

Table 3. Recombination percents of the three genes, ogr, g and li, on chromosome 10.

Phase	No. of fam.	Total plants	ogr-g	g-li	ogr-li
F <sub>2</sub> *	1	506	40.0	17.0	51.5
B *	1	206	53.7	16.5	60.2
F <sub>2</sub> 1)	3	766	21.3	15.0	30.4
B 2)	4	1303	26.5	17.9	44.7
B 3)	5	852	25.6	17.7	43.3

\* came from the female parent of the F<sub>1</sub> plants with the cytoplasmic stripe.

- 1) came from the F<sub>1</sub> normal plant without any striping.
- 2) indicates the use of the female heterozygous parent with the stripe.
- 3) indicates the use of the female heterozygous parent without the stripe.

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#### 1. The inheritance of resistance to brown spot of corn.

A study was designed to investigate the inheritance of brown spot of corn (*Physoderma maydis*). A susceptible inbred (NC7) was crossed with a resistant inbred (GT154) and the following generations derived for study: F<sub>1</sub>, F<sub>2</sub>, F<sub>3</sub>, B<sub>1</sub>, B<sub>2</sub>, B<sub>11</sub>, B<sub>12</sub>, B<sub>22</sub>. Individual plants were examined for brown spot symptoms and given a rating from 0 to 5; 0 being no symptoms and 5 being very badly infected. Data were collected at one location in 1954 and at each of two locations in 1955. The data were analysed using the methods proposed by Powers, Locke and Garrett 1950, and Powers, 1955.

It was found that four or more gene pairs differentiate the parents with respect to brown spot resistance. Several genetic models involving four loci and five loci, each defining the disease reaction of every genotype, were found which were compatible with the F<sub>2</sub> data obtained at each year-location. All of the models which were found to be compatible with the data involved epistasis; i.e., non-additivity between genotypes at certain of the loci. Further evidence of epistasis was

noted when the relative magnitude of the means of the various generations did not agree with the relative magnitude expected under the assumption of no epistasis.

The three genetic models involving five loci found to be compatible with the F<sub>2</sub> data collected at the three year-locations showed a consistent pattern of gene action, although the relative value of the genotypes varied, reflecting a genotype X environment interaction. Assuming these three models were correct, predictions were made concerning the disease reaction of single crosses relative to the disease reaction of their respective parental lines. This indicates that single crosses which are more resistant than either parent, and single crosses which are more susceptible than either parent are to be expected. Furthermore, a single cross more resistant than either parent and a single cross more susceptible than either parent may have one parental inbred in common.

Data obtained on various inbred lines and their single crosses in 1956 are in agreement with the expectations based on the five factor genetic models.

From the point of view of the plant breeder, these results indicate that the brown spot reaction of an inbred line is not a reliable indication of the reaction of single crosses involving that inbred, and the hybrid combinations themselves must be tested for brown spot resistance.

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1. Studies on a mutable system involving chromosome 6.

A yellow mosaic kernel was found on an ear of a yy x YY cross. The resulting plant was selfed and yellow mosaic and white endosperms segregated. The yellow mosaic endosperms are characterized by a white background with yellow spots if the yellow area is small. The large yellow areas may be somewhat irregular in outline. Progeny from the selfed plant were grown and a recessive pale green character segregated. Some of the pale green plants possessed numerous mutant green areas on the pale green (or white) background. These plants in addition to being pale green also have a white sheath and somewhat banded white areas on the leaves. Classification of the pale green character in the seedling stage is good in the field but poor in the greenhouse. However, classification of the character in the mature plant is excellent both in the field and in the greenhouse. The mutable white allele has been designated as y<sup>m</sup> and the mutable pale green allele as pg<sup>m</sup>.