THE EFFECT OF ABNORMAL CHROMOSOME 10 ON TRANSPOSITION OF MODULATOR FROM THE R LOCUS IN MAIZE

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ABSTRACT

Transposition of the non-specific repressor element, Modulator, from the R locus on chromosome 10 in maize, is enhanced by coupling with the K10 segment at a distance of at least 35 map units from R. There is no detectable interaction in the repulsion phase. The K10 effect appears to be relatively greater in the earlier somatic cell generations during ear development. The transposition rate also is affected by the direction of crosses, being somewhat higher on the ears of F1 plants which received the compound mutable R allele from the pollen parent. The significance of the behavior of Modulator and other instability phenomena of higher plants is discussed in relation to chromosome organization.

The hypothesis has been advanced by Brink (1960, 1969) that the unstable genetic repression phenomena in maize associated with controlling elements and paramutation at the R locus result from abnormal functioning of genetic components which are normally concerned with general chromosomal functions, and do not reflect the operation of displaced locus-specific regulators of gene action. In support of this interpretation Brink and coworkers have demonstrated interactions in the coupling phase between paramutation at the R locus and two structural alterations located on the long arm of chromosome 10 distant from the R locus. Insertion of a paramutable R allele into a chromosome bearing the distinctive terminal, heterochromatic K10 segment reduces sensitivity of the allele to paramutation in heterozygotes with Rst (stippled), and the reduction persists, in part, when R is returned by crossing over to a structurally normal chromosome 10. K10 retards but does not block paramutation, and this effect is duplicated by insertion of R into a reciprocally translocated chromosome (T2-10a) with the breakpoint at least 10 map units from the R locus (Brink 1961; Brink and Blackwood 1961; Brink and Notani 1961; Brink 1969).

These interactions favor the view that the metastable genetic repression which characterizes paramutation results from the action at the R locus, not of a gene-specific physiological regulator, but rather of a non-specific displaced fragment of a system normally concerned with more general chromosomal processes.

A similar type of interaction is reported in the present article between the

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K10 segment and transposition of the non-specific repressor element Modulator (Mp) away from the R locus.

MATERIALS AND METHODS

Abnormal chromosome K10: The morphology and properties of the K10 chromosome have been documented by Rhoades (1942, 1952, 1968), EmmelIing (1958), Kikudome (1959), Longley (1945) and Rhoades and Dempsey (1966), and have been summarized briefly by Brink (1969). Relevant to this report are the facts that the K10 segment is at least 35 map units distal to the R locus, that it is known to incite neocentric activity and preferential segregation of heterochromatic knobs on other chromosomes and also to influence closeness of pairing and frequency of crossing over in structural heterozygotes. The abnormal meiotic behaviour of K10 results in its recovery in an average of about 70% of kernels on plants heterozygous for the segment. The interaction with paramutation, a process which occurs in somatic cells, indicates that K10 is also physiologically active during plant development.

The transposable element Modulator, (Mp): Brink and Nilan (1952) found that the variegated pericarp (P<sup>rr</sup>) allele in maize involves association at the P locus of the P<sup>rr</sup> allele, a gene for colored pericarp and cob, with a repressor element, which they termed Modulator. Sectors of red pigmentation on otherwise colorless ears are caused by transposition of Mp away from the P locus, thus permitting expression of the P<sup>rr</sup> gene. Modulator is homologous with McClintock's Activator (Ac) (Barclay and Brink 1954).

Modulator in heterozygous state has no overt effects on plant growth (Brink and Wood 1958), and no major effect on crossing over in adjacent regions (Fradin and Brink 1956). The element may be transposed away from the P locus at any stage of sporophyte or kernel development, giving a wide range of sector sizes and germinal mutation frequencies. Transpositions occur most frequently, however, at late stages of plant development. Transpositions are delayed by increasing dosages of Mp in the genome (Brink and Nilan 1952; Brink 1954), and under certain conditions may be decreased in frequency by a reduction in plant vigor (van SchaiK 1955).

