

UNIVERSITY OF ILLINOIS  
Urbana, Illinois  
Department of Agronomy  
and  
UNITED STATES DEPARTMENT OF AGRICULTURE

1. Location of  $Rf_2$ , a fertility-restoring gene for Texas sterile cytoplasm.

Two dominant complementary genes,  $Rf_1$  and  $Rf_2$ , are required for full restoration of male fertility in the presence of Texas sterile cytoplasm.  $Rf_1$  has been shown to lie between  $d_1$  and  $ts_1$  on chromosome 3 (Duvick, Snyder, and Anderson, 1961, Genet. 46:1245-4).

The following is a portion of the data obtained in recent  $X^2$  tests involving  $Rf_2$  and a series of chromosomal translocations:

Family	Translocation	FT*	FN	ST	SN	Total	P
60-3022	6-9d	1	16	12	5	34	<.01
61-21092	6-10(5519)	58	0	0	40	98	<.01

\*F = fertile, S = sterile, T = translocation heterozygote, N = normal.

Although further tests are required, it appears that  $Rf_2$  is located on the short arm of chromosome 6 at approximately 6S.75, the breakage point of T6-10(5519).

J. B. Beckett

UNIVERSITY OF ILLINOIS  
Urbana, Illinois  
Department of Plant Pathology  
and  
UNITED STATES DEPARTMENT OF AGRICULTURE

1. Symbols for genes for resistance to rust, Puccinia sorghi, Schw.

The discovery of a second major gene locus for resistance to P. sorghi in inbred 25 from Australia (page 51, 1961 M.G.C.N.L.) raises the question of gene nomenclature. In keeping with genetic custom, new gene loci would be identified by a different subscript represented by different numbers; different alleles of the same locus would be identified by different small letters shown as superscripts. The symbol  $rp_2$  has been used to identify the recessive gene in the sweet corn inbred 13-b for resistance to P. sorghi in Argentina (Page 39, 1948 M.G.C.N.L.). Therefore, the symbol  $Rp_3$  is suggested for the locus in inbred 25 identified by rust culture 901aba. Since  $rp_2$  and  $Rp_3$  could easily be confused with  $Rp_2$  present in inbred B38 and with  $Rp_3$  present in inbred K148, especially in verbal communication, it is suggested that the symbol  $Rp_1$  be used for the locus in inbreds GG208R,

B38, K148, etc. located near the end of chromosome 10 (Page 47, 1960 M.G.C.N.L.). The dominant genes for resistance in GG208R, B38, K148, Cuzco, B149, and P. I. 172332, previously designated as  $Rp_1^1$ ,  $Rp_1^2$ ,  $Rp_1^3$ ,  $Rp_1^4$ ,  $Rp_1^5$ , and  $Rp_1^6$  become  $Rp_1^a$ ,  $Rp_1^b$ ,  $Rp_1^c$ ,  $Rp_1^d$ ,  $Rp_1^e$ , and  $Rp_1^f$ , respectively.

A. L. Hooker

2. A gene for resistance to *P. sorghi* present in a resistant source from Mexico

Inheritance studies involving  $F_1$ ,  $F_2$ ,  $F_3$ , and backcross progenies derived from a cross of a rust-resistant inbred M166 from Mexico with the susceptible inbreds B14 and R168 indicate that M166 contains a single dominant gene for resistance to *P. sorghi*. This is indicated by the following number of resistant, segregating, or susceptible progenies when tested with the rust culture 901aba.

Cross	Number of plants or progenies observed			Expected ratio	P value
	Res.	Seg.	Susc.		
(M166 x B14) $F_2$	121	0	30	3:0:1	0.10-0.20
(M166 x R168) $F_2$	89	0	33	3:0:1	0.50-0.70
(M166 x B14) x B14	82	0	67	1:0:1	0.20-0.30
(M166 x R168) x R168	73	0	68	1:0:1	0.50-0.70
(M166 x B14) x M166	141	0	0	all res.	
(M166 x R168) x M166	107	0	0	all res.	
(M166 x R168)	24	40	29	1:2:1	0.30-0.50

Hooker (Page 53, 1961 M.G.C.N.L.) has demonstrated that M185-1 has a single dominant gene for resistance which assort independently of the genes at the  $Rp_1$  locus (Syn. A and B.Y. Dent) and that the single genes in M189 and M212 are either at or closely linked to the  $Rp_1$  locus.

Inbred M166 was crossed with M185-1, M189, M212, and B.Y. Dent. These single crosses were advanced to the  $F_2$  and crossed with the susceptible inbred Oh07K. The following data were obtained in greenhouse tests with rust culture 901aba which is avirulent to the resistant inbreds.