4. Gene exchanges between corn and Tripsacum.

Genetic crossing over is observed at regular frequencies between certain common loci shared by the homeologous chromosomes of corn and Tripsacum. Both crossover products between the lg_1 and gl_2 loci on the short arm of corn chromosome 2 and the long arm of a Tripsacum chromosome have been obtained. All possible crossover classes have been recorded for the known common loci v_5, ra_1, gl_1, and ij on chromosome 7 of corn and 4 of Tripsacum. Exchanges between corn chromosome 9 and Tripsacum 7 or 8 are confined to yg_2 at the distal end of the short arm and bk_2, bm_4 on the long arm (of corn 9). The frequency of these observed gene exchanges is in the order of 1%. It has not been possible yet to use the rate of crossing over to ascertain the order of the different genes on the Tripsacum chromosomes.

Cytological studies have shown that the concerned chromosomes of corn and Tripsacum are different in their lengths and arm ratios. In the addition disomics, they show preferential pairing at pachytene to their respective homologs and because of the apparent lack of meiotic pairing between the corn and Tripsacum chromosomes, the regions involved in the exchanges could not be determined in the materials examined so far. The morphological differences in the pachytene chromosomes of corn and their Tripsacum homeologs, as well as the probable premeiotic exchanges involving regions of different lengths, indicate differences in the arrangement of the common loci on the chromosomes of the two genera.

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

5. A possible elimination of corn chromosome 4 in the hybrid origin of Tripsacum.

Genetic comparisons of six linked loci on corn chromosome 4 to the genome of Tripsacum do not reveal a corresponding assemblage of these loci on any single Tripsacum chromosome. The position of the Su_1 locus in both corn and Tripsacum is close to the centromere but the similarities seem to stop there. The Su_1 chromosome of Tripsacum does not include La to which Su is linked by 11 crossover units on the short arm of corn chromosome 4 nor does it include 4 other loci tested on the long arm. A

different Tripsacum chromosome bears Gl_3 but like the Su-marked Tripsacum chromosome, it does not include La nor three other loci (Bm_3, Ra_3, J_2) 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 pachytenes 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