Mp transposes to many other sites in the genome; but in about ⅔ of the cases, the new site is linked to P. Furthermore, the closer the new site to P, the more likely it is to receive the transposed Mp (van SchaiK and Brink 1959). The frequency of secondary transpositions from these new sites varies widely from case to case. The variegated pericarp (P<sup>rr</sup>Mp) association can be reconstituted by transposition of Mp back to the P locus. New variegation patterns are frequently produced, indicating different relationships of Mp with the locus (Orton and Brink 1966). Frequency of reconstitution of the variegated pericarp allele is a function of the proximity of the P locus to the site of transposed Mp (Orton 1966).

When Mp is transposed to the locus of another known gene (e.g., R or Wx), it conditions a typical, repressed mutable locus of the P<sup>rr</sup>Mp type. Occasionally it becomes effectively fixed at the locus, where it continues to repress gene action but no longer transposes (Brink 1958).

Transposition occurs during a replication cycle, Mp being transposed from one half of a duplicated P<sup>rr</sup>Mp complex to an unduplicated segment of the genome in about ⅔ of cases where it is then reduplicated in the same mitotic cycle (Greenblatt and Brink 1962, 1953; Greenblatt 1966, 1968). Greenblatt (1968) has discussed possible transposition mechanisms, but in the absence of a detailed knowledge of chromosome organization the nature of the phenomenon and the constitution of Mp itself remain obscure. Currently it is suggested that Mp is a small, misplaced segment of the regional parachromatin system (Brink 1960) which has been inserted close to, or within, an otherwise normal gene locus, and has imposed upon the normal "regulator" a state of "super repression" (Fincham and Harrison 1967) from which sporadic escape occurs by loss of Mp from the region. These concepts will be further considered in the discussion.

Stocks and symbols: The strains used in the present experiments carried the residual genotype of the uniform inbred W23 or its hybrids with W22, a second uniform inbred dent corn line.
Mutable Navajo \((mR^{n1})\), isolated by I. M. Greenblatt in stocks carrying variegated pericarp \((Pr^{mp})\) on a reciprocally translocated chromosome, T1-10g, is a bipartite mutable allele consisting of \(Mp\) inserted at the \(R\) (anthocyanin) locus on chromosome 10 (Brink unpublished). That is, \(mR^{n1} = R^{n1}M^{p}\). Navajo \((R^{n1})\) conditions anthocyanin formation in the aleurone layer of the kernel crown, the embryo, and also certain sporophytic tissues including silks and anthers. The combination \(R^{n1}M^{p}\) is non-pigmenting. Kernels carrying \(R^{n1}M^{p}\), however, normally show a spotting pattern on the crown caused by mutations of \(mR^{n1}\) to \(R^{n1}\) at late stages of endosperm development. Whole kernel \(R^{n1}\) mutants carrying germinal \(R^{n1}\) on an \(mR^{n1}\) ear parent, result from transpositions of \(Mp\) during sporophyte development up to meiosis or in the functional megaspore. They may result also from transposition in the embryo sac nucleus destined to form the egg and a polar nucleus. \(R^{n1}\) kernels carrying germinal \(mR^{n1}\) (and vice versa) are formed by transposition of \(Mp\) during certain other stages of embryo sac development. Transpositions in the descendants of the triple fusion nucleus give rise to spotted endosperms only. A transposition occurring in the ear shoot before the formation of floral primordia gives rise to a somatic sector of \(R^{n1}\) kernels derived from a single mutational event. The earlier the mutation, the larger the \(R^{n1}\) sector. Transpositions between formation of floral primordia and early embryo sac development produce whole isolated \(R^{n1}\) kernels.

The alleles \(R^{sc}\), \(R^{sC}\), and \(P^{<}\), conditioning full aleurone color in one, two, or three doses, were used as markers in coupling with the K10 segment. The stable recessive allele \(r^{e}\) conditions absence of anthocyanin pigmentation. “K10” stands for a chromosome 10 bearing the distinctive K10 segment distal to \(Ron\) the long arm. “N10” stands for a normal chromosome 10.

**Crossing procedures:** Two separate experiments were performed to test the effect of the K10 segment on transposition of \(Mp\) from \(mR^{n1}\):

(A) The effect of K10 in repulsion as compared with absence of K10 from the genome. Crosses were carried out as shown in Figure 1.

