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INHERITANCE OF *BALD PALPI* AND *BALD ANTENNA* IN *ANOPHELES ALBIMANUS*[1]

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ABSTRACT. *Bald palpi (bp)* and *bald antenna (ba)* are fully penetrant, recessive, autosomal mutants of *Anopheles albimanus*. These new mutants are visible only in the adult stage, and the expression of *bald antenna* is limited to males. Genetic crosses were used to assign *bald palpi* to the right arm of chromosome 2. *Bald antenna* is loosely linked to *nonstripe (st)* on chromosome 3.

The inheritance and linkage groups for several mutants and enzymes were noted in a recent report by Narang et al. (1981) on *Anopheles albimanus* Wiedemann, the most important vector of human malaria in Central America. We are involved in conducting genetic and cytogenetic studies of *An. albimanus* with the intention of using this information in devising better strategies for the control of this species.

In this present paper, we describe the mode of inheritance of *bald palpi (bp)* and *bald antenna (ba)*, both of which are recessive, autosomal traits expressed only during the adult stage. The expression of *bald antenna* is limited to the male sex.

METHODS AND MATERIALS

Established procedures were employed for rearing and maintenance of the mosquitoes (Rabbani and Seawright 1976, Seawright et al. 1979). An inbreeding scheme was used to obtain the mutants.

Appropriate crosses (Tables 1–6) were used to determine the mode of inheritance and the linkage group for the 2 mutants. Other mutants and stocks used in the linkage study included: *red eye (re)* on 2R (unpublished), *propoxur resistance* (pr^r) on 2R (Kaiser et al. 1979), *T(Y;2R)1*—a male linked translocation (Rabbani and Kitzmiller 1972), and *nonstripe (st)* on 3R (Rabbani and Seawright 1976). Crossing over occurs on the 2 autosomes of both sexes of *An. albimanus* (Kaiser et al. 1979). Sex determination is an XY system in this species, and the male is the heteromorphic sex (Keppler et al. 1973).

RESULTS

Bald palpi (bp) is expressed in both sexes in the adult stage as a lack of scales over the distal half of the maxillary palpi. The proboscis and the palpi of both sexes curve slightly downward, and in cases of

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the extreme expression, they are malformed at the tip. The palpi of homozygotes break off quite easily. This mutant has been observed on numerous occasions during inbreeding experiments that were conducted with a large colony, SANTA TECLA, maintained in our laboratory. Some difficulty was encountered in establishing a vigorous colony of *bp*, because the females that show the best expression of the trait have difficulty in taking a blood meal which is necessary for the development of eggs in this species. For example, out of a sample of 100 females, only 17 were capable of taking a blood meal and only 8 had developed eggs when the ovaries were examined. Characteristically, so few eggs were obtained from *bp* females that the stock was hard to maintain on a simple replacement basis. Eventually, selection for a more moderate expression, recognizable with the aid of low magnification, resulted in the establishment of a more vigorous colony. Although the females are not quite as fit as wild type, both sexes of the *bp* stock can now be used in gene mapping studies.

When a *bp* phenotype was crossed to bp^+, all of the F_1 progeny were normal. The crosses summarized in Tables 1–4 were used to determine that *bp* is a recessive, monofactorial trait. Chi-square analysis of the crosses in Table 1 showed a good fit to the expected ratios of *bp* to bp^+ type. Generally, there was a slight deficiency in the *bp* type, but the deviation was not significant in any of the crosses. There was no linkage between *bp* and *st*, which is on chromosome 3. The crosses in Table 2 showed that *bp* is linked to *re* and pr^r on chromosome 2. Linkage distances were estimated for the combined data of the 2 crosses. These estimates were combined with earlier observations on *green larva (gl)* (Seawright et al. 1979) and *ebony (eb)* (Benedict et al. 1979) to derive the following gene order for mutants on chromosome 2:

eb——*bp*——*gl*——pr^r——*re*.

The linkage estimates for the relationship between *re*, pr^r, and *bp* provided a reliable delineation of the correct gene order, but the reliability of the map distances are partly suspect since there was a deficiency of *re* and pr^s homozygotes in the two crosses (9 and 10). In the case of *re*, this is contrasted to a good fit to the expected ratio in cross 11. Since *re* and pr^s are tightly linked the deficiency in the *re*

Table 1. Summary of crosses showing that *bald palpi (bp)* is a recessive trait.

Cross ♀ × ♂	No. families	Phenotype of progeny bp^+	*bp*	χ^2
(1) *bp* × F_1 (*bp* × bp^+)	15	369	330	2.176
(2) F_1 (*bp* × bp^+) × *bp*	8	255	224	2.006
(3) *bp* × F_1 (bp^+ × *bp*)	11	479	428	2.868
(4) F_1 (bp^+ × *bp*) × *bp*	13	403	357	2.784
(5) F_2 (*bp* × bp^+)	15	965	307	0.508
(6) F_2 (bp^+ × *bp*)	13	897	311	0.357

Table 2. Summary of crosses with *bald palpi (bp)* showing independent assortment from *stripe* (st^+).

