

T. floridanum, and both he and Chaganti (1965) have described the occurrence of chromosomes similar to the one reported now in the complements of T. floridanum. Furthermore, our own data on the cytological map of the Kansas form (Bussey clone) of T. dactyloides, from which this particular chromosome was extracted, indicate that chromosome 9 of its complement is nearly identical to that reported now (vide items 8 & 16).

Preferential pairing of the corn II homologues to the exclusion of the extra tripsacum chromosome(s) is observed at meiosis in both the 20+1 and 20+2 stocks; crossover products involving the two loci tested (Lg Gl) are recovered only at a low frequency among thousands of plants. It would thus appear that the tripsacum chromosome, when transmitted to the progeny, has remained virtually unaltered in most of our materials.

Other differences with Maguire's observations are:

While she reports total pollen sterility in her 21 chromosome plants of the constitution  $2, 2+T^2$  and  $2, 2^T+T^2$ , most of our stocks have been nearly normal and fertile. Crossing over between lg and gl was rare in her material, while we have recovered both the reciprocal products at a low but regular frequency in each of the generations.

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

10. Cytology of  $lg_1 Gl_2$  and  $Lg_1 gl_2$  crossover progenies of a corn-Tripsacum hybrid.

Both of the reciprocal crossovers lg Gl and Lg gl are recovered at a frequency of about 3-5% when the 20+1 Lg Gl plants are selfed. The regularity in the appearance of these phenotypes in each of the generations indicates that crossing over does take place between the short arm of corn chromosome II and the long arm of its tripsacum homeolog (T9), although at a relatively low rate. In the lg Gl plants, over a hundred PMC's at diakinesis show a trivalent frequency of nearly 90%. Analysable pachytene nuclei, however, give a frequency of only a little over 50%. In the remainder the univalent chromosome shows nonhomologous centric associations with the centromeres of corn bivalents. It appears that these associations persist up to and possibly beyond diakinesis and give the appearance of trivalents, which they are not.

When the lg Gl interchanged tripsacum chromosome ( $T^C$ ) formed a trivalent with corn II, the configuration could be resolved into three regions at pachytene: AB: corn segment distally located on  $T^C$ ; BC: the univalent portion in the long arm of  $T^C$ , apparently not involved in the interchange with corn II and therefore possibly unaltered to that extent, and CD: the centromere and the short arm of  $T^C$ , also unrelated to the interchange. While region AB paired uniformly with the corresponding portion in one of the corn II homologues, BC and CD remained asynapsed most frequently; occasional inside pairing (torsion pairing) was noticed to variable degrees in these regions. Illegitimate pairing of the BC and CD segments with the other corn chromosome II was observed in about 20% of these configurations. The average lengths of each of these regions is compared below with the unaltered TT chromosome:

|                      | TT chromosome from<br>20+2 <u>LgGl</u> plants<br>(microns) | $T^C$ chromosome from<br>20+1 <u>lgGl</u> plants<br>(microns) |
|----------------------|--|---|
| Length of long arm:  | 13.2   | AB: 18.3<br>BC: 12.9  |
| Length of short arm: | 7.7  | CD: 7.2   |
| Total length:        | 22.3   | 39.6  |
| Terminal knob:       | present  | absent  |

If the length of the paired region involving the distal portion of normal corn II and its homologue on the  $T^C$  chromosome (region AB) is any indication of the extent of the interchanged segment, it would seem that about 25% of the total length of the normal corn II has been transposed on to the TT chromosome. These data also indicate that the breakpoint for the TT chromosome in this interchange is very near the terminal knob, which would locate the allele Lg in its close proximity; in fact, it is so close that the phenotype Lg or lg can be correlated with the presence or absence of the terminal knob. The  $T^C$  chromosome can therefore be interpreted as a product of unequal crossing over involving segments of different lengths of the two homeologs. Whether this unequal crossing over is the result of pairing between homeologs without exact juxtaposition of the alleles or is due to the alleles being located differently on the two chromosomes needs to be examined. Considering that the total length

of the tripsacum chromosome is about 70% of the short arm of corn II, linkage values other than those obtaining in corn might be expected, although the order of sequence of the common loci could be the same.

Studies on the Lg gl plants have not yielded any meaningful results. The interchanged Tripsacum chromosome in this case had the terminal knob, as expected, and showed inside pairing, illegitimate pairing as well as nonhomologous associations to variable degrees in each cell where it could be identified. The inconsistency in its behaviour at pachytene is attributable to the presence of a sufficiently large segment of corn in an intercalary position. It appears that a small portion proximal to the terminal knob, the region adjacent to the centromere, and the short arm represent the original segments of the tripsacum chromosome, while a greater part of the long arm represents the corresponding intercalary segment of the normal corn II. Intercrosses of the lg Gl and Lg gl plants, which are under study, might yield some information on this aspect.

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

11. The discovery of the booster locus (b) on Chromosome 9 of Tripsacum dactyloides.

In the F<sub>2</sub> segregants from a heterozygous substitution for the corn-tripsacum interchange, homeologous to corn Chromosome IIS, the phenotype of recessive b appeared in the derived homozygotes for the interchange. As the corn marker stock contained only dominant B (lg<sub>1</sub> gl<sub>2</sub> B v<sub>4</sub>), it is apparent that the recessive b allele is contributed by the tripsacum segment along with linked dominants (Lg<sub>1</sub> Gl<sub>2</sub>). The data are as follows:

F<sub>2</sub> for a C-T heterozygous substitution for the homeolog to corn Chromosome II S.

| Color                           | Green                         | Purple           | Purple         |
|---------------------------------|-------------------------------|------------------|----------------|
| Phenotype                       | <u>Lg Gl b</u>                | <u>Lg Gl B</u>   | <u>lg gl B</u> |
| Constitution of Chromosome II ) | C <sup>T</sup> C <sup>T</sup> | C <sup>T</sup> C | C C            |
| No. of plants observed )        | 9                             | 30               | 11             |