Studies of Dotted, a Regulatory Element in Maize III. Transpositions of Dotted and Its Stability at Various Locations *

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<u>Summary</u>. Dotted (<u>Dt</u>) is the regulatory element of a two-unit controlling system in maize. <u>Dt</u> causes the inherited change from the recessive <u>a</u> (colorless) to its dominant allele, <u>A</u> (anthocyanin production), during the development of the stalk, leaves, and endosperm. The mutation events are observed as sectors of color in an anthocyaninless background.

Since its discovery over 40 years ago, <u>Dt</u> has always been found in the terminal knob of the short arm of chromosome 9. This is puzzling because controlling and regulatory elements in general are not located permanently, but change positions (transpose) within the chromosomal complement. To resolve this seeming discrepancy, transpositions were looked for in a homozygous <u>a Dt</u> stock. Because the frequency of aleurone mutations is exponentially related to <u>Dt</u> dosage, a <u>Dt</u> transposition would result in a greatly increased number of dots if the egg or sperm nucleus contained both the transposed <u>Dt</u> and the <u>Dt</u> remaining on chromosome 9. A total of 6 transposed <u>Dt</u>'s (<u>Dt-T</u>) were recovered in this manner.

<u>Dt-TA</u> was found linked to the gene \underline{Y} ("yellow endosperm") of chromosome 6. <u>Dt-TB</u> no longer showed linkage with <u>yg2</u> of chromosome 9, but remains unlocated (the original <u>Dt</u> in this stock is separated from <u>yg2</u> by 6 or 7 cross-over units.). The remaining transpositions (C-F) assorted independently of <u>Dt</u> on chromosome 9.

The transposed <u>Dt</u>'s had the same effect as <u>Dt</u> on the frequency and timing of aleurone mutations. An increase in transposition frequency and losses of <u>Dt-T</u>'s was characteristic of several of the transposed <u>Dt</u>'s. <u>Dt-T</u>'s B-F transposed so frequently that testcross ratios of 7:1 (three <u>Dt</u>'s) and 15:1 (four <u>Dt</u>'s) were observed. No secondary transpositions or losses of Dt-TA were detected. Thus, <u>Dt-TA</u> resembles the original Dt with regard to its transposition frequency and stability.

Introduction

Controlling-regulatory elements in maize have been the subject of intense study in several laboratories for more than 20 years (see Fincham and Sastry 1974, for a recent review). These elements regulate the expression of genes that are directly responsible for a particular phenotype. In some systems, an elementat the gene site effectively changes the expression of the gene (autonomous control). Other systems consist of two elements, one at the gene site and a second at another location (nonautonomous control). In the latter instance, gene activity is initiated by action of the independently located element on the gene-associated element. (According to Peterson's 1970a nomenclature, the gene-associated element is called a controlling element, whereas the independently located entity is a regulatory element. This practice will be used here for clarity.) Several significant features of these systems

have emerged: 1) Changes of the controlled gene usually are from the inactive recessive to the fully active dominant. With autonomous control, the regulatory-controlling element complex leaves the gene site; in the nonautonomous type, the controlling element alone need move away to allow gene expression. 2) These changes normally are stable and are inherited as such in subsequent cell and plant generations. 3) Controlling and regulatory element in general are not located permanently but change positions within the chromosomal complement. 4) As a consequence of this behavior, many genes (probably all) are susceptible to the control of the element(s) of a particular system.

The present study is concerned with the nonautonomous"Dotted"(\underline{Dt}) system, the first in which the control of one gene by another was demonstrated (Rhoades 1938). Subsequently, more detailed analysis of other systems have introduced unsuspected complexities and have indicated that differences in behavior of the various systems are common. Typically \underline{Dt} causes heritable changes of the <u>a</u> gene (colorless aleurone) to its active allele, <u>A</u>

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(purple aleurone), producing a dotted effect on the kernel. The <u>A</u> locus is on chromosme 3 and, when in combination with the controlling element of this system, usually is noted as <u>a-dt</u>. The regulatory element, Dt, however, since its discovery in the 1930's (Rhoades 1936), always has been found in the terminal knob of the short arm of chromosome 9. This suggests a possible difference between <u>Dt</u> and other regulatory elements in maize (e.g., Ac, Activator; Spm, Supressor-Mutator; Md, Modulator; En, Enhancer); i.e., that <u>Dt</u> does not transpose, but remains fixed in position. According to Rhoades (1945) the location of Dt is seven crossover units distal to the yg2 ("yellow green") locus, which resides in the ultimate chromomere. The major goals of this investigation were to determine: 1) if <u>Dt</u> is stationary or moves from one chromosomal location to another and 2) whether such movements, if they occur, affect the stability or modify the activity of <u>Dt</u>.

