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.

Bernard C. Mikula and Steven D. Skopik

DUKE UNIVERSITY
Durham, North Carolina

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:

Plant		Su	su	o/o su	P*	P* (comb. data)	Crossover** value
# 3	self	321	76	19.1	<.01	<.01	38.3%
	BC	248	168	40.4	<.01		40.4%
#11	self	350	97	21.7	>.05	<.01	43.4%
	BC	222	173	43.8	<.05		43.8%
#12	self	334	76	18.5	<.01	<.01	37.1%
	BC	221	176	44.3	<.05		44.3%

* For deviations from 3:1 and 1:1
** Computed for coupling

Crossover values are rather high but comparable to those for high-sugary plants in the same culture.

Since all, or nearly all, of each tassel presumably was composed of cell descendants of a somatic crossover cell, it is suggested that the putative crossing over occurred early in ontogeny--possibly in zygotic mitosis.

Perhaps the use of a third gene such as Ts$_2$ will clarify the situation by making possible a regular four-class backcross test.

H. S. Perry

HARVARD UNIVERSITY
Cambridge, Massachusetts

1. Further data on the components of the tunicate locus.

In a previous News Letter (No. 35) we reported that the two components of the Tu locus which had been separated by crossing over appeared to have slightly different effects. After additional backcrosses to the inbred A158 to render them more nearly isogenic, this is still true. In the summer of 1961 we grew seven strains heterozygous for tu^{h-d}, two of which were 13/16 A158 and five were 29/32 A158. These were compared with ten strains heterozygous for tu^{h-1}, three of which were 5/8 A158 and seven were 29/32 A158.

The two types of heterozygous half-tunicate genotypes could not be distinguished by their tassels or by the external characteristics of the mature ears, but examinations of longitudinal sections of both young and mature ears revealed differences. Pistillate spikelets from plants heterozygous for tu^{h-1} consistently had longer rachillae, slightly thinner lower glumes, and longer and more numerous cupule hairs than those from plants heterozygous for tu^{h-d}. In 71 paired comparisons of longitudinal sections of young ears the two types were consistently distinguishable. However, we cannot yet be certain that the differences are inherent in the two components and are not due to other genes closely linked with them.

P. C. Mangelsdorf