A GENETIC STUDY OF TWO SEX-LINKED RECESSIVE MUTANTS, MARGINAL CELL LESS (MCL) WING AND CUT (CT) WING OF DROSOPHILA ANANASSAE.

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Abstract

The present study was made in order to carry out further genetic investigations of two mutants ct wing and mcl wing isolated by Bogahawatta in 1982. These two mutants were observed to be recessive and sex-linked, but were also seen not to strictly obey Mendelian rules. In the absence of the wild allele the mutants allele behaves in a peculiar manner. Each mutant allele is capable of producing all the types of mutants such as ct wing mcl wing, and ct-mcl wing along with the wild types. The most probable explanation for this peculiar behaviour is that these two allele are unstable.

Introduction

Drosophila ananassae is the most abundant drosophilid species in Asia and Sri Lanka. Genetic studies on this species have been in progress since 1930, particularly in Japan. In Sri Lanka Genetic studies of D. ananassae were started in 1981 by Ratnayake and Bogahawatta with the initiation of a survey of mutant alleles in the wild population and the estimation of their mutant load. (Bogahawatta, 1984).

The present study is a part of this programme. The objective was to carry out further genetic investigations on two visible sex-linked mutations namely, cut (ct) wing and marginal cell less (mcl) wing isolated by Bogahawatta in 1982.

Even though there were no previous records of cut (ct) wing mutants of Drosophila in Sri Lanka, there were five other instances recorded in other parts of the world. (Kikkawa, 1933, 1937; Moriwaki, 1936, 1971) In all the above instances the cut (ct) wing has been recorded as a recessive sex-linked mutant. The marginal cell less (mcl) mutant has not been recorded anywhere in the world before.

In the present study, these two mutants did not strictly obey the Mendelian rules, but it could be inferred that they behave as sex-linked recessive mutants.

Materials and Methods

The cut (ct) wing mutant is clearly distinguishable from the other wing mutants by the appearance of the wing tip which looks as if cut by a pair of scissors. But there are three patterns of this mutant (see Fig. 1) in
Two sex-linked recessive mutants of Drosophila ananassae

the present stock. These three types also differ from each other in the extent of the area of the cut. However, all three types were considered as cut (ct) wing mutants in the present study.

Marginal cell—less (mcl) mutant showed the absence of the marginal cell of the wing. Here too there were variations. (See Fig. 2) Sometimes instead of the entire marginal cell, only a portion of the marginal cell or even the marginal vein was found to be snipped off. In this case, too, all these aberrant types were considered as the mcl mutant.

Perhaps these variants of the two mutants may be due to variabilities in their expressivity.

In order to study the pattern of inheritance of these mutants, the following crosses were made. In each case pair matings were carried out.

Cross 1. – wild type male × ct wing female
2. – ct wing male × wild type female
3. – The wild flies obtained from the cross 2 were intercrossed
4. – wild type male × mcl wing female
5. – mcl wing male × wild type female
6. – The wild type flies obtained from the cross 5 were intercrossed
7. – ct wing male × ct wing female
8. – mcl wing male × mcl wing female
9. – The wild type flies obtained from cross 7 were intercrossed
10. – The wild type flies obtained from cross 8 were intercrossed
11. – wild type male × wild type female (from ct Stock)
12. – wild type male × wild type female (from mcl stock)
   (wild type male flies, were obtained from the wild population
   But wild type female flies in cross 11 and 12 were obtained from
   ct wing and mcl wing mutant stocks respectively.

13. – ct wing male × mcl wing female
14. – mcl male × ct wing female.

The standard culture medium for Drosophila was used and all experimental crosses were carried out at room temperature which ranged from 26°C – 31°C.
Results

The results obtained from the crosses (1 - 14) are presented in the following Table.
### TABLE 1—PHENOTYPES OF THE F₁ AND F₂ PROGENY

<table>
<thead>
<tr>
<th>Cross</th>
<th>Expected</th>
<th>Unexpected</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>wild type</td>
<td>ct wing</td>
</tr>
<tr>
<td></td>
<td>♂️</td>
<td>♀️</td>
</tr>
<tr>
<td>01.</td>
<td>Wild type ♂️ x ct wing ♀️</td>
<td>384</td>
</tr>
<tr>
<td>02.</td>
<td>ct wing ♂️ x wild type ♀️</td>
<td>297</td>
</tr>
<tr>
<td>a 03.</td>
<td>F₁ wild type ♂️ x F₁ wild type ♀️</td>
<td>525</td>
</tr>
<tr>
<td>04.</td>
<td>wild type ♂️ x mcl wing ♀️</td>
<td>357</td>
</tr>
<tr>
<td>05.</td>
<td>mcl wing ♂️ x wild type ♀️</td>
<td>276</td>
</tr>
<tr>
<td>b 06.</td>
<td>F₁ wild type ♂️ x F₁ wild type ♀️</td>
<td>519</td>
</tr>
<tr>
<td>07.</td>
<td>ct wing ♂️ x ct wing ♀️</td>
<td>114</td>
</tr>
<tr>
<td>08.</td>
<td>mcl wing ♂️ x mcl wing ♀️</td>
<td>120</td>
</tr>
<tr>
<td>c 09.</td>
<td>F₁ wild type ♂️ x F₁ wild type ♀️</td>
<td>36</td>
</tr>
<tr>
<td>d 10.</td>
<td>F₁ wild type ♂️ x F₁ wild type ♀️</td>
<td>65</td>
</tr>
<tr>
<td>e 11.</td>
<td>wild type ♂️ x wild type ♀️ (from ct wing stock)</td>
<td>50</td>
</tr>
<tr>
<td>f 12.</td>
<td>wild type ♂️ x wild type ♀️ (from mcl wing stock)</td>
<td>43</td>
</tr>
<tr>
<td>13.</td>
<td>ct wing ♂️ x mcl wing ♀️</td>
<td>53</td>
</tr>
<tr>
<td>14.</td>
<td>mcl wing ♂️ x ct wing ♀️</td>
<td>98</td>
</tr>
</tbody>
</table>