Cross ♀ × ♂	Phenotype of progeny st^+bp^+	st^+bp	$stbp^+$	*stbp*	χ^2 *st*	*bp*	Linkage
(7) F_1 (st^+bp^+ × *stbp*) × *stbp*	*48*	*46*	*61*	*56*	*2.507*	*0.232*	*0.043*
(8) *stbp* × F_1 (st^+bp^+ × *stbp*)	154	161	158	131	1.119	0.662	1.914

Table 3. Results of three-point testcrosses showing linkage relationship of *red eye (re), propoxur resistance (pr^r)*, and *bald palpi (bp)*. Linkage distances in map units were calculated: *re-bp* = 17.61±1.26; *re-pr^r* = 1.53±0.41; *bp-pr^r* = 16.08±1.21.

Cross ♀ × ♂	Phenotype of progeny								χ^2		
	$re^+bp^+pr^r$	$re^+bp^+pr^s$	re^+bppr^r	re^+bppr^s	$rebp^+pr^r$	$rebp^+pr^s$	$rebppr^r$	$rebppr^s$	*re*	*bp*	pr^r
(9) F_1 ($re^+bp^+pr^r$ × $rebppr^s$) × $rebppr^s$	158	0	40	3	3	27	0	130	4.656*	0.623	4.656*
(10) $rebppr^s$ × F_1 ($re^+bp^+pr^r$ × $rebppr^s$)	151	0	23	2	1	15	0	111	7.924*	3.172	7.290*

* $p < .05$, χ^2 test.

Table 4. Results of three-point testcross (8 families) showing linkage relationship between *red eye (re), bald palpi (bp)*, and the breakpoint for *T(Y;2R)1*. Linkage distances in map units were estimated: *re-bp* = 12.16±1.24; *re-T(Y;2R)1* = 33.76±1.78; *bp-TY;2R)1* = 22.60±1.58.

Cross ♀ × ♂	Phenotype of progeny								χ^2	
	re^+bp^+♂	re^+bp^+♀	re^+bp♂	re^+bp♀	$rebp^+$♂	$rebp^+$♀	$rebp$♂	$rebp$♀	*re*	*bp*
(11) *rebp* × F_1 (*rebp* × re^+bp^+ *T(Y;2R)1*	245	75	3	33	45	4	76	218	0.242	2.176

pr^s type could be attributed to a detrimental effect of homozygosity for both genes. Also, as noted for the crosses in Table 1, *bp* homozygotes seem to suffer a slight disadvantage.

Crossing-over between *bp* and *re* was reduced when the *T(Y;2R)1* translocation was included in a backcross (Table 4). Recombinant types were 17.61±1.26% in the crosses shown in Table 3, but when *T(Y;2R)1* was included, crossovers were reduced to 12.16±1.24%. The breakpoint for this male-linked translocation is fairly close to the centromere, and as shown in Table 4 it is located between the centromere and the loci for the 2 mutants.

Bald antenna is expressed in males by a drastic reduction in the number of hairs on the antenna. Generally, *ba* behaved as a typical autosomal, recessive trait as shown in Table 5. *Bald antenna* is loosely linked to *nonstripe* on chromosome 3 as shown in the results of the two-point test crosses listed in Table 6.

Usually, the F_1 progeny of *ba* crossed to ba^+ are normal, but depending on the ba^+ stock as high as 10% of the F_1 males have the *ba* phenotype. For example, when *ba* females were crossed to ba^+ *T(Y;3R)1* males, 10.1% (28 of 276) of the F_1 males had bald antenna, but in a similar cross with the *T(Y;2R)1* stock, all of the F_1 males were normal. In backcrosses of the normal and *ba* F_1 phenotypes to *ba* females, equal numbers of the ba^+ and *ba* phenotypes were observed in the progeny. In a cross of normal phenotype F_1 males (from *ba* × ba^+) to ba^+ females only 4 males of the *ba* phenotype were observed amongst 288 males. Similarly, when *ba* F_1 males were crossed to ba^+ females, 2 of 278 males had the *ba* phenotype. Further work is required to determine whether the variable expression of *ba* in the heterozygote is due to conditioned dominance or dominance modifiers.

DISCUSSION

Narang et al. (1981) reported that a total of 21 loci have been studied for *An. albimanus*. Fifteen visible mutants have been described and assigned to linkage groups, as have 6 enzyme loci. We are involved in the development of chromosome aberrations for use in the synthesis of genetic systems that can be used to control natural populations of this important malaria vector. Ten of the mutants isolated thus far are being used in chromosome manipulation studies; the others are either recessive lethals or not fit enough for practical use as markers.

Females homozygous for *bald palpi* require an abnormally prolonged time to take a blood meal, and in this regard *bp* could be considered a conditional lethal because it is very doubtful that this mutant could survive in a natural situation. In a previous paper, Kaiser et al. (1978) reported several genetic sexing strains of *An. albimanus*, all of which had an inversion—translocation complex, induced by radiation, on the right arm of chromosome 2. The inversions cover the region of 2R where *bp* is located; thus, it would be easy to make a strain consisting of homozygous (*bp*) females and

Table 5. Summary of crosses showing that *bald antenna (ba)* is a recessive trait.

