A RED STRIPE CHARACTER AND ITS INHERITANCE IN *ANOPHELES ALBIMANUS* WIED [1]

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ABSTRACT. The description of a red stripe mutant (*Rd*) in larvae, pupae, and adults of *Anopheles albimanus* Wied. is presented. Despite incomplete penetrance, it was determined that *Rd* is inherited as a single, dominant gene in the same linkage group as *St* at a distance of 15–28 units. A discussion of the penetrance of *Rd* when associated with either *St* or St^+ is also presented.

Morphological mutant markers are being used with increasing frequency in research on genetic control of insects (Davidson 1972, Wright and Pal 1967). Although several markers have been identified in *Culex fatigans* Wied. and *Aedes aegypti* L., there is a paucity of such markers reported in anophelines. Only one mutant, a white stripe character, has been studied in *Anopheles albimanus* Wied. (Georghiou et al. 1967). In this investigation we describe a new character, red stripe, and report on its mode of inheritance.

MATERIALS AND METHODS

MOSQUITO STRAINS. The following strains of *A. albimanus* were used:

(1) White stripe (*St*), a strain originating on Haiti and true breeding for a dorsal white stripe character in the larva (Georghiou et al. 1967)

(2) Non-stripe (St^+), was collected in Panama by L. E. Rozeboom in 1936 and provided by the Gorgas Memorial Laboratory, Balboa Heights, Panama.

(3) Red stripe (*Rd*), a mutant discovered in a collection obtained from Hacienda Melara, Department of La Libertad, El Salvador, in June, 1970 (Ariaratnam and Georghiou 1971).

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Table 1. Crosses involving red stripe and segregation of phenotypes obtained.

Cross	Parental phenotype	Total examined	Progeny phenotype (%)						
			1° *Rd*	2° *Rd*	3° *Rd*	Total *Rd*	*St*	*St*⁺	*RdSt*
1	*St* ♀ x *Rd* ♂	3,015	...	...	...	82.5[a]	17.5	...	...
2	*St* ♀ x *Rd* ♂	3,424	5.3	72.1	18.8	96.2	3.8	...	...
3	*St* ♀ x *Rd* ♂	2,069	0.7	80.9	17.7	99.3	0.7	...	...
4	*St*⁺ ♀ x *Rd* ♂	1,330	10.5	62.2	0.8	73.5	...	26.5	...[b]
5	(*St* ♀ x *Rd* ♂) ♀ x (*St* ♀ x *Rd* ♂) ♂	7,011	0.1	15.4	9.9	25.4	20.2	0.2	54.2
6	(*St* ♀ x *Rd* ♂) ♀ x *St*⁺ ♂	11,960	...	...	...	18.5[a]	47.2	33.1	1.2
7	(*St* ♀ x *Rd* ♂) ♀ x *Rd* ♂	13,714	...	...	...	50.9	3.9	0.3	44.9
8	(*St*⁺ ♀ x *Rd* ♂) ♀ x *St*⁺ ♂	6,932	4.0	20.1	...	...	...	75.9	...
9	*St*⁺ ♀ x (*St*⁺ ♀ x *Rd* ♂) ♂	257	4.3	31.1	...	...	...	64.6	...

[a] Unclassified as to 1°, 2° or 3°.
[b] 1° *Rd* 2.2%; 2° *Rd* 41.4%; 3° *Rd* 10.6%.

DESCRIPTION OF MUTANT. The red stripe character, *Rd,* was found to be present in both larvae and pupae but with variable intensity of expression. In its full expression it is designated as 3°*Rd*. A slightly lighter red is referred to as 2° *Rd,* while the 1°*Rd* variation differs from both 3° and 2°*Rd* in that its expression may be limited to only the posterior portion of the 1st abdominal segment or can be faintly discernible on the lateral edges of, at most, four segments.

The red stripe character in the adult is not easily detectable because of metallic-gold hairs which cover the abdominal surface. Upon manipulation of the specimen in relation to the light source, one observes two parallel red lines which extend down the median dorsal surface of the abdomen. The lines were generally more evident in females, probably due to their larger size. No evidence of the red stripe character was seen on the thorax.

An initial check of the homogeneity of the red stripe character among offspring showed a 100% penetrance of *Rd* (3° and 2°*Rd* only) in the colony.

MATINGS. Nine crosses were performed as indicated in Table 1. They involved either 100–200 or 5–20 individuals of each sex depending on whether a sample or all of the progeny were to be examined. Only larvae with the highest expression of *Rd* were used for crossing. Sexing was facilitated by the isolation of pupae in 20 ml shell vials. The adults were introduced in a cage progressively over a period ranging from one day to two weeks.

