Table 3 - A158TF6 Crosses

Cross	F	S	P for 1:1	P for heterogeneity
A158TF5(69-1) x A	72	80	.50	
AT7 x 69-1	75	76	.90	
	147	156	.60	.70
A158TF6(69-4) x (WF9 x Oh51A)	94	70	.06	
(WF9T7 x Oh51A) x 69-4	63	53	.35	
	157	123	.04	.60
(A158TF6(69-5) x (WF9 x Oh51A)	85	90	.80	
(WF9T7 x Oh51A) x 69-5	59	47	.25	
	144	137	.70	.25
3 families combined:				
TF x N	251	240	.60	.15
T x TF	197	176	.28	.60
	448	416	.28	.60

Table 4 - Oh51ATF6 Crosses

Cross	F	S	P for 1:1	P for heterogeneity
Oh51ATF6(81-11) x(WF9 x Oh51A)	55	83	.02	
(WF9T7 x Oh51A) x 81-11	64	94	.02	
	119	177	<.001	.85
Oh51ATF6(81-3) x A	78	91	.30	
AT7 x 81-3	103	63	<.01	
	181	154	.14	<.01
2 families combined:				
TF x N	133	174	.02	.25
T x TF	167	154	.60	<.01

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3. Pollen transmission of T restorer genes by plants with sterile (T) and normal (N) cytoplasm.

A second aspect of restorer gene behavior investigated was a comparison of the segregation ratios produced by heterozygous ($\underline{Rf_1}\underline{rf_1}$) restorer male parents possessing T and normal (N) cytoplasm. The T and N restorer male parents were produced as follows: restored sterile lines of A158, Oh51A, and Kr which had been backcrossed 4 or 5 generations, selfed 3 or 4 generations, and shown by test crosses to be homozygous for the restorer genes (T $\underline{Rf_1}\underline{Rf_1}\underline{Rf_2}\underline{Rf_2}$) were crossed reciprocally with the respective normal lines (i.e. N $\underline{rf_1}\underline{rf_1}\underline{Rf_2}\underline{Rf_2}$) to give the two kinds of families, T $\underline{Rf_1}\underline{rf_1}\underline{Rf_2}\underline{Rf_2}$ and N $\underline{Rf_1}\underline{rf_1}\underline{Rf_2}\underline{Rf_2}$. In any given reciprocal cross the same two plants were used as parents. The original source of the restorer genes for A158 and Kr was Ky21, and the source for Oh51A was I153.

Pollen from the T $\underline{Rf_1}\underline{rf_1}$ and N $\underline{Rf_1}\underline{rf_1}$ (both are homozygous $\underline{Rf_2}\underline{Rf_2}$) plants was applied to the silks of various T sterile testers. The sterile testers were also crossed with the normal (N $\underline{rf_1}\underline{rf_1}$) lines of A158, Oh51A and Kr to determine the degree of restoration brought about by the genotypes of the test crosses in the absence of the $\underline{Rf_1}$ restorer gene. Progenies of the latter crosses contained either all sterile plants or sterile and fertile plants which produced little or no pollen. Consequently partial fertile offspring in the test crosses were classified as sterile.

Results are shown in Table 5. In the case of A158 there is no evidence for a difference in the behavior of A158NF and A158TF restorers, either in individual test crosses or in the combined results for the two types of crosses.

With Oh51A the crosses to C106T12 x A158 suggest a possible difference between the NF and TF restorers, the segregations in the families being almost exactly reversed. The combined totals for the T x NF and T x TF crosses do not give a significant X^2 for heterogeneity between the two kinds of crosses, but the families in the T x NF category give a poor fit for homogeneity.

None of the individual test crosses with the Kr restorers shows a significant difference between the NF and TF plants. The two kinds of crosses as groups also do not show a significant difference. However, the pooled T x TF crosses may contain a significant excess of fertile plants (P = .03), but the six families are of doubtful homogeneity (P = .07). Combining the results from all T x NF and all T x TF crosses gives 776 fertile and 700 sterile plants, a segregation with a P value of .05. There is thus a suggestion that Kr $\underline{Rf_1}\underline{rf_1}$ restored steriles produce an excess of fertile plants when used as pollen parents, but there is no evidence for a difference between NF and TF restorers.

Table 5. A158N Rf_1rf_1 and A158T Rf_1rf_1

Sterile tester ♀	T x NF F	T x NF S	P for 1:1	T x TF F	T x TF S	P for 1:1	P for heterogeneity TxNF, TxTF
AT7	81	81	>.99	75	76	.93	.95
WF9T7 x Oh51A	70	59	.35	122	100	.14	.85
WF9T7 x W22	53	56	.90	88	80	.50	.60
Totals:	204	196	.70	285	256	.25	.60
P, heterogeneity, families			.60			.55	

Oh51A N Rf_1rf_1 and Oh51A T Rf_1rf_1

Sterile tester ♀	T x NF F	T x NF S	P for 1:1	T x TF F	T x TF S	P for 1:1	P for heterogeneity T x NF, TxTF
B8T7 x Oh43	85	74	.40	84	78	.70	.75
"	71	92	.10	77	81	.75	.35
WF9T7 x W22	85	83	.85	84	81	.80	.98
C106T12 x A158	71	92	.10	92	76	.22	.04
Totals:	312	341	.25	337	316	.40	.22
P, heterogeneity, families			.15			.70	

Kr N Rf_1rf_1 and Kr T Rf_1rf_1

Sterile tester ♀	T x NF F	T x NF S	P for 1:1	T x TF F	T x TF S	P for 1:1	P for heterogeneity T x NF, TxTF
WF9T7 x W22	74	60	.25	94	65	.03	.50
WF9T11 x 38-11	83	70	.30	80	77	.75	.60
C103T11 x Hy	76	80	.75	87	61	.03	.08
C106T12 x A158	74	74	>.99	78	81	.80	.85
C103T12	31	36	.60	32	42	.25	.85
KrT9	29	31	.85	38	23	.06	.12
Totals:	367	351	.55	409	349	.03	.27
P, heterogeneity, families			.60			.07	

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1. Multiple conversion of R-locus expression in one generation.

R. A. Brink and his students have demonstrated that the expression of the R-locus can be altered by passing the R allele through a heterozygote with certain pattern alleles such as R^{st} and R^{mb} (stipple and marble). More recently, it was shown (PNAS 47:566) that R-locus expressions could be progressively converted to lighter and lighter phenotypes by passing R-alleles through pattern allele heterozygotes successively. That is, when RR^{mb} heterozygotes were crossed to $R^{st}R^{st}$(light) to yield in the next generation $R'R^{st}$ and $R'R^{st}$(light) heterozygotes (prime is used here to indicate the number of pattern alleles with which R has been heterozygous), the testcrosses of these last heterozygotes gave R'' phenotypes which were significantly lighter than R' controls removed from the RR^{mb}, RR^{st} and RR^{st}(light) heterozygotes.