Materials and Methods

Detection and analysis of <u>Dt</u> transpositions

The investigation of transpositions of <u>Dt</u> ("<u>Dotted</u>") was suggested by Dr. Marcus M. Rhoades, who supplied the <u>aaDtDt</u> stock used in this study (Fig.1). The <u>A</u> gene is concerned with anthocyanin formation and is located on chromosome 3. The standard recessive allele <u>a</u>, which normally prevents anthocyanin coloration, responds to <u>Dt</u> on chromosome 9 to form purple <u>A</u> sectors on a colorless background (Rhoades 1938). Because of absence of complementary plant color factors in the stock supplied for these tests, the <u>aDt</u> phenotype was expressed only in the aleurone layers of the kernels. Kernels with exceptionally high numbers of dots, believed to possess a transposed <u>Dt</u> in addition to the standard <u>Dt</u>, were selected for analysis.

Two criteria were used as evidence of transpositions of \underline{Dt} from its usual location on chromosome 9: 1) a segregation of 3 dotted: 1 dotless kernels in a backcross, or 15 dotted: 1 dotless in an F_2 population the expected ratios for the independent segregation of duplicate factors; and 2) loss of linkage between <u>Dt</u> and yg2 ("yellow green") loci which are normally separated by 7 recombinational units (Rhoades 1945). Plants suspected of having a transposed \underline{Dt} were crossed to an Aa-m, dt Yg2 dt yg2 stock (obtained from Dr. Gerald Neuffer, University of Missouri) and either self-pollinated or testcrossed to $\underline{a-m} \underline{a-m}$, dt yg2 dt yg2 plants. The <u>a-m</u> allele mutates 406 times as frequently as does a (Nuffer 1961) and greatly facilitated the classification of dotted and dotless kernels in these crosses. The dotted-green progeny (Dt Ig2) from testcrossed and self-pollinated ears were grown and testcrossed again to obtain offspring segregating for only the transposed Dt or for Dt on chromosome 9. Chi-square analysis of the factor segregations and for linkage was carried out according to standard methods (see Mather 1951).

The transposed <u>Dt</u>'s were labelled <u>Dt-TA</u>, <u>Dt-TB</u>, etc., in order of their isolation. Previously described "Dotted" loci have been designated <u>Dt</u> (chromosome9), <u>Dt2</u> (chromosome 6), and <u>Dt3</u> (chromosome 7) (Nuffer 1955).

Results

Detection of <u>Dt</u> transpositions

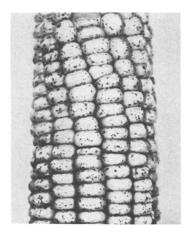
A search was made for transpositions of <u>Dt</u> in a homozygous <u>a Dt</u> stock that had been maintained for several generations by self-pollinating or sib-crossing. The mutation frequency of the <u>a</u> gene was uniformly high in this stock (Fig.1). Because the frequency of aleurone mutations is exponentially related to <u>Dt</u> dosage (Rhoades 1938, 1941), a <u>Dt</u> transposition would result in a greatly increased number of dots if the egg or sperm nucleus contained both the transposed <u>Dt</u> and the <u>Dt</u> remaining on chromosome 9. The endosperm of maize kernels is triploid; thus, the normal <u>Dt</u> dosage of 3 could be increased to 4 if transposition took place in the pollen parent, or to 5 if it occurred in the egg parent (Fig.2).

1255 <u>aaDtDt</u> plants were self-pollinated and the progeny ears were examined. Several kernels had significantly greater mutation rates of the <u>a</u> gene than did the rest of the kernels (Fig.3). Individuals in a stock established from these exceptional kernels were crossed as pollen parent (P₁) to <u>A a-m</u> dt Yg2 dt yg2 plants. The F₁'s, <u>a-m a</u> and heterozygous for whatever <u>Dt</u>'s might be present, were testcrossed (as egg parent) by a homozygous <u>a-m</u> dt yg2 stock or self-pollinated.

