

behavior in ion-exchange columns, etc.) indicate that cardinalic acid is an 8-ester of xanthurenic acid (Fig. 2).

Fifteen double mutants for eye-color, all of them carrying the mutation cardinal, were tested for the presence of cardinalic acid. This compound was only found in the cases where the other mutation allowed the accumulation of at least normal amounts of xanthurenic acid. This fact seems to indicate that xanthurenic acid is a precursor in the biosynthesis of cardinalic acid.

References: Danneel, R. & B. Zimmermann 1954, Z. Naturf. 9b:788-792; Ferre, J. 1983, "Accumulation of kynurenic acid in the "cinnabar" mutant of *D. melanogaster* as revealed by thin-layer chromatography, Insect Biochem. 13:289-294; Umebachi, Y. & K. Tsuchitani 1955, J. Biochem. (Tokyo) 42:817-824.

Table 1. Distribution of *Drosophila* fauna collected from Sampaje Ghats during August 1981.

Sites:	1	2	3	4	5	6	7	8	TOTAL
<u>SUBGENUS SOPHOPHORA</u>									
<i>D.malerokotliana</i>	28	-	6	1	80	122	20	11	268
<i>D.bipectinata</i>	-	-	-	-	91	311	7	-	409
<i>D.nagarholensis</i>	-	54	-	-	-	-	-	-	54
<i>D.nigra</i>	-	-	-	-	5	1	-	-	6
<i>D.parabipectinata</i>	-	-	-	-	-	2	-	-	2
<i>D.jambulina</i>	-	-	-	-	-	2	-	-	2
<i>D.sahyadrii</i>	-	-	-	-	-	1	-	-	1
<u>SUBGENUS DROSOPHILA</u>									
<i>D.n.nasuta</i>	3	20	8	3	74	151	55	34	348
<i>D.s.neonasuta</i>	-	3	1	3	12	53	1	-	73
* <i>D.neoiimmigrans</i>	14	34	-	-	51	18	27	-	144
TOTAL	45	111	15	7	313	661	110	45	1307
# species per site	3	4	3	3	6	9	5	2	

*New species described by the authors.

Table 2. Distribution of *Drosophila* fauna collected from Shiradi Ghats during June 1982.

Sites:	1	2	3	4	5	6	7	8	9	TOTAL
<u>SUBGENUS SOPHOPHORA</u>										
<i>D.malerkotliana</i>	100	201	164	15	24	8	26	57	29	624
<i>D.bipectinata</i>	76	94	72	-	5	2	6	13	78	346
<i>D.takahashii</i>	3	2	-	1	-	-	-	-	-	6
<i>D.eugracilis</i>	-	1	5	-	-	-	-	-	-	6
<i>D.nagarholensis</i>	-	-	2	-	-	-	1	-	-	3
<i>D.rajasekari</i>	-	-	-	-	-	-	-	-	2	2
* <i>D.barbarae</i>	-	-	1	3	-	-	2	-	-	6
<u>SUBGENUS DROSOPHILA</u>										
<i>D.n.nasuta</i>	8	17	22	8	19	4	7	30	2	117
<i>D.s.neonasuta</i>	5	13	-	-	1	-	1	-	-	20
<i>D.brindavani</i>	-	-	-	-	-	-	-	-	12	12
* <i>D.daruma</i>	-	-	3	-	-	-	-	-	-	3
TOTAL	192	328	269	27	49	14	43	100	123	1145
#species per site	5	6	7	4	4	3	6	3	5	

*Species reported for the first time from INDIA.

Gai, P.G. & N.B. Krishnamurthy. University of Mysore, India. Studies on the *Drosophila* fauna from Sampaje and Shiradi Ghats, Karnataka, India.

The Western Ghats is known to harbour a number of *Drosophila* species because of its excellent ecogeographic conditions. It offers a rich abode for a variety of *Drosophila* species because of its luxuriant flora and varied climatic conditions. Though some parts of the Western Ghats of India have been investigated for *Drosophila* fauna (Sreerama Reddy & Krishnamurthy 1971; Hegde & Krishnamurthy 1980; Prakash & Sreerama Reddy 1978 & 1979), yet several areas of the ghats remain to be surveyed.

Hence, the present collection trips were undertaken to Sampaje and Shiradi Ghats, which form part of the Western Ghats during August 1981 and June 1982, respectively. Collections were made both by fermenting banana bait and sweeping methods.

Table 1 shows the distribution of *Drosophila* species from Sampaje Ghats, whereas Table 2 shows the distribution from Shiradi Ghats.

Table 1 shows a total of 1307 flies trapped from eight spots. A total of 10 species were recorded, out of which 7 species represent the Subgenus *Sophophora* and the remaining 3 species represent

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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References: Bock, I.R. & M.R. Wheeler 1972, *Studies in Genetics VII*, Univ. of Texas Publ. 7213:1-102; Hegde, S.N. & N.B. Krishnamurthy 1980, DIS 55:60; Prakash, H.S. & G. Sreerama Reddy 1978, *Entomon* 3(1):85-90; Prakash, H.S. & G. Sreerama Reddy 1979, *Entomon* 4(1):73-76; Sreerama Reddy, G. & N.B. Krishnamurthy 1971, DIS 47:116.

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