

<u>Su^d Source</u>	<u>No. Kernels</u>	<u>% Su^d as female</u>	<u>Related No. kernels</u>	<u>% Su^d as male</u>	<u>Unrelated No. kernels</u>	<u>% Su^d as male</u>
67-268-2	526	6.85	638	14.3	378	11.9
-3	408	6.40	199	15.6	---	----
-4	771	8.85	486	19.1	124	13.7
-5	611	6.37	911	16.6	252	11.5
-6	575	7.25	---	no tassel	---	----
-7	486	7.20	500	13.0	237	17.3
-8	644	6.06	461	15.4	259	17.7
-9	564	4.97	533	18.3	387	10.3
-10	639	5.31	548	17.1	---	----
Ave. female = 6.58%		Ave. male = 16.0%		Ave. male = 13.7%		

The expected frequency of Su^d on selfing would be the sum of male and female transmissions minus half of the frequency of double unions of Su^d. Using the above data from reciprocal crosses with the combined average for the two Su^d male crosses, we have as follows:

$$\begin{aligned} \text{Expected on selfing} &= 15 + 6.6 - \left(\frac{6.6 \times 15}{2}\right) \\ \text{Expected on selfing} &= 18.8\% \end{aligned}$$

This expected frequency of the Su^d phenotype on selfing is almost identical to the observed (19%) reported in the previous item for self-pollinations.

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7. Morphology of the Tripsacum chromosome carrying the homeolog for su of corn.

Galinat and Mangelsdorf (MNL 40:99-100) have reported a genetic comparison of some of the 18 possible addition monosomics of corn in which the different Tripsacum chromosomes carry the dominant alleles for some of the known recessives on different corn chromosomes. This report represents the preliminary cytological comparison of one of these Tripsacum chromosomes (referred to as the Su^d chromosome) that covers the recessive allele at the su locus on the short arm of chromosome 4 of corn. As already reported the Su^d chromosome does not cover either la on the short arm or gl₃ on the long arm (MNL 41:119). Additional evidence now indicates that gl₂ on the long arm also is not covered by the Su^d chromosome.

The material studied was from two related lines of addition disomics (67-258 & 67-259 in this item and 67-260 following). The homozygosity for the extra chromosome pair from Tripsacum in these two stocks originated independently within the selfed progenies of 20+1 families stemming originally (six generations back) from a single 20+1 plant. The Su^d chromosome was selected among the segregates from the second backcross of (4n su g corn X 4n T. dactyloides Fla.) X su gl₃ corn to su gl₃ corn.

The morphological features of the Su^d chromosome ascertained from 10 pachytene nuclei are given in Table 1. Synapsis at pachytene between the two homologues is complete, regular and normal. With a total length of 29.28 microns, the Su^d chromosome is shorter than chromosome 10 of corn but is similar to it in its arm ratio of 2.8:1.0. The relative lengths and arm ratios of the ten corn chromosomes from these nuclei agree fairly well with the data of Longley (see Rhoades, J. Heredity 41:59-67; 1950).

Table 1
Morphology of the *Tripsacum* chromosome at pachytene in the corn-*Tripsacum* hybrid derivatives: Stock 67-258 & 259 ($2n = 20+2$)

Sl. No.	Length in Microns			Arm ratio
	Short arm	Long arm	Total	
1	7.2	24.8	33.3	3.4:1.0
2	5.4	17.1	23.9	3.3:1.0
3	5.4	18.0	24.8	3.3:1.0
4	6.8	18.0	27.0	2.7:1.0
5	6.8	18.0	26.1	2.7:1.0
6	7.7	20.3	29.3	2.7:1.0
7	9.0	22.5	33.8	2.5:1.0
8	9.0	24.8	34.7	2.8:1.0
9	6.8	18.0	26.1	2.7:1.0
10	9.0	22.5	33.8	2.5:1.0
Mean	7.31	20.40	29.28	2.79:1.0
SE	0.432	0.951	1.34	---

Longley (J. Agric. Res. 54:835-862; 1937), Ting (Bot. Mus. Leaflet. Harvard Univ., 19:97-108; 1960), Chaganti (Bussey Institution of Harvard Univ., Cambridge, Mass. 1-93; 1965) and Tantravahi (MNL 41:52-57; 1967) have reported the pachytene chromosome morphology in four *Tripsacum* species in all. The Su^d chromosome derived from a $4n$ *T. dactyloides* and described now in the corn genome, when compared on the basis of the two diagnostic criteria (total length and arm ratio) with the above reports, has no similarities with any of the chromosomes described for *T. floridanum* by Longley (1937) and Chaganti (1965). However, it resembles chromosomes 11 and 12 described for *T. australe* by Ting (1960) and chromosome 10 of *T. maizar* and chromosome 9 of the tetraploid *T. laxum* recorded by Tantravahi (1967) as can be seen from data presented in Table 2.

Table 2
Morphological features of the pachytene chromosomes of different *Tripsacum* species comparable to the Su^d chromosome in corn-*Tripsacum* addition disomics ($2n = 20+2$)

Species	Chromosome No.	Length (microns)			Arm ratio	Author & Year
		Short arm	Long arm	Total		
<u>T. australe</u>	11	7.98	23.52	32.60	2.9:1	Ting, 1960
<u>T. australe</u>	12	8.19	21.36	31.00	2.5:1	Ting, 1960
<u>T. maizar</u>	10	7.81	21.87	31.25	2.8:1	Tantravahi, 1967
<u>T. laxum</u>	9	10.40	21.84	33.80	2.5:1	Tantravahi, 1967
<u>T. dactyloides</u>	*	7.31	20.40	29.28	2.8:1	Present study

* Su^d chromosome

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8. Synaptic affinities and altered morphology of the *Tripsacum* chromosome from addition disomics of corn.

The morphological features of the Su^d chromosome present in plants of a second addition disomic line (67-260) are given in Table 1 together with similar data from the related stocks (67-258 & 259) reported earlier.

When these two Su^d chromosomes, occurring in different but related $20+2$ stocks are compared, a change in the position of the centromere from submedian (arm ratio 2.8:1.0) to nearly subterminal (arm ratio 4.4:1.0), thus altering the chromosome morphology, becomes evident. Considering that these two types of Su^d chromosomes had a common origin from $20+1$ addition monosomics, the altered morphology could be ascribed to (a) a deletion of a part of the short arm or (b) a possible crossing over and chromatid exchange between the *Tripsacum* chromosome and any one of the corn chromosomes in one or more of the preceding generations. From the regular and complete pairing at pachytene as well as the occurrence of only bivalents in the later stages of meiosis I, it appears that in either case, the chromosome is homozygous for the alteration, the situation in this case being different from the $20+1$ stocks of Maguire (Genetics, 45:195-209 & 651-664; 1960) where she found evidence of complete synapsis in chromosome 2 heterozygous for the ZT interchange segment. In the absence of readily distinguishable markers like, for example, the terminal knob for the *Tripsacum* chromosome isolated by Maguire (Genetics, 42:473-486; 1957), it would be difficult to readily locate the corn chromosome involved in