

the Subgenus *Drosophila*. *D. bipectinata* formed the bulk of the catch, followed by *D. n. nasuta*, *D. malerkotliana* and *D. neoimmigrans*. The remaining species were found in lesser numbers. *D. neoimmigrans* is a new species belonging to the *Immigrans* species group.

Table 2 reveals a total of 1145 flies collected from nine spots. A total of 11 species were recorded out of which 7 species represent the Subgenus *Sophophora* and the remaining 4 species represent the Subgenus *Drosophila*. *D. malerkotliana* formed the bulk followed by *D. bipectinata* and *D. n. nasuta*. The remaining species were found in lesser numbers. It is quite interesting to note that *D. barbara* (Bock and Wheeler 1972) and *D. daruma* (Okada 1956) are the two species which are herein reported for the first time from India.

The collection data reveals that the flies belong either to the *melanogaster* species group or *immigrans* species group. This is in conformity with the suggestions of Bock and Wheeler (1972) who are of the opinion that both these species group are in abundance in South East Asia.

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Gerasimova, T.I. Institute of Molecular Genetics, USSR Academy of Sciences, Moscow, USSR. Superinstability of insertion mutations at the *cut* LOCUS in *Drosophila melanogaster*.

An unstable ct^{MR2} allele associated with a characteristic phenotype (sharply cut wings) was earlier obtained with the help of the male recombination factor (Gerasimova 1981). The present paper is analysis of normal (ct^+ revertants) and mutant (other *ct* alleles) derivatives of the ct^{MR2} allele. The author has analyzed

43,800 ct^{MR2} chromosomes and selected 58 wild-type revertants in a homozygous ct^{MR2}/ct^{MR2} stock and after the crosses $\varnothing XX/Y \times \sigma ct^{MR2}/Y$. All of them were tested for stability. As a result three groups of ct^+ revertants were identified: stable, unstable and superunstable. There were no new *ct* mutants in the progeny of stable revertants. No less than 10,000 chromosomes were analyzed for each stable revertant. Among the 58 revertants there were 11 stable ones, six of which carried mutations in genes *y*, *w*, *cm*, *sn*, *m*, *g*. Unstable revertants proved to be the most numerous category (43 out of 58). Their progeny regularly displayed *ct* mutants similar to ct^{MR2} , e.g., there were mutant transitions from ct^{MR2} to ct^+ and back to ct^{MR2} . The frequency of these transitions was about 10^{-4} . In superunstable revertants such transitions occurred with a much higher frequency (about 0.5), 4 of the 58 ct^+ revertants were superunstable. The ct^{+40} revertant was thoroughly analyzed. The progeny of 20 ct^{+40}/Y males individually crossed to XX/Y females was investigated for six generations. The overall number of wild-type males was 1485, that of mutant males was 1430. Thus ct^{+40} maintained its property of superinstability for a number of generations. A similar splitting phenomenon was observed in various crosses, proving that autosome modifiers have no influence on superinstability. Superinstability is most probably an allele-specific property of the revertants of the third kind. Superunstable mutations were also found among the new *ct* alleles derived from ct^{MR2} . Apart from reversions to the wild type, the ct^{MR2} allele is characterized by the formation of a series of new unstable *ct* alleles. Superunstable ones have been found among them. From the ct^{MR2} mutant (sharply cut wings) the author obtained the ct^{MRPN10} mutant (multiple incisions at the wing's edge). Among 26,000 ct^{MRPN10} chromosomes, 3 independent ct^{MRN} mutations were found (two small incisions at the wing's edge). All three mutations were superunstable. The ct^{MRN1} allele was studied best of all. In the progeny of a cross between one ct^{MRN1}/Y male and XX/Y females about half of the males were ct^{MRN1}/Y and the other half were ct^{MRPN10}/Y . In this case superinstability was also maintained in the line of generations. In each generation the progeny of 10 to 20 ct^{MRN1} males individually crossed to XX/Y females was analyzed. 15 generations were thus studied. The overall number of ct^{MRN1} males was 3946 and that of ct^{MRPN10}/Y males was 3850.

Analysis of the three kinds of ct^+ revertants and of the new unstable *ct* alleles suggests that the mobile element integrated in the *cut* locus, which has been called the *MR* transposon, can be excised (stable revertants), inverted (unstable revertants) or change its position within the *cut* locus (the new *ct* alleles). The inversions are in some way strongly enhanced

in superunstable revertants. In superunstable ct^N mutants the MR transposon has an enhanced ability to move within the cut locus. This ability of the MR -transposon to change its orientation and position with a high frequency indicates that under certain conditions the MR -transposon may become a controlling element that regulated the genes by switching their activity.

