CUBITUS INTERRUPTUS, A NEW GENOVARIATION OF THE FOURTH CHROMOSOME OF *DROSOPHILA* *MELANOGASTER*

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The new genovariation here described was discovered in the Normal Florida line in February, 1930, simultaneously at the INSTITUTE OF EXPERIMENTAL BIOLOGY in Moscow and at the CENTRAL GENETICS STATION of Narcomzem (Department of Agriculture). At the CENTRAL GENETICS STATION, the gene-variation was named cubitus interruptus (c_i) and it was called cubitus incompletus in the genetics laboratory of the INSTITUTE OF EXPERIMENTAL BIOLOGY.¹

FIGURE 1.

PHENOTYPE OF THE GENOVARIATION

The mutant character consists of one or of several interruptions of the fourth-longitudinal vein (cubitus). Sometimes, additional interruptions are observed in the fifth-longitudinal vein and in the posterior cross vein, which, at times, is even entirely lacking. Sometimes also, the cubitus and

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the second cross vein are crooked, and frequently the cubitus is thickened and ragged at the basis. The drawings of six wings in figure 1 give a clearer demonstration of the comparatively strong invariability in the expression of this character. The manifestation of the character in the lines obtained at the CENTRAL GENETICS STATION was complete (100 percent). In the lines of the INSTITUTE OF EXPERIMENTAL BIOLOGY there were inbred cultures where the average manifestation of the character was 98 percent. It is necessary to note that in some lines the percentage of the character manifestation was considerably lower, this being evidently due to the difference of the genotypical medium. The character is very often asymmetrical in its expression, and is sometimes lacking on one of the wings.

GENETIC ANALYSIS

In F_1 from crosses of the new mutation with normal lines (Florida and Caucasus Gelendzhik) exclusively normal individuals, in males as well as in females, were obtained (see table 1). Hence it follows that the new genovariation is recessive and not sex-linked. In F_2 a ratio very near to 3:1 was obtained (see table 1).

TABLE 1

CROSSES	F_1	F_2
♀ c_i × ♂ Normal Florida	1,302 Normal	2,317 Normal: 641 c_i
♀ Normal Florida × ♂ c_i	365 Normal	(3.13:0.87)
♀ c_i × ♂ Caucasus Normal	353 Normal	2,557 Normal: 786 c_i
♀ Normal Caucasus × ♂ c_i	185 Normal	(3.06:0.94)
Total	2,205 Normal	4,874 Normal: 1,427 c_i (3.09:0.91)

For determining in which of the autosomes the c_i gene is situated, the following dominant mutations were used as indicators: for the second chromosome, Lobe 2 (L^2) and Star (S), and for the third, Dichaete (D). As a result of the backcrosses of the F_1 heterozygotes with the double recessives, the data presented on tables 2 and 3 were obtained. In these data the relative lowness of the numbers of c_i and the relative highness of the corresponding not- c_i class (for example, 556 > 363) is probably due to strong overlapping of the c_i character with the not- c_i phenotype. This

TABLE 2
Male backcrosses for chromosome II.

c_i	L^2	$c_i L^2$	NORMAL
363	595	387	556
c_i	S	$c_i S$	Normal
99	203	157	217

TABLE 3
Male backcrosses for chromosome III.

c_i	D	$c_i D$	NORMAL
337	307	296	505

suggests that the stocks in which the expression is 100 percent or 98 percent have modifying genes which strengthen the manifestation.

It is seen from these tables that the flies obtained in the male backcrosses were of 4 phenotypes, which shows that no linkage exists either with the second or with the third chromosome characters. One supposition remained possible, that of the gene c_i being linked with fourth-chromosome characters. To verify this hypothesis a cross was made between homozygous c_i , flies and homozygous flies of the fourth-chromosome character eyeless (Russian mutant allelomorph). All the flies obtained from this cross (527 in number) were normal, as was to be expected, both the genes being recessive, and the flies of this generation being heterozygous by both genes. In the second generation, a segregation into 3 phenotypes, in the proportion of 2 Normal: 1 e_y^R : 1 c_i was expected, and was realized, as table 4 shows.

TABLE 4
F₂ from the cross of $c_i \times e_y$.

NORMAL	c_i	e_y^R	$e_y^R c_i$
3,220	1,422	1,008	0

If the gene c_i were not carried in the fourth chromosome, we ought to have received four phenotypes in the ratio of 9 Normal: 3 c_i ; 3 e_y^R : 1 $e_y^R c_i$. Since no phenotype $e_y^R c_i$ was obtained the data prove that the c_i gene is carried in the fourth chromosome. One of the authors of the present paper (G. G. TINIAKOF) has obtained through crossing over in the fourth chromosome between eyeless (Russian) and c_i , a stock of $e_y^R c_i$.

We had the opportunity of demonstrating this stock to BRIDGES on his visit to our Institute in January, 1932, and he confirmed our classification. He also stated that this is the first definite evidence of crossing over in the fourth chromosome. His own experiments had given apparent crossing over (0.9 between eyeless and bent), but some of this apparent crossing over was undoubtedly due to non-disjunction instead and he had not excluded the possibility that all of it was due to non-disjunction and that perhaps the fourth chromosome was too short to give the usual kind of crossing over. With the $e_y^R c_i$ stock further work is now being carried on for testing the amount of crossing over between the genes in question. The results will be published later.

SUMMARY

The new character here described is due to a recessive gene in the fourth chromosome in *Drosophila melanogaster*. The gene causes varying breaks and abnormalities in the veins of the wing, principally in the cubitus and occasionally in the analis and in the posterior cross vein. In some lines the genovariation c_i has a complete manifestation (100 percent) while in other lines it is 98 percent or lower; in the F_2 from out-crosses it may be as low as 75 percent. This probably means that the high manifestation stocks have intensifying modifiers which are separated from c_i in the segregation. Definite evidence that crossing over occurs in the fourth chromosome between the loci *eyeless* (Russian) and c_i was obtained.