after gamma-irradiation. Pre-treatment of the D-32 males with caffeine does not modify this picture. However, pre-treatment with actinomycin-D (other things being equal) significantly enhances the occurring of the chromosome yellow mutations and reduces the yield of the gene ones. It would appear that the transformation of the pre-mutational lesions into chromosomal damages and less effective repair of the latter have both simultaneously taken place. These taken together (our own data and the well-known fact that actinomycin-D is bound with GC-repeats of DNA) argue that the chromosome changes, except for VV^g, are initiated by the damages of the repetitive DNA sequences surrounding and/or interspersing the functional genetic unit. Therefore, as it follows from our own experimental data with neutrons (see Table), the quality (mode and perhaps density) of initial lesions predetermines the occurrence of rearrangements also. Thus both factors (i.e., the feature of the initial lesions determined by the radiation quality and the nature of the primarily damaged DNA sequences) appear to be decisive in the processing of the radiation-induced chromosome changes of all kinds.

However, the modifying effect of some other variables studied prove to be new and unpredictable. In particular, the combined irradiation by neutrons and gamma-rays (consecutive or simultaneous in the case of ^{252}Cf) increases the yield of VV^g, but not a chromosome alteration. On the other hand, in the gamma-irradiated c(3)G post-meiotic male germ cells (repair-deficient mutant as proposed by Watson 1972), there was a very marked decrease in the frequency of the VV^g in comparison with that in the gamma-irradiated wild-type germ cells.

One obvious question that needs to be answered is whether these variatioins in the specific-locus radiomutability are conditioned by the variables as such or are due to the feature of the locus studied. To answer this question, the spectrum and frequency of visibles for another loci will need to be studied under the same experimental conditions. Such genetical and cytogenetical analysis of the white, black and cinnabar mutations scored simultaneously with yellow ones is in progress now.

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References: Alexandrov, I.D. 1984, Mutation Res. 127:123-127; Watson, W.A.F. 1972, Mutation Res. 14:299-307.

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Studies on bristle number in hybrids between strains of **D.capricorni** from Brazil.

Drosophila capricorni is related to the "willistoni" species group but distinguishable from each other in externally visible characters (Dobzhansky 1951). It usually prefers cooler and humid regions. In Brasil, it extends from northern part to the southern most state. It has rarely been found in the summer while it occurs in abundance during the winter season (pers. comm. from Prof. A.R. Cordeiro), and was confirmed partly by our data.

The object of the present research work was to examine the variance of bristle number in parental, F_1's and F_2 classes. For this purpose, several strains of **D.capricorni** were collected in July 1978 and February 1979 from Itatiaia (Resende, RJ), and were maintained in the laboratory as isofemale lines. A total of 13 strains (six from July 1978 and seven from the year 1979; these lines were maintained at 18°C for 540 and 980 days, respectively, before the commencement of the investigation) were utilized for the research work. Crosses in various combinations between strains (within and between the year of collection) were made to yield F_1 and F_2 classes. A total of 60 parental and 60 F_1's; 60 parental and 60 F_2 classes were analyzed at each of the two temperatures: 18° and 25°C. The parental and F_1's were placed simultaneously at each temperature, using 50 eggs for each of the five or more replicates. Similar procedure was followed for the parental and F_2 classes. The bristle number on 4th and 5th sternites, and the left and right esternopleurals were counted on the same individual in both sexes for each of the parental, F_1 and F_2 classes. In general, 8-10 males and 8-10 females from each of the three to six replicates for each class were examined. (However, there were cases where the sample size was very small which did not alter the final results.) The variance of the difference in bristle number between 4th and 5th sternites, and between left-right esternopleurals was computed. It was observed that the F_1's or F_2's had either equal, greater or smaller value of the variance when compared with their parental classes. However, in general, no significant difference in variance between parental and F_1's, and between parental and F_2's was observed for each sex at each temperature. Thus, these results indicated that the F_1's and F_2's were developmentally as buffered (stable/homeostatic) as their parental classes for the number of bristles examined even though the strains utilized in this experiment were maintained for the two different periods.

