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.

A further question remained; could the amount of change produced in two generations by the above method of progressive conversion be registered on the R-locus expression in a single generation by using more than one pattern allele.

A trisomic, $r^{r}R^{st}r^{g}_{I}$ (the allele r^{g}_{I} was a colorless mutant of R^{st} recovered by R. B. Ashman and capable of R-locus conversion), was crossed to the inbred RR homozygote to yield the $R^{st}r_{I}R$ trisomic as well as $R^{st}R$, $r_{I}R$ and rR disomic heterozygote controls. The above trisomics and disomics were testcrossed for comparison of R' and R'' phenotypes. The amount of pigment produced in the endosperm was scored by matching kernels against a series of 23 standard kernels ranging from "zero" or colorless to complete pigmentation. Mean scores for 50 kernels from each ear are recorded below. The results show significantly lighter R'' expressions from the trisomic as compared with any of the R' kernels from the disomic controls.

$R^{st}Rr^{g}_{I}$	$R^{st}R$	Rr^{g}_{I}	Rr^{r}
R''	R'	R'	R
3.26	8.24	6.52	18.96
4.10	8.98	11.28	18.60
4.64	6.76	10.10	19.80
3.66	10.86	16.04	19.00
2.06	9.58	8.52	18.00
3.08	11.12	10.36	20.12
4.80	10.86	11.86	
3.86	10.54	10.10	
3.56	13.98		
3.48			

Thus it is possible to influence R-expressions by progressive treatments over several generations or by using more than one pattern allele in a single generation.

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1. Somatic crossing over ?

Cross: $\frac{Su\ \ ga}{Su\ \ ga} \times \frac{su\ \ Ga}{su\ \ Ga}$

F_1 zygotes (expected): $\frac{Su\ \ ga}{su\ \ Ga}$

In one of three cultures containing F_1 plants of this origin were three plants which behaved in an unexpected manner. From selfing and from back-crossing (pollen to Ga ga su su plants) the following distributions were obtained: