5) The western area occupies the western foot of Mt. Fuji. Corn introduction to this area is comparatively recent. The growing area is not so wide. Corn growers are careless in corn management. There were three races. Plants and leaves were remarkably small. The ear was also small and conical, and had many kernel-rows containing small kernels, generally arising in a high position on the stalk. The variability of characters within a race was very conspicuous. It is assumed that repeated contaminations of the Caribbean corn with a primitive race of pop corn have occurred. Such a race has from old times been native to this region, essentially similar to the race "Lady Finger" grown in Latin America. No cytological examination was made on any races in this area.

2. A recessive mutant producing male sterility.

Two male sterile plants appeared in certain populations heterozygous for ra_1-gl_1-ii, a chromosome 7 linkage tester which has been preserved by sib-crosses in the breeding fields of our institute. One male sterile was called "A28" and the other "A29". These two mutants behaved similarly so far as the results of crossing experiments were concerned. In the present work, two stocks of different sources, a chromosome 7 linkage tester marked by ra_1-gl_1-ii and a multiple tester (Mangelsdorf's or Randolph's), were used as pollinators to be crossed with the male steriles. F_1 plants resulting from a cross with the multiple tester were all normal in a total of 1072, whereas two F_1 populations involving the chromosome 7 linkage tester were composed of a few male-sterile plants in addition to normal ones. One of these was an F_1 derived from the cross of a ms plant and consisted of 209 normal and 5 ms plants; the other F_1 was derived from a cross of a normal plant heterozygous for ms and gave 617 normal and 9 ms plants. The present sterile mutation, like that reported in 1950 by Prof. M. M. Rhoades in his paper on cytoplasmic male sterility, may also be induced by the genes, ra_1-gl_1-ii, especially ii.

From the data obtained on F_2 and backcross segregations, it seems highly probable that the present sterility is controlled by a single recessive allele. However, a significant discrepancy from the expected ratio of 3:1 or 1:1 was frequently encountered between (1) sterile stocks (A28 and A29), (2) different fields planted, (3) generations of sterility induced, and (4) different pollinators. At present the genetical cause is unknown. Out crosses were all made using the male sterile as the female parent. The cytoplasm in all crossing progenies should therefore have been transmitted from the sterile parent only. Whether the discrepancy is caused by such a cytoplasmic effect or not will be further studied.

At any rate, it may be assumed from the data in Table 2 and 3 that a gene governing the present case of male sterility is located on chromosome 4 with approximately 40% of recombination with su_1.

Table 2. F_2 data on the linkage detection of male sterility (x) in the repulsion phase of segregation.[1)]

Chr. no.	Marker gene (y)	Families	F_2 Individuals					X^2	P
			XY	Xy	xY	xy	Total		
1	bm_2	37	3476	936	1688	499	6588	2.7904	0.10*
2	lg_1	37	3469	934	1695	490	6588	1.2678	0.3-0.2
3	A_1	11	716	735	314	303	2068[2)]	0.4139	0.7-0.5
4	su_1	36	2973	1336	1756	422	6487	99.0611**	0.01
5	pr	6	290	136	132	50	1719	1.1905	0.3-0.2
6	Y_1	3	332	114	247	105	798	1.7944	0.2-0.1
7	ra_1	1	64	21	27	9	121	0.0012	0.95-0.99
8	j_1	37	3698	693	1816	331	6538	0.1458	0.8-0.7
9	wx	34	1896	1009	1157	549	4611	3.1305	0.10-0.05
10	g_1	37	3321	1080	1637	550	6588	0.2907	0.5-0.3

[1)] Nine of the F_2 populations listed above came from a cross of male-sterile hybrids with two multiple linkage testers, Mangelsdorf's and Randolph's, and the one involving linkage group 7 was from a cross with a single linkage tester marked by the three well-known genes, $\underline{ra}_1$-$\underline{gl}_1$-$\underline{ij}$.

[2)] This is the total of two F_2 progenies, one of which was heterozygous for three aleurone color genes, $\underline{A}_1$ $\underline{a}_1$, $\underline{C}$ $\underline{c}$ and $\underline{R}$ $\underline{r}$, all resulting from crosses with Mangelsdorf's tester, while the other was heterozygous for the alleles, $\underline{A}_1$ $\underline{a}_1$ and $\underline{C}$ $\underline{c}$, from Randolph's tester.

Table 3. Linkage relation of male sterility to the gene, su_1, in the repulsion phase of 36 F_2 families.

Pedigree used	Fam.	F_2 segregation					X^2 for linkage			Recombination value
		+	su	ms	su.ms	Total	Total	Deviation(1)	Heterogeneity	
1. A29-234	16	1125	558	860	222	2765	58.0738(16)**	50.4246**	7.6492(15)	40.84±1.59%
2. A29-236	15	1458	566	659	154	2837	54.7261(15)**	0.2224	54.5047(14)**	42.86±1.54%
3. A29-239	5	390	212	237	46	885	34.0094 (5)**	15.9749**	18.0345 (4)**	35.49±2.92%
Total	36	2973	1336	1756	422	6487	146.8094(36)**	99.0611**	47.7483(35)*	41.21±1.02%
1 + 3	21	1515	770	1097	268	3650	92.0832(21)**	83.0576**	9.0256(20)	39.74±1.39%

Numerals given in parentheses are the number of the "Degrees of Freedom (DF)" for X^2.