Such tests of original high dot isolate A revealed two ears segregating two <u>Dt</u>'s, whereas 40 ears segregated one (Table 1). Similarly, only six ears of a total of 67 segregated two <u>Dt</u>'s in backcrosses or selfpollinations involving isolate B. The χ^2 values (Table 2) are consistent with the hypothesis that two unlinked <u>Dt</u>'s were segregating. The deviations of B-53 and B-60 from a 15:1 ratio do not detract from the conclusion because ears clearly are segregating <u>Dt</u> at more than one location.

Original isolates A and B most likely represent transpositions of the <u>Dt</u> gene from its mapped position on chromosome 9 to an unlinked site. The transposed <u>Dt</u> genes will be referred to as <u>Dt-TA</u> and <u>Dt-TB</u>.

The small number of ears in Table 1 with segregations of both <u>Dt</u> and <u>Dt-TA</u> or <u>Dt-TB</u> is puzzling. Half of the F_1 plants should have segregated two <u>Dt</u>'s if <u>Dt-T</u> were heterozygous (and <u>Dt</u> homozygous) in the dotted P_1 , and all should have segregated two <u>Dt</u>'s if



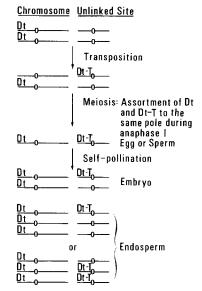


Fig.1. A self-pollinated ear of the <u>aaDtDt</u> stock used to isolate transpositions and losses of \underline{Dt}

Fig.2. Method by which \underline{Dt} dosage is increased in \underline{aaDtDt} plants after its transposition from chromosome 9 to an unlinked site

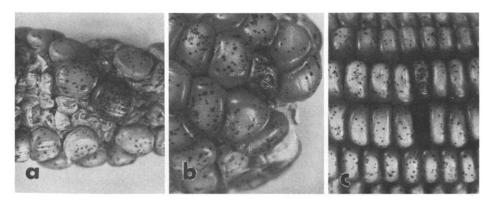


Fig.3. Single highly dotted kernels shown on the parent ears. Subsequent crosses demonstrated that the increased dotting frequencies were due to transpositions of \underline{Dt} to other locations. a) \underline{Dt} -TE, b) \underline{Dt} -TE, c) \underline{Dt} -TF

the P_1 plants were <u>DtDt</u>, <u>Dt-TDt-T</u>. The gene <u>yg2</u> ("yellow green"), closely linked to Dt, segregated in 55 of the 101 plants that segregated only one <u>Dt</u>. In all these, there was close linkage between the two genes. Therefore, the dotted P_1 plants were homozygous <u>Dt</u>. The unexpected low recovery of the transposed <u>Dt</u>'s could have been due to unequal transmission of the <u>Dt-T</u>-bearing chromosome and its homologue in the pollen parent (P_1) or to instability of the <u>Dt-T</u> gene itself. These alternatives cannot be distinguished without closely linked markers.

Analysis of <u>Dt-TA</u>

Linkage of $\underline{Dt-TA}$ with \underline{Y} ("yellow endosperm") on chromosome 6 was suggested by the nonrandom association of <u>Dt</u> and <u>Y</u> phenotypes on a 3 <u>Dt</u>:1 <u>dt</u> testcross ear (Table 1). The relationship was unclear, however, because of the presence of the independently segregating <u>Dt</u>. Dotted (<u>Dt</u>) kernels with yellow endosperm (Y) were selected, and the resulting plants were crossed again to an a dt yg2y tester to obtain progeny lacking <u>Dt</u>.

