is true for seeds carrying other stippled derivatives. The results are reported in the following table.

Table 2

Reversion rate of different stippled derivatives in germinal and somatic tissues

Allele tested	#seeds scored	Germinal revertants	x 10^{-3}	Half-seed sectors	x 10^{-3}	Quarter-seed sectors	x10^{-3}
Stippled	1397	6.6	4.7	11	3.9	26	4.6
Smoky	3672	3.1	0.8	45	6.1	72	4.9
Light smoky	4080	0.0	0.0	0	0.0	4	0.3

These data suggest that when the frequency of reversion is expressed as reversion rate per cell per generation, it is possible to group the alleles into 3 categories:

1. The stippled allele exhibiting the same chance of reversion for all the cells and at different times of the development.

2. The smoky allele exhibiting an increase of approximately 5 times in its somatic reversion rate when compared to that in the germ cells.

3. The light smoky allele with high stability both in the germ cells and at the first cell divisions during endosperm development.

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2. Paramutagenic action of some stippled derivatives.

The various stippled derivatives can be distinguished by means of different criteria such as their capacity to induce paramutation and their reversion rate toward $\underline{R}^{sc}$ in somatic and germ cells (see previous note). The first criterion is particularly important in relation to the problem of the genetic basis of paramutation. In fact, the mosaic phenotype of the aleurone, conditioned by $\underline{R}^{st}$, could be controlled by a genetic component associated with the $\underline{R}$ region that is also responsible for inducing paramutation. Accordingly, one should find that any genetic alteration leading to a change in the stippling pattern is coupled with an alteration in its paramutagenic potentialities. This possibility has been tested by comparing the paramutagenic capacity of $\underline{R}^{st}$ and $\underline{R}^{n.c.}$ that differ markedly in their phenotypic expression. This test has been accomplished by crossing standard stippled and nearly colorless sib plants with a homozygous $\underline{R}^{r}/\underline{R}^{r}$ stock and then testcrossing them on W23 $\underline{r}^{g}/\underline{r}^{g}$. Individual testcross kernels were scored for pigmentation according to the standard matching technique (see Brink et al., 1960).

From each testcross ear 42 kernels of the appropriate genotype were scored. Since in testcross ears obtained from the cross W23 $\underline{r}^g\underline{r}^g$ x W22 $\underline{R}^{n.c.}$ $\underline{R}^r$, kernels of the two genotypic classes overlap in phenotype, the two classes were separated retrospectively by germinating the seeds after scoring. The results of such a comparison are reported in Table 1.

Table 1

Means of aleurone color scores for $\underline{R}^{rl}\underline{r}^g$ $\underline{r}^g$ kernels from W23 $\underline{r}^g$ $\underline{r}^g$ x W22 $\underline{R}^r$ $\underline{R}^{st}$ ♂ matings in comparison with those of $\underline{R}^{rl}\underline{r}^g$ $\underline{r}^g$ kernels from W23 $\underline{r}^g$ $\underline{r}^g$ ♀ x W22 $\underline{R}^r$ $\underline{R}^{n.c.}$ ♂ matings

Allele tested	# ears scored	Mean aleurone color score	Standard error	Estimated t value (1)
Stippled	15	2.37	0.124	0.533 n.s.
Nearly colorless	15	2.45	0.087	

(1) n.s. = non significant

No significant difference in level of paramutagenic action between the two classes is detected by the test. These data suggest that there is no straight relationship between the phenotype of the two stippled alleles tested and their paramutagenic potentialities. As previously mentioned, the various stippled derivatives were first isolated following introduction of Mp into the genome of a homozygous $\underline{R}^{st}/\underline{R}^{st}$ stock. Furthermore, it has been noticed that the addition of increasing doses of Mp in a homozygous $\underline{R}^{st}/\underline{R}^{st}$ stock determines an approximately linear increase in the $\underline{R}^{st} \longrightarrow \underline{R}^{sc}$ reversion rate (Gavazzi, 1967). Because of this interaction of Mp with the stippled expression, it seemed appropriate to establish whether the association of a given stippled allele with the Modulator can also affect its paramutagenic capacity. This has been accomplished by determining the paramutagenic action of $\underline{R}^{n.c.}$ and $\underline{R}^{sc}$ individuals isolated from an ear that was segregating for Mp. Each $\underline{R}^{sc}$ and $\underline{R}^{n.c.}$ sib plant has been crossed with a homozygous $\underline{R}^r$ $\underline{R}^r$ stock and then testcrossed on W22 $\underline{r}^g/\underline{r}^g$. The resulting testcross kernels have been scored with the same procedure adopted in the previous test. At the same time, pollen from each plant under test has been put on a $\underline{C}^I\underline{-Ds}/\underline{C}^I\underline{-Ds}$ $\underline{R}^g/\underline{R}^g$ tester stock in order to check its Mp constitution. For each allele thus tested two sublines were derived differing in their Mp constitution. The results of this paramutagenicity test are here reported.

