

In both types of single cross hybrids the defective cytoplasm isolate markedly depressed yield in comparison with the same hybrid made with either of the other two cytoplasm types, but hybrids having maize and normal teosinte cytoplasm did not differ from each other.

Since both isolates of perennial teosinte cytoplasm were made from the same original classical clone of teosinte, E16515, it seems apparent that a cyto mutation must have occurred during the process of transferring the Wf9 nucleus, but examination of remnant seeds and field records gives no further information.

Further work is in progress to insert the B37 nucleus into the two teosinte cytoplasm types, and this work has reached the BC-3 level of recovery. Since recoveries of B37 having the defective cytoplasm show essentially the same phenotype noted in Wf9, it is evident that the defective character of the cytoplasm is not restored by association with B37 nuclear factors. However, some differences are evident in the two backgrounds: male sterility and nearly all the chlorophyll striping are relieved in the B37 material. The defective cytoplasm described here differs from the classical S cytoplasm in its drastic reduction of plant size in all environments, and also in its production of partial kernel abortion.

D. L. Shaver

3. Inheritance of resistance to Sugar Cane Mosaic Virus (SCMV) in Calif.

SCMV is a serious threat to corn production in the Great Central Valley. In parts, resistance is a simple necessity. Johnson Grass is the principal alternate host, from which it is transferred to corn by the Green Peach Aphid. It is also easily transferred by mechanical inoculation.

In breeding for resistance, it is found to be fairly easy to develop multigenically resistant strains as derivatives from parents having tolerance and/or partial resistance. Other strains of corn seem to have a single dominant gene type of resistance. An experiment was undertaken to establish data from which to test the single gene idea, and to determine if allelism exists between the presumed single gene types.

On the basis of breeding experience, two susceptible, and four single gene resistant lines were selected:

Susceptible inbreds

01 02

Resistant inbreds11 33
22 44

The following F_2 and backcross data were obtained in the 1973 disease nursery at Tulare:

<u>Progeny</u>	<u>Resistant</u>	<u>Susceptible</u>	<u>P</u> (Based on single gene .001**idea)
01 x 44 F_2	357	270	
11 x 22 F_2	674	6	
11 x 33 F_2	683	3	
11 x 44 F_2	470	11	
22 x 33 F_2	510	13	
22 x 44 F_2	463	7	
33 x 44 F_2	666	20	
(01 x 02)01	0	322	
(01 x 02)02	1	381	
(11 x 01)01	122	141	.300
(22 x 01)01	201	210	.200
(33 x 01)01	177	191	.500
(44 x 01)01	165	190	.200
(11 x 02)02	265	275	.999
(22 x 02)02	219	192	.200
(33 x 02)02	231	242	.200
(44 x 02)02	175	212	.100

There is a tendency towards an excess of susceptible plants which tends to make the P values seem too high, and made one very high indeed. But it should be explained that many of the plants scored as susceptible were in reality only slightly infected. "Resistant" plants, especially when heterozygous at the resistance locus, often show mosaic symptoms at times, but they still have essential resistance and usually recover later. The heterozygosity factor is more than sufficient to account for all the low P values reported here.

F_2 data indicate that all four resistant parents have allelic genes for resistance.

Added evidence for the single gene idea comes from numerous projects in which resistance is routinely transferred to susceptible lines. In extended, continuous backcrossing, the resistance factor continues to segregate as a unitary, essentially dominant gene. However, since, for example, resistance deriving from inbred 11 is clearly more potent during the advanced backcross generations than that from the other three sources, it seems clear that there is an allelic series at the resistance locus.

In recovering a few lines with resistance, the potency of the added gene seems to fade away upon reaching about BC₄ or BC₅. This is thought to be due to the fact that these exceptional lines lack complementary genes necessary for the expression of resistance. Added evidence for this explanation comes from the fact that inbred 44, while it has been found to be a source of excellent single gene resistance, is uniformly susceptible in its original state.

The dependence of the expression of the SCMV gene upon complementary genes is exactly parallel to the dependence of the Rf₁ - Rf₂ restoration system upon complementary loci, first noted by Shaver (MNL 30:160, 1956). It is again interesting to note that the inheritance of resistance to SCMV can appear perfectly simple, or relatively complex, depending entirely upon the type of material being observed. We propose the designation, Scm for the SCMV resistance locus.

D. L. Shaver

DEPARTMENT OF SCIENTIFIC AND INDUSTRIAL RESEARCH
PLANT PHYSIOLOGY DIVISION
Palmerston North, New Zealand

1. Maize genetics studies by protoplast fusion.

Use has been made of several lines of the well-documented chloroplast mutations and nuclear controlled chloroplast deficiencies of maize in studies to demonstrate genetic complementation by protoplast fusion. Because of the difficulty of initiating mitosis in fused protoplast heterokaryons, it was hoped that the appearance of chlorophyll