

LOW LEVELS OF GENETIC DIFFERENTIATION IN MOSQUITO (*Culex quinquefasciatus*) POPULATIONS FROM RECIFE, PERNAMBUCO, BRAZIL

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ABSTRACT

An allozymic survey of five populations of *Culex quinquefasciatus* (Diptera; Culicidae) in Recife, Pernambuco, Brazil, revealed very low levels of genetic differentiation in malate dehydrogenase, isocitrate dehydrogenase and phosphoglucosmutase loci, judging from the low values of F_{ST} found. An explanation is proposed, based on seasonal change in population size, sanitation conditions and urban transport.

INTRODUCTION

Culex quinquefasciatus is a mosquito that presents a high reproductive rate, in regions with high temperatures, high levels of humidity and long rainy seasons, along with poor hygiene conditions. Several biochemical-genetics studies have been made of *Culex* (Iqbal *et al.*, 1973; Narang *et al.*, 1977; Cheng and Hacker, 1979; Pryor *et al.*, 1980; Bhalla and Narang, 1981; Pryor and Ferrell, 1981) but only a few have considered population genetics problems. It is the major vector for Bancroftian filariasis an endemic disease in northeastern Brazil (Medeiros *et al.*, 1992). In Recife, Pernambuco, Brazil though many city districts have similar optimum conditions for this species' development, inhabitants of some of those districts have significantly higher levels of infection than others (Medeiros *et al.*, 1992). The higher the number of bites, the more adjusted one would assume this mosquito to be to local conditions (Curtis and Feachem, 1981). This could affect genetic differentiation.

MATERIAL AND METHODS

We attempted to characterize and compare *C. quinquefasciatus* populations from different districts, through an allozymic survey. The sample was constituted of specimens captured with light traps in five different city districts of Recife within an eight km range from one another. According to researchers from the Aggeu Magalhães (CPqAM-FIOCRUZ), four of them had a high level of infection (Coque, Mustardinha, Jardim São Paulo and Casa Amarela) and only Boa Viagem presented a low level (Dreyer, 1987). The allozymic systems tested were: malate dehydrogenase, E.C. 1.1.1.37 (MDH); phosphoglucosmutase EC 5.4.2.2. (PGM); malic enzyme EC 1.1.1.40 (ME) and isocitrate dehydrogenase, EC 1.1.1.42 (IDH) (May, 1992), totalizing six loci. For each district, and for each enzymatic system, 38 to 119 specimens were studied. Electrophoresis was performed with starch gel for MDH, and polyacrylamide gel (7%) for the other enzymes. Buffer and staining procedures followed Harris and Hopkinson (1977) standards. Homogenates were prepared through squashing techniques, using an acrylic plate in an ice bath. The migration conditions were: 7 V/cm, 4°C, and five hours for each system. Because of laboratory and/or collection conditions, it was not possible to analyze every system for each district. All electrophoretic procedures used as a control the abdomen homogenate from a bug lineage, *Dysdercus maurus* (Hemiptera). Statistics for the allelic

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frequencies were standard and the fixation index (F_{st}) determined according to Weir and Cokerhan (1984).

RESULTS AND DISCUSSION

Gene frequencies are given in Table I. Electrophoretic patterns are presented in Figure 1. MDH and IDH, respectively, exhibited two loci. IDH (IDH1 and IDH2) similarly to PGM, had anodal mobility while MDH showed both anodal (MDH1) and cathodal (MDH2) migrations. Systems ME and IDH2 were monomorphic, in all the districts surveyed, along there were homozygous types for ME*1 allele (relative mobility, MR = 1.6) and IDH2*1 (MR = 0.4). For the districts Mustardinha and Jardim São Paulo, the locus MDH1 had two alleles (MDH1*1 and MDH1*2), with similar frequencies. In Boa Viagem district, the same loci were monomorphic, with all the specimens homozygous for allele MDH1*2. This allele was also the most frequent one in all other populations. Locus MDH2, however, was monomorphic for MDH2*1 in Mustardinha and Jardim São Paulo, while in Boa Viagem it was polymorphic. In Coque, Mustardinha and Jardim São Paulo, locus IDH1 was monomorphic, with all the specimens homozygous for IDH1*1, with the exception of one specimen from Coque which was heterozygous (IDH1*1/IDH1*2). The IDH1*2 allele was a rare variant in this district. In Boa Viagem this locus was