Table 3, cross 1, shows the total numbers of progeny from 13 ears in which <u>Dt-TA</u> was linked to <u>Y</u> of chromosome 6 and showed no association with <u>Yg2</u> of chromosome 9. The linkage χ^2 values of <u>Dt-TA</u> and <u>Y</u> (Table 4) for each ear (not shown) and for total data (χ^2 total = 291.519) were highly significant. On the other hand, the χ^2 values testing linkage of <u>Dt-TA</u> and <u>Yg2</u> on the same ears were not significant, indicating inde-

Table 1. Summary of progeny from F_1 plants of $\frac{a}{a} \frac{Dt}{dt} \frac{Dt-T}{dt}$ constitution that were self-pollinated

or testcrossed (× a-m dt). Listed are the number of plants that segregated 1:1 (one \underline{Dt} segregating) and 3:1 (two \underline{Dt} 's segregating) for the testcrosses or 3:1 (one \underline{Dt} segregating) and 15:1 (two \underline{Dt} 's segregating) for the self pollinations

	Testcrosses	Self-pollinations
	$1:1(1\underline{Dt}) 3:1(2\underline{Dt})$	3:1 (1 <u>Dt</u>) 15:1 (2 <u>Dt</u>)
<u>Dt-TA</u> <u>Dt-TB</u>	22 1 22 3	18 1 39 3

Table 2. Analysis of ears deviating significantly from the expected ratios for the segregation of one \underline{Dt} : χ^2 test of the hypothesis that two independently segregating \underline{Dt} 's were present in some F_1 plants. Segregation of 2 \underline{Dt} 's at independent locations yields ratios of 3 \underline{Dt} : 1 dt in a testcross or 15 \underline{Dt} : 1 dt in an F_2 population

					χ^2 for a <u>Dt</u> :dt segregation of:					
Reference Number	Cross*	Dt	dt	Total	3:1 (2 <u>Dt</u> 's)	S	15:1 (2 <u>Dt</u> 's)	S		
Ta-1	t	331	127	458	1.820	n.s.		· · · · · · · · · · · ·		
TA-24	S	481	39	520			1.387	n.s.		
TB-5	t	267	98	365	0.666	n.s.				
TB-13	t	197	76	273	1.173	n.s.				
TB-25	t	354	121	475	0.057	n.s.				
TB-44	s	566	28	594			2.392	n.s.		
TB-53	s	405	40	445			5.697	P=.025010		
TB-60	S	484	16	500			7.938	P=.005001		

* t = testcross; s = self-pollination

Tested at the five per cent level of significance

pendent assortment of these two genes. The recombination data (Table 3) place <u>Dt-TA</u> in chromosome 6, about 39 recombination units from y.

Six sibling plants of those listed in Table 3, cross 1, are characterized by linkage of <u>Dt</u> with <u>Yg2</u> of chromosome 9 (cross 2). No association of <u>Dt</u> with <u>Y</u> of chromosome 6 was found. Highly significant linkage χ^2 's were obtained for joint segregation of <u>Dt</u> and <u>Yg2</u> (Table 4, number 2).

Thirty-five of a total of 50 plants in which \underline{Dt} - was segregating 1:1 showed linkage of \underline{Dt} and \underline{Y} . An excess of plants with \underline{Dt} -TA was expected because \underline{Y} kernels were selected for testing. The result is in contrast to the low recovery of \underline{Dt} -TA in the F_1 generation (Table 1). This discrepancy may have occurred, however, because \underline{Dt} -TA was introduced by the pollen parent, whereas plants giving rise to the progenies in Tables 3 and 4 were crossed as the egg parent. Competition of \underline{Dt} -TA and \underline{dt} -TA pollen grains due to a linked gametophyte factor could account for the low transmission of \underline{Dt} -TA in the pollen parent. Competition between megaspores does not occur.

Analysis of <u>Dt-TB</u>

The data of Table 3, cross 3 together with the linkage χ^2 values of Table 4, no. 3 show that <u>Dt-TB</u> was segregating independently of both <u>Yg2</u> in chromosome 9 and <u>Y</u> in chromosome 6. This clearly demonstrates the transposition of <u>Dt</u> from its position on chromosome 9 to some other location in the chromosomal complement. Unlike <u>Dt-TA</u>, however, <u>Dt-TB</u> was not linked to Y of chromosome 6.

Confirmation of <u>Dt</u> location on chromosome nine

Table 3, cross 4 and accompanying χ^2 Table 4, no. 4 record the joint segregation of <u>Dt</u> and <u>Yg</u> in sibling ears with no <u>Dt-TB</u>. The highly significant linkage χ^2 values reflect the tight linkage of <u>Dt</u> and <u>Yg2</u>. The combined data of Table 3 crosses 2 and 4, giving a total population of 6,468 plants, place <u>Dt</u> 6.0 crossover units from <u>Yg2</u>. This agrees well with the value of 7.1 found by Rhoades (1945).

