# DEEP THROAT, A SEX LINKED MUTANT OF *CULEX TRITAENIORHYNCHUS*

RICHARD K. SAKAI AND RICHARD H. BAKER

Pakistan Medical Research Center, 6, Birdwood Road, Lahore, Pakistan and International Health Program
University of Maryland School of Medicine, 660 West Redwood Street, Baltimore, Maryland 21201,
U.S.A.

ABSTRACT. The genetics of an ethyl methanesulfonate-induced mutation, *deep throat* (*dt*), was investigated. Experimental data indicate that *dt* is recessive and sex-linked. The gene sequence is $dt$-$go$-$w^{re}$-$M$ and the recombination frequencies are as follows: $dt$-$go = 15.02\%$; $dt$-$w^{re} = 23.28\%$, and $dt$-$M = 37.65\%$. This mutant currently represents one terminal marker on linkage group I which is approximately 39 map units in length.

During an experiment with ethyl methanesulfonate to induce temperature-sensitive lethals (Sakai and Baker, 1974) in the mosquito, *Culex tritaeniorhynchus* Giles, a number of morphological mutations were recovered. Among these was a mutant in which there was a large gap on the ventral side of the head between the two eyes which made the mosquito appear to have a greatly elongated, deep "throat" (Fig. 1). Previous to this study, more than 25 individual mosquitoes had been isolated with similar phenotypic expressions, but on further breeding experiments, the variants did not seem to have a simple genetic basis. However, the mutant recovered after the chemical treatment was established as a true-breeding strain although its expression is somewhat variable. This paper reports the genetic and linkage experiments of this mutant, designated *deep throat, dt*.

MATERIALS AND METHODS. The following mutants were used to investigate the inheritance of *dt*: (1) *golden* (*go*)—a recessive sex-linked mutant in which the mosquito's cuticle and scales are a bright golden-yellow (Baker, 1968) and (2) *rose eye* ($w^{re}$)—a recessive sex-linked mutant in which the eyes are bright rose (Baker and Sakai, 1973). A number of strains were synthesized incorporating various combinations of the three mutants, *dt, go* and $w^{re}$. Mass matings were done for all crosses, but egg rafts were isolated and reared individually (each egg raft thus represents the offspring of a single female). The larvae were fed liver powder daily. In this mosquito sex is determined as if by a single allelic pair, *m* and *M,* for which females are homozygous, *m/m,* and males heterozygous, *m/M.*

RESULTS AND DISCUSSION. The results of the parental crosses suggest that *dt* is recessive and also confirm that *go* and $w^{re}$ are also recessive (Baker, 1968; Baker and Sakai, 1973) as only wild type females and males were observed among the progeny (Table 1).

Table 1. Summary of parental crosses

| Proposed Parental Genotype* | $F_1$ Progeny | |
|---|---|---|
| | +♀ | +♂ |
| $\frac{+\ +\ +\ \mathrm{m}}{+\ +\ +\ \mathrm{m}}$ ♀ X $\frac{\mathrm{dt}\ \mathrm{go}\ +\ \mathrm{m}}{\mathrm{dt}\ \mathrm{go}\ +\ \mathrm{m}}$ ♂ | 182 | 165 |
| $\frac{\mathrm{dt}\ \mathrm{go}\ +\ \mathrm{m}}{\mathrm{dt}\ \mathrm{go}\ +\ \mathrm{m}}$ ♀ X $\frac{+\ +\ +\ \mathrm{m}}{+\ +\ +\ \mathrm{M}}$ ♂ | 224 | 219 |
| $\frac{\mathrm{dt}\ +\ +\ \mathrm{m}}{\mathrm{dt}\ +\ +\ \mathrm{m}}$ ♀ X $\frac{+\ \mathrm{go}\ +\ \mathrm{m}}{+\ \mathrm{go}\ +\ \mathrm{M}}$ ♂ | 214 | 214 |
| $\frac{+\ \mathrm{go}\ +\ \mathrm{m}}{+\ \mathrm{go}\ +\ \mathrm{m}}$ ♀ X $\frac{\mathrm{dt}\ +\ +\ \mathrm{m}}{\mathrm{dt}\ +\ +\ \mathrm{M}}$ ♂ | 178 | 187 |
| $\frac{+\ +\ +\ \mathrm{m}}{+\ +\ +\ \mathrm{m}}$ ♀ X $\frac{\mathrm{dt}\ +\ \mathrm{re}\ \mathrm{m}}{\mathrm{dt}\ +\ \mathrm{re}\ \mathrm{M}}$ ♂ | 274 | 317 |
| $\frac{\mathrm{dt}\ +\ \mathrm{re}\ \mathrm{m}}{\mathrm{dt}\ +\ \mathrm{re}\ \mathrm{m}}$ ♀ X $\frac{+\ +\ +\ \mathrm{m}}{+\ +\ +\ \mathrm{M}}$ ♂ | 292 | 288 |
| $\frac{\mathrm{dt}\ +\ +\ \mathrm{m}}{\mathrm{dt}\ +\ +\ \mathrm{m}}$ ♀ X $\frac{+\ +\ \mathrm{re}\ \mathrm{m}}{+\ +\ \mathrm{re}\ \mathrm{M}}$ ♂ | 295 | 290 |
| $\frac{+\ +\ \mathrm{re}\ \mathrm{m}}{+\ +\ \mathrm{re}\ \mathrm{m}}$ ♀ X $\frac{\mathrm{dt}\ +\ +\ \mathrm{m}}{\mathrm{dt}\ +\ +\ \mathrm{M}}$ ♂ | 278 | 272 |