Table 2

Means of aleurone color scores for $\underline{R}^{rl}\ \underline{r}^{g}\ \underline{r}^{g}$ kernels from $\underline{r}^{g}\underline{r}^{g} \times \underline{R}^{r}\ \underline{R}^{n.c.}$ (with or without Mp) matings in comparison with those of $\underline{R}^{rl}\ \underline{r}^{g}\ \underline{r}^{g}$ kernels from $\underline{r}^{g}\underline{r}^{g} \times \underline{R}^{r}\ \underline{R}^{sc}$ (with or without Mp) matings

Allele tested	Mp constitution	# ears scored	Mean aleurone color score	Standard error
Nearly colorless	1 Mp	9	3.73	0.204
Nearly colorless	0 Mp	10	3.48	0.203
Self-colored	0 Mp	19	2.50	0.097
Self-colored	1 Mp	19	2.32	0.103

In the following table the results of an analysis of variance from the paramutation scores presented in Table 2 are reported.

Table 3

Analysis of variance of the paramutagenic action of $\underline{R}^{n.c.}$, and $\underline{R}^{sc}$ with and without Mp in their genome (A = $\underline{R}^{n.c.}$ with Mp; B = $\underline{R}^{n.c.}$ without Mp; C = $\underline{R}^{sc}$ without Mp; D = $\underline{R}^{sc}$ with Mp)

Source of variation	Degrees of freedom	Sum of squares	Mean square	F value (1)
Between genotypes	3	18.489	6.163	24.01**
A vs. B	1	0.300	0.300	1.17 n.s.
C vs. D	1	0.315	0.315	1.23 n.s.
AB vs. CD	1	17.873	17.873	69.63**
Within genotypes	53	13.604	0.256	
Total	56	32.938	0.573	

(1) n.s. = non significant ($P > 0.05$)
** = highly significant ($P < 0.01$)

This analysis shows that the $\underline{R}^{sc}$ and $\underline{R}^{nc}$ alleles differ significantly in their capacity to induce paramutation. On the other hand, the introduction of Mp into their genomes does not alter their paramutagenic potentialities. The data here presented indicate that:

1. The paramutagenic action of $\underline{R}^{sc}$ is significantly higher than that of $\underline{R}^{n.c.}$

2. The introduction of Mp in the $\underline{R}^{st}$ genome, while exhibiting an effect upon the stippled phenotype, does not seem to be associated with a change in its paramutagenicity.

The data so far obtained suggest that two functions exhibited by the unstable R alleles, i.e. their capacity to induce paramutation and their production of a variegated phenotype in the aleurone, do not have a common genetic basis. On the contrary the data point to the existence of two independent components associated with the R locus governing these different functions. The paramutagenic capacity of other stippled derivatives and the relationship between paramutagenic potential of $\underline{R}^{st}$ and crossing over in its adjacent regions are now under investigation. The accomplishment of these tests will allow a more general formulation of the conclusions here presented.

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3. Phenotypic stability in maize.

The phenotypic expression of the genotype may vary with environmental conditions and the kind and the amount of that variation cannot be the same for all genotypes. Many efforts have been made to study the genetic control of variability of the phenotypic stability. The object of this study was to examine the phenotypic stability of different genotypes in relation to the effect of plant spacing. This effect is of great interest in plant breeding and in research concerned with the nature of gene action involved in determining quantitative traits.

The aims of this work are twofold: (1) to obtain information about the possibility of selecting strains to be used with high plant density and (2) to get additional information on the genetic control of variation of phenotypic stability.

Sixty-four genotypes from a complete set of diallel crosses between eight inbred lines formed the experimental material. They have been planted at three different levels of plant density, namely 5, 7 and 9 plants per m^2. The experimental design was the following: two blocks were divided into three plots, one for each level of plant density. For each plot, five plants of each family were used. In order to distribute equally the competition effect between genotypes, a single plant randomization was used. The measurements taken in the field were the following: flowering time (tassel), plant height, leaf width and length. Parental and F_1 means of all characters considered for each level of plant density are presented in Table 1. The variance between densities provides an inverse measure of the stability over the range of environmental variation considered in this experiment (Griffing and Langridge, 1963). This parameter was estimated for each family in both blocks. The logarithms of the estimated variances (Sheffe, 1949) have been used for diallel analysis of variance (Table 2) according to the model of Hayman (1954).