(B) The effect of K10 in coupling as compared with absence of K10 from the genome. Crosses were carried out as shown in Figure 2. Six independently occurring crossovers of \(mR^{n1}\) into the K10 chromosome were identified using the mating system shown in Figure 2. For each crossover ear found with distinctly more than 50% spotted kernels \((mR^{n1}K10/r^{e}N10)\), a non-crossover sib ear with a normal distribution of spotted kernels \((mR^{n1}N10/r^{e}N10)\) was selected at random for subsequent use as a control.

**Collection and processing of data:** Data collected from test and control ears in the above experiments consisted of (a) the number of \(R^{n1}\) kernels (mutant selections), (b) the number and sizes of somatic sectors of 2 or more \(R^{n1}\) mutant kernels, and (c) the number of \(mR^{n1}\) kernels. Only healthy, well-filled ears were used.

The percent of \(R^{n1}\) kernels (relative to the total \(R^{n1} + mR^{n1}\) kernels) is a combined measure of both the mutation rate and the time at which mutation occurs (i.e., sector size). Complete separation of these components was not feasible for several reasons: (a) It was not possible to identify the mutations according to the particular cell generation in which they occurred. (b) In the ears from the heterozygous plants used \((mR^{n1}/r^{e})\), large somatic sectors tended to be broken up by meiotic segregation into more than one apparent mutant patch. This phenomenon gives the effect of an apparent increase in mutation rate. (c) Chance associations of single kernel mutants give apparent sectors which influence the apparent timing of mutation events. With the above difficulties in mind, a partial separation of the rate and timing components was attempted.

A measure of the mutation rate was sought by calculating the percentage of single kernel events, representing transpositions in the limited number of cell generations from the formation of floral primordia to early embryo sac development:

\[
\text{Percent single events} = \frac{\text{isolated single kernel events}}{mR^{n1} + \text{total events}}
\]

The denominator represents a total number of kernels corrected approximately for the fact that kernels which are already part of a somatic sector are no longer available for mutation.
Ears with distorted segregation. >50% purple kernels.

TESTS

CONTROLS

FIGURE 1.—Crosses used in the test of K10 in repulsion (A).

Measures of timing were sought in the mean sector size ($R^{n1}$/events), the ratio of single kernel to multiple kernel events, and the frequency of ears carrying sectors larger than 2 kernels. (Chance associations of 3 or more single kernel mutation events would be expected to be extremely rare.)

Statistical procedures utilized were: weighted t-test for samples of unequal size (Steel and Torrie 1960, p. 74); standard analysis of variance with subsampling (Steel and Torrie 1960, p. 142); analysis of variance adjusted for unequal sub-class numbers by weighting of means (Snedecor and Cochran 1967, p. 483); Mann-Whitney-Wilcoxon non-parametric test (Steel and Torrie 1960, p. 405). For all analyses ears were assumed to be equal in size. Data consisting of small percentages were transformed to $\sqrt{x + \frac{1}{2}}$ before analysis by the t-test or analysis of variance.

RESULTS

A. The effect of K10 in repulsion: The median frequencies of $R^{n1}$ kernels (mutant selections) for test and control ears are shown in section (A) of Table 1. The populations of ears were somewhat more variable with respect to $mR^{n1}$ to
Ears with distorted segregation. >50% purple kernels.

Non-crossovers

\[
\begin{array}{cccc}
\text{mr}^{nj} N_{10} & \text{RK10} & \text{rr}^{g} N_{10} \\
\text{spotted} & \text{purple} & \\
\end{array}
\]

Crossovers

\[
\begin{array}{cccc}
\text{RN10} & \text{mr}^{nj} K_{10} \\
\text{rr}^{g} N_{10} & \text{rr}^{g} N_{10} \\
\text{purple} & \text{spotted} \\
\end{array}
\]

Identification of crossovers

\[
\begin{array}{cccc}
\text{♀♀} & \times (\text{W23}) & \frac{\text{rr}^{g} N_{10}}{\text{rr}^{g} N_{10}} & \text{♂♂} \\
\end{array}
\]

