Summary:

In the presence of the paramutagenic gene c^{IP}, the following mutational sequences have been obtained: $C^i \longrightarrow c^{im}$ and $c^i \longrightarrow c^{Im}$.

In the absence of the paramutagenic c^{IP} gene, the following mutational sequences have been obtained: $c^{im} \longrightarrow c^{iR}$, $c^i \longrightarrow c^{Im}$, and $c^{im} \longrightarrow C^{iR} \longrightarrow c^{im2}$. Symbols: C^i, c^I, c^I = standard alleles; m = first mutation; m2 = second mutation; R = reversion.

The present results may be interpreted in accordance with the hypothesis already described (MNL 40:62, 1966) as an excessive replication of DNA segment(s) of the paramutagenic gene c^{IP}. This segment(s) could have the power of self duplication and interaction with the C locus either in an attached or in a free state, not necessarily released into the cytoplasm. These findings suggest the possibility that a gene of a higher organism may originate episome-like particles.

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1. Pale phenotypes at the A_2 locus.

A number of distinct pale phenotypes, representing a wide spectrum of qualitative differences in anthocyanin coloration, have been isolated at the A_2 locus. These arose from a newly induced unstable a_2 mutant, a_2 m(1 1511), but are themselves stable. They fall into a sequential series of pigment types from very light pales to darker shades. (Other phenotypes representing unrelated forms of phenotypic expression have also been isolated.)

Differences in pale phenotypes may be due to one of two alternatives: (1) differential placement of the I(nr)* element (Peterson, 1966) within the A_2 locus - the position hypothesis or (2) qualitative differences in the composition of the I(nr) element - the composition hypothesis. The position hypothesis may be tested by subjecting pales of different origin to crossover tests. Differential placement would be expected to yield full color types.

It is interesting to note that in a study of the a_1 - Dt system, Professor Rhoades found novel types at the a_1 locus that had not previously been recorded in natural populations. Similar types of variants have arisen at the A_2 and Wx loci following their exposure to the Ac-Ds system (McClintock, 1951). It is evident that systems such as a_1 - Dt, Ac-Ds and En-I can significantly influence types of variation originating at a locus.

*I(nr) = suppresses gene action but does not respond to En.

2. En control of an a_2 mutable.

A number of unstable genes have been isolated in En- containing stocks. The new mutables originated from dominant alleles (MGCNL 40:64). One of them, $a_2^{m(1\ 1511)}$ has been shown to be under the control of Enhancer (En). A wide assortment of pattern types (differences in time and frequency of mutation events) has been identified. The relationship to En is based on a correlation between the presence of a_2^m and concomitant mutability in a tester a_1 allele, either $a_1^{m(r)}$ or a_1^{m-1}, both known to respond to En. The following tests are employed to demonstrate this relationship.

Cross #1 $a_2^m/-, A_1/A_1 \times A_2/A_2, a_1^{m(r)} Sh/a_1^{m(r)} Sh$

Cross #2 $A_2/a_2^m, A_1/a_1^{m(r)} \times A_2/A_2, a_1^{m(r)} Sh/a_1^{ml} sh$ (En tester)

selected phenotypes: mutable types
non-mutable types

(The F_1 type, $A_2/a_2^m\ A_1/a_1^{m(r)}$, in Cross #2 utilized in a cross with an En tester is also crossed to an a_2 tester to verify the presence of the a_2^m allele.) The selected and separated phenotypes resulting from Cross #2 are tested by an a_2 tester (Cross #3).

Cross #3: mutable types resulting from Cross #2 x a_2 bt

non-mutable types resulting from Cross #2 x a_2 bt

Progeny Cross #2	Separated x a_1 into			
	mutable		non-mutable	
Progeny of Cross #3	I mutable	II non-mutable	III mutable	IV non-mutable
5 1039	11	3	0	7
5 1041	19	2	0	3
5 1044	19	0	0	7
5 1047	11	2	0	8
5 1050	12	0	1	8

Although not all selected a_1-mutable types (and therefore known to carry En) were mutable for a_2 (see column II), only 1 of the non-mutable was found to be mutable for a_2 (column III). This is presently being tested since a low frequency mutable type would escape detection in the a_1 test.

The non-mutable types in Column II are probably $\underline{a}_2^{m(nr)}$ types and crosses with an $\underline{a}_2^{m(r)}$ (a colorless $\underline{a}_2$ that will respond to $\underline{En}$) will test this.

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1. Genetic studies involving homozygous T6-9e: The location of $\underline{Y}_1$ with respect to the break point in chromosome 6 and a reduction in crossing over observed in chromosome 9.

Patterson (1958, Maize Genet. Coop. News Letter 32:54-66) reported on linkage relations of T6-9e (6L.18, 9L.24) in which he indicated that the break point in 6 was probably proximal to $\underline{Y}_1$. This break point position has been confirmed by testcrossing plants homozygous for the translocation and heterozygous at the $\underline{Y}_1$ and wx loci. If the break point on 6 is proximal to $\underline{Y}_1$, wx and $\underline{Y}_1$ should be linked in the homozygous translocation plants. If the break point is distal to $\underline{Y}_1$, independent assortment should be observed. Table 1 gives the results of the testcross.

Table 1

Testcross data of plants homozygous for T6-9e and heterozygous at the $\underline{Y}_1$ and wx loci ($\frac{\underline{Y}_1\ \underline{T}\ \underline{wx}}{\underline{Y}_1\ \underline{T}\ \underline{Wx}}$).

Direction of cross	Phenotypes				% C.O.
	White waxy	Yellow starchy	White starchy	Yellow waxy	
F_1 as males	913	948	34	23	
F_1 as females	919	857	22	24	
	1832	1805	56	47	2.8%

The data indicate that the break point in chromosome 6 is proximal to $\underline{Y}_1$ and that about 3% crossing over takes place between wx and $\underline{Y}_1$. Since the cytological distance between waxy and the break point in chromosome 9