



**A GENETICAL STUDY OF SOME MUTANTS OF  
DROSOPHILA ANANASSAE; Doleschall**

by

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ABSTRACT

Drosophila ananassae was used for the determination of spontaneous mutation rate in Sri Lanka in a previous study (Bogahawatte, 1984). The present work was carried out to study the inheritance patterns of four autosomal mutants and two sexlinked mutants obtained in the above study at the Dept. of Zoology, University of Sri Jayewardenepura, Nugegoda, Sri Lanka. These mutants were bw (brown eye), "cnt" (contracted wing), hl (hooked leg), mcl (marginal cell-less wing) and ct (cut wing).

This organism was selected for genetical studies as it is found locally and is easier to breed than D. melanogaster.

Initially some experiments were carried out with the purpose of building up double and triple mutant colonies.

Of the above mutants bw, "cnt" and hl are autosomal mutants and of them only brown eye (bw) mutant showed 100% agreement with Mendelian rules and it is concluded to be an autosomal recessive gene and the line is pure.

According to Bogahawatte (1984), "cnt" gene is autosomal



recessive. However, when "cnt" was out crossed it gave rise to only Curled wing flies. When it is inter-crossed it gave rise to only "cnt" flies and inter-crosses of Curled wing flies gave rise to wild type, Curled wing and contracted wing flies in 1:2:1 ratio. Therefore my results show conclusively that there is no "cnt" gene but that the "cnt" phenotype is simply the homozygous form of the Curled (Cu) gene. They also show the variable expressivity and incomplete penetrance.

For hooked leg (hl) mutants, it is concluded that though it is autosomal recessive according to the inheritance pattern, it shows variable expressivity and incomplete penetrance. Their viability is also low.

The sex-linked mutants were cut wing (ct) and marginal cell-less wing (mcl) whose inheritance patterns were complex. Each sex-linked mutant when out-crossed or inter-crossed could produce mcl, ct, mclct and wild type flies in a variable frequency. In order to explain the aberrant data the following possibilities, namely, pseudo-allelism, conditional mutants and movable genetic elements have been discussed. Pseudo-allelism probably is not the concept that could be used to interpret the aberrant results because the recombinant types and wild types in the progeny appear in larger numbers than would be the case with pseudo-alleles. Also they appear in widely varying proportions in different test crosses. The concept of the

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