* $\mathrm{re} = w^{re}$

Table 2. Summary of backcrosses to heterozygous females

| Cross | Proposed Parental Genotype** | | | f* | ♀ | | | | | | ♂ | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | + | dt | go | re | dt go | dt re | + | dt | go | re | dt go | dt re |
| A | $\frac{+\ +\ +\ m}{dt\ go\ +\ m}$ | X | $\frac{dt\ go\ +\ m}{dt\ go\ +\ M}$ | 6 | 167 | .. | .. | .. | 100 | .. | 145 | .. | .. | .. | 132 | .. |
| B | $\frac{dt\ go\ +\ m}{+\ +\ +\ m}$ | X | $\frac{dt\ go\ +\ m}{dt\ go\ +\ M}$ | 6 | 130 | .. | .. | .. | 84 | .. | 130 | .. | .. | .. | 82 | .. |
| C | $\frac{dt\ +\ +\ m}{+\ go\ +\ m}$ | X | $\frac{dt\ go\ +\ m}{dt\ go\ +\ M}$ | 6 | .. | 156 | 151 | .. | .. | .. | .. | 160 | 112 | .. | .. | .. |
| D | $\frac{+\ go\ +\ m}{dt\ +\ +\ m}$ | X | $\frac{dr\ go\ +\ m}{dt\ go\ +\ M}$ | 6 | .. | 151 | 114 | .. | .. | .. | .. | 152 | 119 | .. | .. | .. |
| E | $\frac{+\ +\ +\ m}{dt\ +\ re\ m}$ | X | $\frac{dt\ +\ re\ m}{dt\ +\ re\ M}$ | 10 | 259 | .. | .. | .. | .. | 165 | 227 | .. | .. | .. | .. | 176 |
| F | $\frac{dt\ +\ re\ m}{+\ +\ +\ m}$ | X | $\frac{dt\ +\ re\ m}{dt\ +\ re\ M}$ | 5 | 106 | .. | .. | .. | .. | 49 | 98 | .. | .. | .. | .. | 75 |
| G | $\frac{dt\ +\ +\ m}{+\ +\ re\ m}$ | X | $\frac{dt\ +\ re\ m}{dt\ +\ re\ M}$ | 9 | .. | 184 | .. | 179 | .. | .. | .. | 181 | .. | 186 | .. | .. |
| H | $\frac{+\ +\ re\ m}{dt\ +\ +\ m}$ | X | $\frac{dt\ +\ re\ m}{dt\ +\ re\ M}$ | 9 | .. | 160 | .. | 177 | .. | .. | .. | 164 | .. | 190 | .. | .. |

* Number of families tested.

** $re = w^{re}$

Table 3. Summary of backcrosses to heterozygous males.

