

5. Recessive resistance to P. sorghi.

F₁, F₂, and backcross data obtained in greenhouse tests during January, 1961, indicate that resistance to culture 928bb of P. sorghi is controlled by three independent loci in inbreds (A277 x 41.2504B)-1-47-1-1-1-1 and Midland-125-3-1-3-5-1. These inbreds are highly resistant to rust culture 928bb while F₁'s with the susceptible inbred B14 are susceptible. The highest degree of resistance appears to be due to the completely recessive condition. The proposed type of gene action is as follows:

<u>Genotype</u>	<u>Rust reaction</u>
First dominant gene	Susceptible
Second dominant gene	Susceptible in absence of dominant gene 3
Third dominant gene	Intermediate (inhibits dominant gene 2, but not gene 1)
Multiple recessive	Highly resistant.

The following data support the above hypothesis:

<u>Cross</u>	<u>No. of plants observed</u>			<u>Expected ratio</u>	<u>P Value</u>
	<u>Res.</u>	<u>Inter.</u>	<u>Susc.</u>		
(A277 x 41.2504B) x B14 F ₂	3	17	86	1:12:51	.30-.50
[(A277 x 41.2504B) x B14] x (A277 x 41.2504B)	11	27	63	1:2:5	.80-.90
Midland 125 x B14 F ₂	1	9	71	1:12:51	.10-.20
(Midland 125 x B14) x Midland 125	8	24	61	1:2:5	.50-.70

Inbreds (A277 x 41.2504B) and Midland 125 give differential and reciprocal reactions with various cultures of P. sorghi and on this basis must be regarded as having different genotypes for rust resistance.

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6. Location of genes determining resistance to Puccinia sorghi in corn inbred selection (Oh45 x W92)-2-5-2.

Studies on the inheritance of resistance to corn leaf rust, Puccinia sorghi, have demonstrated that the resistance in Cuzco,

GG208R, K148, E38, B49 and P.I. 172332 is due to 6 distinguishable alleles at the Rp locus on the short arm of chromosome 10. An analysis of another source of resistance, (Oh45 x W92)-2-5-2, had indicated that this source has 2 or more genes determining resistance and none of these is allelic with the series in chromosome 10. For example, segregations in progenies from B14 x (Oh45 x W92)-2-5-2, where B14 is the susceptible parent, indicate that more than one gene pair is segregating. F3 progenies from K148 x (Oh45 x W92)-2-5-2 have indicated that (Oh45 x W92)-2-5-2 has 2 or more genes and that none of these is allelic to K148. Thus far, only one dominant gene has been found in K148.

Selection (Oh45 x W92)-2-5-2 (resistant) was crossed with a series of translocation stocks and the single crosses were crossed with waxy B14 (susceptible) where waxy was used as the marker gene, or a susceptible sweet corn where sugary was the marker gene. The translocation stocks have the waxy gene where chromosome 9 is involved and the sugary gene where chromosome 4 is involved. The translocations are in M14 which is susceptible to all cultures of rust used in the study. Although all of the translocations show susceptibility in the field there may be some variation among them in genes affecting resistance because they have not all been backcrossed to M14 an equal number of times.

The table given below summarizes the translocation stocks used, breakage points, rust cultures, segregation counts and calculated X^2 values. The translocation breaks do not include all arms but in most chromosomes the location of breakage is such that linkage would be detected except for genes near the end of the chromosome. Chromosome 7 was not included because the progenies obtained did not segregate for waxy. Seedling tests giving counts of resistant and susceptible plants were made in the greenhouse using rust cultures 90lab and 917a, both of which are avirulent to (Oh45 x W92)-2-5-2 but virulent to the translocation stocks, waxy B14 and the sugary stock.

The X^2 values were calculated using Fisher's formula

$$X^2 = \frac{(ad-bc)^2 N}{(a+b)(a+c)(b+d)(c+d)}$$

for one degree of freedom. The continuity

correction was applied only in the case of T4-9b. Continuity corrections were not applied in other cases because they would not have changed the interpretations.

