CHAPTER VII

THE LOCATION OF GENES IN RELATED SPECIES

DE VRIES' mutation theory quite apart from its special interpretation discussed in an earlier chapter postulates that "elementary" species are made up of a large number of identical genes; and that their differences are due to different recombinations of these genes. The more recent work on hybridizing related species has furnished evidence bearing on this theory.

The most obvious way to study the problem would be to cross species and determine in this way, if possible, whether they are made up of the same number of homologous genes, but several difficulties stand in the way. Many species cannot be crossed, and some of those that can be crossed produce sterile hybrids. Nevertheless, a few species are fertile *inter se,* and some of them also give fertile hybrids. Even then, another difficulty arises, namely, the identification in the two species of the characters that behave as Mendelian pairs; for the differences that serve to distinguish one species from another species are dependent on a multitude of factors in each case. In other words, it is rare to find two well-marked species in which any single difference is due to one differential factor. Mutant differences of recent origin in one or in both species must be resorted to for the necessary evidence.

There are several cases in plants and two at least in animals where species having mutant types have been

crossed with other species, and produced fertile offspring. These, when inbred, or back-crossed, have furnished the only crucial evidence concerning the allelomorphic relation of genes in different species.

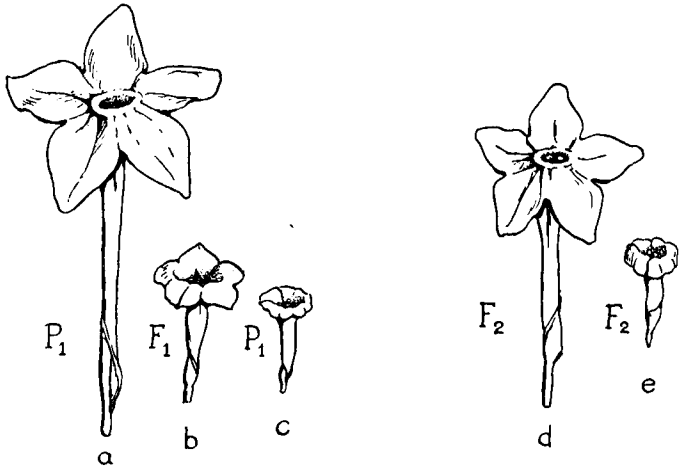

FIG. 53.

Cross between two species of tobacco, Nicotiana Langsdorffii and N. alata. In a and c the two original types of flowers are shown, and in b the hybrid type. In d and e, two of the recovered types in F_2 are shown. (After East.)

East crossed two species of tobacco, Nicotiana Langsdorffii and N. alata (Fig. 53). One plant with white flowers was a mutant type. Despite the wide variability of many characters in the second generation, the white flowers appeared in one-fourth of the individuals of this generation. The mutant gene of one species behaved toward a gene of the other species in the same way as it behaves with its own normal partner.

Correns crossed Mirabilis Jalapa with M. longiflora. A recessive mutant of Jalapa (chlorina) was used. This

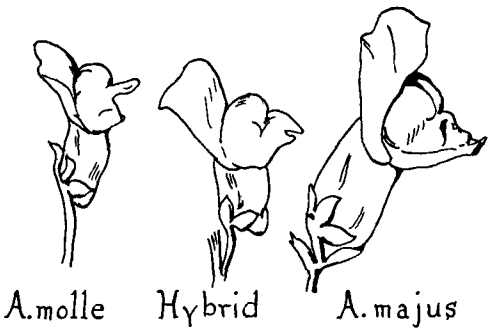

FIG. 54.

Two species of snapdragon, Antirrhinum molle and A. majus with the hybrid between them. (After Baur.)

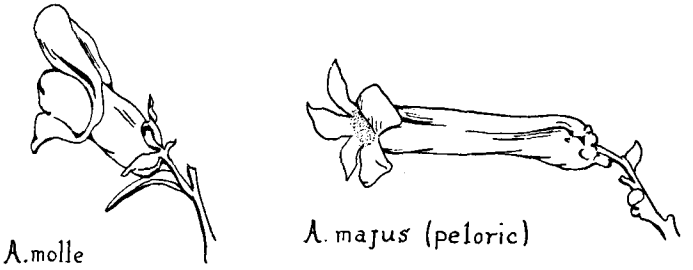

FIG. 55.

A bilateral type of flower of Antirrhinum molle by a peloric type of A. majus, which, when crossed, gives the hybrid "wild" type seen below. (After Baur.)

character reappeared in almost one-quarter of the individuals in the second generation.

