UNIVERSITY OF ILLINOIS
Urbana, Illinois
Departments of Agronomy and Plant Pathology

1. Cytoplasmic susceptibility to Helminthosporium maydis in the U.S.

In 1970, southern corn blight caused by Helminthosporium maydis developed to a major disease of the U.S. corn crop. This was due to the appearance and widespread distribution of a new race of H. maydis which has been named race T.

Race T is unique in that it produces a pathotoxin that is highly specific for the T cms (Texas) cytoplasm widely used in seed production in the U.S. Race T reproduces rapidly and attacks the leaf, leaf sheath, husk, shank, ear, seedling, and sometimes stalk tissue of the plant. It spread from Florida west to Texas and north to Canada during the summer of 1970.

All "normal" cytoplasms (not male-sterile) are resistant to race T. The same is true for the S cms, C cms, and a number of other cytoplasms for male-sterility. The same nuclear genes for resistance to the old race O of H. maydis condition partial resistance to race T when interacting with T cms cytoplasm.

With the exception of symptom expression, the U.S. situation is similar to the experience in the Philippine Islands reported in 1961 and subsequent years.

A. L. Hooker

ILLINOIS STATE UNIVERSITY
Normal, Illinois
Department of Biological Sciences

1. The use of monosomy to detect genes altering recombination in Zea mays.*

The r_{x-1} deficiency in maize induces an extremely high frequency of monosomes in Zea mays (Satyanarayana, unpublished). With this system, I have obtained at least three confirmed cases of monosomy for 8 of the

*Partially supported by A.E.C. Contract No. AT(11-1)-2121.

10 chromosomes (all possible monosomes except monosomes for chromosomes 3 and 5). A report on this system which produces monosomes will be published in the near future. Since monosome 3 has been produced through the interaction of a knob on chromosome 3 with a B chromosome (Rhoades, Dempsey, and Ghidoni, 1967, Proc. Nat. Acad. Sci. 57: 1626-32), monosomy for 9 of the 10 chromsomes in maize has been confirmed. This is the first time that a series of this type has been obtained in a higher diploid organism.

In a monosomic plant, an entire chromosome is present in the hemizygous condition. Plants monosomic for a specific chromosome can be compared with their diploid sibs. If a gene on this chromosome exhibits dosage effect, a difference will be found between these two types for the trait being analyzed. Thus, one can screen <u>all</u> of the genes on a given chromosome at the same time by comparing monosomic and disomic sibling plants. Given 10 monosomic plants, it is possible to screen the entire genome. This is a new method for screening the genome, and it analyzes all genes on a given chromosome at the same time. One can in this way observe gene loci without inducing mutations!

The above approach is being utilized to study several different classes of genes. Of special interest are genes affecting recombination. Monosomic plants are being generated utilizing the $\underline{r}_{x-1}$ deficiency which are heterozygous for linked genes in chromosome 2 and the amount of recombination in the monosomes is being compared with recombination in diploid sibs.

One especially vigorous monosomic 8 plant was used both as a male and female parent in crosses this past summer. The amount of recombination in this plant and in diploid sibling plants is presented in the following table:

Comparison of Recombination in Monosomic 8 and Diploid Sibs

Female Parent	Male Parent	Population	% Recombination
$\underline{ws}_3\ \underline{gl}_2$	Monosome 8		
	$\underline{Ws}_3\ \underline{Gl}_2/\underline{ws}_3\ \underline{gl}_2$	1696	28.07
$\underline{ws}\ \ \underline{gl}$	Diploid Sibs		
	$\underline{Ws}\ \ \underline{Gl}/\underline{ws}\ \ \underline{gl}$		
	Plant 1	500	23.3*
	Plant 2	580	23.8*
	Plant 3	149	19.5*
	Plant 4	393	21.9*
	Total Diploid Sibs	1622	22.75**
Monosome 8, $\underline{Ws}\ \underline{Gl}/\underline{ws}\ \underline{gl}$ Diploid Sib	$\underline{ws}\ \ \underline{gl}$	94	29.8
$\underline{Ws}\ \underline{Gl}/\underline{ws}\ \underline{gl}$	$\underline{ws}\ \ \underline{gl}$	295	28.1

X^2 Contingency tests of the above using Yates correction factor.

*Significantly different from monosome 8 used as a male at the 5% level.

**Significantly different from monosome 8 used as a male at the 0.5% level.

It can clearly be seen that recombination in the monosomic 8 plant is distinctly higher than in diploid sibling control plants when they were used as males. No difference was detected when the plants were used as maternal parents, but only a limited amount of data is available from the monosomic plant as a maternal parent. The difference in recombination values between the monosomic 8 plant and its diploid siblings might be attributed to two causes:

A. A gene or series of genes are present on chromosome 8 which in one dose allows more recombination than in two doses.

B. The difference could be due to an interchromosomal effect, i.e., more recombination occurs in chromosome 2 in the absence of recombination in chromosome 8. To distinguish between these two

alternatives, similar tests will be conducted with additional monosomes 8 and other monosomes this coming summer.

A relaxation of recombination inhibition might be of tremendous economic importance since an increase in recombination would permit breaking up of linkage groups and allow more variability in the plants.

David F. Weber

2. The use of monosomy to detect genes for lipid biosynthesis in Zea mays.*

Monosomes generated by the $\underline{r}_{x-1}$ deficiency are being used in a study to detect major genes or gene complexes for lipid biosynthesis in Zea mays embryos. This paper describes the procedure of study. In monosomes generated by the $\underline{r}_{x-1}$ deficiency, there is a non-correspondence between the chromosome numbers of the embryo and endosperm, thus monosome generation must take place in the post-meiotic megaspore divisions of the embryo sac. In other words, a monosomic embryo is not accompanied by monosomic endosperm.

The line carrying the $\underline{r}_{x-1}$ deficiency in this study has been maintained in inbred W22 for many generations. $\underline{R}/\underline{r}_{x-1}$ heterozygotes in inbred W22 were crossed by a second inbred, Mangelsdorf's multiple chromosome tester ($\underline{bm}_2$; $\underline{lg}_1$; $\underline{a}_1$; $\underline{su}_1$; $\underline{pr}$; $\underline{y}_1$; $\underline{gl}_1$; $\underline{j}_1$; $\underline{wx}$; $\underline{g}_1$). The F_1 kernels carrying the $\underline{r}_{x-1}$ deficiency were dried until the water content of the kernel was below 4.5 per cent. The lipid content of each kernel was determined with wide line nuclear magnetic resonance spectroscopy. The NMR analysis was conducted as described by Alexander et al. (1967, J. Am. Oil Chem. Soc. 44:555-558). Although the chromosome number of the endosperm and embryo do not correspond, this would not alter the results because virtually all of the free lipid is concentrated in the embryo of the kernel (Brunson, Earle, and Curtis, 1948, Agron. J. 40:180-185).

Over 2,300 kernels have been scanned individually with the NMR to date. Since it is impossible to detect monosomic kernels, all of the kernels had to be scanned by the NMR and then planted. The monosomic

*Partially supported by A.E.C. Contract No. AT(11-1)-2121.