Table 3. Analysis of <u>Dt-TA</u> and <u>Dt-TB</u>. Testcross data of $\frac{Dt}{dt} \frac{Yg2}{yg2} \frac{Y}{y}$ plants from progeny segregating two independent <u>Dt</u>'s. The total numbers of progeny are listed only for ears that segregated 1<u>Dt</u>:1dt. In these cases <u>a Dt</u> was linked with <u>Yg2</u> of chromosome 9, <u>Y</u> of chromosome 6, or assorted independently of either of these two genes. χ^2 analysis of the data is found in Table 4.

No.	Cross	No. ears	Dt Yg	Dt yg	dt <u>Yg</u>	dt yg	Total	Dt Y	<u>Dt</u> y	dt Y	dt y	Total
1.	$\frac{\text{Dt-TA Y}}{\text{dt} y} \frac{\text{Yg2}}{\text{yg2}} \stackrel{\heartsuit \times \text{dt yyg2}}{} \stackrel{\diamondsuit}{}$	13	1328	1352	1341	1313	5334	1744	1094	1080	1711	1529
2.	$ \frac{\text{Dt Yg2}}{\text{dt yg2}} \frac{\text{Y}}{\text{y}} \stackrel{\heartsuit \times \text{dt y yg2 } \checkmark}{(\text{siblings of those in No. 1})} $	6	958	68	66	1006	2092	532	513	547	543	2135
3.	$\frac{\mathrm{Dt-TB}}{\mathrm{dt}} \; \frac{\mathrm{Yg2}}{\mathrm{yg2}} \; \frac{\mathrm{Y}}{\mathrm{y}} \; \stackrel{\diamondsuit{\times}{} \mathrm{dt} \; \mathrm{y} \; \mathrm{yg2} \; \stackrel{\diamondsuit{\times}{} \mathrm{y} \; \mathrm{dt} \; \mathrm{y} \; \mathrm{y} \; \mathrm{y} \; \stackrel{\diamondsuit{\times}{} \mathrm{dt} \; \mathrm{y} \; \mathrm{y} \; \mathrm{y} \; \stackrel{\diamondsuit{\times}{} \mathrm{dt} \; \mathrm{y} \; \mathrm{y} \; \mathrm{y} \; \stackrel{\diamondsuit{\times}{} \mathrm{y} \; \mathrm{y} \; \frac{\mathrm{y} \; \mathrm{y} \; \mathrm{y} \; \mathrm{y} \; \mathrm{y} \; \frac{\mathrm{y} \; \mathrm{y} \;$	8	695	633	749	754	2831	648	707	710	816	2881
4.	$ \begin{array}{c} \underline{\mathrm{Dt}} \mathrm{Yg2} \\ \mathrm{dt} \mathrm{yg2} \end{array} \frac{\mathrm{Y}}{\mathrm{y}} \stackrel{\mathbb{Q}}{\to} \times \mathrm{dt} \mathrm{y} \mathrm{yg2} \overset{\mathbb{C}}{\to} \\ (\mathrm{siblings} \mathrm{of} \mathrm{those} \mathrm{in} \mathrm{No.} 3) \end{array} $	16	2067	123	135	2051	4376					

Analysis of <u>Dt-TC</u>, <u>Dt-TD</u>, <u>Dt-TE</u>, and <u>Dt-TF</u>

Four other kernels with high mutation rates of \underline{a}_1 to \underline{A}_1 were tested and found to result from <u>Dt</u> transpositions. Plants heterozygous for one or more <u>Dt</u>'s were crossed as egg and pollen parents to the <u>a-m dt</u> stock of Neuffer to introduce an allele that is highly mutable in the presence of <u>Dt</u>: <u>ag Dt</u>? <u>dt Dt-T</u>? <u>dt × a-m a-m dt dt</u>.

Table 5 summarizes the segregations of the <u>Dt</u>'s in these crosses. The presence of $3\underline{Dt}:1\underline{dt}$ ratios in each is evidence for the segregation of two independent <u>Dt</u>'s.

