After observing that only the homozygous substitution plants for the C-T interchange were green (b) in the above F_2 (69-294 to 300), it was realized that all previously isolated homozygous substitutions for this interchange C-T chromosome were also b.

The discovery of the b locus on chromosome 9 of T. dactyloides increases the number of loci held in common with the short arm of corn II to six.

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12. Multiple homeologies of chromosome 9 of Tripsacum dactyloides.

In some of the microsporocytes from 20+2 Lg Gl plants, chromosome 9 of T. dactyloides is seen to be occasionally associated at pachytene with corn chromosome X in addition to its association with corn II S. Sometimes, the otherwise homomorphic pair of this extra chromosome is found to be deficient for a greater part of its long arm including the terminal knob and the corresponding segment is found attached, as a univalent, to the short arm of corn X. Less frequently, the distal knobbed univalent portions of both these pairs also show homologous pairing in these regions, and in related stocks the terminal knob of tripsacum 9 is found in the short arm of corn X. The breakpoints for these interchanges, which seem to be confined to a few nuclei, are estimated to be in the proximal half of the long arm of the tripsacum chromosome and in the distal portion of the short arm of corn X. Spontaneous breakage (fragmentation) and reunion is ruled out because of the somewhat regular, but low, frequency with which such configurations appear among the pachytene nuclei. Further, identical pachytene associations and altered chromosome types have been observed in the Lg Gl homeolog extracted independently from T. floridanum (vide item 17). From these observations it seems reasonable to assume that there exist some unidentified homeologies between tripsacum chromosome 9 and corn X, in addition to its already known affinities to the short arm of corn II, and that the alterations in the form of these chromosomes is not due merely to breakage and reunion of the concerned segments.

It is already verified cytologically that the two loci $\underline{Su}_1$ and $\underline{Gl}_3$ of corn chromosome IV occur on two different tripsacum chromosomes. In the present case, it seems that a single tripsacum chromosome has loci belonging to different linkage groups in corn. Considering the quite different chromosome numbers and the cytological maps, perhaps a reasonable amount of redistribution of their common loci might be expected in these two genera.

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13. Recombination potential between chromosome VII of corn and its homeolog from T. dactyloides.

As previously reported, one of the tripsacum chromosomes is partly homeologous to chromosome VII of corn and is capable of covering the recessives $\underline{v}_5$, $\underline{ra}_1$, $\underline{gl}_1$ and $\underline{ij}$. Plants carrying one or a pair of these extra chromosomes were backcrossed to the male corn parent and the combined segregation data for three loci tested are given in table 1.

By virtue of the irregular transmission of the tripsacum chromosome, certain basic assumptions have to be made in an interpretation of the segregation data for the parental as well as the recombinant characters. First, the dominant phenotypes are expressed only when the original tripsacum chromosome (TT) or its interchanged products (C^T or T^C) are included in the genome. With regular meiotic events observed for the corn (CC) or the corn-tripsacum interchange (C^T) chromosomes, recombinants of the higher order in each class of crossovers are regarded as due to the transmission of the C^T chromosomes; the number of reciprocal crossovers revealed in each of the three classes, being dependent upon the irregular transmission frequency of the corresponding T^C chromosome, would appear in less than the equal numbers normally expected. With the noninclusion of the T^C for any of these classes, there would be a corresponding enhancement of the recessive phenotypes; likewise when both the interchanged chromosomes C^T and T^C are included in the same gamete there would be an increase in the expression of all the dominants which would cover up the phenotypic expression of the crossover recessives. It is therefore considered that both of the observed parental combinations,