
Mean	50	10	1.99	45.00%	0.384	0.505

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

Number of alleles ranged from 1.92 to 2.07 with a mean of 1.99. The percentage of polymorphic loci ranged from 40.00% to 50.00% with a mean of 45.00% and the mean observed heterozygosity ranged from 0.320 to 0.452, with a mean of 0.384. The mean expected heterozygosity ranged from 0.488 to 0.527, with a mean of 0.505. Six loci showed significant departure from Hardy-Weinberg equilibrium (Table-1). The percentage of polymorphic loci was found to be similar in the populations of MS and DF as well as in VM and SW population. Thus it seems that the flies collected from MS and DF are genetically very similar. Nei's genetic identity (I) and distance (D) values, further corroborates this fact as highest genetic identity (I=0.983) values were observed between the samples collected from MS and DF (Table. 3). This may perhaps 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 (29).

Table 3.
Genetic identity (I) and genetic distance (D) among house flies in spatial collections.

(I)

Population	MS	VM	DF	SW
MS	-	0.853	0.983	0.806
VM	0.159	-	0.867	0.742
DF	0.017	0.143	-	0.757
SW	0.216	0.298	0.298	-

(D)

$$I = Jxy/\sqrt{Jx\ Jy}$$
$$D = -\ln I$$

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.

Wright's F statistics further supports the fact that very little genetic variation has occurred among house fly populations analyzed in the present study. Except ACPH-1 and EST-3 all the other loci reveal inbreeding ($F_{is}>F_{st}$) (Table 4).

Table 4.
Wright's F statistics for all the variable loci.

Loci	F_{is}	F_{st}
ACPH-1	-0.140	0.767
ACPH-2	0.341	0.008
EST-1	0.480	0.399
EST-2	-	-
EST-3	0.161	0.223
G6PD-1	0.479	0.021
G6PD-2	0.235	0.005

A persistent excess of heterozygosity was observed only in ACPH-1 ($F_{is=}$ -0.140) in spatial collections. Kimura and Crow (30) have opined that a negative F_{is} value is indicative of random mating. Thus, it seems plausible that the house fly populations surveyed in the present study are characterized by a high level of inbreeding.

ACKNOWLEDGEMENT

Thanks are due to, Head, Department of Zoology (UGC-SAP and DST-FIST scheme sponsored), University of Allahabad, for providing all the necessary facilities.

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