A detailed analysis of those plants segregating more than 3<u>Dt:1dt</u> as the pollen and (or) egg parent is presented in Table 6. Plant no. 3, involving Dt-TC, segregated 7 Dt: 1 dt whether used as pollen or egg parent. Two independent transposed <u>Dt</u>'s evidently were present in addition to Dt. Plant 4 segregated 3 Dt: 1 dt when used as egg parent and 7 Dt: 1 dt in the reciprocal cross. A second transposition may have occurred in a sector of the plant including the tassel. Evidence for more than one transposed <u>Dt</u> was found with <u>Dt-TD</u> in plants nos. 5 and 6 and with Dt-TF in plant no.8. Plant no. 7 segregated 15 Dt: 1 dt in the testcross, the expected ratio for 4 independent Dt genes. The ratios obtained on several ears were intermediate between expected ratios (nos.1, 2, 5, 6, 8), whereas segregations from several of the reciprocal crosses were 3:1 or 7:1. Transpositions evidently were occurring frequently; intermediate ratios could result from transpositions in sectors of the ear or tassel and (or) transpositions producing linkage between two <u>Dt</u>'s.

Secondary transpositions of <u>Dt-T</u>'s or additional transposition of the original <u>Dt</u> led to a search for multiple transpositions among discarded progenies segregating for <u>Dt-TA</u> and <u>Dt-TB</u>. No segregations greater than 3:1 were found for <u>Dt-TA</u> crosses, but two ears involving <u>Dt-TB</u> contained kernels in the proportion $7 \underline{Dt}: 1 \underline{dt}$.

Stability of the <u>Dt</u> gene

More than 1200 self-pollinations of stocks homozygous for a and Dt were made to detect transpositions. Some of the resultant ears contained a very low percentage of dotless kernels, whereas in others, there was a ratio of 3 dotted to 1 dotless. Dotless kernels were not expected on the basis of random distribution of dots inasmuch as the frequency of aleurone mutations in these stocks was uniformly high (Fig.1). Nevertheless, almost 9 % (34 + 41/861) of self-pollinated ears in a <u>Dt Dt</u> stock had dotless kernels (Table 7). Presumably, dotless kernels originated from changes in either or both parental contributions to the endosperm. If the alteration involved one parent only, the immediate kernel phenotype would be dotted, followed by a segregation of the dotted and dotless phenotypes in the next generation, or it would be dotless because of a lower mutation rate with decreased dosage of Dt or a. A change in both the egg and the pollen parent would give rise directly to a dotless kernel.

The <u>a</u> allele frequently changes in certain stocks to a stable form $(\underline{a-s})$ unable to mutate to <u>A</u>₁ (or only with a low frequency) in the presence of <u>Dt</u> (Rhoades

Table 4. χ^2 analysis of the data in Table 3. Values were calculated for $\underline{Dt}:dt$, $\underline{Yg2}:yg2$, and $\underline{Y}:y$ factor pair segregations and for the joint segregation of \underline{Dt} with either $\underline{Yg2}$ or \underline{Y} . A χ^2 - sum (the sum of the χ^2 's, for individual ears -- the individual ears are not listed in Table 3 for the sake of brevity), the χ^2 to-tal (the values listed in Table 4), and χ^2 - heterogeneity (χ^2_s - χ^2_{τ})

		x²	x²
No.	*	<u>Dt</u> :dt	<u>Y</u> :y
1.	χ^{2} - Sum	6.506	12.597
	χ^{2} - Total	0.039(P=.98)	0.064(P=.98)
	χ^{2} - Heterogeneity	6.467(P=.98)	12.533(P=.54)
2.	χ_{2}^{2} - Sum	4.633	1.086
	χ_{2}^{2} - Total	0.948(P=.87)	0.248(P=.76)
	χ^{2} - Heterogeneity	3.685(P=.65)	0.838(P=.9)
3.	χ^{2}_{2} - Sum	15.515	16.065
	χ^{2}_{2} - Total	10.150(P=.055001)	9.450(P=.005001)
	χ^{2} - Heterogeneity	5.365(P=.76)	6.615(P=.54)
4.	χ^{2} - Sum	12.080	17.988
	χ^{2}_{2} - Total	0.003(P > .9)	0.179(P=.76)
	χ^{2} - Heterogeneity	12.077(P=.76)	17.809(P=.32)