Baur crossed two species of snapdragon, Antirrhinum majus and A. molle (Fig. 54). He used at least five

FIG. 56.

Types of F_2 flowers from the cross shown in Fig. 55. (After Baur.)

mutant types of A. majus and recovered them in the second generation in the expected number of individuals (Fig. 55 and 56).

Detlefsen crossed two species of guinea pigs, Cavia porcellus and C. rufescens. The hybrid females (the hybrid males are sterile) were mated to C. porcellus males

with mutant characters, seven in all. The mutant characters were inherited in the same way as in C. porcellus. This result again shows that the two species carry some identical loci. The results do not show, however, that identical mutants exist in the two species, for no mutant races with characters similar to those of porcellus have been studied.

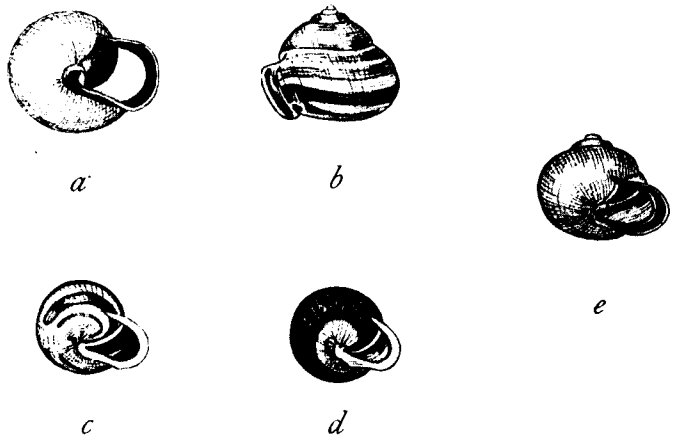

FIG. 57.

a, Helix nemoralis, 00000, yellow, Zurich type; *b*, ditto 00345, reddish (Aarburger type); *c*, typical H. hortensis, 12345; *d*, ditto; *e*, hybrid 00000. (After Lang.)

One of the clearest cases where the characters of one species behave toward the characters of the other species in the dominance-recessive relation as do the same character-pairs within the species is described by Lang in his experiments with two wild species of snail, Helix hortensis and H. nemoralis (Fig. 57).

There are two wild species of Drosophila that are so much alike externally that they were put into the same species. One is now called D. melanogaster, the other D.

simulans (Fig. 58). Careful scrutiny shows them to be different in many ways. They cross with difficulty and the hybrids produced are completely sterile.

Forty-two mutant types are now known in D. simulans. These fall into three linkage groups.

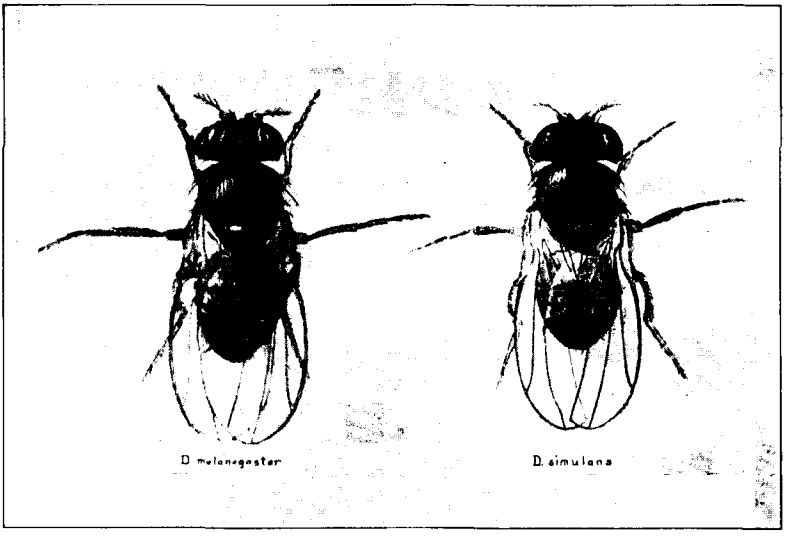

FIG. 58.

Drosophila melanogaster to the left, and D. simulans to the right; both males.

Twenty-three of these recessive mutant genes in simulans are recessive in the hybrid, and 65 recessive mutant genes of melanogaster have also been shown to be recessive in the hybrid. This result means that each species carries the standard or wild type gene of each of the recessive genes of the other species.