Counts of resistant and susceptible seedlings in the segregating progenies suggest the presence of one to 4 genes for resistance. This apparent variation in number of gene pairs segregating is probably due to differences in genotypes among the translocation stocks used. For example, in the tests using culture 917a, the data indicate that 4 complementary genes are involved in T1-9, T2-9b and T4-9b: 3 complementary genes may be segregating in T5-9c, T8-9d and T9-10b: and

Counts of seedlings resistant and susceptible to rust cultures 917a and 90lab in normal starch and mutant (waxy or sugary) classes in progenies of ((Oh45 x W92)-2-5-2 x translocation) x waxy B14 or x sugary.

Translocation	Position of breaks	Rust culture	Number of seedlings				X ² Values
			Normal starch Resistant	Normal starch Susceptible	Mutant Resistant	Mutant Susceptible	
T1-9 (wx)	1L. 19-9S. 20	917a	3	53	3	55	0.002
		90lab	18	42	26	33	2.526
T2-9b (wx)	2S. 18-9L. 22	917a	4	55	2	56	0.667
		90lab	6	53	4	50	0.267
T3-9c (wx)	3L. 09-9L. 12	917a	5	50	5	53	0.008
		90lab	5	54	7	52	0.371
T4-9b (wx)	4L. 90-9L. 22	917a	8	55	1	58	3.908*
		90lab	36	76	28	88	1.808
T4-9g (wx)	4S. 27-9L. 27	917a	25	35	10	51	9.398**
		90lab	63	59	27	77	15.447**
T1-4a (su)	1L. 51-4S. 69	917a	15	44	8	45	2.253
		90lab	30	85	12	96	8.171**
T4-5j (su)	4L. 21-5L. 36	90lab	34	26	12	40	12.986**
T4-8a (su)	4S. 59-8L. 19	90lab	20	40	8	49	5.980*
T5-9a (wx)	5L. 69-9S. 17	90lab	25	33	16	37	1.983
T5-9c (wx)	5S. 07-9L. 10	917a	12	49	4	62	5.334*
		90lab	37	77	14	103	14.092**
T5-9 (wx)	5L. 06-9L. 07	917a	20	41	2	61	18.621**
		90lab	17	100	6	76	2.454
T6-9 (wx)	6L. 13-9ct.	917a	15	44	13	46	0.187
		90lab	20	45	11	47	2.265
T8-9d (wx)	8L. 09-9S. 16	917a	6	53	7	51	0.107
		90lab	7	54	3	46	0.942
T9-10b (wx)	9S. 13-10S. 40	917ab	9	52	6	55	0.684
		90lab	6	53	1	58	2.430

* significant at the 5% level
 ** significant at the 1% level

2 complementary genes may be segregating in T4-9g, T6-9 and T1-4a. Similar segregations may be followed through for 90lab, but since the number of genes segregating in some progenies is not always the same as for 917a it is evident that resistance to 90lab is determined by genes at different loci.

The X^2 values indicate linkage between resistance to 917a and non waxy in T4-9b, T4-9g, T5-9c and T5-9. Since none of the other stocks involving chromosome 9 shows a significant X^2 value it may be assumed that chromosomes 4 and 5 in (Oh45 x W92)-2-5-2 carry genes that determine resistance to 917a. T1-4a did not show linkage, thus the gene in chromosome 4 is probably to the right of 4S.27 and too far from 4S.69 to show linkage. In tests using culture 90lab, linkage between resistance and non waxy or non-sugary is indicated in T4-9g, T1-4a, T4-5j, T4-8a and T5-9c. Since T5-9 (5L.09) and T5-9a (5L.69) do not show linkage but T5-9c (5S.07) and T4-5j (5L.36) indicate linkage, it seems likely that the linkage in T4-5j is in chromosome 4 and not chromosome 5. Other translocations involving chromosomes 8 and 9 did not show linkage. Therefore, chromosome 5 apparently carries a gene for resistance to 90lab in its short arm and chromosome 4 has a gene near to the centromere. The linkage relationships between resistance and translocation breakage points indicate the genes determining resistance to 917a are not the same as those giving resistance to 90lab. This is in agreement with data obtained in previous tests of F_3 progenies from K148 x (Oh45 x W92)-2-5-2. Selection (Oh45 x W92)-2-5-2 may have additional genes affecting resistance to 90lab and 917a but escaped detection due to arms not being adequately covered.

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