A SEX-LINKED MUTANT, HOOKED LEG, IN *AEDES* (*FINLAYA*) *TOGOI*

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ABSTRACT. A new recessive mutant, hooked leg (*h*), was discovered from an inbred strain of *Aedes togoi*. Tarsi of hindlegs in the mutant are bent sharply like hooks and the hindlegs of some homozygotes for *h* are sometimes broken off by hooking onto the pupal skins upon emergence. Homozygotes exhibit complete penetrance with almost uniform expression. The midlegs of the homozygotes are also slightly affected.

Linkage studies indicated that the *h* allele is located between the *m* (sex allele) and *s* (straw-colored larva) loci on linkage group I and that the recombination distances are 16.5 map units for *m-h*, 39.0 for *h-s*, and 42.4 for *m-s*.

The mosquito *Aedes* (*Finlaya*) *togoi* (Theobald) occurs mainly on the Pacific east coast of Asia, but recently has been collected from the Pacific coast of Canada (Meredith and Phillips 1973, Trimble and Wellington 1979) and U. S. A. (Belton 1980). This species can be a natural or experimental vector of various species of filarial worms (Tadano 1977).

To date 5 mutant genes have been described for linkage group I in the mosquito; they are *n* (notch wing), *rd* (reddish eye), *m* (sex), *dv* (disturbed venation), and *s* (straw-colored larva) (Tadano 1976,

1977, 1979a,b). The gene arrangement and recombination distances on this linkage group are: *n*-(32)-*rd*-(0)-*m*-(approximately 25)-*dv* -(5)-*s*.

A new sex-linked mutant, hooked leg (*h*), was found during routine rearing of this species. Tarsi of hindlegs in this mutant were bent sharply like hooks (Fig. 1); those of the midlegs were also slightly affected. Hindlegs of the homozygotes for *h* were sometimes lost upon emergence because of adhesion to the pupal skins. This allele was recessive and exhibited complete penetrance as well as almost constant expression. The *h* phenotype appeared similar to those of the *th* (tarsi-hooked) mutant of *Ae. aegypti* (Linn.) (McClelland 1962, Craig and Hickey 1967), and of the *cl* (curved leg) mutant of *Culex tritaeniorhynchus* Giles (Baker and Sakai 1973).

This paper gives linkage data on the *h* mutant gene.

MATERIALS AND METHODS

Three wild-type strains and 2 genetic marker strains were employed for this study. The wild-type strains, MUR, MNZR, and NGSK, were collected at Miura City and Manazuru Town, Kanagawa Prefecture, and Nagasaki City, Kyushu, respectively. One marker strain carried the *s* (straw-colored larva) allele on linkage group I, and the other strain the *y* (yellow larva) on group III.

Mass crosses were done for all experiments, but single blood-fed females were isolated from the experimental cages into individual plastic cups for oviposition. Larvae from each egg batch were separately reared as a family, and the phenotypic scores were recorded for each family.

RESULTS AND DISCUSSION

Six crosses were conducted in this study (Table 1). Crosses A and B were

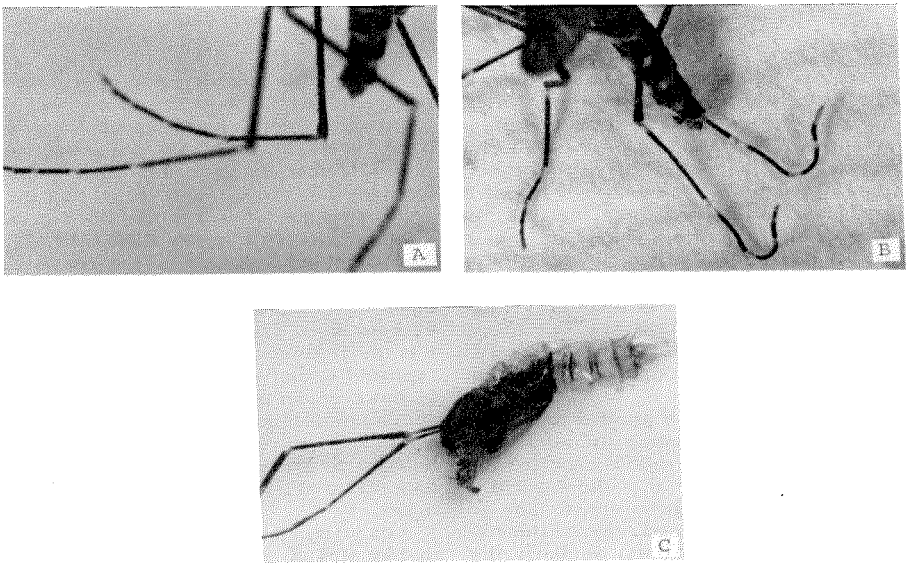

Fig. 1. A, wild-type leg; B, hooked hindleg (*h*), also note the affected middle leg; C, *h* legs adhering to the puparium.

