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Phosphoglucomutase (PGM) polymorphism in natural populations of Drosophila melanogaster

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SEZIONE III

(Botanica, zoologia, fisiologia e patologia)

Genetica. — *Phosphoglucomutase (PGM) polymorphism in natural populations of* Drosophila melanogaster (*). Nota di GIOVANNI TRIPPA, CLAUDIA BARBERIO, ADA LOVERRE e DOMENICO ARCUDI, presentata (**) dal Socio G. MONTALENTI.

RIASSUNTO. — È stata studiata la distribuzione del polimorfismo elettroforetico per la fosfoglucomutasi (PGM) in sette popolazioni naturali di *Drosophila melanogaster*; i campioni sono stati raccolti in Puglia e in Sicilia durante il periodo Settembre–Ottobre 1971. Le sette popolazioni esaminate sono tutte polimorfiche per almeno due alleli, Pgm^A e Pgm^B. Oltre a questi due alleli già descritti ne sono stati trovati quattro nuovi, Pgm^C, Pgm^D, Pgm^E e Pgm^F. L'osservazione che gli stessi alleli, Pgm^A e Pgm^B, siano i più frequenti in tutte le popolazioni esaminate viene discussa in relazione all'idea di una prolungata azione della selezione.

INTRODUCTION

Until recently genetic polymorphism was identified mostly, if not entirely, at a morphologic or clinical or functional level, thus the genetic variations which failed to express themselves at such phenotypic levels rather far from the primary effect of the gene (that is, the majority of the gene variations) went overlooked. Moreover, there was no way of identifying a gene besides that of finding at least two alternative alleles of that gene.

Although a method of measuring the extent of genetic variation was lacking *in principle*, the fact that the observed genetic variation was very low, gave rise in the long run to the "general impression" that genetic polymorphism is a rare phenomenon.

Moreover, owing to the relatively crude methods available for detecting the phenotypic variations, the genotypic variations which were identified were usually of such an extent as to make it reasonable to believe that most, if not all, the genetic variations, were selectively relevant: not too much room was left for the neutral mutations. Two trends, one emphasizing the impact of the genetic load and the other that of the genetic flexibility, developed. Though both of them assumed that the genetic variation was, as a rule, relevant for selection, they arrived at opposite conclusions as far as the *extent* of the genetic variation was concerned.

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(**) Nella seduta del 16 giugno 1972.

Now that the occurrence of a very large genetic variation is out of the question (Shaw, 1965; Harris, 1966; Lewontin and Hubby, 1966; O' Brien and Mac Intyre, 1969; Selander *et al.*, 1970; Kojima *et al.*, 1970) the debate is by no means less fierce than before but the subject of the dispute has changed. There is the tendency, for explaining the microevolution, to switch from the old " naïve panselectionism " (as Kimura and Ohta call the old theories) to the panneutralism of Kimura and Ohta (1971) (evolution by genetic drift instead than by selection). The origin of this radical change of ideas might be recognized especially in the fact that the bulk of genetic variation which is presently being identified is an electrophoretically detectable variation, that is a variation which might well be thought to be selectively neutral.

There are two possible general approaches for trying to evaluate the relative relevance of these two factors (selection and genetic drift) in the causation and maintenance of genetic variations: a purely speculative approach and an experimental approach, which could be a direct or an indirect one. The direct approach, consisting in a series of comparisons between the relative fitnesses of the relevant genotypes for a suitable number of genetic polymorphisms, is practically unfeasible both from a technical point of view and at the level of interpretation of the results (selection or co-selection). The indirect and most recent approach consists in the search for a series of expected consequences of a *prolonged* action of selection. They could be a constancy from year to year of certain gene frequencies in natural populations though submitted to strong genetic drift (bottle neck) every year; a nonrandomness in the distribution of certain electrophoretic properties (Bulmer, 1971); the occurrence of some general rules in the distribution of gene frequencies in different natural populations, such as for example that the same allele(s) is the most common one in every population examined (for instance, this has been usually observed in Man). The latter approach has been the one adopted in the present paper.

This communication is a comparative study of electrophoretic phosphoglucomutase (PGM) polymorphism in seven natural Italian populations of *Drosophila melanogaster*.

Materials and Methods

Samples of seven natural populations of *Drosophila melanogaster*, collected during September–October 1971 in Puglia (Otranto, Castellaneta and Corato) and in Sicily (Ranna, Pedalino, Vittoria and Archi), were examined.

The PGM electrophoretic phenotypes of single adult flies were determined according to the technique of Spencer *et al.* (1964), adapted by Trippa *et al.* (1970) to single fly homogenates.

Before the PGM phenotype determination, all the males were crossed with females homozygous for a known *Pgm* allele.

RESULTS

The Pgm alleles found in the present survey.

