

3. Two new alleles of the E gene found in teosinte.

Three alleles of the E gene, \underline{E}^F , \underline{E}^N , and \underline{E}^S , have been found in maize. In a study of 550 strains of maize from South and Central America, we found that the \underline{E}^N allele was the most common and the \underline{E}^F allele the least common. Two other alleles, \underline{E}^L and \underline{E}^R , have been found in some teosinte strains. \underline{E}^L and \underline{E}^R specify enzymes with electrophoretic migration rates intermediate between the enzymes specified by \underline{E}^F and \underline{E}^N , and \underline{E}^N and \underline{E}^S , respectively. The teosinte heterozygotes $\underline{E}^L/\underline{E}^R$ form a hybrid enzyme with an intermediate migration rate just as do the maize heterozygotes. A hybrid enzyme is also found in the \underline{E}^F maize \underline{E}^R teosinte hybrid plants. Other hybrid crosses are presently being made for further tests.

We have tested eight teosinte lines supplied by Dr. P. C. Mangelsdorf. Chapingo, Chilpancingo, Chalco, Arcelia, and Huixta carry only the alleles found in maize, \underline{E}^F , \underline{E}^N , or \underline{E}^S , while the Lake Retana, Florida, and El Valle teosintes carry only the new alleles \underline{E}^L or \underline{E}^R . Dr. Mangelsdorf has pointed out the interesting comparison that the latter three teosinte lines are quite Tripsacoid. Surprisingly, this esterase is not found in young Tripsacum seedlings. We have tested two species, T. floridanum and T. dactyloides. At the moment we cannot tell whether the absence of the enzyme is due to absence of the E gene or simply a different distribution of gene activity in the life cycle of Tripsacum.

Drew Schwartz

OHIO AGRICULTURAL EXPERIMENT STATION

Wooster, Ohio

Department of Agronomy

1. Evidence for linkage of genes for stalk-rot susceptibility with genes located in chromosomes 7 of inbreds Mo21A and NC34.

Translocation studies (Agron. Jour. 49:197-201) have shown that major genes for resistance to Helminthosporium turcicum leaf blight are located in the short arms of chromosomes 7 of inbreds Mo21A and NC34. Tests designed to locate these genes more precisely were grown at Columbus, Ohio, using a chromosome 7 marker gene stock. Plants from the backcrosses ($\underline{o}_2 \underline{v}_5 \underline{ra}_1 \underline{gl}_1$ x Mo21A) x $\underline{o}_2 \underline{v}_5 \underline{ra}_1 \underline{gl}_1$ and ($\underline{o}_2 \underline{v}_5 \underline{ra}_1 \underline{gl}_1$ x NC34) x $\underline{o}_2 \underline{v}_5 \underline{ra}_1 \underline{gl}_1$ were inoculated with ground leaf inoculum of H. turcicum. Difficulties of classification made the gene \underline{v}_5 unusable.

Leaf blight failed to reach a high level of disease incidence by rating time. Although it appeared doubtful that good differences in disease reaction could be obtained, individual plants from each of the backcrosses were scored for H. turcicum. Statistical analyses of the data failed to show any significant differences between the various gene classes for H. turcicum reaction.

A natural infestation of stalk rot, most likely Gibberella zeae, caused many of the plants to die prematurely. These were noted as dead plants since it was difficult, as well as impracticable, to score them for leaf blight.

In working up the data, it became apparent that the greater proportion of dead plants occurred in the dominant parental classes. Frequency distributions for each of the gene classes of the two backcrosses are shown in Table 1. Chi-square tests for independence of dead and living plants in the parental classes yielded values with probabilities of occurrence well beyond the 0.50 per cent point. The data indicate that genes for stalk-rot susceptibility are linked with the dominant alleles of o_2 ra_1 gl_1 located in or near the short arms of chromosomes 7 of inbreds Mo21A and NC34.

Table 1. Frequency distributions by genetic classes of living and dead plants and the P values for chi-square tests of independence for the backcrosses (o_2 ra_1 gl_1 x Mo21A) x o_2 ra_1 gl_1 and (o_2 ra_1 gl_1 x NC34) x o_2 ra_1 gl_1 .

Genetic class	Mo21A Backcrosses			NC34 Backcrosses		
	Plants: living	Plants: dead	x^2 for independence	Plants: living	Plants: dead	x^2 for independence
	No.	No.	P value	No.	No.	P value
o_2 ra_1 gl_1 + + +	356 243	44 161	<0.005	339 209	75 185	<0.005
o_2 + + + ra_1 gl_1	39 34	10 11	≤0.50	25 45	16 9	<0.05
+ + gl_1 o_2 ra_1 +	4 4	4 0		5 4	10 1	
+ ra_1 + o_2 + gl_1	1 6	0 1		0 0	0 0	

W. R. Findley, Jr.
E. J. Dollinger

PENNSYLVANIA STATE UNIVERSITY
University Park, Pennsylvania
Department of Agronomy and Computation Center

1. Parthenogenesis.

During 1959, 290 plants of the "Pa G-100 Synthetic" were bagged before silk emergence to prevent pollination in an attempt to follow up the report of S. H. Yarnell dealing with parthenogenesis in corn. The "Pa G-100 Synthetic" was constituted from numerous early to extremely early lines, mainly of Ottawa, Canada, and Wisconsin origin.

Seeds per ear developed under the bags varied from 0 to 239. A frequency distribution suggested random development of seeds that might have represented pollen contamination carried by insects or wind.