

INHERITANCE OF ORANGE PUPA AND PHOSPHOGLUCOMUTASE IN THE MOSQUITO *ARMIGERES SUBALBATUS*

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The mosquito genus *Armigeres* includes approximately 50 species. *Armigeres subalbatus* (Coquillett) has a distribution range throughout Asia from Korea through Pakistan (Knight and Stone 1977). Except for *Ar. subalbatus*, no species belonging to this genus has been cytogenetically examined. This species was reported to have three haploid chromosomes, all metacentric (Sinoto and Suzuki 1943).

This is a first genetic report for *Ar. subalbatus* on three markers: a morphological mutant (orange-pupa), the sex locus, and a phosphoglucumutase (PGM; E. C. 2. 7. 5. 1) locus. The mosquito was collected at Takashima, Saga Prefecture, Japan. The mutant orange-pupa (*op*), the *Pgm*^F (fast phosphoglucumutase allele: see below), and the *op Pgm*^S (orange-pupa, slow *Pgm* allele) lines were isolated from the Takashima strain. Rearing methods were similar to those of *Aedes togoi* (Theobald) (Tadano 1977) with the following exceptions: the eggs were hatched before drying of egg papers, larvae were reared in tap water instead of saline water, and adults were maintained in 30 x 30 x 20 cm cages. In backcross experiments, single families from single females were separately reared in plastic boxes, and the phenotypes were scored separately for each family.

Electrophoresis of phosphoglucumutase was

carried out by means of agar gels (Tadano 1986). Only adult homogenates were subjected to electrophoresis, since larvae and pupae did not give clear electrophoretic bands.

The *op* (orange-pupa) body color gene was recessive to wild type (dark green pupa) and best expressed in the pupal stage, although it also is apparent in larvae. The penetrance of this gene is excellent, with constant expressivity. The PGM activity patterns on agar gels were consistent in all lines of this mosquito, exhibiting only one banding zone located at about 3-4 cm from the electrophoretic origin. This zone contained only two alleles in all lines which were subject to electrophoresis, named fast (*F*) and slow (*S*) alleles according to their mobility (Fig. 1). The *F* allele produced two bands, of which one was faint, anodic to the other principal band. However, the *S* allele yielded only one band. Thus, the *F/S* heterozygotes exhibited a three-banded pattern. In many *Anopheles* species, each allele for PGM displays a single, discrete band, while in *Anopheles claviger* (Meigen), *An. maculipennis* Meigen, *Culex quinquefasciatus* Say, *Aedes albopictus* (Skuse), and *Ae. togoi* (Theobald), each PGM allele produces two bands (for a review, Tadano 1986). Therefore, the *Pgm* alleles in *Ar. subalbatus* were unique in that one allele displayed two bands and the other only one band.

Four backcrosses (Table 1) were made to determine linkage relationships among *op*, *Pgm* and sex locus. The sex-determining genotype was hypothesized to be *m/m* for femaleness and *M/m* for maleness, as in other culicine mosquitoes. All the backcross data herein are consistent with this hypothesis.

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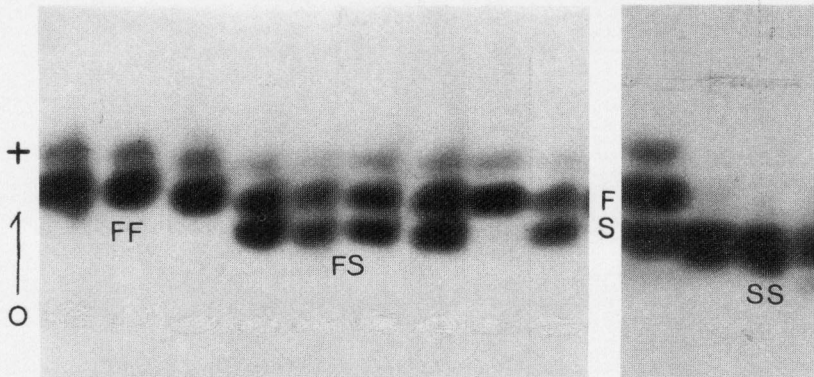


Fig. 1. Electrophoretic patterns of phosphoglucumutase (PGM) in *Armigeres subalbatus*.

Table 1. Results of backcrosses in *Armigeres subalbatus*.

Phenotype	Cross A: $op \text{♀} \times (+ \text{♀} \times op \text{♂})$ Cross B: $op \text{♀} \times (op \text{♀} \times + \text{♂})$ Cross C: $(+; Pgm^F \text{♀} \times op; Pgm^S \text{♂}) \text{♀} \times op; Pgm^S \text{♂}$ Cross D: $op; Pgm^S \text{♀} \times (+; Pgm^F \text{♀} \times op; Pgm^S \text{♂})$		Phenotype	C*	D*
	A	B			
♀ <i>op</i>	3	204	♀ <i>op Pgm^{S/S}</i>	32	0
♀ +	67	1	♀ <i>op Pgm^{F/S}</i>	22	3
♂ <i>op</i>	47	10	♀ + <i>Pgm^{S/S}</i>	34	57
♂ +	6	198	♀ + <i>Pgm^{F/S}</i>	26	63
Sum	123	413			
Families pooled	2	6	♂ <i>op Pgm^{S/S}</i>	16	57
Map units between sex (<i>M/m</i>) and <i>op</i>	7.3 ± 2.4	2.7 ± 0.8	♂ <i>op Pgm^{F/S}</i>	28	54
			♂ + <i>Pgm^{S/S}</i>	34	0
			♂ + <i>Pgm^{F/S}</i>	20	3
			Sum	212	237
			Families pooled	4	4
			Map units between sex (<i>M/m</i>) and <i>op</i>	X	2.5 ± 1.0

* χ^2 values testing for linkage between *Pgm* and either *op* or sex (*M/m*) were: 2.72 between *Pgm* and *op* in C; 0.34 between *Pgm* and *op*, and 0.34 between *Pgm* and sex (*M/m*) in D. All χ^2 values indicate that *Pgm* assort independently of either *op* or sex ($P > 0.05$).

Segregation of alleles in each cross was tested by χ^2 and showed the 1:1 ratio ($P \gg 0.05$) with one exception—cross A produced more wild-type offspring (73 individuals) than *op* (50 individuals) ($0.05 > P > 0.02$). In crosses A and B, linkage between *op* and sex (*M/m*) was clear, with recombination units (\pm SE) of 2.7 ± 0.8 to 7.3 ± 2.4 . Additionally, cross D gave 2.5 ± 1.0 units between *M/m* and *op* (χ^2 for linkage = 213.6, $P \ll 0.01$). Cytologically, the sex chromosomes in this species have not been confirmed to be homomorphic as in *Aedes* and *Culex* species (Rai and Hartberg 1975, Barr 1975), but the genetic basis for sex determination in *Ar. subalbatus* seems to be fundamentally the same as that in *Aedes* and *Culex*. Crosses C and D suggested that *Pgm* is inherited independently of the *M/m*—*op* chromosomal region.

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