

## INHERITANCE OF THE STRIPE TRAIT IN *ANOPHELES FREEBORNI*

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The morphological marker stripe (*St*), which appears as a broad, light, dorsal stripe in larvae and pupae, has been reported for a number of anopheline species in the subgenera *Anopheles*, *Cellia* and *Nyssorhynchus* (Kitzmiller and Mason 1967). Genetic studies on the inheritance mechanism of this trait are limited to only a few species. In *An. albimanus* Wiedemann (Georghiou et al. 1967, Rabbani and Seawright 1976) and *An. quadrimaculatus* Say (Coggeshall 1941, French and Kitzmiller 1963), the stripe character appears to have simple inheritance as an autosomal dominant over the nonstripe trait (*st*). Mitchell and Seawright (1984a) reported a red stripe *St<sup>rd</sup>* mutant in natural populations of *An. quadrimaculatus*. Genetic crosses of red stripe with stripe and nonstripe showed these to be members of an allelic series. The *St<sup>rd</sup>* trait is codominant with *St*, and both are dominant over *st*. During the course of a study on the population genetics of *An. freeborni* Aitken, we have seen many larvae and pupae that bear a similar white dorsal stripe. We also found much variability in the expression of stripe among individuals in laboratory culture; similar findings were reported by Rabbani and Seawright (1976) for *An. albimanus*.

Easily scored morphological markers are useful in linkage relationships and genetic mapping studies (French and Kitzmiller 1964, Narang and Seawright 1982). There are no published reports on the inheritance of morphological characters for *An. freeborni*. This study reports on the results of crosses made to determine the genetic basis of nonstripe and stripe in this

species.

The stripe character has been found in populations collected from various locations in California and Washington. The strain of *An. freeborni* used in this study originated from mosquitoes collected in the Sacramento Valley, California. A homozygous stripe (*St*) isolate was established by selecting and inbreeding only those individuals which showed the greatest degree of expression of the trait in successive generations. Each parental (stripe and nonstripe) line was considered homozygous only after it had bred true for at least 3 generations. Individual females that were inseminated and blood-fed were placed in plastic vials containing water and filter paper linings. Eggs were allowed to hatch in the vials, and larvae were subsequently transferred to enamel pans. Larvae were reared in enamel pans (30 × 18 × 5 cm) and fed a 1:1:1:3 mixture of liver powder, yeast, hog chow and guinea pig chow. Adults were maintained in gallon-size containers with screen-top lids and provided with cotton soaked in a 10% sugar-water solution. Control crosses and reciprocal parental crosses between stripe and nonstripe phenotypes were done. The F<sub>1</sub> hybrids were crossed with each other (monohybrid crosses) as well as backcrossed to nonstripe parental types. Fourth instar larvae were scored for the stripe character, and the sex of all pupae of each phenotype was determined.

All the F<sub>1</sub> progeny from the reciprocal parental crosses (Table 1) had the stripe character. When the F<sub>1</sub> progeny were inbred, the F<sub>2</sub> progeny from each cross produced stripe (*St*) and

Table 1. Summary of crosses showing that stripe (*St*) is a dominant autosomal trait in *Anopheles freeborni*. None of the chi-square values is significant at  $P = 0.05$ .

Cross	No. families	Stripe		Nonstripe		Total	$\chi^2$	
		F	M	F	M		<i>St</i>	Sex
1. <i>st/st</i> × <i>st/st</i>	5	0	0	195	172	367		1.44
2. <i>St/St</i> × <i>St/St</i>	4	166	135	0	0	301		3.19
3. <i>St/St</i> × <i>st/st</i>	4	142	117	0	0	259		2.41
4. <i>st/st</i> × <i>St/St</i>	6	190	174	0	0	364		0.70
5. <i>St/st</i> × <i>St/st</i>	10	254	240	99	90	683	2.50	0.77
6. <i>st/St</i> × <i>st/St</i>	5	156	150	61	51	418	0.72	0.61
7. <i>st/St</i> × <i>st/st</i>	3	68	63	72	81	284	1.70	0.06
8. <i>st/st</i> × <i>st/St</i>	5	129	117	123	132	501	0.16	0.02
9. <i>St/st</i> × <i>st/st</i>	4	109	97	108	101	415	0.02	0.87
10. <i>st/st</i> × <i>St/st</i>	4	81	87	87	95	350	0.56	0.56

nonstripe (*st*) individuals in a 3:1 ratio, respectively ( $P = 0.05$ ). Backcrosses of *St/st* and *st/St* males and females to the *st/st* parental line also produced the phenotypic frequencies expected for a dominant *St* allele. In all instances, stripe segregated independently of sex.

All the results of the crosses are consistent with the hypothesis that a dominant *St* allele is located on 1 of the 2 autosomal chromosomes. The stripe locus has been located on chromosome 2 (linkage group II) in *An. (Cellia) stephensi* Liston (Sakai et al. 1974) and on chromosome 3 (linkage group III) in both *An. (Nyssorhynchus) albimanus* (Rabbani and Seawright 1976) and *An. (Anopheles) quadrimaculatus* (Mitchell and Seawright 1984b). The latter is closely related to *An. freeborni* based on morphological, chromosomal and crossing studies (Kitzmiller et al. 1967), and it is probable that the stripe locus is located on the same chromosome in both species.

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