Table 1. Results of all crosses performed throughout this study.

Cross	Parental genotype ♀	×	♂	Phenotype of offspring: Female ++	Female +h	Female s+	Female sh	Male ++	Male +h	Male s+	Male sh	Families pooled	Total
A	$\frac{+\ m}{h\ m}$	×	$\frac{+\ m}{h\ m}$	861	106	—	—	644	402	—	—	12	2013
B	$\frac{s\ +\ m}{+\ h\ m}$	×	$\frac{s\ +\ m}{+\ h\ M}$	124	18	59	0	77	60	53	19	5	410
C	$\frac{s\ h\ m}{+\ +\ m}$	×	$\frac{s\ h\ m}{s\ h\ M}$	93	22	9	65	102	10	25	76	4	402
D	$\frac{s\ h\ m}{s\ h\ m}$	×	$\frac{s\ h\ m}{+\ +\ M}$	25	77	17	116	131	15	85	34	5	500
E	$\frac{s\ h\ m}{s\ h\ m}$	×	$\frac{+\ +\ m}{s\ h\ M}$	402	38	261	63	80	244	64	400	15	1552
				Female ++	Female +h	Female y+	Female yh	Male ++	Male +h	Male y+	Male yh		
F	$\frac{y\ h\ m}{y\ h\ m}$	×	$\frac{y\ h\ m}{+\ +\ M}$	47	140	48	165	165	39	171	47	7	822

heterozygotes × heterozygotes; crosses C through F were the reciprocal testcrosses. In each of the 6 crosses, the segregation of alleles were examined for the 1 : 1 or 1 : 3 ratio by chi-square tests of the pooled data. Chi-square tests in crosses A and B indicated that the sex and *h* alleles segregated at the expected 1 : 1 and 1 : 3 ratios, respectively, but *s* individuals were fewer than expected ($P < 0.01$). The χ^2 values estimated for crosses C through F suggested that alleles in crosses C to F segregated at a 1 : 1 ratio, but that in cross C there were significant deficiencies of both *h* and *s* individuals.

Again, χ^2 tests were applied to examination for linkage among the alleles. In cross A, a 1 : 1 : 3 : 3 ratio is expected for *h*♀ : h ♂ : + ♀ : + ♂ if the *h* allele is inherited independently of sex. The χ^2 value (= 212.9) obtained rejected this hypothesis (d.f. = 3, $P < 0.01$). Similarly, the χ^2 values, estimated in crosses C to F (Table 2), also provided strong evidence of sex-linkage for both *h* and *s*.

Recombination units calculated for *m* (sex) - *s*, *m* - *h*, and *s* - *h* are shown in parentheses in Table 2. The three-point testcross data (D and E) revealed that the gene order is *m* - *h* - *s*, and that the *h* locus is located closer to the sex allele than to *s*. The weighted averages of the recombination units, calculated from the D and E data, were 16.5 for *m* - *h*, 39.0 for *h* - *s*, and 42.4 for *m* - *s*. The map distance for *m* - *s* was much longer than that (ca. 30 units) reported earlier (Tadano 1977). In cross C, however, an unusually low level of recombination (16.4 ± 1.8 map units) was observed between *h* and *s*. The heterozygous females showed a recombination rate of less than half of that of the males.

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Table 2. Chi-square values testing for linkage between *m*, *s*, *h*, and *y*, and recombination units between linked loci.

Cross	Linkage (map units)			
	m–s	*m–h*	*s–h*	*h–y*
C			181.30 (16.4±1.8)	
D	6.73 (44.2±2.2)	202.25 (18.2±1.7)	25.09 (38.8±2.2)	
E	41.52 (41.8±1.3)	723.04 (15.9±0.9)	74.39 (39.1±1.2)	
F		257.42 (22.0±1.4)		0.82*

Figures in parentheses are recombination units ± standard errors.
* All values except this are significant ($P < 0.01$).

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