Preparation of crossover and non-crossover families by reciprocal crosses

\[
\begin{array}{cccc}
\text{♀♀} & \times (\text{W23}) & \frac{\text{rr}^{g} N_{10}}{\text{rr}^{g} N_{10}} & \text{♀♀} \\
\text{♂♂} & \\
\end{array}
\]

Ears with normal segregation of \(\text{mr}^{nj} N_{10}/\text{rr}^{g}\)  

Ears with distorted segregation of \(\text{mr}^{nj} K_{10}/\text{rr}^{g}\)

**CONTROLS**  

**TESTS**

\(R^{nj}\) mutations than those of experiment (B) below, but no consistent effects of K10 on the mutability of \(mr^{nj}\) in the repulsion phase were detected.

**B. The effect of K10 in coupling:** The median frequencies of \(R^{nj}\) kernels for
TABLE 1

The frequency of mutant Rnj kernels on ears carrying mRnj

<table>
<thead>
<tr>
<th>Experiment</th>
<th>Linkage and derivation of mRnj</th>
<th>Number of ears</th>
<th>Median(^2) percent of Rnj kernels</th>
</tr>
</thead>
<tbody>
<tr>
<td>(A)</td>
<td>(mRnjN10) RK10 tests</td>
<td>56</td>
<td>3.81 ns(^3)</td>
</tr>
<tr>
<td></td>
<td>(mRnjN10) controls</td>
<td>97</td>
<td>2.60</td>
</tr>
<tr>
<td>(B)</td>
<td>(\delta) (mRnjK10) tests</td>
<td>56</td>
<td>7.98</td>
</tr>
<tr>
<td></td>
<td>(\delta) (mRnjN10) controls</td>
<td>86</td>
<td>5.53 ***</td>
</tr>
<tr>
<td></td>
<td>(\varphi) (mRnjK10) tests</td>
<td>110</td>
<td>5.97 ***</td>
</tr>
<tr>
<td></td>
<td>(\varphi) (mRnjN10) controls</td>
<td>166</td>
<td>4.81</td>
</tr>
</tbody>
</table>

\(^1\) In experiment (B) comparable sets of data were obtained by reciprocal crosses with mRnj derived through the male or female gamete.
\(^2\) The median is a better estimate of mutability than the mean, which is strongly affected by the rare occurrence of large somatic sectors. The indicated differences between populations were actually tested using means of transformed data which are not shown here.
\(^3\) Not significant (P ~ 0.5) Mann-Whitney-Wilcoxon non-parametric test of original data, and weighted t-test of data transformed to \(x + \frac{1}{2}\).

Highly significant enhancements of mutability by coupling with K10, and also by derivation of mRnj through the male side of crosses, are indicated by both parametric and non-parametric tests.

Similar enhancements of mutability in the cell generations between initiation of floral primordia and early embryo sac development are shown in Table 2 and Figure 4.

TABLE 2

The frequency of whole single kernel mutations on ears carrying mRnj in coupling with K10 and on mRnj control ears which lack K10

<table>
<thead>
<tr>
<th>Linkage and derivation of mRnj</th>
<th>Number of ears</th>
<th>Mean percent single events relative to &quot;total mutable kernels&quot;(^2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(\delta) (mRnjK10) tests</td>
<td>56</td>
<td>5.24 ***</td>
</tr>
<tr>
<td>(\delta) (mRnjN10) controls</td>
<td>86</td>
<td>4.78 ***</td>
</tr>
<tr>
<td>(\varphi) (mRnjK10) tests</td>
<td>110</td>
<td>4.48 ***</td>
</tr>
<tr>
<td>(\varphi) (mRnjN10) controls</td>
<td>166</td>
<td>4.02 **</td>
</tr>
</tbody>
</table>

\(^1\) Correction of the total number of kernels as explained under MATERIALS AND METHODS.
\(^2\) Highly significant (P < 0.01) data transformed to \(\sqrt{x + \frac{1}{2}}\) before analysis of variance by weighted means.
Sector size was found to be increased by coupling with K10, using a non-parametric test, but in this case no significant effect of the direction of the cross was detected (Table 3 and Figure 5).