RESULTS AND DISCUSSION

ALLELISM BETWEEN *Rd* AND *St*. Crosses 1, 2, 3 and 4 were made to test red stripe against the non-stripe and white stripe alleles of the *St* locus. In Cross, 1, 525 of 3015 larvae sampled (17.5%) did not show the red stripe character. Subsequently, Crosses 2 and 3 were a repetition of the *Rd* x *St* cross and showed only 3.8% and 0.7% larvae, respectively, without the red stripe. White stripe (*St*) was present in all offspring larvae examined in

each cross. This agrees with data reported by Georghiou et al. (1967), who showed *St* to be dominant to non-stripe (*St*$^+$). In Cross 4 the red stripe was present in 73.5% of the larvae, the rest being non-stripe. Thus *Rd* is apparently dominant over *St*$^+$. The incomplete penetrance noted above will be dealt with later in the discussion.

Before examining the possibility of allelism between the *Rd* and *St* loci, Cross 5 was performed to ascertain whether *Rd* is a monogenic or polygenic character. The results (Table 1, Cross 5) provided no evidence of polygenic inheritance. Since no gradations in the expression of the character occurred which could not be explained by biological variation (2° *Rd*) or reduced expressivity of the mutant character (1°*Rd*), it was felt that *Rd* is determined by a single, dominant gene. The possibility of *Rd* being allelic to the *St* locus may also be discounted, since the backcross (*St* ♀ x *Rd* ♂) to *St*$^+$ (Cross 6) produced four classes instead of two that would be expected if the genes were allelic. These results differ from preliminary findings of Mason (1967), who believes that a red stripe mutant in *Anopheles gambiae* is of polygenic inheritance.

It will be noted that the data for segregation of phenotypes in Cross 6 (backcross to *St*$^+$) showed 19%:47%:33%:1% segregation of red stripe, white stripe, non-stripe, and red and white stripe, respectively. Because of the deviation from a 1:1:1:1 segregation ratio, linkage of *Rd* and *St* was suspected.

LINKAGE AND PENETRANCE TESTS. Evidence of linkage between *Rd* and *St* was sought from an F2 progeny (Cross 5). It was felt that if *Rd* and *St* were indeed linked, one would expect 1:2:1 segregation of *Rd:RdSt:St,* as well as 3:1 ratios for *Rd:rd* and *St:St*$^+$. Chi-squire values for the 1:2:1 and the 3:1 (*Rd:rd*) showed highly significant deviations from the expected (χ^2=91 and 86, respectively). However, the Chi-square for 3:1 (*St:St*$^+$) showed a good fit with a value of 0.842. What is unusual about the significant Chi-squares is the greater than expected percentage of *Rd/St* (~54%) and *Rd* (~26%) offspring. This is contrary to expectation based upon the F1 progeny in which only 96.2% showed both the *Rd* and *St* characters. However, two recombinant classes *Rd/St* and *Rd* could account for the observed deviations, since any expected reduction of *Rd/St* and *Rd* would be masked by recombinant larvae. If the expected for *Rd/St* is ~48% (i.e. 0.5 x 96%) and for *Rd* 25%, the percentage of recombinations is 7% (6% *Rd/St* and 1% *Rd*.) Additional evidence for the occurrence of recombinants is the presence of 0.2% (16 of 7011) *St*$^+$ larvae.

Incomplete penetrance of *Rd* when associated with *St* is indicated from Crosses 1,2,3, and 7. In the progeny of Crosses 1–3 the range of *Rd* penetrance is 82.5% to 99.3% In Cross 7, a backcross to the *Rd* colony, since the recombinants were not differentiable from parental types, all larvae are expected to be either *Rd* or *Rd/St*. The observed 4.2% not belonging to either class must be a result of reduced penetrance of *Rd*. Since Crosses 2,3 and 7 all indicate a penetrance of 96–99%, it is likely that these results better reflect the true degree of penetrance of *Rd* in association with *St*.

In the case of *Rd* vs. *St*$^+$, a lower degree of *Rd* penetrance is noted. Cross 4 resulted in only 73.5% *Rd* individuals. Of these, 62.2% were 2°*Rd* with only 0.8% showing full expression (3°*Rd*) of *Rd*. A backcross to the St$^+$ colony using 2° *Rd* larvae (Cross 8) yielded only 24.1% of progeny with the marker (no 3°*Rd* were found). A second backcross (Cross 9) utilizing 2°*Rd* types from Cross 8 yielded 35.4% *Rd*. Therefore the degree of penetrance of *Rd* when associated with *St*$^+$ ranges from 48.2% (Cross 8) to 70.8% (Cross 9) to 73.5% (Cross 4).

The strength of linkage between *St* and *Rd* loci may be determined using backcross data from Cross 6. Approximately 52% of this population are *Rd* and *St*$^+$ phenotypes, a percentage of which are *Rd* individuals misclassified as *St*$^+$. Using

the various penetrance percentages, the calculated crossover values [e.g. 52% — (0.52 x 48% x 100) +1%, *Rd/St* recombinants] show that *St* and *Rd* are 15–28 units apart.

Reasons for incomplete penetrance are largely speculative and in this case it might be attributed to modifiers affecting the pigment-producing pathways. Perhaps it is sex-related, since different levels of *Rd* penetrance occurred in the reciprocal backcrosses (Crosses 8 and 9).

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