Fig. 1 shows besides the three phenotypes PGM A, PGM AB and PGM B previously described (Trippa, 1970) four new PGM phenotypes which will be thereafter referred to as PGM AC, PGM AD, PGM AE and PGM AF (Trippa *et al.*, 1972).

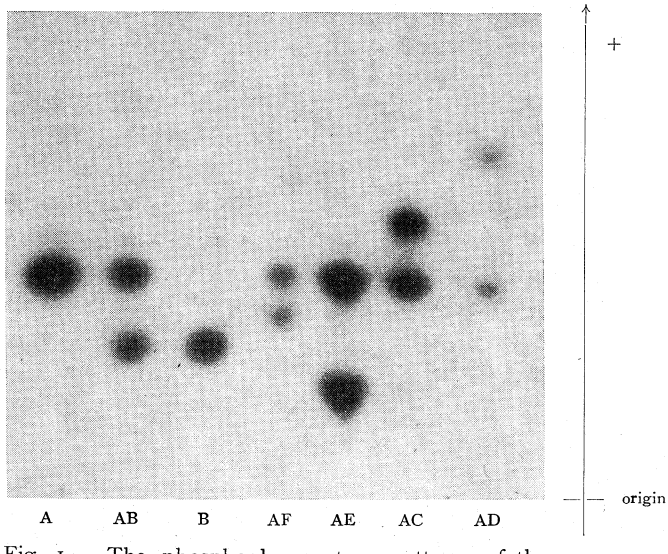

Fig. 1. – The phosphoglucomutase patterns of the different genotypes observed in the present survey.

The alleles (1) Pgm^C, Pgm^D and Pgm^E have been recovered, brought to homozygosity and maintained as laboratory stocks, while the attempts to bring to homozygosity the Pgm^F allele have been unsuccessful (this allele is at present maintained as a TM2/Pgm^F balanced stock).

No obvious quantitative differences between the new and the common alleles appeared on the visual inspection of the heterozygous variant patterns.

Population data.

Table I shows that all the seven populations examined are polymorphic for at least two alleles, the Pgm^A and the Pgm^B.

All the testable populations turned out to be in Hardy–Weinberg equilibrium for the Pgm^A and Pgm^B alleles.

(1) The frequencies of the PGM phenotypic classes were the expected ones in all the progenies of those males that turned out to be carriers of new *Pgm* alleles.

Discussion

Table I shows that in all the populations which have been examined the Pgm^A allele is the most frequent one. However, the frequency of the other common allele, the Pgm^B is so variable that the degree of heterozygosity ranges from 0.016 to 0.33.

It would be very interesting to ascertain whether or not the single frequencies and the interpopulation differences are maintained from year to year. If it turns out that this is the case the hypothesis that these allelic differences are due to selection (or to co-selection) will become extremely likely.

Table I.

The percent frequencies of alleles and the degree of heterozygosity for the Pgm *locus in samples of seven natural populations of* Drosophila melanogaster *collected in Southern Italy.*

Populations	Number of tested individuals	Percent frequencies of alleles						Degree of heterozygosity
		Pgm^A (1)	Pgm^B (1)	Pgm^C	Pgm^D	Pgm^E	Pgm^F	
1. Castellaneta . .	213	90.6	8.3	0.7	0.2	—	0.2	0.17
2. Otranto	296	93.2	5.4	0.5	0.8	—	—	0.13
3. Corato	233	94.4	5.2	0.2	—	0.2	—	0.11
4. Ranna	206	94.7	4.1	1.0	0.2	—	—	0.10
5. Pedalino	162	94.1	5.9	—	—	—	—	0.11
6. Vittoria	46	79.3	20.7	—	—	—	—	0.33
7. Archi	200	99.2	0.8	—	—	—	—	0.016

(1) The standard errors of the frequencies of the Pgm^A allele (which are practically the same as those of the Pgm^B) were for the seven samples: 1 : ± 1.38; 2 : ± 1.03; 3 : ± 1.06; 4 : ± 1.10; 5 : ± 1.31; 6 : ± 4.22; 7 : ± 0.44.

As far as the other alleles are concerned, owing the small size of the present subsamples, it is not possible for each of them to decide if it is a common or a variant allele. Relevant for this question would be the finding of the same allele or pattern of alleles in the same population (on the basis of a geographical criterion only) after a long period of time.

A further point concerns the question if the less common alleles, showing the same electrophoretic behaviour in different populations, do so because

they are the same alleles or because they are different alleles with the same electrophoretic behaviour.

The answer to this question can be considered, in a way, a by-product of the solution of the previous question. In fact, if one of the less common alleles shows itself as a common allele the most likely explanation is that it is the same in all the tested populations; on the contrary, if it turns out to be just a variant, it appears likely that it is represented by different iso-electrophoretic variant alleles in the different populations.

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