On the other hand the inbred Pa 422P appears to have two genes exhibiting complementary action for resistance to the MDM virus. When the cross Pa 422P x Pa 887P was selfed, the F_2 segregated in a ratio that appeared to fit a ratio of 9 resistant to 7 susceptible. A population of 400 seedlings gave 216 resistant and 184 susceptible. The X^2 probability for a 9:7 ratio for this is .30 - .50. Another inbred, Oh 7B, also appears to have 2 genes with complementary action for resistance. Further tests of both Pa 422P and Oh 7B are being conducted to verify the validity of these results.

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1. DNA from Black Mexican sweet corn.

We reported previously that the base ratios of DNA from young kernels of lines of Black Mexican sweet corn with and without B-chromosomes differed from those of a white inbred line. Other workers have failed to find these abnormal ratios using leaf material. Our determinations were repeated using material from young seedlings and leaves and mature husks in addition to kernels. The methods used are described in detail elsewhere.

The results are given in Table 1.

Table 1
Base composition of DNA-preparations of three lines of *Zea mays*

Composition in moles per cent (Average of 2 or more determinations)

Material	% C + G
K64--commercial white dent inbred	44.0
Black Mexican Sweet Corn with no B-chromosomes: leaves	44.0
husks	45.0
seedlings	42.0
kernels (10 days after pollination) colorless	44.5
kernels (>14 days after pollination) colored	55.0
Black Mexican Sweet Corn with B-chromosomes	
leaves	46.0
husks	42.0
seedlings	43.0
kernels (10 days after pollination) colorless	46.0
kernels (>14 days after pollination) colored	70.0

It is hypothesized that a deoxyribonucleotide which forms a complex with the DNA via a specific agent is responsible for the peculiar base composition. The synthesis of the atypical DNA from Black Mexican Sweet Corn appears to depend on the stage of kernel development and probably coincides with the time of pigment development. The abnormal base ratios reported previously are presumably not related to heterochromatin content.

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1. A new striate mutant on chromosome 10.

A new mutant type was isolated which has longitudinal white stripes that parallel the leaf veination from early seedling stage onward. This mutant arose in M_2 segregating material from the combined chemical mutagen treatment of ethyl methanesulfonate followed by diethyl sulfate to the seed of a multiple marker stock used in mutation experiments. This character is recessive and very similar to Waseca stripe (*sr*$_2$) in chromosome 10 which was described by Joachim and Burnham (1953) MNL 27:66. Classification is good in the seedling and mature plant stage and pollen and ears are produced on most plants.

Intercrosses were made with homozygous recessive *sr*$_2$*sr*$_2$ stocks obtained from Dr. R. A. Brink. There were no striate individuals among 193 F_1 plants from eight crossed ears.

The mutant was crossed to a waxy marked chromosome-nine translocation series involving all chromosomes and F_2 waxy seeds were screened. All F_2 populations showed normal 3:1 segregation except those involving the *wx* 9-10b interchange (9S.13, 10S.40) in which the following data were collected in ten families. Waxy seeds gave 349 normal : 12 striate plants. These data indicate that the mutant is located close to the interchange point on the short arm of chromosome 10, whereas the Waseca stripe (*sr*$_2$) gene has been placed distal to *R* on the long arm of chromosome 10. The symbol, *sr*$_3$, has been assigned tentatively to this new mutant.

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2. A compact plant gene located on chromosome 1.

This mutant was given to this station by Allan Caspar of the Blandy Experimental Farms. The mutant produces seedlings which have very wide and