a, b, c, d, The wild flies obtained from the crosses 02, 05, 07, 08 were intercrossed respectively.
e, f, wild type male flies were obtained from the wild population. But wild type female flies in cross.
11 and 12 were obtained from ct wing and mcl wing mutant stock respectively. Results of all crosses carried out in this study.
As ct is a sex-linked recessive mutant, from the cross 1 (wild type male x ct wing female) only ct males and wild females are expected in the F₁ generation. But the results show that apart from ct males, mcl, ct-mcl and wild type males too have appeared. However, the percentage of the females is as expected. In the reciprocal cross (ct male x wild female), only wild type males and females were obtained as expected. In cross 3 all F₂ female progeny are wild type, whereas the males are of all types with wild type males predominating. ct wing and ct-mcl wing mutants show more or less the same percentages.

These results also appear very similar to obtained with the mcl wing mutant. (cross 4-6)

It can be concluded from these data that both mutants ct wing and mcl wing behave more or less similarly in their inheritance patterns. The phenotypic expression of the two mutants are completely suppressed in the presence of the wild allele. When the wild allele is not present, the phenotypic expression varies. The phenotypes can be ct wing, ct-mcl wing, mcl wing or even wild type.

Cross 7 and 8 clearly show that the F₁ progeny of the ct wing and mcl wing colonies comprised the various mutant forms: ct, ct-mcl, and mcl. Further in both these colonies wild type flies too appear in the F₁ generation. However, the ratios of the 4 phenotypes appearing in the F₁ generation differ in the two mutant types.

In the ct wing colony, the percentage occurrence of ct wing and ct-mcl wing phenotypes in the F₁ generation, is comparatively higher than that in mcl colony, whereas in the mcl colony mcl wing and wild type phenotypes occur at a higher percentage.

The remarkable feature of the results of crosses 7 and 8 is the appearance of wild flies in the F₁ generation. In crosses 9-12, the data clearly show that these wild flies are not true breeders for the wild character. They are indeed homozygotes for the respective mutant characters but not fully expressing them phenotypically.

**Discussion**

ct wing and mcl wing are two visible mutants of *Drosophila ananassae* isolated in Sri Lanka by Bogahawatta in 1982. The ct wing mutant is clearly distinguishable from the other wing mutants by the appearance of the wing tip which looks as if cut by a pair of scissors. The mcl wing mutant character is where the marginal cell of the wing is entirely or in part missing.

The results of the present study clearly indicate that the two mutants ct wing and mcl wing are recessive and sex-linked. The phenotypic expression of these mutants are clearly marked by the presence of alternative wild alleles.
In the absence of respective wild alleles the phenotypic expressions of the mutant types were variable. Both \( ct \) wing and \( mcl \) wing alleles in the absence of the wild counterparts produced all types of mutants \( ct \) wing, \( ct-mcl \) wing, \( mcl \) wing. They also produced wild types.

**Table 11 — Percentage of \( F_1 \) phenotypes of crosses 7 & 8**

<table>
<thead>
<tr>
<th>Cross</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( ct ) wing ( mcl ) wing wild type ( ct-mcl ) wing</td>
</tr>
<tr>
<td>( 7 - ct ) wing ( \alpha \times ct ) wing ( \varphi )</td>
<td>26.4 21.7 0.5 1.2 3.5 6.0 20.2 20.6</td>
</tr>
<tr>
<td>( 8 - mcl ) wing ( \alpha \times mcl ) wing ( \varphi )</td>
<td>0.8 1.3 32.1 39.8 12.5 9.6 2.4 1.3</td>
</tr>
</tbody>
</table>

The mutant allele at the \( ct \) locus in the absence of the wild allele gave rise to more \( ct \) wing and \( ct-mcl \) wing flies, whereas the allele at \( mcl \) locus gave rise to more \( mcl \) wing and wild flies. In both these cases the wild offspring produced can be considered as pseudo-wild phenotypes, because when intercrossed, they themselves behaved as homozygotes of the respective mutant types. The \( ct-mcl \) double mutant too acts as \( ct \) wing and \( mcl \) wing mutants but with slight changes in the percentage occurrence of the same phenotypes (\( ct \) wing and \( ct-mcl \) wing).

Therefore, it is possible to consider these two mutants as being due to a single mutant gene whose phenotypic appearance is seen to differ.

The most probable mechanism that can explain the peculiar mode of inheritance of this single mutant is Gerasimova's (1983) description which was given to explain the mutation at the \( ct \) locus of \( D. melanogaster \). According to him the induced \( ct^{p}\cdot mR^2 \) mutant allele of \( D. melanogaster \) can change into \( ct^{+} \) (wild type) with time. Therefore, according to these revertants 3 groups were recognized by him as stable, unstable, and superunstable mutants.

He further reported that new \( ct \) alleles could not be obtained from stable groups, but could be obtained from the other two groups in a few generations of inbreeding.

In the present case too, it became evident that this single mutant behaves as an unstable mutant expressing itself as \( mcl \), \( ct-mcl \) or even as wild type.

The fact that such unstable genes are present have been recently demonstrated at the molecular level with regard to the white-eye mutant in \( D. melanogaster \). (Bingham et al. 1982).
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References