| Gross | Proposed Parental Genotype** | | | f* | ♀ | | | | | | ♂ | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | + | dt | go | re | dt go | dt re | + | dt | go | re | dt go | dt re |
| M | $\frac{\text{dt go + m}}{\text{dt go + m}}$ | X | $\frac{\text{+ + + m}}{\text{dt go + M}}$ | 28 | 679 | 123 | 13 | .. | 201 | .. | 251 | 13 | 139 | .. | 451 | .. |
| N | $\frac{\text{dt go + m}}{\text{dt go + m}}$ | X | $\frac{\text{dt go + m}}{\text{+ + + M}}$ | 20 | 145 | 0 | 66 | .. | 261 | .. | 396 | 86 | 3 | .. | 85 | .. |
| O | $\frac{\text{dt go + m}}{\text{dt go + m}}$ | X | $\frac{\text{dt + + m}}{\text{+ go + M}}$ | 20 | 105 | 364 | 52 | .. | 4 | .. | 3 | 153 | 291 | .. | 55 | .. |
| P | $\frac{\text{dt go + m}}{\text{dt go + m}}$ | X | $\frac{\text{+ go + m}}{\text{dt + + M}}$ | 10 | 5 | 81 | 102 | .. | 22 | .. | 29 | 231 | 41 | .. | 3 | .. |
| Q | $\frac{\text{dt + re m}}{\text{dt + re m}}$ | X | $\frac{\text{+ + + m}}{\text{dt + re M}}$ | 10 | 296 | 72 | .. | 2 | .. | 45 | 64 | 3 | .. | 95 | .. | 219 |
| R | $\frac{\text{dt + re m}}{\text{dt + re m}}$ | X | $\frac{\text{dt + re m}}{\text{+ + + M}}$ | 20 | 113 | 9 | .. | 150 | .. | 392 | 603 | 164 | .. | 4 | .. | 65 |
| S | $\frac{\text{dt + re m}}{\text{dt + re m}}$ | X | $\frac{\text{dt + + m}}{\text{+ + re M}}$ | 10 | 129 | 225 | .. | 42 | .. | 4 | 3 | 41 | .. | 258 | .. | 87 |
| T | $\frac{\text{dt + re m}}{\text{dt + re m}}$ | X | $\frac{\text{+ + re m}}{\text{dt + + M}}$ | 10 | 2 | 57 | .. | 284 | .. | 96 | 119 | 322 | .. | 79 | .. | 3 |

* Number of families tested.

Table 2 summarizes the data of the backcrosses of the heterozygous females. In all these crosses the sex ratio did not depart significantly from the expected 1:1. However, in crosses A-F there were significant and highly significant departures from the expected 1:1 ratio between the mutant markers and their respective wild type alleles. This suggests that under the conditions of the experiment, the mutant markers used (particularly *dt* and *go*) were characterized by lower viabilities than their wild types alleles. Linkage is indicated among *dt, go,* and $w^{re}$ by highly significant linkage chi squares. Moreover, no recombination was observed among these markers, which is in agreement with earlier reports of complete linkage in females of this species (Baker and Rabbani, 1970; Baker and Sakai, 1974).

Table 3 summarizes the data of the backcrosses of the heterozygous males. In almost all these crosses there were significant departures from the expected 1:1