Sixteen dominant genes have also been tested. All but one produced nearly the same effect in the hybrid that they produce within their own species. This means that

sixteen normal genes are recessive to the dominant mutant genes of the other species.

Mutants of simulans have been mated to mutants of melanogaster. In twenty cases tested, the mutant character proved to be the same.

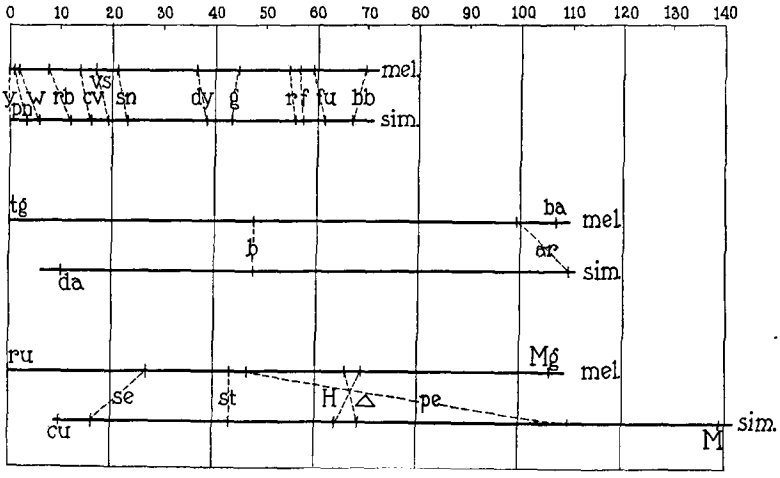

FIG. 59.

Chart showing, above, the corresponding loci of identical mutant genes of the first or X-chromosome in Drosophila melanogaster and in D. simulans, similarly, in the middle, of the second chromosome; and, at the bottom, of the third chromosome. (After Sturtevant.)

This last result establishes the identity of the mutants in the two types, and enables one to discover whether they lie in the same linkage series, and in the same relative position in each series. The chart (Fig. 59) shows by the connecting dotted lines the relative position of the loci of identical mutants so far worked out by Sturtevant. In chromosome-I there is a remarkable agreement. In chromosome-II only two identical loci have been determined. In chromosome-III the agreement is not complete. It can

probably be explained on the assumption that a large section of this chromosome has been reversed, and the corresponding loci are in inverse order.

These results of Sturtevant's are not only important in themselves, but help to make probable the view that similar mutants in different species that occupy the same relative position in the linkage series, are identical mutants, but unless their identity can be tested by crossing,

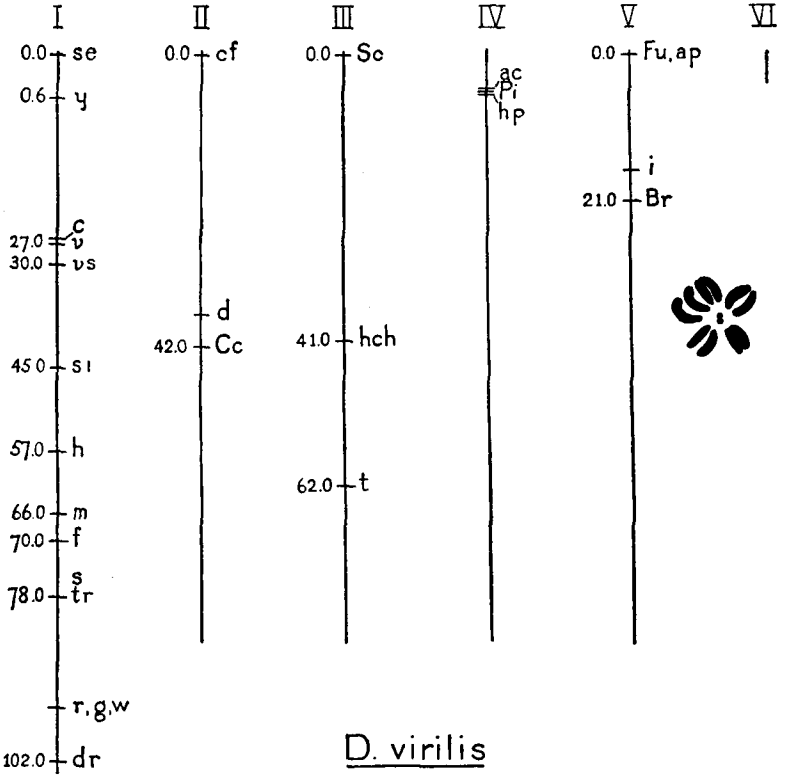

FIG. 60.

