

Segregations for Lesion Type to H. turcicum in the Field

Cross	Observed number			P values	
	Highly Res.	Res.	Susc.	1:2:1	3:1
W37A x H52 F ₂	24	50	26	0.95-0.98	0.80-0.90
W37A x 187-2 F ₂	16	58	25	0.05-0.10	0.95-0.98
B14 x EES647 F ₂	15	53	24	0.10-0.20	0.80-0.90
187-2 x EES647 F ₂	14	48	29	0.05-0.10	0.10-0.20
B14 x EES650 F ₂	24	49	25	0.98-0.99	0.90-0.95
187-2 x EES650 F ₂	20	48	21	0.70-0.80	0.70-0.80

Segregations for Lesion Type to H. turcicum in Corn Seedlings

Cross	Observed number			Expected ratio	P value
	Highly Res.	Res.	Susc.		
R168 x Pop 35 F ₂	21	54	16	1:2:1	0.10-0.20
W153R x Pop 35 F ₂	24	41	28	1:2:1	0.30-0.50
B14 x Pop 35 F ₂	13	51	17	1:2:1	0.05-0.10
(B14 x Pop 35) B14	0	34	31	0:1:1	0.70-0.80
B14 (B14 x Pop 35)	0	42	56	0:1:1	0.10-0.20
(B14 x Pop 35) Pop 35	49	46	0	1:1:0	0.70-0.80
(R168 x Pop 35) Pop 35	55	55	0	1:1:0	> 0.99
(W153R x Pop 35) Pop 35	45	48	0	1:1:0	0.70-0.80

In addition to the selections reported, other corn types have been located which express chlorotic lesions when infected by H. turcicum. Inheritance studies of these are underway as well as tests to determine if the genes present in any of the selections can be distinguished from the gene Ht.

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2. Additional gene loci for resistance to Puccinia sorghi.

Rust resistant inbreds 178 and 191 were crossed to the rust susceptible inbreds B14 and R168. The single crosses were advanced to the F₂ generation and backcrossed to the susceptible inbred. The following seedling data indicate that each line has a single dominant gene for resistance to culture 901aba P. sorghi.

Cross	F ₂ generation			Backcross generation		
	R	S	P value (3:1)	R	S	P value (1:1)
178 x B14	81	13	0.01-0.02	57	55	0.80-0.90
178 x R168	89	35	0.30-0.50	55	65	0.20-0.30
191 x B14	83	25	0.50-0.70	71	78	0.50-0.70
191 x R168	92	36	0.30-0.50	75	75	> 0.99

Line Mex 185 having a single dominant gene for resistance (Pages 53-54, 1961 M.G.C.N.L.) was crossed with lines Syn A having gene Rp_1^c and NN14 having gene Rp_3 for resistance to *P. sorghi*. Line Mex 185 was also crossed with line 178. Lines 178 and 191 were crossed with BY Dent. BY Dent has gene Rp_1^c . These single crosses were advanced to the F_2 generation and also crossed with susceptible inbreds (test-cross populations). The following seedling data for reaction to *P. sorghi* culture 901aba were obtained:

	F_2 populations			Test-cross populations		
	R	S	P value (15:1)	R	S	P value (3:1)
Mex 185 x Syn A	100	12	0.05-0.10	95	36	0.50-0.70
Mex 185 x NN14	118	6	0.50-0.70	82	19	0.10-0.20
Mex 185 x 178	67	5	0.80-0.90	67	28	0.30-0.50
178 x BY Dent	127	9	0.80-0.90	87	37	0.20-0.30
191 x BY Dent	436	0	< 0.01	894	9	< 0.01

These data suggest that the gene in Mex 185 is not at Rp_1 or Rp_3 and therefore is at a new locus. It is suggested that this locus in line Mex 185 be designated as Rp_4 . The locus in line 178 assort independently of Rp_1 and Rp_4 . We do not know yet if the gene assort independently of Rp_3 . The gene in line 191 is linked to Rp_1 with a recombination value of 0.01. It is suggested that the locus in 191 be designated Rp_5 .

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3. Location of genes determining resistance to Puccinia sorghi in lines Mex 185 and 178.

Translocation stocks with waxy or sugary marker genes were used in linkage tests with the dominant genes for resistance to *P. sorghi* in the corn inbreds Mex 185 and 178. A list of the translocation stocks used, breakage points, and methods of study were given in the 1961 M.G.C.N.L. pages 55-58. In all cases except for the chromosomes listed below, the linkage was negative or inconsistent.

Translocation	Number of seedlings				χ^2 values
	Normal Starch		Mutant		
	R	S	R	S	
	(Mex 185 crosses)				
T1 - 4a (su)	178	39	26	117	88.309**
T4 - 8a (su)	128	30	19	115	129.553**
	(178 crosses)				
T3 - 9c (wx)	113	13	19	129	160.971**

These data were confirmed with field tests of other progenies. It appears that the gene Rp_4 in Mex 185 is on chromosome 4 and that the gene in 178 is on chromosome 3.

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