Frequencies of ears with sectors larger than two kernels are shown in Table 4. Coupling with K10 very significantly increases the occurrence of larger sectors, and a smaller but significant increase is caused by passing \( mR^{n} \) through the male side of crosses.

That the enhancement of single kernel and multiple kernel mutational events by coupling with K10 does not merely reflect a constant increase in the probability of \( Mp \) transposition from the \( R \) locus in any given cell generation is indicated by the comparisons shown in Table 5. As compared with the controls which lack K10 in the genome, K10 in coupling gives an approximately 50 percent increase in the ratio of large multiple kernel events to single kernel events, suggesting a greater effect in the earlier somatic cell generations during ear shoot development. A similar but much smaller (10%) effect of the direction of the cross also
Figure 4.—Frequency distributions of individual ears with respect to percent of single kernel \( R^{ij} \) mutational events. (a) Test ears. \( mR^{ij}K10 \ \delta^{-} \)-derived. (b) Control ears. \( mR^{ij}N10 \ \delta^{-} \)-derived. (c) Test ears. \( mR^{ij}K10 \ \Omega^{-} \)-derived. (d) Control ears. \( mR^{ij}N10 \ \Omega^{-} \)-derived.

Table 3

<table>
<thead>
<tr>
<th>Linkage and formation of ( mR^{ij} )</th>
<th>Number of ears</th>
<th>Median sector size 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \delta ) ( mR^{ij}K10 ) tests</td>
<td>56</td>
<td>1.22 ( **2 )</td>
</tr>
<tr>
<td>( \delta ) ( mR^{ij}N10 ) controls</td>
<td>86</td>
<td>1.11 ( 2 )</td>
</tr>
<tr>
<td>( \Omega ) ( mR^{ij}K10 ) tests</td>
<td>110</td>
<td>1.20 ( **2 )</td>
</tr>
<tr>
<td>( \Omega ) ( mR^{ij}N10 ) controls</td>
<td>166</td>
<td>1.06 ( 2 )</td>
</tr>
</tbody>
</table>

1 The mean sector size was calculated for each individual ear. The medians of the four mean sector size distributions are presented in the table in preference to the distribution means because the means are strongly affected by the infrequent occurrence of ears with large somatic sectors.

2 Highly significant \( (P < 0.01) \) Mann-Whitney-Wilcoxon non-parametric test.

3 Not significant \( (P = 0.4) \) Mann-Whitney-Wilcoxon test.

4 Not significant \( (P = 0.2) \) Mann-Whitney-Wilcoxon test.
Mean Number of Kernels per Event

**FIGURE 5.**—Frequency distributions of individual ears with respect to mean number of $R^{n_j}$ kernels per mutational event (mean sector size). (a) Test ears, $mR^{n_j}K10$ $\delta$-derived. (b) Control ears, $mR^{n_j}N10$ $\delta$-derived. (c) Test ears, $mR^{n_j}K10 \varphi$-derived. (d) Control ears, $mR^{n_j}N10 \varphi$-derived.

**TABLE 4**

*Frequencies of individuals with sectors larger than 2 kernels among ears carrying $mR^{n_j}$ in coupling with K10 and among control $mR^{n_j}$ ears which lack K10*

<table>
<thead>
<tr>
<th>Linkage and derivation of $mR^{n_j}$</th>
<th>Number of ears</th>
<th>Mean percent ears carrying sectors larger than 2 kernels</th>
</tr>
</thead>
<tbody>
<tr>
<td>($\delta$) $mR^{n_j}K10$ tests</td>
<td>56</td>
<td>59</td>
</tr>
<tr>
<td>($\delta$) $mR^{n_j}N10$ controls</td>
<td>86</td>
<td>23</td>
</tr>
<tr>
<td>($\varphi$) $mR^{n_j}K10$ tests</td>
<td>110</td>
<td>37</td>
</tr>
<tr>
<td>($\varphi$) $mR^{n_j}N10$ controls</td>
<td>166</td>
<td>17</td>
</tr>
</tbody>
</table>