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References: Gerasimova, T.I. 1981, *Molec. Gen. Genet.* 184:544.

Gerasimova, T.I. Institute of Molecular Genetics, USSR Academy of Sciences, Moscow, USSR. Simultaneous reversion of two unstable alleles at the carmine and cut loci in Drosophila melanogaster.

The unstable ct^{MR2} allele carrying within the cut locus a mobile element called the MR -transposon is a strong mutator which causes new unstable mutations both at the cut locus itself and in other genes (Gerasimova 1981). Among the derivatives of the ct^{MR2} allele there is a double mutant with the cm^{MR1} and ct^{MR1} and ct^{MRpN1}

mutations in the X-chromosome. The ct^{MRpN1} mutation has a phenotypic expression that differs from ct^{MR2} , hence the MR -transposon occupies a different site within the cut locus. The cm^{MR1} mutation was not complementary to the standard cm mutation. The cm/cm^{MR1} flies had brown eyes. The homozygous stock $cm^{MR1} ct^{MRpN1}$ was analyzed for reversions. The following revertants were found among 30,000 individuals: eight $cm^{MR1} ct^+$, two $cm^+ ct^{MRpN1}$, two $cm^+ ct$, one $cm^+ ct^+$, four $w cm^+ ct^+$, one $y cm^+ ct^+$, one $y w cm^+ ct^+$ and sixteen $cm^+ ct^+ sn$. The first two types of revertants resulted from inversions at one locus (either $cm^{MR1} \rightarrow cm^+$ or $ct^{MRpN1} \rightarrow ct^+$). $cm^+ ct$ carried a reversion at cm and a new ct mutation other than ct^{MRpN1} . One $cm^+ ct$ revertant was tested for stability. Among 9500 flies no ct^+ revertants or new ct mutations were found. Hence $cm^+ ct$ most probably contain a deficiency at the cut locus due to an inaccurate excision of the MR transposon, i.e., $cm^+ ct$ are double revertants ($cm^{MR1} \rightarrow cm^+$, $ct^{MRpN1} \rightarrow ct^+$). All the other revertants had reversions at both loci; in most cases the double revertants carried new mutations at y , w , and, preferentially, sn . Thus about 70% of all revertants were double. A similar kind of double reversion had earlier been discovered by M.D. Golubovsky at the clw and sn loci (1979). The double reversion of unstable mutations always raises the question of whether both loci have kept their initial location or have come closer together as a result of some rearrangements, such as, say, inversions. The cm locus occupies position 18.9 (6E6) and cut is at 20.0 (7B3-4), i.e., they are separated by 1.1 morganids or 20-22 bands. Analysis of the polytene chromosomes in $cm^{MR1} ct^{MRpN1}$ mutants and in $cm^{MR1} ct^{MRpN1} / ++$ heterozygotes did not reveal any anomalies in the 6E-7B region. An attempt was made to separate the cm and ct loci by crossing-over. For that purpose crossing-over was analysed in $cm^{MR1} ct^{MRpN1} / ++$ / $y + + sn lz$ females. Among 3593 male offspring, there were 273 $y cm ct$, 246 $y sn lz$, 2 $cm ct sn lz$, 15 y , 4 $cm sn lz$, 11 $y ct$. The crossing-over between cm and ct was 0.5% (1.1% in the map), that between ct and sn was 0.4% (1% in the map). Thus the cm - ct - sn crossing-over was approximately halved. The fact that it was reduced to the same extent in the cm - ct region and in the ct - sn region indicates that ct is at equal distances from the cm and the sn loci. The reduced crossing-over may be a specific feature of the cm^{MR1}/ct^{MRpN1} chromosome, for the crossing-over between y and cm is also reduced and amounts to 14.4% (519/3593) or 18.9 in the map.

These results suggest that both loci have most probably kept their location. Another explanation may be found in the specificity of the $cm^{MR1} ct^{MRpN1}$ reversion. Different unstable ct and ct^+ alleles are characterized by different mutant transitions and different reversion frequencies, which seems to be the result of altered functions of the MR transposon: excision and transposition, change of position and orientation. These functions are altered in different ways in different alleles (Gerasimova in press). In the $cm^{MR1} ct^{MRpN1}$ stock the transposon has an enhanced ability for transpositions. 71% of all revertants are the result of transposition of the MR -transposon from the cm and ct loci to other genes. In the ct^{MR2} stock such transpositions occur far less frequently and account for 5 to 10% of all revertants. Double reversion itself, as has been shown for repressor protein mutations at Tn3 in E.coli enhancing Tn3 translocations in the transposition (Chow 1979).

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