We were unable to detect any chromosome damage induced by atrazine in exposed seedlings. Breaks induced by atrazine in meiotic chromosomes of barley have been reported; however, the plants were exposed to 1000 ppm (Wuu, K. D., and W. F. Grant, Cytologia 32:31-41, 1967).

We propose to extend this bioassay to include the effects of long term growth after an initial exposure to a pesticide. Maize pollen grains can be used to detect chromosome damage and forward and reverse mutation rates. The amount of pollen abortion can be used as an index of chromosome aberrations; if a proximal mutagen causes breaks in meiotic chromosomes, we could monitor these effects over an exposure concentration gradient by the increase in pollen abortion. Forward and reverse mutation rates could be measured on populations based on 10^5 to 10^6 pollen grains by studying mutation rates at the waxy locus. We have experiments in progress that should determine whether or not the above suggestions are feasible.

We contend that this bioassay could be used routinely by industry to test the agricultural chemicals they produce prior to their introduction into the environment. We believe that such information is essential in making rational decisions concerning agriculture and its ecological impact. (Partially funded by a D. F. Jones Fellowship, Research Corporation, New York).

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Topographical structure of the R region in R-ch complexes — Recombination studies involving a number of R-ch isolates revealed that the R region in these stocks consists of a number of closely linked discrete genetic units, each controlling anthocyanin pigmentation in a plant part or tissue. Recombinational analyses in the testcross progenies from G R-ch/g r-g heterozygotes of five cherry isolates show the following linkage relationships among the anthocyanin traits: pigmentation in aleurone (S), anther (P), silk (Si) and pericarp (Ch) (Table 1). Probable gene sequences in these isolates can be constructed as:

Ecuador R-ch: G - S - P - Ch - Si
New Mexican R-ch: G - Si - S - Ch - P, or g - P - Ch - Si - S
Standard R-ch: G - Si - Ch - S - P
Pueblo R-ch: G - S - Ch - Si - P
P.C. 150 R-ch: G - S - Ch - Si

In addition to these four anthocyanin traits, pigmentation in glume (Glm), auricle (Au), leaf margin (Lm), nodal ring (Nr) and coleoptile (Co) appear to be controlled by independent discrete units. Leaf color factor (Lc) expression was poor and

Table 1. Recombination percentages among g and four anthocyanin traits in five R-ch isolates.

Interval	Ecuador R-ch	New Mexico R-ch	Standard R-ch	Pueblo R-ch	Peru Corongo R-ch*
g-S	15.13	14.71	13.58	15.02	12.43
g-P	16.52	13.97	16.02	16.06	-
g-Si	17.83	13.54	13.21	14.36	13.09
g-Ch	17.23	14.84	16.17	14.55	14.34
S-P	0.55	1.32	0.89	2.60	-
S-Si	2.00	0.39	1.19	1.03	2.39
S-Ch	1.52	0.72	0.97	1.06	2.20
P-Si	1.68	1.14	2.36	1.71	-
P-Ch	1.25	0.99	2.65	1.94	-
Si-Ch	1.07	0.42	0.64	0.46	0.39

*Peru Corongo #150 R-g, no anther color.

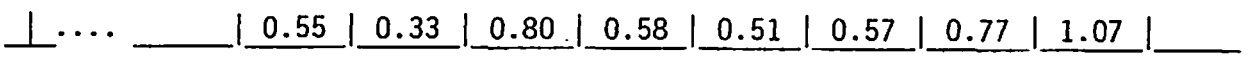
erratic in Delhi conditions and its relationship with these anthocyanin traits could not be established. However, recombinations among these traits and between these and the four established components P, S, Si and Ch were regularly obtained (Table 2). Intercrosses between different isolates or between segregant classes

Table 2. Recombination percentages among various anthocyanin distribution traits in two R-ch isolates.

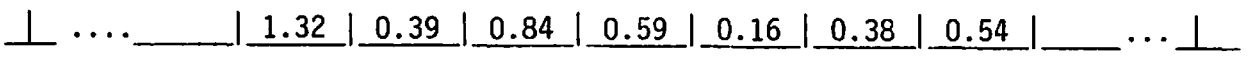
	Ecuador R-ch	New Mexico R-ch1		Ecuador R-ch	New Mexico R-ch1
Population	13,750	3,072	Ch-Nr	0.77	0.54
S-Glm	0.93	1.40	Glm-Au	0.85	0.59
S-Au	1.06	0.46	Glm-Lm	0.65	1.22
S-Lm	0.87	0.89	Glm-Nr	0.84	1.57
S-Nr	1.17	0.95	Au-Lm	0.51	0.16
P-Glm	0.33	1.16	Au-Nr	0.57	0.73
P-Lm	0.65	1.37	Lm-Nr	0.55	1.33
P-Au	0.87	0.77	S-Co	0.72	-
P-Nr	0.86	1.70	P-Co	0.80	
Si-Glm	1.65	0.84	Si-Co	1.61	
Si-Au	1.33	0.06	Ch-Co	1.12	
Si-Lm	1.35	0.87	Glm-Co	0.80	
Ch-Glm	1.20	0.75	Au-Co	0.72	
Ch-Au	0.89	0.49	Lm-Co	0.58	
Ch-Lm	0.98	0.38	Nr-Co	0.68	

of the same isolate result in complementation in "trans" position, indicating that this cluster of genes does not form a pseudoallelic series. They are rather independent but closely linked genes carrying out the same function with different times of action. They may be termed "para-allelic" (Laughnan, J. R., Am. Nat. 86:109, 1952). Mutation studies to examine these findings are in progress.

Strong negative interference and consequent high coincidence values were obtained in the majority of the three-point tests. This may be explained by a high degree of effective pairing in this region due to homology of the component segments. It can be postulated that various members of the gene cluster at the R region in R-ch complexes might have originated as tandem repeats through unequal crossing over. Two or more genes thus assembled together would acquire altered functions through mutation or position effect. On the basis of three-point data, tentative maps for the R region in Ecuador R-ch and New Mexican R-ch1 isolates are constructed as below:



Ecuador R-ch



New Mexican R-ch1

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Characterization of the Spf and Dil factors of the spotted-dilute R system —

To explain the aleurone spotting behavior in the unstable R alleles designated as "spotted-dilutes" (R-sd), Sastry and Kurmi (MNL 44:101) postulated the presence of two dominant modifiers, Dil (diluting factor) and Spf (spotting factor). Our studies involving two isolates, R-sd2 and R-sd4, confirm these postulations. Homozygous R-sd plants on selfing occasionally yield intense, spotted and dilute kernels in addition to the spotted-dilute kernels. Data from selfing and testcrossing heterozygous R-sd/r plants involving isolates R-sd-4 are presented in Tables 1 and 2.

Segregation of Dil was regular in the majority of ears, showing 3:1 ratios on selfing and 1:1 on testcrossing. The other factor, Spf, however, did not exhibit regular Mendelian behavior and consideration of its linkage with R does not fully explain the erratic segregation pattern. Segregation of both Dil and Spf in R-sd2 stocks was more irregular, not conforming to the 1:1 ratio in most of the ears obtained in the testcrosses.

Selfing of heterozygous dilutes of the R-sd4 isolate (R Dil/R dil) yielded dilute and non-dilute (intense) kernels in a 3:1 ratio, confirming that the diluting factor is a dominant independent modifier of the S component of the R locus and is not concerned with the spotting phenomenon. Linkage data obtained by crossing R-sd stocks with the waxy translocation series and selfing or testcrossing