Cross ♀ × ♂	No. families	Phenotype of progeny			χ^2	
		ba^+♂	*ba*♂	♀	*ba*	*sex*
(1) *ba* × F_1 (*ba* × ba^+)	18	288	261	581	1.328	0.906
(2) F_1 (*ba* × ba^+) × *ba*	9	143	157	348	0.326	3.555
(3) *ba* × F_1 (ba^+ × *ba*)	43	557	508	1212	2.254	9.490[a]
(4) F_1 (ba^+ × *ba*) × *ba*	23	378	341	745	1.904	0.462

[a] $p < .01$; χ^2 test.

Table 6. Summary of crosses that demonstrate linkage between *stripe* (st^+) and *bald antenna* (*ba*). Percent crossingover between st^+ and *ba* was 37.00±1.44.

Cross ♀ × ♂	No. of families	Phenotype of progeny						χ^2			Linkage
		Male			Female						
		ba^+st^+	ba^+st	$bast^+$	*bast*	st^+	*st*	*st*	*ba*	*sex*	*ba-st*
(5) *bast* × F_1 (*bast* × ba^+st^+	9	85	45	39	63	129	104	1.692	3.379	0.002	17.655
(6) *bast* × F_1 (ba^+st^+ × *bast*)	32	242	136	135	213	406	376	2.231	1.239	2.231	46.634
(7) F_1 (ba^+st^+ × *bast*) × *bast*	8	56	37	24	51	93	80	0.073	1.928	0.036	12.595

heterozygous (bp/bp^+) males. If the males, which would be heterozygous for the aberration complex as well as *bp*, were released and mated successfully with a field population, they would pass the aberration complex to their sons and the *bp* gene to their daughters. In subsequent generations, the frequency of *bp* homozygotes would approach 0.5 depending on the near fixation of the aberration complex which is dependent on the release ratio and the duration of releases. Seawright et al. (1979) used computer simulations to test theoretically the effect of releasing male-linked translocations on a natural population. They showed a fairly rapid decline in the theoretical population when they released males heterozygous for a male-linked translocation. The combination of male-linked translocations with *bp* and other traits with reduced viability would cause a larger genetic lethal load and thus a more rapid decline in a target population.

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ECOLOGICAL STUDIES OF MOSQUITOES IN BANANA LEAF AXILS ON CENTRAL LUZON, PHILIPPINES[1]

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ABSTRACT. *Aedes poicilius* and *Ae. flavipennis* were the 2 most abundant mosquito species found breeding in the leaf axils of wild banana, *Musa errans botoan*, at 3 different study sites on Clark Air Base, Philippines. Breeding of both species was continuous from June to March depending on the study site. Populations peaked at the height of the SW monsoon in August and September. *Aedes poicilius* and *Ae. flavipennis* immatures survived the dry season in wet detritus at the base of axils and in the few axils retaining some free water. It appeared that *Ae. flavipennis* had a faster development rate and a better immature survival than did *Ae. poicilius*. Neither species was more prevalent at a particular axil location within the banana trees sampled, and the 2 species frequently coexisted in individual axils. The distribution of both species among banana trees conformed to the negative binomial model. Other species uncommonly associated with *Ae. poicilius* and *Ae. flavipennis* in axils included: *Ae. albopictus*, *Armigeres magnus*, *Ar. subalbatus*, *Malaya genurostris* and *Toxorhynchites splendens*.

INTRODUCTION

Water retained in the leaf axils of various *Musa* spp. common to the Philippines has been reported as a habitat for certain mosquito species (Knight and Laffoon 1946, Baisas et al. 1960). The most extensive studies of mosquitoes inhabiting axils in the Philippines have been conducted in the abaca (*Musa textilis* Nee) growing regions of southern Luzon and in the more southerly islands of the archipelago (Baisas et al. 1960, Cabrera 1969, Cabrera and Valeza 1972, Wenceslao et al. 1972, Cabrera and Valeza 1978). The primary impetus behind these studies has been the use of *Musa* axils by *Aedes poicilius* Theobald, an important vector of *Wuchereria bancrofti*. The areas in which *Ae. poicilius* has been implicated as a vector of human filariasis are characterized by even rainfall patterns (Cabrera 1969). In contrast to these areas, Clark Air Base (AB) and the rest of Central Luzon have distinct wet and dry seasons which strongly influence the availability of water for leaf-axil-breeding mosquitoes. Central Luzon is also essentially free of endemic bancroftian filariasis (Cabrera 1969).

The only data on mosquito larvae found in *Musa* axils from the Clark AB area are contained in the accounts of Dowell et al. (1965) and Baisas et al. (1960). In these taxonomically-oriented surveys, larval collecting was not accom-

[1] The opinions and assertions contained herein are those of the authors and are not to be construed as views of the Department of the Air Force.

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