

Thus, despite the fact that the parents were selected to provide a maximum range of expression in pollen grain diameter, the differences observed in 1972 were not sufficiently large to permit a genetic analysis. Banerjee and Barghoorn (Maize Genetics Coop. News Letter 45:244-245, 1971) reported that position of the flower on the tassel, size of the anthers, time of anthesis and anther dehiscence and water deprivation cause variability in maize pollen grain size. Rumbaugh and Whalen (Maize Genetics Coop. News Letter 46:171-172, 1972) noted real differences in pollen grain size when the same plants were sampled on successive days. The results of the 1972 research indicated the sensitivity of this trait to environmental influences and the difficulties inherent in a genetic analysis of pollen grain size.

M. D. Rumbaugh
R. H. Whalen

UNIVERSITY OF SYDNEY
Sydney, New South Wales, Australia
Department of Agricultural Botany

1. Linkage relations of opaque-7 with marker loci in linkage group 10.

Linkage relations of the opaque endosperm, high lysine mutant previously reported to be in linkage group 10 (M.N.L. 45: 184, 1971), and now designated opaque-7, have been determined in testcrosses involving the marker loci : R (aleurone color), Mst (modifier of Stippled), G₁ (plant color) and Lc (leaf color). The locus of opaque-7 is situated about 25 recombination units to the right of the R locus on the linkage map of chromosome 10.

In testcrosses of $\underline{R}^x\text{O}_7/\underline{r}^g\text{O}_7$ heterozygotes, the recombination value varied from $.224_{\pm}.02$ to $.333_{\pm}.01$. Differences in recombination value between families were significant and there was a significant tendency for recombination in microsporogenesis to be more frequent than recombination in megasporogenesis. Recombination values of $.244_{\pm}.02$ and $.264_{\pm}.02$, $.245_{\pm}.01$ and $.333_{\pm}.01$, $.296_{\pm}.01$ and $.319_{\pm}.01$ among female and male gametes,

respectively, were obtained in three sets of reciprocal testcross matings.

In plants heterozygous for abnormal 10 (K10), recombination between \underline{R} and \underline{O}_7 was greatly reduced, the recombination values being 0.004 in $\underline{R}^{nj} \underline{Cudu} \underline{O}_7$ K10/ $\underline{r}^g \underline{o}_7$ k10 heterozygotes and 0.0136 in $\underline{R}^g \underline{O}_7$ K10/ $\underline{r}^g \underline{o}_7$ k10 heterozygotes.

Three point testcross data, involving \underline{R}^f (Ecuador) $\underline{Lc} \underline{O} / \underline{r}^g \underline{lc} \underline{o}$, and $\underline{R}^{st} \underline{M}^{st} \underline{O} / \underline{r}^g \underline{m}^{st} \underline{o}$ heterozygotes, and classifications of $\underline{G} \underline{R}^f \underline{o} / \underline{g} \underline{r}^g \underline{O}$ selfed matings, which establish the sequence of loci in this region of the linkage map of chromosome 10, are given below:

(a) Loci: $\underline{R} \underline{Lc}$ and \underline{O}

Mating: $\frac{\underline{R}^f(\text{Ecuador}) \underline{Lc} \underline{O}}{\underline{r}^g \quad \quad \underline{lc} \underline{o}} \quad \begin{matrix} \text{oo} \\ \text{++} \end{matrix} \times \frac{\underline{r}^g \underline{lc} \underline{o}}{\underline{r}^g \underline{lc} \underline{o}} \quad \begin{matrix} \text{oo} \\ \text{oo} \end{matrix}$

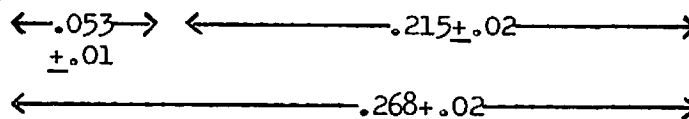
No. of families classified	No. of plants							
	$\underline{R}^f \underline{Lc} \underline{O}$	$\underline{R}^f \underline{Lc} \underline{o}$	$\underline{R}^f \underline{lc} \underline{o}$	$\underline{R}^f \underline{lc} \underline{O}$	$\underline{r}^g \underline{Lc} \underline{o}$	$\underline{r}^g \underline{Lc} \underline{O}$	$\underline{r}^g \underline{lc} \underline{O}$	$\underline{r}^g \underline{lc} \underline{o}$
2	106	37	6	1	nil	9	37	106

Total

Linkage Map:

302	\underline{R}^f	\underline{Lc}				\underline{O}	

Recombination values:



(b) Loci: \underline{G} , \underline{R}^f , and \underline{O}

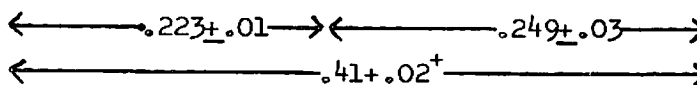
Mating: $\underline{G} \underline{R}^f \underline{o} / \underline{g} \underline{r}^g \underline{O}$ selfed.