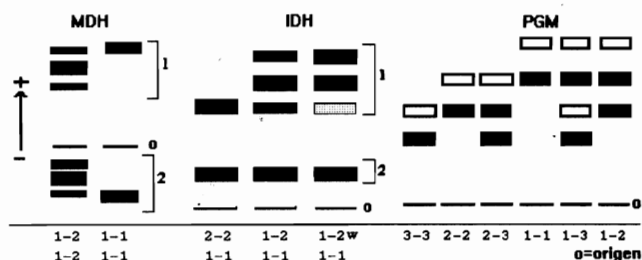


Figure 1 - The electropherograms showing the allozyme patterns for MDH, IDH and PGM in *C. quinquefasciatus* populations of Recife, Pernambuco, Brazil.

polymorphic for three alleles: IDH1*1, IDH1*2 and IDH1*2w (w = weak). Amongst the six loci studied, PGM was the most polymorphic, presenting three alleles: PGM*1, PGM*2, and PGM*3 in all populations. The comparative data analysis, in the three districts, did not reveal significant differences. Hardy-Weinberg analysis, in each district and in each system, indicated a deviation in data from Coque for PGM ($\chi^2 = 7,633$; d.f. = 3; $P < 0.001$); excess of heterozygous PGM*1/PGM*3.

Electrophoretic patterns and gene frequency distribution revealed some genetic differences amongst the populations; and in Boa Viagem some new alleles were

Table I - Allelic frequencies in the *Culex* populations of Recife, Pernambuco, for the MDH1, MDH2, IDH and PGM allozymes.

Loco	Allele	COQ	MUS	JSP	BVG	CAM	F_{ST}
MDH1	1	0.0138	0.0156	0.0288	0.0000	---	0.0018
	2	0.9862	0.9844	0.9712	1.0000	---	
N		113	51	38	119		
MDH2	1	---	1.0000	1.0000	0.9939	---	0.0000
	2	---	0.0000	0.0000	0.0061	---	
N			52	47	82		
IDH	1	0.9956	1.0000	1.0000	0.9619	---	0.0292
	2	0.0044	0.0000	0.0000	0.0212	---	
	2w	0.0000	0.0000	0.0000	0.0169	---	
N		113	51	38	119		
PGM	1	0.2000	0.2300	---	---	0.2264	0.0313
	2	0.5190	0.5500	---	---	0.4623	
	3	0.2810	0.2200	---	---	0.3113	
N		105	50	---	---	53	

COQ = Coque, MUS = Mustardinha, JSP = Jardim São Paulo, BVG = Boa Viagem, CAM = Casa Amarela.

found. The *C. quinquefasciatus* population in Coque, Mustardinha, Jardim São Paulo and Casa Amarela, where the human population had a high level of microfilaremia, is genetically different from that observed in Boa Viagem, where microfilaremia is lower.

Contrary to expectations, *C. quinquefasciatus* data from Recife seem to indicate that populations are not becoming significantly different, according to the F_{ST} values obtained (Table I). It could be presumed that, as during the rainy season the city canals are flooded, exchange eggs is facilitated. But, eggs do not resist these conditions. Mosquito dispersion is carried out by car, bus or another means of transport. That exchange must cause the deviation found in the PGM locus, where there is a surplus of heterozygous types without diminishing the homozygous ones. It would also support the hypothesis that the differences found among the populations, considering loci MDH1, MDH2 and IDH1, are due to genetic drifting. Only 25% of the houses have a sewage system and/or septic cesspits. These conditions favour the oviposition of mosquitoes, especially during the rainy season and apparently favor genetic variability maintenance of *C. quinquefasciatus* populations in Recife.

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RESUMO

Uma investigação utilizando alozimas de cinco populações de *Culex quinquefasciatus* do Recife, Estado de Pernambuco, Brasil, revelou índices de diferenciação genética muito baixos a julgar pelos valores de F_{ST} encontrados para os locos de malato desidrogenase, isocitrato desidrogenase e fosfoglicomutase. Uma explicação com base nas variações sazonais, condições de saneamento básico e transporte urbano, é proposta.

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