A CASE OF REARRANGEMENT OF GENES IN DROSOPHILA[1]

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Seven mutant genes of Drosophila simulans have been shown to be allelomorphic to previously known mutant genes of D. melanogaster.[2] Five of these lie in the X-chromosome, and a study of their linkage relations was shown to indicate that the sequence of the five loci concerned is the same in both species, and that the percentages of crossing over in comparable regions, while not indentical, is still not very different. The other two allelomorphic mutant genes, scarlet and peach, lie about 3 units apart in the third chromosome of melanogaster; in simulans they lie in the same chromosome (which is thus identified as the third one), but they were found to be at least 45 units apart.

More recently two more mutant genes of simulans that lie in the third chromosome have been studied. One of these, dachs,[3] lies to the left of scarlet; the other, deltoid,[4] lies between scarlet and peach. The latter, since it makes possible the detection of a portion of the double crossovers, has resulted in a more accurate determination of the scarlet peach distance. The map based on the linkage relations of these four loci (not corrected for unobservable double crossing over) is shown in figure 1.

Both of the new mutant types, dachs and deltoid, resemble previously known mutant types in D. melanogaster. Dachs in melanogaster lies in the second chromosome; it is accordingly not surprising that tests have shown it not to be allelomorphic to dachs simulans. Deltoid resembles delta melanogaster. Since both genes are dominant, the usual test of allelomorphism could not be applied; but each has also a recessive lethal effect, and crosses of delta melanogaster by deltoid simulans have shown that the hybrids that receive both mutant genes do not develop. It follows that the two genes are allelomorphic. The map of the melanogaster third chromosome, including the known ends and the three loci occupied by parallel mutations, is shown in figure 2.[5]

A comparison of figures 1 and 2 shows that *the three identical loci are not in the same sequence in the two species.*

Mr. D. E. Lancefield has obtained evidence suggesting a similar rearrangement of genes in the X-chromosome of D. obscura. His results were obtained before those here reported, but are not yet published. Since D. obscura has not yet been crossed with any other species, the evidence for identity of loci is not conclusive in this case.

The only analogous case so far reported appears to be that briefly described by Bridges[6] under the name of "vermilion duplication." In

this case a section from near the middle of an X-chromosome of D. melanogaster appears to have broken loose and attached itself to the left-hand end of a normal X-chromosome. Weinstein[7] has shown that such an occurrence might lead to a change of sequence of identical loci such as is here reported. If we suppose that the simulans third chromosome was originally constituted as is that of melanogaster, the situation as we now find it may be supposed to have arisen as follows: A section, including the peach locus, broke loose and attached itself near the right-hand end of a normal third chromosome. After this condition had become established the peach locus near the middle of the chromosome mutated or became "deficient," so that in effect the peach locus was moved to the right end of the chromosome. Such an interpretation will account for the observed facts.[8]

There is, however, another possible method whereby the same result might be supposed to have been brought about, viz., by the simple inversion of a section of a normal chromosome. Such an accident seems not unlikely to occur at the stage of crossing over. If we suppose a chromosome to occasionally have a "buckle" at a crossing over point, it is conceivable that crossing over might be followed by fusion of the broken ends in such a way as to bring about an inversion of a section of chromosome.

Either of the two suppositions discussed will account for the observed results, but they should lead to different relations for other loci in the same chromosome; it is hoped that further work will lead to the discoveryof additional parallel mutations, so that the maps may be studied in more detail.

If an inversion of the kind suggested above occurred within a species, then individuals bearing one normal chromosome and one chromosome with an inverted section would probably show no crossing over in the region in question, since it seems probable that synapsis in this region would be abnormal or absent. It would also be not surprising if crossing over in adjacent regions was decreased. But individuals homozygous for the inverted section would be expected to show free crossing over again, since there should now be no difficulty at synapsis.

The relations indicated are those that have actually been found in the cases of the two "crossover genes" in melanogaster known as C_{III}[9] and C_{IIr}.[10] These "genes" both cause, in individuals heterozygous for them, the disappearance of crossing over in the immediate regions where the "genes" themselves lie, and a considerable reduction of crossing over in neighboring regions. In individuals homozygous for either of these "genes," however, the percentage of crossing over rises to (or beyond) that found in "normal" individuals. Experiments are now under way in an attempt to determine if these "genes" are really simply inverted chromosome sections, but it will probably be a long task to definitely settle the matter.

The demonstration of a change in sequence of identical loci that is here reported makes the identification of parallel mutations in species that cannot be crossed even more difficult than it has previously seemed; for identity of sequence in a group of identical loci now appears not to be necessarily expected.

0.0	dachs
14.2	scarlet
39.0	deltoid
76.5	peach

FIGURE 1

0.0	roughoid
41.5	scarlet
44.5	peach
63.5	delta
101.0	minute–23

FIGURE 2

[1] Contribution from the Carnegie Institution of Washington.

[2] Sturtevant, A. H., *Genetics*, **6**, 1921 (63, 179).

[3] Discovered by Prof. T. H. Morgan.

[4] Discovered by Dr. C. B. Bridges.

[5] This map is based on the more extensive one published by Bridges in these PROCEEDINGS.

[6] Bridges, C. B., *J. Gen. Physiol.*, **1**, 1919 (645).

[7] Weinstein, A., these PROCEEDINGS, **6**, 1921 (625).

[8] It is, of course, possible to invert this interpretation by supposing the simulans situation to be the original one.

[9] Muller, H. J., *Amer. Nat.*, **50**, 1916 (103, 284, 350, 421), and Sturtevant, A. H., *Carnegie Inst. Wash. Publ.*, No. 278, 1919 (305).

[10] Sturtevant, A. H., these PROCEEDINGS, **3**, 1917 (555), and *Carnegie Inst. Wash. Publ.*, No. 278, 1919 (305).

A REMEASUREMENT OF THE RADIATION CONSTANT, h, BY MEANS OF X-RAYS

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Since the discovery of the fact[1] that the continuous X-ray spectrum has a short wave-length limit, which obeys the quantum law, a number of experimentors have used this phenomenon to determine the value of h.[2] In its application to X-rays the quantum law may be expressed by the equation

$$Ve = h\nu, \qquad (1)$$

where V represents the maximum difference of potential in the X-ray tube through which the electrons fall, e, the charge carried by each electron, ν, the frequency of vibration corresponding to the short wave-length limit of the spectrum, and h, Planck's action constant. Evidently a measurement of V and ν gives us the ratio of h to e, and from this we get h, if we suppose e to be given by other experiments. Blake and Duane[3]