

The breakpoints of Inversion 2a are thus between gl_2 and B in the short arm and between Ht and Ch in the long arm. There is an indication that lg_1-gl_2 recombination may be increased in stocks homozygous for Inversion 2a.

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2. Mapping studies of Rp_3 .

In the 1964 MNL (p. 66), Hooker and Russell reported that a dominant gene for resistance to *Puccinia sorghi* present in line 178 showed linkage with T 3-9c (3L.09; 9L.12). This gene later proved to be allelic to Rp_3 . In the data they reported, in plants heterozygous for T 3-9c, wx and Rp_3 showed 11.7% recombination (32/274).

Further efforts to determine the map position of Rp_3 yielded the following information:

(a) In greenhouse classifications: $d_1 - Rp_3 = 51/288 = 17.7\%$ recombination

(b) In field classifications (255 plants): d_1 23.1 Lg_3 7.1 Rp_3
└────────── 27.1 ─────────┘

(c) In greenhouse classifications (244 plants):

Rp_3 3.3 gl_6 25.8 lg_2
└────────── 28.3 ─────────┘

(d) Progeny of the following cross were scored in the field in 1967:

	+ + +	X		+ +	Rp_3	
				Lg_3	Rg	+
P	+	+	Rp	202		
	Lg	Rg	+	233		
						$Lg_3 - Rg = 17/456 = 4.1\%$
1	+	Rg	+	7		
	Lg	+	Rp	10		
						$Lg_3 - Rp_3 = 21/456 = 5.0\%$
						$Rg - Rp_3 = 4/456 = 0.9\%$
2	+	+	+	4		
	Lg	Rg	Rp	0		
						Order: $Lg_3 - Rg - Rp_3$
			Total	456		

At right above are indicated the recombination values based on the data as recorded. However, the four wild-type plants tabulated as region 2 recombinants in the table may represent contaminants, since no contamination marker was present in the male parent and hence their origin could not be verified. The occurrence of $Rg Rp_3$ progeny would have established the

