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 (yg_2, C_1, sh_1, bz_1, wx, gl_{15}, bk_2, and bm_4) 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:	Bz_1 Gl_{15}	Bz_1 gl_{15}	bz_1 Gl_{15}	bz_1 gl_{15}	Total
No. recovered	219	17	14	233	483

Contrary to our expectations there were no other crossovers for the rest of the tested loci, with exception of two crossover individuals showing the waxy (wx) phenotype. Suppression of crossing over as well as differences in gene sequence and/or their map distances on the tripsacum chromosome seem to be the plausible explanations for the lowered value of 6.6% recombination observed in our testcross. Further tests are in progress.

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15. The possible occurrence of a gene for asynapsis (as)in chromosome 5 of T. dactyloides.

Both the 20+1 and 20+2 chromosome plants, carrying one or two extra tripsacum chromosomes homeologous to corn IX marked with 8 recessives, show near normal fertility and seed set. In contrast, their 20 chromosome derivatives, representing homozygous substitutions for all dominants from tripsacum, were either partly or totally sterile. The results of 276 self-pollinations of homozygous substitutions are summarized below:

a) No. of pollinations (69-651 to 69-700):	276	
b) No. of ears without any kernels:	177*	(64.1%)
c) No. of ears with kernel set:		
(i) greater than 50%:	16	(5.8%)
(ii) less than 50%:	83	(30.1%)

*Of these, 40 ears were from 11 rows in which all the plants selfed, without exception, gave no kernels.

Cytological studies made from samples collected at random from either the same plants or related ones revealed partial or total asynapsis of one or more bivalents at pachytene, variable frequencies of univalents at diakinesis and metaphase I, their uneven segregation at anaphase I, and associated irregularities at meiosis II, resulting in abortive spores. The univalent frequencies ranged from 0 to 20 per cell in different plants or in different sister nuclei of the same plant. The average univalent frequencies and the degree of kernel set in the