* corresponds to the number in Table 3

Table 5. Summary of analysis of <u>Dt-TC</u>, <u>Dt-TE</u>, and <u>Dt-TF</u>. Testcrosses were made of <u>Dt</u> plants from progenies that segregated two independent <u>Dt</u>'s. The number of plants segregating 1,2, or more <u>Dt</u>'s is listed for each isolate. Each plant was used as a pollen and egg parent unless indicated. χ^2 analysis was carried out for each cross

Transposition	Number of plants that segregated						
isolate	1 <u>Dt</u> : 1 dt	3 <u>Dt</u> : 1 dt	greater than 3 <u>Dt</u> :1dt as ♀ or ♂ parent				
Dt-TC	3	4	4				
Dt-TD	3	7	3				
Dt-TE	5 *	6 *	0				
Dt-TF	5 *	7*	1				

* crossed as egg parent only

1945). Consequently, dotless kernels of separate origin were crossed to the testers listed in Table 8 to determine the cause of the lack of mutability. Crosses of seven of the eight dotless stocks with dt dt plants carrying the standard <u>a</u> allele or the highly mutable <u>a-m</u> found by Nuffer (1961) produced only dotless kernels (families 2-8): similar crosses involving the remaining stock (family no.1) resulted in a low frequency of dotted kernels. When crossed with a-sDt (the <u>a-s Dt</u> stock has dotless aleurones inasmuch as a-s does not mutate in the presence of <u>Dt</u>), all the dotless stocks gave F , kernels with aleurone mutations, with the exception of family no.6, which produced ears with all dotless kernels, ears segregating for dotted and dotless, and ears with only dotted kernels. Thus, a dottable <u>a</u> allele was present in the dot-

less stocks, and the loss of mutability was attributed to loss of <u>Dt</u> activity. Additional crosses involving family no.6 substantiated the finding that both a mutable and a stable a allele were present. It is possible that the loss of <u>Dt</u> activity was coincident with a mutation of a to a-s. It is not known whether the families 2-8 have an inactive <u>Dt</u> allele or whether they had an actual physical loss of <u>Dt</u>. Numerous sibling crosses of the dotless stocks (Table 8) as well as self-pollinations and crosses with a-m dt have produced no reactivation of Dt. The chromosomes 9 of these families, when observed at pachynema, appeared to be normal and had the small terminal knob characteristic of <u>Dt</u> stocks. Several losses of \underline{Dt} and one mutation of \underline{a} to a-s accounted for the occurrence of dotless kernels on otherwise <u>a a Dt Dt</u> ears. The apparent discrepancy

χ^2 Yg2:yg2	χ ² <u>Dt-Y</u> Linkage	χ ² Dt-Yg2 Linkage	Degrees of Freedom
13.275	316.605	21.589	13
0.003(P > .9)	291.519(P < .0005)	0.507(P=.54)	1
13.272(P=.43)	25.086(P=.025010)	21.082(P=.050025)	12
4.941	2.091	1613.421	6
1.499(P=.32)	0.105(P=.87)	1611.327(P < .0005)	1
3.442(P=.76)	1.986(P=.98)	2.094(P=.98)	5
11.940	9.073	7.015	8
1.148(P=.32)	0.767(P=.43)	1.586(P=.32)	1
10.792(P=.21)	8.306(P=.43)	5.429(P=.76)	7
17.988		3412.715	16
0.179(P=.76)		3404.844(P<.001)	1

Table 6. χ^2 analysis of segregation of <u>Dt</u> greater than 3 <u>Dt</u>: 1 dt among those listed in Table 5