1 Highly significant ($P < 0.01$) analysis of variance.
2 Significant ($0.01 < P < 0.025$) analysis of variance.
TABLE 5

Ratios of multiple kernel to single kernel mutations on ears carrying mRnj coupled with K10 and on mRnj control ears which lack K10

<table>
<thead>
<tr>
<th>Linkage and derivation of mRnj</th>
<th>Number of ears</th>
<th>Mean percent multiple events</th>
<th>Mean percent single events</th>
</tr>
</thead>
<tbody>
<tr>
<td>(♂) mRnj K10 tests</td>
<td>56</td>
<td>0.054</td>
<td></td>
</tr>
<tr>
<td>(♂) mRnj N10 controls</td>
<td>86</td>
<td>0.037</td>
<td></td>
</tr>
<tr>
<td>(♀) mRnj K10 tests</td>
<td>110</td>
<td>0.044</td>
<td>46% increase</td>
</tr>
<tr>
<td>(♀) mRnj N10 control</td>
<td>166</td>
<td>0.029</td>
<td>52% increase</td>
</tr>
</tbody>
</table>

1 Multiple events involving sectors larger than two kernels.

is indicated by comparison of lines 1 and 3, and lines 2 and 4 in the body of Table 5.

DISCUSSION

The data show that transposition of Modulator from the R locus is enhanced by coupling with the K10 segment situated at a distance equivalent to at least 35 map units from R. There is no detectable interaction of mRnj and K10 in the repulsion phase. Although a complete separation of rate and timing components of the mutational data has not been made, the K10 effect appears to be relatively greater in the earlier somatic cell generations during ear development. This coupling phase interaction of K10 with a genetic instability phenomenon in somatic cells is consistent with the interpretation of Brink (1969) that the coupling phase effect of K10 on R paramutation is also a process related primarily to somatic tissues.

Sensitivity of Mj transposition to residual genotypic and physiological influences is indicated by the differences in overall mean frequencies of mutant kernels obtained from the two sequences of crosses in the absence of K10. Compare the controls for section A in Table 1 (2.60%) with the controls for section B (5.53% and 4.81%).

An unexpected finding was a small differential effect of direction of the cross on frequency of mutant kernels on ears produced by the resulting F1 plants (K10 present, or absent). Mutants were consistently somewhat more numerous on the ears of F1 plants which had received mRnj from a pollen parent. It appears, therefore, that either there is an interaction between Mj transposition and the cytoplasm, or the passage of mRnj through a male gametophyte predisposes the complex to enhanced mutation in the late developmental phase of the succeeding sporophyte generation. A long term sexual transmission effect of the latter type would indicate a persistent, self-replicating modification of gene action. It is theoretically feasible that in the absence of relevant physiological signals such a state might persist from its induction until the next period of major genetic reorganization, in this case the meiosis terminating the succeeding sporophyte...
MAIZE CYTOGENETICS

A sexual transmission effect on pigmentation by the standard $R^r$ allele in the triploid endosperm immediately following double fertilization has been established by Kermicle (1970).

The results reported here for transposition of $Mp$ from the $R$ locus, together with previous work in this laboratory on the instability phenomena of $Mp$ at the $P$ locus, and also paramutation at the $R$ locus, have led to a point of view summarized in the paragraphs following.

The chromosomes of eukaryotes are complex organelles with three major levels of function. These are: (a) the replication and transcription of genetic information; (b) the precise regulation of transcription at each individual locus at its assigned stage in ontogeny; and (c) the regulation of general chromosomal processes such as coiling and condensation, centric activity and divisional movements, meiotic pairing, positioning in relation to the nuclear envelope, and so forth.

The purely cytological terms "euchromatin" and "heterochromatin" have proved to be insufficient and ambiguous whenever attempts have been made to identify the above processes with chromosomal components. For example, although transposable elements share certain properties with phenomena known to be associated with visible heterochromatin, cytological evidence for heterochromatin at loci controlled by transposable elements is not at hand. Brink (1960) has proposed a functional terminology by means of which these ambiguities may be avoided while awaiting the allocation of functions to precise molecular structures. It was suggested that the chromosome consists of two basic functional components: orthochromatin, which comprises the structural genes, and is constant; and parachromatin, regulatory components that vary in response to ontogenetic signals. Parachromatin can be further subdivided into two categories: First, locus-specific parachromatin, which responds in each particular case only to the specific activation signal for the gene with which it is conjoined, and collectively represents the regulators of ontogenetical gene action; and secondly, regional parachromatin which forms a pervasive system of elements throughout the genome, controls general chromosomal processes, and is non-specific in its action upon individual genes.

