1. <u>Evidence in support of a linkage between factors located on chromosome three and one of two complementary factors which restore fertility to cytoplasmic male sterile corn.</u>

From a study of the progenies of a series of Sterile Normal x Fertile Marker crosses (News Letter 28:31-33, 1954) this author suggested that duplicate genes were controlling the inheritance of pollen production. Although this data conformed also to the supposition that the fertility restoring (FR) genes could have been complementary in their action, this possibility was not mentioned. A series of F_2 segregating populations from these initial crosses (Table 1) later indicated that the FR genes we indeed complementary in their action. From somewhat similar studies, Duvick (News Letter 28:35-36, 1954) and Brunson (News Letter 28:39, 1954) explained their results on the basis of the action of two complementary genes.

Table 1. Fertile and sterile segregates from sterile normal x fertile marker F_2 populations

	Sterile x Marker	Chrom. Marked	Fertile	Sterile	Chi-Sqs. for 9:7 Ratios	P
$C1C6^{T6}$	x Coop 51-80	1	108	72	1.0285	0.50-0.20
	x Coop 50-32					
	Population 1	1	202	171	0.6660	0.50-0.20
	Population 2	1	203	181	1.7884	0.20-0.10
	Population 3	1	146	119	0.1380	0.95-0.50
	x Coop 49-26	3	129	84	1.7207	0.20-0.10

An analysis of F_2 data obtained from the cross $C106^{T6}$ x Coop 50-32 has suggested that a linkage exists between factors located on chromosome three and one of two complementary genes which restored fertility to the cytoplasmic male sterile line. This particular cross was made in the repulsion phase. The marker line was homozygous recessive for d, ts_4, and lg_2. Table 2 shows the segregation for FR genes and ts_4, Table 3 shows the segregation for FR genes and d, and Table 4 shows the segregation for FR genes and lg_2. Linkage intensities calculated by the product method indicated that here was less than 1% crossing over between the FR gene and ts_4, 21% crossing over between the FR gene and d, and 36% crossing over between the FR gene and lg_2. The markers, ts_4 and d, were linked with approximately 31% crossing over; ts_4 and lg_2 were linked with 25% crossing over; and d and lg_2 were linked with 35 crossing over. The linear arrangement of these loci and the units between them may be illustrated as follows:
d--21-FR--10--ts_4-25--lg_2.

If the FR gene is approximately 21 units from d, it should also be approximately 36 units from lg_2. The distance between the FR gene and lg_2 is approximately 36 units. The distance between the FR gene and ts_4 is apparently somewhat in error. The data indicate, however, that the FR gene is located approximately 21 units from d and not more than 10 units from ts_4.

Table 2. Segregation for FR Genes and ts_4

Segregating Classes	No.	Chi-Square Values	
Normal Fertile	87	Chi-sq. for total (27:21:9:7)	11.5707*
Normal Sterile	73	Chi-sq. for FR segregation (9:7)	0.2286**
ts_4 Fertile	42	Chi-sq. for ts_4 segregation (3:1)	2.6289***
ts_4 Sterile	11	Chi-sq. for linkage	10.7132*

* P = <0.01
** P = 0.95-0.50
*** P = 0.50-0.20

Table 3. Segregation for PR Genes and d

Segregating Classes	No.	Chi-Square Values	
Normal Fertile	97	Chi-sq. for total (27:21:9:7)	8.6081*

Normal Sterile	73	Chi-sq. for FR segregation (9:7)	0.0452**
d Fertile	33	Chi-sq. for d segregation (3:1)	0.0601**
d Sterile	10	Chi-sq. for linkage	8.5028***

* P = 0.05-0.02
** P = 0.95-0.50
*** P = <0.01

Table 4. Segregation for FR genes and lg_2

Segregating Classes	No.	Chi-Square Values	
Normal Fertile	89	Chi-sq. for total (27:21:9:7)	4.8027*
Normal Sterile	66	Chi-sq. for FR segregation (9:7)	0.0861**
lg_2 Fertile	40	Chi-sq. for lg_2 segregation (3:1)	1.1264***
lg_2 Sterile	18	Chi-sq. for linkage	3.5902****

* P = 0.20-0.10
** P = 0.95-0.50
*** P = 0.50-0.20
**** P = 0.10-0.05

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