

It is already verified cytologically that the two loci Su_1 and $G1_3$ 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 v_5 , ra_1 , gl_1 and 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,

Ij, Ra, Gl and ij, ra, gl, are somewhat enhanced to the extent that the two reciprocally interchanged chromosomes are included in the same gamete on the one hand, and on the other to the extent to which the interchanged T^C chromosomes, in each of the crossover classes, are eliminated from the functional gamete. In a population of 663 plants classified for these three loci, the transmission frequency of the chromosome with the tripsacum centromere (T or T^C) is found to be 25.6%. The theoretical probability calculated on this basis is taken into account in giving the expected values for the parental combinations, while the reciprocal crossovers in each class, involving the T^C chromosome are taken as being about equal to the maximum observed values for the corresponding reciprocal on the C^T chromosome.

Table 1

Backcross data for *Tripsacum* homeolog to corn chromosome VII
(66-376 to 434A)

(The theoretically expected data are not based on the known linkage values for corn chromosome VII but represent figures assumed to be the minimum probability for the unknown genetic content of the *Tripsacum* chromosome.)

	Chromosome type	Phenotype	No. observed	No. expected (theoretical)	Percent
Parental:	{ CC	ij ra gl	395	347	70.44
	{ TT	Ij Ra Gl	163	120	
Crossover I	{ C^T	Ij ra gl	24	24	7.24
	{ T^C	ij Ra Gl	7	24	
Crossover II	{ C^T	Ij Ra gl	66	66	19.77
	{ T^C	ij ra Gl	0	66	
Double crossover, I & II	{ C^T	Ij ra Gl	8	8	2.41
	{ T^C	ij Ra gl	<u>0</u>	<u>8</u>	
		Total	663	663	

Reduction or absence of phenotypes governed by T^C is due to its elimination and to that extent ij ra gl are enhanced; masking of the recessive crossover phenotypes by the inclusion of both C^T and T^C in the same gamete results in an increased value for the triple dominant Ij Ra Gl phenotypes. In addition, we have also to contend with some degree of suppression of crossing over due to nonhomologous pairing between the tripsacum and corn homeologs. Therefore, while these recombination data do not reflect the actual crossover frequencies, they do reflect the recombination potential and the probable difference in gene sequence. It seems that the Gl and Ij loci are in an inverted order between these two chromosomes. What is more important to recognize now is that despite their generic differentiation, morphologically as well as cytologically, these two forms are capable of genetic exchange. With refinement of the techniques in experimentation and selection of the proper material, it should be possible eventually to construct a comparative genetic map of tripsacum.

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14. The gene sequence of the Tripsacum homeolog to corn chromosome IX.

A comparison of the gene sequence of chromosomes which are homeologous between corn and tripsacum is possible when the heterozygous substitution is backcrossed to the marker stock of corn. The initial substitution chromosome derived from tripsacum is frequently an interchange chromosome which may not reflect its original structure. However, in the case of the tripsacum homeolog to corn IX, an early evaluation of its genetic content on an 8 recessive marker stock (yg₂, C₁, sh₁, bz₁, wx, gl₁₅, bk₂, and bm₄) made possible the selection and development in the heterozygous substitution of a noncrossover tripsacum chromosome for backcrossing to the tester stock. The data given below are based on the bronze and glossy-15 loci, which are separated by 38 crossover units spanning the centromere in maize.

Phenotype:	<u>Bz₁ Gl₁₅</u>	<u>Bz₁ gl₁₅</u>	<u>bz₁ Gl₁₅</u>	<u>bz₁ gl₁₅</u>	<u>Total</u>
No. recovered	219	17	14	233	483