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SHORT WING, A RECESSIVE MUTANT ON CHROMOSOME 1 IN *CULEX TRITAENIORHYNCHUS*

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ABSTRACT. A recessive, sex-linked mutant, short wing (*sw*), was isolated from a strain which contained an induced translocation. Genetic crosses revealed that the gene sequence is w^{re}

(rose eye) - $sw - M$ (sex) and the recombination frequencies are as follows: $w^{re} - sw = 7.3\%$, $sw - M = 5.9\%$ and $w^{re} - M = 13.2\%$.

During routine culling of a strain of *Culex tritaeniorhynchus* containing an autosomal translocation, a number of individuals with short wings were found. The wings of these individuals were greatly shortened and broadened with very prominent venation; in addition, the segments of the legs were usually shorter and thicker than the wild type. The larvae and pupae of this mutant appear to develop normally, but there is considerable mortality during and shortly after emergence of the imago. Some of the adults are unable to extricate their legs from the pupal case while others seem unable to fly from the surface of the water and consequently drown. A pure line of short wing was

selected without the presence of the translocation. The morphological characteristics as well as the viability problems associated with this mutant are similar to those of the short wing mutant in *Aedes aegypti* (Uppal et al. 1976). The results of the genetic analysis of short wing (*sw*) in *Cx. tritaeniorhynchus* are reported.

MATERIALS AND METHODS

The following strains of *Cx. tritaeniorhynchus* were used in the crosses:

1) Balloki—a wild type strain colonized from Balloki Headworks with the M^1 sex allele (Baker and Sakai 1976).

2) rose (w^{re})—this strain contains the

recessive linkage group I mutant, rose eye (Baker and Sakai 1973).

3) short wing (*sw*)—the short wing mutant strain.

4) rose, short wing (*w^{re}sw*)—this strain is homozygous for rose and short wing.

The crossing procedures as well as the rearing and handling of the eggs, larvae,

pupae and adults were as described previously (Baker and Sakai 1973).

RESULTS AND DISCUSSION

Table 1 is the summary of crosses done to elucidate the inheritance of short wing, and Table 2 the frequency of crossing over among linked loci.

Table 1. Results of crosses to determine the inheritance of *sw*

Cross	Proposed Parental Genotype		F*	Progeny Phenotype**							
				♀				♂			
				+	re	sw	re sw	+	re	sw	re sw
A	$\frac{+ + m}{+ + m}$	$\times \frac{re sw m}{re sw M^1}$	3	180	0	0	0	200	0	0	0
B	$\frac{re sw m}{re sw m}$	$\times \frac{+ + m}{+ + M^1}$	5	365	0	0	0	393	0	0	0
C	$\frac{+ sw m}{+ sw m}$	$\times \frac{re + m}{re + M^1}$	4	208	0	0	0	219	0	0	0
D	$\frac{re + m}{re + m}$	$\times \frac{+ sw m}{+ sw M^1}$	5	222	0	0	0	205	0	0	0
E	$\frac{+ + m}{re sw m}$	$\times \frac{re sw m}{re sw M^1}$	5	111	0	0	114	117	0	0	93
F	$\frac{re sw m}{+ + m}$	$\times \frac{re sw m}{re sw M^1}$	4	122	0	0	96	116	0	0	99
G	$\frac{+ sw m}{re + m}$	$\times \frac{re sw m}{re sw M^1}$	2	0	80	53	0	0	68	79	0
H	$\frac{re + m}{+ sw m}$	$\times \frac{re sw m}{re sw M^1}$	5	0	230	195	0	0	212	218	0
I	$\frac{re sw m}{re sw m}$	$\times \frac{+ + m}{re sw M^1}$	10	445	31	0	37	27	0	34	356
J	$\frac{re sw m}{re sw m}$	$\times \frac{re sw m}{+ + M^1}$	10	24	0	30	282	416	19	0	9
K	$\frac{re sw m}{re sw m}$	$\times \frac{+ sw m}{re + M^1}$	9	1	32	323	35	41	389	31	1
L	$\frac{re sw m}{re sw m}$	$\times \frac{re + m}{+ sw M^1}$	9	40	473	28	0	0	21	416	30

* F = number of families tested.

** re = *w^{re}*

Table 2. Recombination frequencies in males

Cross	% combination in males		
	re - sw	sw - M	re - M
I	6.99 ± 0.84	6.88 ± 0.83	13.87 ± 1.13
J	6.28 ± 0.87	4.23 ± 0.72	10.51 ± 1.10
K	9.14 ± 0.99	7.62 ± 0.91	16.76 ± 1.28
L	6.94 ± 0.80	4.86 ± 0.68	11.80 ± 1.02

In Table 1, A-D are reciprocal crosses among the parental strains. The progeny from all the crosses were wild type, indicating that *sw* is recessive and confirming the previous observation that *w^{re}* is also recessive (Baker and Sakai 1973). Crosses E-H are backcrosses of heterozygous females to *w^{re} sw* males. The highly significant chi-squares ($P < .01$) testing for independent segregation between *w^{re}* and *sw* indicate linkage between these two loci. Sex linkage cannot be determined in females as they are the homogametic sex in *Cx. tritaeniorhynchus*. Moreover, since there is generally no crossing over in females, (and none were found in these crosses) recombination frequencies can only be calculated from male data. In the three point backcrosses of heterozygous males to *w^{re} sw* females, highly significant linkage chi-

squares ($P < .01$) were found for *w^{re}, sw* and *M* (sex). Table 2 is a summary of the observed recombination frequencies among the three loci. The gene sequence is *w^{re} - sw - M* and the recombination frequencies from the pooled data are as follows: *w^{re} - sw* = 7.3%; *sw - M* = 5.9% and *w^{re} - M* = 13.2%.

ACKNOWLEDGMENT

This work was supported by Grant No. AI-10049 from the National Institute of Allergy and Infectious Diseases, NIH. We appreciate the technical help of Messrs. M. Saghir, N. Hussain, I. Zafar, M. Tahir, L. Chaudhari, Z. Ahmad, I. Chughtai, M. Ali, M. Rais, and M. Ali, and the assistance of the U.S. Agency for International Development in Pakistan.

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