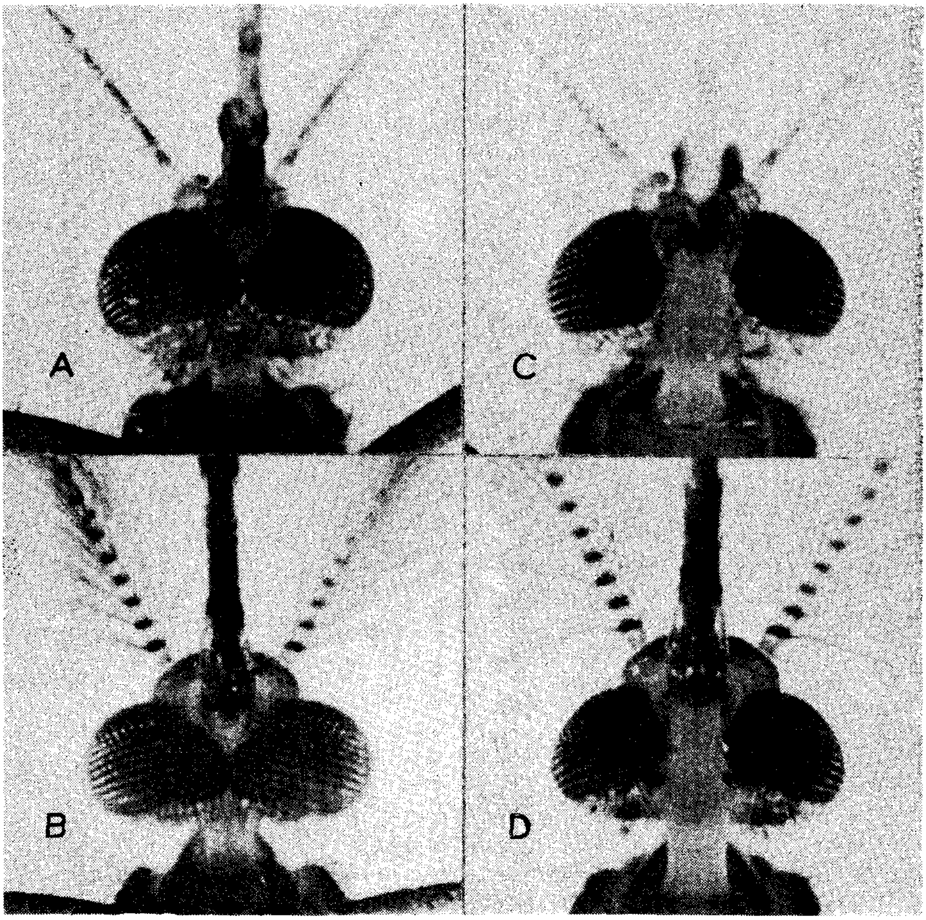

Figure I. A. Wild type female. B. Wild type male.
C. *dt* female. D. *dt* male.

Table 4. Linkage $\chi^2$ analysis of backcrosses to heterozygous males and females

| Cross | *dt-go* | *dt-re* | *dt-M* | *go-M* | *re-M* |
|---|---|---|---|---|---|
| A | 544.0** | ...... | ...... | ...... | ...... |
| B | 426.0** | ...... | ...... | ...... | ...... |
| C | 579.0** | ...... | ...... | ...... | ...... |
| D | 536.0** | ...... | ...... | ...... | ...... |
| E | ...... | 827.0** | ...... | ...... | ...... |
| F | ...... | 328.0** | ...... | ...... | ...... |
| G | ...... | 730.0** | ...... | ...... | ...... |
| H | ...... | 691.0** | ...... | ...... | ...... |
| M | 895.42** | ...... | 104.47** | 446.74** | ...... |
| N | 514.23** | ...... | 74.17** | 318.40** | ...... |
| O | 467.62** | ...... | 85.89** | 354.05** | ...... |
| P | 305.09** | ...... | 54.91** | 125.52** | ...... |
| Q | ...... | 256.66** | 74.79** | ...... | 405.31** |
| R | ...... | 477.14** | 177.50** | ...... | 833.28** |
| S | ...... | 149.11** | 46.24** | ...... | 470.06** |
| T | ...... | 283.25** | 70.27** | ...... | 480.66** |

** $P<0.01$.

ratio for sex as well as the other three mutant markers. These observations are in general agreement with the results obtained for the backcrosses of the heterozygous females in which the mutant markers were also characterized by lower viabilities. The linkage $\chi^2$ analysis confirms the presence of linkage among *dt*, *go*, and $w^{re}$ and in addition indicates the linkage of all three markers to *M*, sex (Table 4). The data indicate that the gene sequence is *dt-go-*$w^{re}$*-M* and the recombination frequencies are as follows: $dt\text{-}go=15.02\%$, $dt\text{-}w^{re}=23.28\%$, and $dt\text{-}M=37.65\%$ (Table 5). Thus, the genetic map of the smallest pair of chromosomes in the genome of *Culex tritaeniorhynchus* is now approximately 39 map units in length, with Delta, *D* (Baker and Sakai, 1972) at position 0.0 and *dt* at position 38.6. Delta is closely linked to *M* (0.3 map units).

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Table 5. Recombination among *dt*, *go*, *re*, and *M*.

| Cross | *dt-go* | *dt-re* | *dt-M* | *go-M* | *re-M* |
|---|---|---|---|---|---|
| M | 15.40±0.83 | ....... | 40.96±1.14 | 25.56±1.01 | ....... |
| N | 14.88±1.10 | ....... | 37.24±1.50 | 22.36±1.29 | ....... |
| O | 16.26±1.15 | ....... | 36.90±1.50 | 20.64±1.26 | ....... |
| P | 11.48±1.41 | ....... | 36.77±2.13 | 25.29±1.92 | ....... |
| Q | ....... | 21.61±1.46 | 35.93±1.70 | ....... | 14.32±1.24 |
| R | ....... | 21.80±1.07 | 34.53±1.23 | ....... | 12.73±0.86 |
| S | ....... | 28.26±1.60 | 39.67±1.74 | ....... | 11.41±1.13 |
| T | ....... | 22.87±1.35 | 37.53±1.56 | ....... | 14.66±1.14 |
|  | 15.02±0.54 | 23.28±0.65 | 37.65±0.52 | 23.65±0.63 | 13.24±0.53 |

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