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Stability of frequencies of phosphoglucomutase alleles in Culex pipiens breeding in ecologically different environments

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Genetica. — *Stability of frequencies of phosphoglucomutase alleles in* Culex pipiens *breeding in ecologically different environments.* Nota di LUCIANO BULLINI, MARIO COLUZZI, ANNA PAOLA BIANCHI BULLINI e LUIGI RENNA, presentata [*] dal Socio G. MONTALENTI.

RIASSUNTO. — Vengono studiate le frequenze alleliche per il locus fosfoglucomutasi (PGM) in otto diverse popolazioni della zanzara *Culex pipiens*. Alcune delle popolazioni studiate sono tra loro geograficamente isolate, si sviluppano in ambienti ecologicamente molto diversi e presentano considerevoli fluttuazioni nelle dimensioni (originate anche da trattamenti con insetticidi). La notevole stabilità nelle frequenze alleliche nelle diverse popolazioni suggerisce che la selezione naturale sia il fattore principale nel mantenimento del polimorfismo enzimatico. Il meccanismo del vantaggio dell'eterozigote sembra fornire una soddisfacente spiegazione dei nostri dati. L'uniformità genetica osservata in ambienti molto diversi dal punto di vista ecologico sembra indicare l'assenza di relazioni semplici tra varianti enzimatiche e i fattori ecologici considerati.

INTRODUCTION

Culex pipiens Linn. is one of the most widely distributed mosquito species since it occurs the world around between latitudes of 60° N and 40° S. Various forms have been described showing biometrical differences and variably combined biological characters such as autogeny and anautogeny, stenogamy and eurigamy, anthropophily and ornithophily, homo- and heterodinamy. Moreover, it is well known the existence of cytoplasmic sterility between certain populations (Laven [1]). The breeding places of this euryecious species are ecologically much differentiated being represented by polluted and unpolluted waters such as springs, wells, cisterns, tanks, sewers, waterdrains and various kinds of ponds even in connection with rivers.

A previous study of the phosphoglucomutase (PGM) electrophoretic variants in an urban population of *Culex pipiens* from Rome showed the existence of a polymorphism involving three codominant alleles of the autosomal gene *Pgm* (Bullini *et al.* [2]). The aim of this paper is to compare the allele frequencies at the phosphoglucomutase locus in natural populations of *Culex pipiens* breeding in different environmental situations.

MATERIAL AND METHODS

The material examined consists in samples from eight Italian populations of *C. pipiens* (see Table I). Only two of these populations (from S. Oliva and Monticelli) can be referred to the type form of *C. pipiens* breeding in

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(*) Nella seduta del 9 dicembre 1972.

unpolluted water and showing pronounced ornithophily, very rare occurence of autogeny and stenogamy, winter diapause at the adult stage. The remaining six populations (from Castagneto Marina, Pontecorvo, Ceccano, Canino, Roma and Latina) appeared *molestus*-like with various degrees between the typical urban form *molestus* and the rural *pipiens* (Rioux and Pech [3]; La Face [4]; Valenti and Coluzzi [5]). They were found to breed in tanks with rain water (Roma, Canino and Castagneto Marina), in polluted water drains (Pontecorvo and Latina) and in polluted ponds near the Sacco river (Ceccano).

TABLE I

Distribution of PGM *alleles in population samples of* Culex pipiens *from Italy.*

LOCALITY	Number of individuals examined	PGM ALLELE FREQUENCIES					
		Pgm^{A}	Pgm^{B3}	Pgm^{B2}	Pgm^{B1}	Pgm^{C}	Pgm^{D}
Castagneto Marina, Livorno	220	—	0.0455	—	0.8409	0.1136	—
Monticelli, Frosinone	1409	0.0025	0.0500	0.0075	0.8190	0.1199	0.0011
Ceccano, Frosinone	187	—	0.0615	—	0.8048	0.1257	0.0080
Pontecorvo, Frosinone	148	0.0034	0.0405	—	0.8074	0.1453	0.0034
S. Oliva, Frosinone	162	0.0031	0.0555	—	0.8241	0.1111	0.0062
Canino, Viterbo	704	0.0043	0.0575	—	0.7955	0.1406	0.0021
Roma	314	0.1545	—	—	0.6974	0.1481	—
Latina	754	0.0053	0.0345	0.0053	0.8415	0.1101	0.0033

The mosquitoes were collected at the preimaginal stages and were tested five-ten days after emergence. The breeding and electrophoretic techniques were the same as those reported in previous papers (Bullini *et al.* [2] and [6]).