All known instances of instability in flowering plants together with V-type position effects (Lewis 1950) and X-chromosome inactivation (Lyon 1968) can be interpreted in terms of the normal or abnormal action of regional parachromatin. For example, the non-specific repression by controlling elements and the spreading effect of this action along the chromosomes to adjacent genes in certain cases suggest that these elements belong to the category of regional parachromatin rather than to locus specific parachromatin. They may, in fact, be displaced fragments of the regional parachromatin system.

If there exists a chromosomal component such as regional parachromatin, distributed throughout the genome, but concerned with only a few general chromosomal processes such as condensation, pairing, etc., we might expect it to consist of a small number of different components each repeated many times. The rap-
idly reassociating fraction of eukaryote DNA first reported by BRITTEN and KOHNE (1968) is an obvious candidate. Support for the dispersion of such repetitive sequences through the bulk of the DNA comes from the work of THOMAS et al. (1970).

The central problem in the resolution of data from unstable loci in flowering plants may be the distinction between effects of regional parachromatin governing general chromosomal processes, which may be subject to fragmentation and transposition, and locus-specific parachromatin, which is concerned with the controlled ontogenetical expression of individual genes (BRINK 1969).

The insufficiency of the cytological term heterochromatin was also recognized by SCHMID (1967). He divided heterochromatin into constitutive heterochromatin including all segments of the genome which were permanently heterochromatic in all cells of the life cycle, and facultative heterochromatin which represented inactivated and condensed segments of the euchromatin. The centric heterochromatin of many organisms such as Drosophila belongs to the constitutive category, and “Lyonised” mammalian X chromosomes to the facultative category. There is evidence that the formation of facultative heterochromatin by condensation may be an effect of prior gene inactivation (LYON 1968) rather than the cause of genetic repression. SCHMID’S subdivisions of heterochromatin are still basically cytological, and do not correspond to BRINK’S functional subdivisions. For example, the formation of SCHMID’S facultative heterochromatin represents the action of BRINK’S regional parachromatin system on the orthochromatin which it pervades.

A useful and generally applicable model for unstable loci was proposed by FINCHAM and HARRISON (1967) to account for mutability of the pal<sup>Cre</sup> allele in Antirrhinum majus. In this system it is postulated that the structural gene has an accessory component which regulates its normal expression (corresponding to an element of BRINK’S locus-specific parachromatin). The mutable allele in its unmutated condition shows no activity because the regulator has lost its ability to respond to the physiological trigger which would normally activate the gene. This super-repressed state is self-replicating, as are the normally repressed and switched-on states. Mutations represent sporadic escapes from the super-repressed condition (which do not always lead, however, to a fully functional normal allele). If the gene escapes from super-repression in a cell where it would not normally be expressed it remains in the normally repressed condition, so that the resultant sector is not immediately visible.

Even with the present limited knowledge of chromosomal organization it is possible to visualize several mechanisms by which a gene regulator might be prevented from responding to its normal physiological trigger in such a way that the state is self-replicating but escape is possible: (a) adjacent foreign heterochromatin ( locus specific, or regional, parachromatin), e.g., transposable element phenomena (McCLINTOCK 1956); V-type position effects (LEWIS 1950); (b) adjacent foreign euchromatin (orthochromatin), e.g., simple position effects (SVURTEVANT 1925); (c) over-replication or structural modification of a nearby segment unrelated to the gene, e.g., paramutation (BRINK 1960); (d) duplication
or structural modification of the regular component at a locus; (e) duplication of the entire gene region.

Thus a number of similar but not necessarily homogeneous instability phenomena might be related through this concept of self-replicating super-repression of a normal regulator component.

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LITERATURE CITED


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