Chart of the location of the mutant genes in the six chromosomes of Drosophila virilis. (After Metz and Weinstein.)

as in the case of D. melanogaster, and D. simulans, there may always remain some doubt as to their identity, because similar mutant types that are not identical are

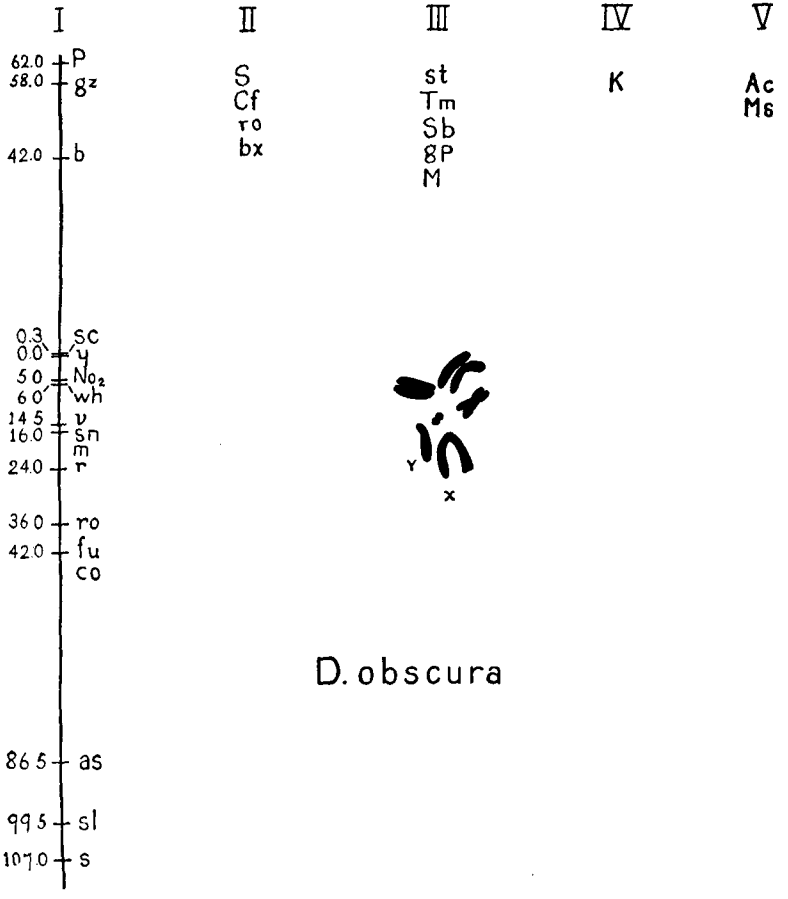

FIG. 61.

Chart of the location of the mutant genes in the chromosomes of Drosophila obscura. The loci corresponding with those of D. melanogaster are sc=scute, y=yellow, No_2=Notch, wh=white. (After Lancefield.)

known, and sometimes these lie near together in the same linkage group.[1]

In two other species of Drosophila the work has progressed to a point where the comparisons are at least very interesting. In Drosophila virilis, Metz and Weinstein have determined the location of several mutant genes, and Metz has compared the order of the series with that of D. melanogaster. The chart (Fig. 60) shows that there are five apparently similar mutants in the sex-chromosome that stand in the same order as those of melanogaster, *viz.*, yellow (y), cross-veinless (c), singed (si), miniature (m), forked (f).

Another species, Drosophila obscura, has a genetic sex-chromosome twice as long as that of melanogaster (Fig. 61). It is probably significant that the four characteristic mutant types, yellow, white eyes, scute, and notch wings, that lie in the middle of this long sex-chromosome, are identical with the same mutant characters of D. melanogaster that lie at the end of the shorter sex-chromosome of melanogaster and simulans. The interpretation of this relation is still being carefully studied by Lancefield.

These and other results should make us extremely cautious in drawing phylogenetic conclusions from inspection alone of the chromosome groups; for, it follows from the Drosophila evidence that very closely related species may have their genes arranged in a different order in the same chromosomes. Similar groups of chromosomes may at times contain different assortments of genes. Since it is the genes, and not the chromosomes as such, that are important, the final analysis of the hereditary construction must be determined by genetics rather than by cytology.

[1] By taking into account more than a single effect of each gene the identification may be made more probable.