A *WHITE THORAX* MUTANT AND ITS RELATIONSHIP IN AN ALLELIC SERIES IN *ANOPHELES ALBIMANUS* WIEDEMANN[1,2]

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ABSTRACT. A strain of *Anopheles albimanus* Wiedemann with white pigmentation on the dorsum of the thorax in larvae and pupae was selected. Genetic crosses were made with this mutant marker, *white thorax* (st^w), which showed it to be part of an allelic series with *stripe* (st^+) and *non-stripe* (*st*). The st^+ character is completely dominant over st^w, and *st* is recessive to both st^+ and st^w.

INTRODUCTION

The importance of *Anopheles albimanus* Wiedemann as a vector of malaria has prompted studies aimed at developing genetic control systems. The most promising of these, compound chromosomes and homozygous translocations, require a thorough genetic knowledge of the species and necessitate sophisticated crossing schemes which utilize mutant markers. Recently, we have isolated and characterized several mutant markers in *An. albimanus*, and in this communication we describe the larval and pupal marker, *white thorax* (st^w). *White thorax* is a member of an allelic series that includes *stripe* (st^+) and *non-stripe* (*st*), previously described by Rabbani and Seawright (1976). It is recessive to st^+ and dominant over *st*.

MATERIALS AND METHODS

During field investigations of natural populations of *An. albimanus* in El Salvador in 1979, larvae were observed that had a white spot on the dorsum of the thorax. The limited incidence of this variant in the wild populations prevented colonization at that time. However, several strains of *An. albimanus* from El Salvador are maintained in our laboratory. The SANTA TECLA strain was screened

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for 1 week (27 trays with ca. 3,000 larvae/tray), and 1 larva exhibiting a white thorax similar to that seen in natural populations was found. The subsequent adult female was mated with the recessive mutant *non-stripe*, and the F_1 progeny were inbred to establish a vigorous colony of *white thorax* (st^w) individuals from the F_2 generation.

The stocks used in crosses were:
(1) SANTA TECLA—This stock, which was colonized in El Salvador in 1975, is comprised of *tan larva* (gl^+) and *normal palmate* (rp^+); it also contains approximately equal numbers of st^+ and *st*, both of which are numerous in the field.
(2) WILD—This stock is homozygous for gl^+, rp^+, and st^+.
(3) GL RP ST—This stock is homozygous for the recessive markers *green larva (gl)*, *reduced palmate (rp)*, and *st*.

Our rearing procedures were similar to those used by Rabbani and Seawright (1976) except that a 2% suspension of TetraMin® was substituted for liver-yeast. Also, crosses involving the recessive mutant *reduced palmate* were reared at 25 ± 0.5°C for production of good gene expression in this temperature-sensitive mutant (Seawright et al. 1979b). Adults were maintained on 10% sucrose and held at 85 ± 5% RH and 25 ± 1°C. Females were blood-fed on guinea pigs.

We made the appropriate crosses (Table 1) between the stock containing *white thorax* ($gl^+gl^+\ rp^+rp^+\ st^wst^w$) and *gl rp st* to assign st^w to a linkage group. *Green larva* is on chromosome 2 (Seawright et al. 1979a) and *reduced palmate* is on chromosome 3 (Seawright et al. 1979b). Crossingover occurs on the autosomes of both sexes of this mosquito so we utilized both hybrid males and females in the backcrosses.

The mode of inheritance and status of st^w in an allelic series with st^+ and *st* was determined by crosses to the WILD and SANT TECLA stocks (Table 2).

RESULTS AND DISCUSSION

The st^w deviant found in the SANTA

Table 1. Summary of crosses with *white thorax* (st^w) that demonstrate independent assortment with *green larva (gl)* on chromosome 2 and linkage with *reduced palmate (rp)* on chromosome 3. of *An. albimanus*.

Crosses ♀ X ♂	Phenotypes								Total	χ^2				
	st^w				st					Monofactorial inheritance			Linkage	
	gl^+		gl		gl^+		gl							
	rp^+	rp	rp^+	rp	rp^+	rp	rp^+	rp		st^w	gl	rp	st^w—gl	st^w—rp
F_1 (+ +st^w X $glrpst$) X $glrpst$	137	20	135	20	25	129	32	154	652	1.20	1.38	0.06	1.77	321.7[a]
F_1 ($glrpst$ X + +st^w) X $glrpst$	120	28	122	33	39	106	32	110	590	0.43	0.03	2.20	0.17	180.1[a]
$glrpst$ X F_1 (+ +st^w X $glrpst$)	104	15	97	21	20	70	27	104	458	0.56	3.49	3.15	3.85	186.2[a]
$glrpst$ X F_1 ($glrpst$ X + +st^w)	127	26	132	30	38	118	35	118	624	0.06	0.06	2.56	0.23	214.7[a]
Total	488	89	486	104	122	423	126	486	2324					

[a] $p = < 0.01$.