In addition, we looked for the pattern for frequency for the phenotypic variance. For this purpose, the variance values for the difference in esternopleural bristle number were grouped into three class intervals: 0-1, 1-2, and >2, for parental, F_1 and F_2 classes for each sex at each temperature. At each temperature the major part of the variance values in both the sexes occurred in the central class (1-2). The frequency in the case of the females grouped in the class greater than two was larger when compared with those of the males at either temperature. On comparing the class interval >2 between temperatures, a slight increase at 18° was observed than at 25°C for each sex. However, no specific pattern on this aspect could be noticed in the case of the crosses made between the two periods of collection. Comparison of the parental with F_1's yielded almost homogeneity for the frequencies in each of the three classes of variance. Overall, F_2's grouped in the central class, 1-2, were in larger number when compared with those of F_1's for each sex at 18°C. No consistent pattern for such a comparison was observed at 25°C.

Likewise, the values of the variance for the difference in bristle number between the two sternites were also classified, into three classes: 2-6, 6-10, and >10, in order to search for pattern. At 25°, the majority of the phenotypic variance for the parental, F_1's and F_2's occurred in the central class (6-10) for each sex. While at 18°, such a frequency was spread into two classes (2-6 and 6-10), indicating a reduced number of phenotypic variances in the class greater than 10 at this temperature. No concludable pattern was observed for the comparison of F_1's or F_2's with their parental classes. The other aspects are under investigation.

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Reference: Dobzhansky, Th. 1951, in:Genetics and the Origin of Species, 3d ed rev, Columbia Univ, New York.

Andrews, K. and C. Chihara. University of San Francisco, California, USNA. An overproducer of a third instar urea-soluble cuticle protein in **Drosophila melanogaster.**

Third instar larvae of **Drosophila melanogaster** show a standard electrophoretic pattern for the urea-soluble cuticular proteins (Fristrom et al. 1978; Chihara et al. 1982) (Figure 1, lanes 1 and 4). The bands are designated from slowest (top) to fastest (bottom) as L_3CP-1, 2, 2a, 3, 4, 5, 6, 7, 8, respectively.

The overproducer variant of L_3CP-5 (named L_3CP5^{op}) was isolated from an Austin Species Center stock acquired from Kuala Lumpur, Malaysia. Several rounds of pair matings produced a stock which gave consistently dark bands at the position of protein 5, (125 samples). The intensity of the variant L_3CP-5 was checked against wild type using a gel scanner with integrator. The density of the L_3CP-5 band relative to the L_3CP-4 band of both stocks was compared and the following ratios were obtained (Figure 1):

5^{op}: Mean density ratio of Bands 5:4 = 1.95(±0.65):1 ;n = 67
+/+: " " " " " = 0.97(±0.13):1 ;n = 7

The L_3CP5^{op} variant is at least partially dominant. When it was crossed to wild type the 5 band remained visibly darker than the wild type. This can also be seen in the crosses described below.

To make sure the darkened 5 band was due to overproduction of L_3CP-5 and not to the introduction of a new protein with the same electrophoretic mobility, the L_3CP5^{op} variant was crossed with, and then backcrossed to, a recessive mutant known as omega. Omega is a putative processing gene whose product, when inactive, results in the non-processing of L_3CP-5; as a result, L_3CP-5 migrates much more slowly than wild type L_3CP-5. This slow band is designated as the omega band (Figure 1, lanes 2 and 3).

Density comparisons between the L_3CP-omega band and L_3CP-4 were made as above (Fig. 2).

Omega/omega: Mean density ratio of omega:4 = 1.04:1, with a high value of 1.40 and a low of 0.84. This is comparable to the values for +/+, bands 5:4 shown above.

5^{op} omega/5^{+} omega: Mean density ratio of Omega:4 = 2.4:1, with a high of 3. and a low of 1.83 (Fig. 1, lane 5).

Wild type omega recombinant: Mean density ratio of Omega:4= 1.25:1, with a high of 1.67 and a low of 0.83.

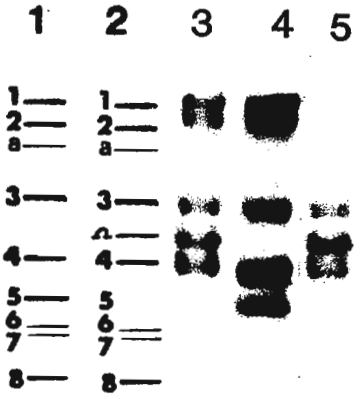

Figure 1. **Lane 1:** Schematic wild type banding pattern with numbers. **Lane 2:** Schematic omega homozygote pattern. **Lane 3:** Homozygous omega with wild type for gene 5. **Lane 4:** Typical wild pattern. **Lane 5:** L_3CP5^{op} heterozygote with homozygous omega, note dark omega band.