

different Tripsacum chromosome bears Gl₃ but like the Su-marked Tripsacum chromosome, it does not include La nor three other loci (Bm₃, Ra₃, J₂) on the long arm of corn chromosome 4. Possibly these loci are distributed among the different chromosomes in the Tripsacum genome.

In connection with our hypothesis that Tripsacum is an ancient amphidiploid of wild corn and Manisuris with genomes of 9 pairs derived from each parent, we suggested that corn chromosome 8 could be the one that is eliminated in the genome of Tripsacum. This was based on the apparent deficiency in known functional loci on corn chromosome 8. The lack of a Tripsacum linkage group corresponding to that of corn chromosome 4 is in contrast to observations with loci on corn chromosomes 7 and 9 and the loci on the short arm of corn 2. This suggests that the "lost" chromosome for Tripsacum is more likely to be corn chromosome 4 rather than chromosome 8.

Further studies on the identity of chromosomes showing haploid pairing in maize (Chaganti, 1965) might be revealing.

W. C. Galinat
B. G. S. Rao

6. Numerical and structural variations of the Tripsacum homeolog for corn chromosome 9 in different derivatives.

Among the progenies being grown to study the linkage groups of dominants contributed by the Tripsacum homeolog for corn chromosome 9, individuals are encountered with variable chromosome number and structure of the Tripsacum chromosome. All of these were derived from the descendants of one addition monosomic plant ($2n = 20 + 1$). After isolation they were either selfed or backcrossed to the recessive corn parent. The observed meiotic behavior in the different families is briefly reported here.

1. Numerical Variation:

(a) Addition monosomics ($2n = 20 + 1$):

The Tripsacum chromosome can always be recognized in pachytene by the presence of a large terminal knob on one of its arms. Usually it does not pair with any of the corn chromosomes and remains a univalent. All such univalents show inside pairing (nonhomologous pairing) to variable extents. The centromere and its other morphological features are

not distinct. A low percentage of PMC's from the same source showed two or three of these chromosomes within a nucleus; these, however, remained univalents without any synaptic affinities. The reason for the apparent loss of pairing amongst them is not known. Such exceptional PMC's are possibly derived from irregular segregation of the division products of the extra chromosome in the mitoses immediately preceding the differentiation of PMC's. Except in such cases, 10 bivalents and a univalent are observed at Diakinesis and Metaphase I. Occasionally $9_{II} + 1_{III}$ are seen. The univalents at anaphase I show precocious divisions and one or both the chromatids move to one of the poles.

(b) Addition disomics ($2n = 20 + 2$):

The extra pair shows complete and normal pairing at pachytene. Its morphology is described in item 2. In certain exceptional PMC's heteromorphic bivalents involving chromosomes of unequal lengths are seen (see item 7). Associations other than 11_{II} or $10_{II} + 2_I$ have not been observed in the later stages. Orientation of the extra bivalent at metaphase I is irregular. Numerical nondisjunction or delayed disjunction, probably related to disturbed centric activity of the extra bivalent is frequent at anaphase I.

(c) Aneuploids with $20 + 3$ and $20 + 4$ chromosomes are also recorded. Obviously these are the products of a sporadic fertilization of gametes with more than the expected $10 + 1$ chromosomes. The more frequent chromosome associations at Diakinesis are: $10_{II} + 3_I$ or $11_{II} + 1_I$ and $2_{III} + 9_{II}$ or $1_{III} + 10_{II} + 1_I$ respectively. The expected irregularities in orientation on the metaphase I plate and segregation at anaphase I are observed.

(d) Substitution stocks:

Plants with $2n = 20$ chromosomes and showing all the 8 known dominants of Tripsacum have been recognized. Though normally 10_{II} are observed at diakinesis and metaphase I, PMC's showing $9_{II} + 2_I$ or $8_{II} + 4_I$ and occasionally $1_{IV} + 8_{II}$ or $1_{III} + 8_{II} + 1_I$ have been observed in different individuals. It has not yet been possible to ascertain the nature of substitution, whether by the elimination of the entire corn chromosome 9, its function being taken over by the Tripsacum homeolog, or by a segmental interchange involving the Tripsacum segment carrying

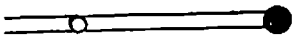
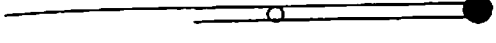
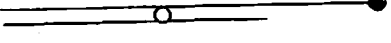
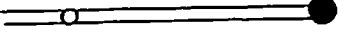
	<u>Plant No.</u>	<u>2n No.</u>
	68-286-1	20+2
	68-271-10	20+0
	68-270-2	20+0
	68-270-9	20+0

Fig. 1. Variability in the structure of the Tripsacum homeolog for corn chromosome 9 in different progenies.

the dominants. Similarly the corn chromosomes involved in the higher associations could not be identified at pachytene. The occurrence of these higher associations, however, suggests that the Tripsacum chromosomes are probably homeologous to at least one chromosome pair other than 9 within the corn complement; a spontaneous reciprocal translocation unrelated to the Tripsacum chromosome pair is also a possibility, which needs to be confirmed.

II. Structural Variations:

The terminal knob on the long arm and the relatively short short arm of the Tripsacum chromosome are so distinctive that its presence, intact or recombined, can be readily recognized in the corn complement. Some of the chromosome types observed in different plants are compared with the original form in Fig. 1. These forms apparently represent the Tripsacum or corn homeologs which have undergone mutual interchanges (primary, secondary, or tertiary) during the previous generations. It is not yet known if and how far they are stable and would be inherited. Considering the relatively high sterility observed in these plants some of them at least are lethal and are likely to be eliminated.

B. G. S. Rao
W. C. Galinat
P. Chandravadana