RESULTS AND CONCLUSIONS

The formal genetics of the PGM variants were carried out by a series of crosses and backcrosses with one or both parents known. These showed in the material of *C. pipiens* examined the occurence of six codominant alleles including the three previously observed (Bullini *et al.* [2]). These alleles were designated Pgm^{A}, Pgm^{B3}, Pgm^{B2}, Pgm^{B1}, Pgm^{C}, Pgm^{D} in order of increasing mobility (for details on this nomenclature see Bullini and Coluzzi [7]). Some of the 21 possible phenotypes are shown in fig. 1. The distribution of PGM alleles in the population samples studied is reported in Table I. The eight populations were found polymorphic for 3-6 alleles, the most frequent being in all samples *Pgm*^{B1}. The phenotype expressed by this allele at the homozygous state showed an intermediate electrophoretic mobility. The relative frequencies of the alleles appeared nearly undifferentiated over our study area in spite of the low dispersal ability of the species and the above quoted environmental heterogeneity. The apparent absence of certain rare alleles in some of the populations could depend on the sample size.

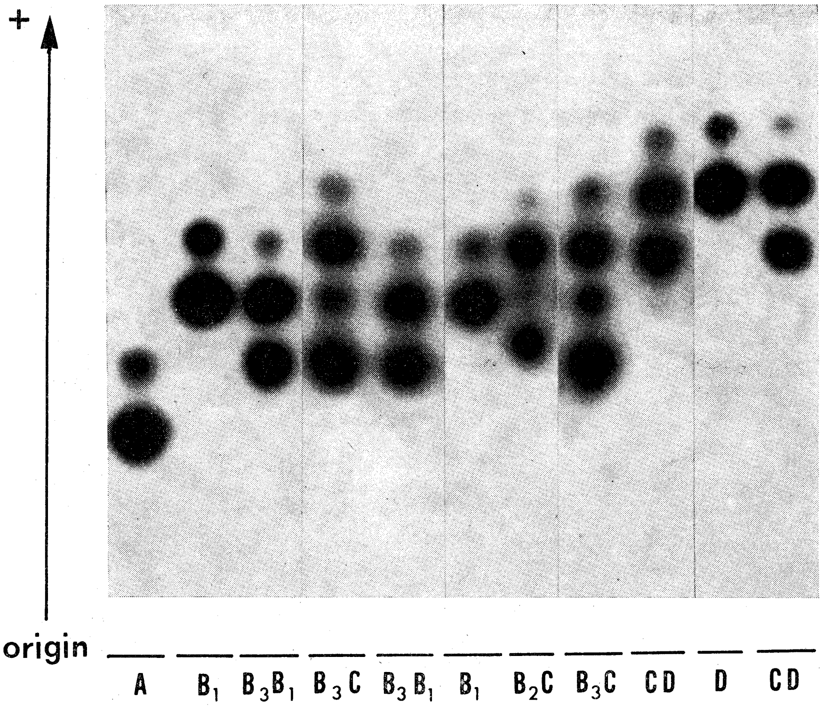

Fig. 1.

The remarkable stability in allele frequencies observed in these populations of *C. pipiens*, some of which geographically fairly well isolated among them and showing large fluctuations in size (originated also by insecticide treatments), suggest natural selection as a factor mantaining the enzymatic polymorphism in agreement with other recent reports (Ayala *et al.* [8], [9]; Burns and Johnson [10]; Bullini and Coluzzi [11]; Lakovaara and Saura [12], [13]; Prakash *et al.* [14]). The mechanism of heterozygous advantage appears to provide a satisfactory explanation of our data.

The genetic uniformity recorded over environments ecologically differentiated for various factors (dependent on degree and type of pollution in the breeding places, structure of the larval biocenose, availability of different hosts for blood meal, etc.) should indicate the lack of simple relationships between PGM enzyme variants and the ecological factors considered.

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