Table 2. Summary of crosses showing that *white thorax* (st^w) is a member of an alleleic series with *stripe* (st^+) and *non-stripe* (*st*) and that st^w is recessive to st^+ and dominant to *st* in *An. albimanus*. The χ^2 values are not significant.

Crosses ♀ X ♂	Phenotypes st^+	st^w	*st*	Total	χ^2
F_1 ($st^w st^+$) X st[a]	138	159	0	297	1.48
F_1 (st^+ X st^w) X *st*	215	235	0	450	0.89
st X F_1 (st^w X st^+)	164	196	0	360	2.84
st X F_1 (st^+ X st^w)	167	169	0	336	0.01
F_1 (st^w X *st*) X st[b]	0	229	214	443	0.51
F_1 (*st* X st^w) X *st*	0	215	197	412	0.79
st X F_1 (st^w X *st*)	0	240	261	501	0.88
st X F_1 (*st* X st^w)	0	199	190	389	0.21

[a] For these crosses the WILD stock was the source of st^+.
[b] For these crosses the SANTA TECLA stock was the source of *st*.

TECLA strain was crossed to *st* and ca. 50% of the F_1 progeny exhibited the new phenotype. These were inbred and a homozygous st^w strain was selected over several generations. The appearance of the white pigmentation, which is located on the dorsal side of the thorax of pupae and 3rd- and 4th-stage larvae, is similar to that of st^+. However, the abdomen of st^w individuals lacks the white pigmentation of st^+ larvae and is more similar in appearance to that of *st* (Figure 1).

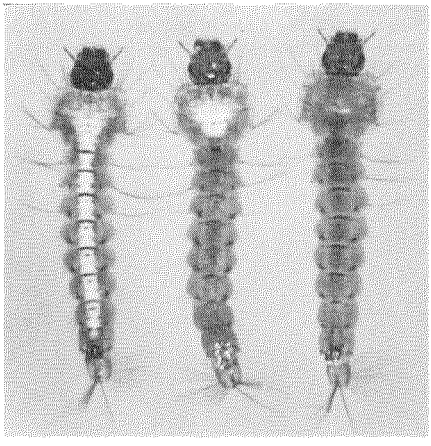

Fig. 1. A comparison of the phenotypes of an allelic series in *An. albimanus: stripe* (left); *white thorax* (middle); *non-stripe* (right).

The results of the crosses shown in Table 1 demonstrate independent assortment between st^w and *gl* on chromosome 2 and linkage between st^w and *rp*, which is on chromosome 3. Using the maximum likelihood method (Mather 1957) on the combined data from the 4 crosses in Table 1, we estimated the map distance between st^w and *rp* to be 18.97 ± 3.3 units. This is similar to the distance of 17.1 ± 0.9 map units observed between *st* and *rp* by Seawright et al. (1979b). Rabbani and Seawright (1976) and Kaiser et al. (1981) have established that *st* is on the right arm of chromosome 3.

When st^w and st^+ homozygotes were crossed, all the F_1 progency were wild type (st^+). The appropriate backcrosses demonstrated the recessive, monofactorial relationship of st^w to st^+. However, crosses between st^w and *st* homozygotes resulted in only st^w F_1 progeny; backcrosses showed the recessive, monofactorial nature of *st* to st^w (Table 2).

The physical appearance of the 6 genotypes constituting the allelic series was observed in both larvae and pupae. The 3 genotypes expressed as st^+ were identical in appearance in both stages, as were the 2 genotypes expressed as st^w, which demonstrates the complete penetrance of both the st^+ and st^w alleles. The *stst* phenotype is completely distinguishable from the other 2 phenotypes in the larval and pupal stages, and none of the

phenotypes are expressed in the adult stage.

We are primarily interested in developing genetic control methods for *An. albimanus*, especially compound chromosomes and homozygous translocations, and the use of mutant markers is essential in detecting new aberrations, maintaining aberrant strains, and following crossing schemes. The addition of the st^w mutant has provided the first allelic series in *An. albimanus*. *Stripe* and *st* were previously described by Rabbani and Seawright (1976). Other important genetic markers in *An. albimanus* are: 1) larval marker—*reduced palmate* (Seawright et al. 1979b); 2) larval and pupal marker—*green larva* (Seawright et al. 1979a) and *brown larva (br)* (unpublished data); 3) larva, pupa and adult marker—*red eye (re)* (unpublished data) and *white eye (we)* (unpublished data); 4) egg, larva, pupa and adult marker—*propoxur resistance* (pr^r) (Kaiser et al. 1979); 5) adult marker—*bald palpi (bp)* (unpublished data).

The presence of an allelic series in *An. albimanus* has provided us with a useful tool in the maintenance of autosomal heterozygous translocations. For example, a translocation marked with st^w can be maintained as $st^w st$ for several generations without cytological verification, yet it remains recessive to st^+, which is essential in some of our crosses used to detect compound chromosomes.

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