No. of ears classified	No. of seedlings*								Total
	$\underline{G} \underline{R}^f \underline{O}$	$\underline{G} \underline{R}^f \underline{o}$	$\underline{g} \underline{R}^f \underline{O}$	$\underline{G} \underline{R}^f \underline{o}$	$\underline{G} \underline{r}^g \underline{O}$	$\underline{G} \underline{r}^g \underline{o}$	$\underline{g} \underline{r}^g \underline{O}$	$\underline{g} \underline{r}^g \underline{o}$	
4	557	288	98	43	107	2	164	18	1277

Linkage Map:

	\underline{G}		\underline{R}^f			\underline{O}

Recombination values:



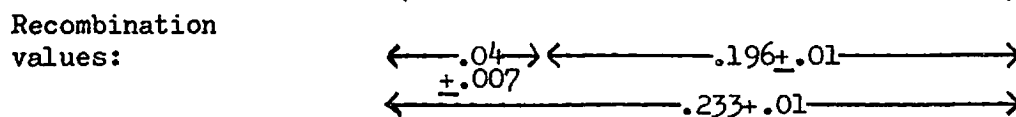
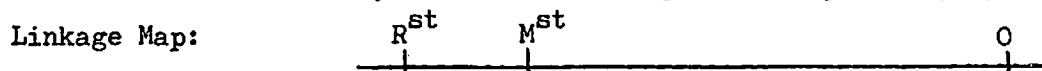
*Data obtained by classification of green (\underline{G}) vs golden (\underline{g}) plant color in the seedling stage.

⁺Recombination value not corrected for occurrence of double crossovers.

(c) Loci: \underline{R}^{st} \underline{M}^{st} and \underline{O}

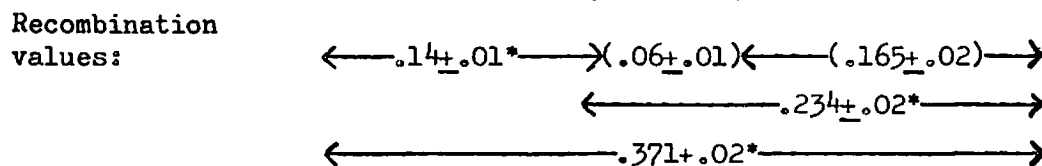
Mating: $\frac{G \underline{R}^{st} \underline{M}^{st} \underline{O}}{g r^g m^{st} o} \overset{oo}{++} \times \frac{g r^g m^{st} o}{g r^g m^{st} o} \overset{oo}{\nearrow}$

Family	No. ears classified	Number of kernels:						Total
		$\underline{R}^{st} \underline{M}^{st} \underline{O}$	$\underline{R}^{st} \underline{M}^{st} o$	$\underline{R}^{st} m^{st} o$	$\underline{R}^{st} m^{st} \underline{O}$	$r^g \underline{O}$	$r^g o$	
K765	7	445	116	27	3	136	479	1206
K766	3	206	48	5	-	71	222	552
Totals	10	651	164	32	3	207	701	1758



In addition, the following four point testcross data, obtained by classification of four ears produced by the above mating, confirms the sequence of loci as being \underline{G} , \underline{R}^{st} , \underline{M}^{st} and \underline{O} .

Kernel phenotype:	Number of individuals of:											
	$\underline{R}^{st} \underline{M}^{st} \underline{O}$	$\underline{R}^{st} \underline{M}^{st} o$	$\underline{R}^{st} m^{st} o$	$\underline{R}^{st} m^{st} \underline{O}$	$r^g \underline{O}$	$r^g o$	Total					
Plant color:	\underline{G}	\underline{g}	\underline{G}	\underline{g}	\underline{G}	\underline{g}	\underline{G}	\underline{g}	\underline{G}	\underline{g}	\underline{G}	\underline{g}
	181	32	42	1	14	1	2	-	167	41	172	554



*additive recombination values

K. S. McWhirter