# ISOLATION OF A VIABLE HOMOZYGOUS TRANSLOCATION STRAIN IN *ANOPHELES CULICIFACIES*

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ABSTRACT. A viable homozygous translocation strain has been isolated in *An. culicifacies* using genetic and cytogenetic techniques. The strain has been outcrossed to the standard Sattoki strain and has been successfully reisolated in a wild type background.

During the course of an experiment to induce, isolate and characterize chromosomal aberrations in *Anopheles culicifacies* (Baker et al. 1978), an attempt was made to isolate homozygous strains of the induced aberrations. Initially a true-breeding line of a pericentric inversion on the X chromosome, *In(X)1*, was isolated (Baker et al. 1978). Repeated attempts to isolate other homozygous aberration lines were unsuccessful although in one complex aberration line, *In(3L)T(2R,3L)1*, a few homozygous females were detected cytologically (Baker et al. 1978). In mitotic configurations, this aberration is seen as an unequal exchange between chromosomes 2R (long arm) and 3 with the longer segment from 2R translocated to 3. In the ovarian nurse cell polytene chromosomes almost all of 2R (break point:19C) has been exchanged with a large part of 3L (break point:39A; see the ovarian polytene map of Saifuddin et al. 1978). Therefore, centromere 3 of the translocated chromosome is included in the longest chromosome of the complement. In addition the translocated segment of 3L included a small paracentric inversion between 41A and 42A (for mitotic and polytene configurations see Baker et al. 1978). This paper reports the successful isolation of a homozygous strain from *In(3L)T(2R,3L)1* herein designated as *T-1*.

## MATERIALS AND METHODS

To facilitate isolation of *T-1*, two eye color mutants, rose eye (*re*, chromosome 1; Sakai et al. 1977) and maroon eye (*ma*, chromosome 2; Sakai et al. 1979) were used. All crosses were done in a rose eye

background as maroon eye can be classified with certainty only in newly emerged adults. However, in a rose eye background, *re/re; ma/ma* individuals have pink eyes and *re/re; ma/+* and *re/re; ++* individuals have rose eyes. The *T-1* chromosome carried the wild type allele of maroon but in preliminary crosses there was approximately 28% crossing over between the aberration and the maroon locus. Females and males heterozygous for *T-1* and *ma* but homozygous for *re* were mass mated, and individual females were isolated for egg laying. Selection in future generations was done under the following assumptions:

1) *T-1/+* X *T-1/+* matings would produce sterilities greater than 60% (sterility = unhatched eggs/total eggs).
2) *T-1* + X +/+ = 35–40% sterility.
3) *T-1/T-1* X *T-1/T-1* = 0 –15% sterility.
4) +/+ X +/± = little or no sterility.

All families showing 0–15% sterilities were reared individually. If all adults from a family had rose eyes, the mitotic or ovarian polytene chromosomes were examined from 3–5 females by methods previously described (Saifuddin et al. 1978). Families with 35–40% sterility were discarded. Individuals with rose eyes from families with 60% or greater sterility were combined and mass mated and their progeny were again selected on the basis of sterility.

## RESULTS

The mitotic chromosomes from more than 700 ovaries were examined during 7 generations of selection from families showing little sterility before a homozygous line was established. After cytogenetic confirmation, various matings involving this aberration were made (Table 1). The sterility of the homozygous strain (12.32%) was slightly greater than those of the homozygous females and males crossed to Sattoki individuals and approximately 2 times that of the standard Sattoki strain (5.27%). Heterozygous males were characterized by somewhat higher sterility (42.47%) than heterozygous females (35.64%).

Table 1. Observed sterilities of the translocation in various homozygous and heterozygous combinations.

| Parental Genotypes* ♀ ♂ | No. of families | Total Eggs | Larvae | % Sterility |
|---|---|---|---|---|
| $\frac{\pm}{+} \times \frac{\pm}{+}$ | 36 | 7394 | 7004 | 5.27±0.26 |
| $\frac{T\text{-}1}{T\text{-}1} \times \frac{T\text{-}1}{T\text{-}1}$ | 228 | 28980 | 25408 | 12.32±0.19 |
| $\frac{\pm}{+} \times \frac{T\text{-}1}{T\text{-}1}$ | 41 | 4654 | 4220 | 9.32±0.43 |
| $\frac{T\text{-}1}{T\text{-}1} \times \frac{\pm}{+}$ | 16 | 1918 | 1718 | 10.43±0.70 |
| $\frac{\pm}{+} \times \frac{\pm}{T\text{-}1}$ | 99 | 14361 | 8262 | 42.47±0.41 |
| $\frac{+}{T\text{-}1} \times \frac{\pm}{+}$ | 121 | 17508 | 11269 | 35.64±0.36 |

* T-1 = translocation; + = wild type.

It is interesting to note that the paracentric inversion on 3L was not fixed simultaneously with the establishment of homozygosity for the translocation, but continues to segregate within the strain. This may account for the low level of sterility observed in the homozygous strain. The aberration has been outcrossed and has recently been reisolated in the Sattoki wild type background. This strain is now being assessed for suitability for a release program either alone or in combination with other aberrations as double translocation heterozygotes. Moreover, the nearly whole arm exchanges between 2R and 3L may be useful as part of a capture system for compound autosomes.

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