No.	Dotted/dt 약 × dt/dt ♂				χ^2 for a <u>Dt</u> :dt segregation of:							
	and reciprocal	Dt	dt	Total	1:1	S	3:1	S	7:1	S	15:1	S
1	<u>Dt-TC-1</u> reciprocal	322 163	69 53	391 216	163.706 56.010	***	11.273	*** n.s.	9.471	**		
2	<u>Dt-TC-2</u> reciprocal	385 132	94 41	479 173	176.787 47.867	***	7.383 0.156	** n.s.	22.228	***		
3	<u>Dt-TC-3</u> reciprocal	340 177	44 29	384 206	228.167 106.330	***	37.556 13.107	***	0.381 0.469			
4	Dt-TC-4 reciprocal	226 190	73 34	299 224	78.291 108.643	*** ***	0.055	n.s. ***	1.469	n.s.	01 504	***
5 6	<u>Dt-TD-1</u> reciprocal Dt-TD-2	388 191 340	51 17 44	439 208 384	258.699 145.558 228.167	***	41.932 31.410 37.556	***	0.313 3.560 0.381	n.s. n.s. n.s.	21.584 1.313 2.639	n.s.
7	reciprocal Dt-TD-3	260 402	61 23	321 425	123.368	***	6.157 86.972	¥ ***	2.639	n.s. ***	_	
8	reciprocal Dt-TF-1	156 328	10 66	166 396	128.410 174.223	***	31.880 14.298	***	6.365 6.511	* *	0.014	n.s.
	reciprocal	254	38	292	159.781	***	22.374	***	0.070	n.s.		

* Five percent level of significance

** One percent level of significance

*** One tenth percent level of significance

between this result and those of Rhoades (1941) and Peterson (1953), who attributed the dotless kernels to mutations, of <u>a</u> to <u>a-s</u>, possibly is the result of sampling errors inherent in small populations. It may be also that the stocks used contained different states of the <u>a</u> and(or) <u>Dt</u> alleles where changes to the inactive <u>a-s</u> and losses of <u>Dt</u> occurred at different rates.

A number of crosses of the type <u>a a Dt Dt</u> $? \times$ <u>a a dt dt</u> \circ were made. Four ears in a total of 40 had dotless kernels that were randomly distributed and not in clusters. The proportion of dotless kernels was large on some ears, but never accounted for half the kernels. Dotless kernels also were observed on ears of the reciprocal crosses. Thus, in these plants, independent losses of <u>Dt</u> (or loss of <u>Dt</u> activity) must have occurred after divergence of the cell lines forming individual ovules in the female parent. In the pollen parent, however, one cannot distinguish be-

<u>a a Dt Dt</u> family	Number of plants segregating 3 <u>Dt</u> :1dt	Number of plants giving a low frequency of dt kernels (1-10%)	Number of plants with all dotted kernels	Total number of plants
63-1, selfed	7	12	147	166
63-2, selfed	3	0	85	88
63-3, selfed	12	8	201	221
63-4, selfed	3	4	42	49
63-5, selfed	0	0	84	84
63-6, selfed	5	9	157	171
63-7, selfed	6	8	68	82
	36	41	784	861

Table 7. Number of ears bearing dotless kernels which arose from self-pollinations of homozygous \underline{aDt} stocks

Table 8. Phenotypes of kernels resulting from crosses between dotless types of different origin and tester strains. The dotless types were derived from the selfed progeny of homozygous \underline{Dt} stocks

No.		Phenotype of kernels						
	Dotless families	× <u>a</u> * sh2 dt	$\frac{\times}{a-m} * dt a$	× <u>a-s</u> * Dt	imes sib (No. of crosses)			
1	741	a few	a few	all				
		kernels	kernels	kernels				
		dotted	dotted	dotted				
2	743		dotless	dotted	dotless (6)			
3	744	dotless	dotless	dotted	dotless (4)			
4	745	dotless	dotless	dotted	dotless (3)			
5	747	dotless	dotless	dotted	dotless (7)			
6	748	dotless	dotless	dotless	dotless (2)			
				ordotted +				
7	749	dotless	dotless	dotted				
8	1255	dotless	dotless	dotted	dotless (2)			

*a, the standard allele that responds to <u>Dt</u>

a-m, a highly mutable a allele described by Nuffer (1961)

a-s, an a allele that does not respond to Dt

+ The ears testing individual sib plants were completely dotted, completely dotless, or segregated 1:1

tween frequent independent losses of \underline{Dt} and a single event involving a sector of the tassel.

Associations of "changes in state" with <u>Dt</u> transpositions

McClintock (1951) found that a "change in state" of an element often was associated with its transposition. Differences in either the physical attachment or in the chromosomal environment affected the activity of the element. Consequently, kernels carrying the transposed <u>Dt</u>'s were examined for changes in <u>Dt</u> activity. The effect of <u>Dt-TA</u> and <u>Dt-TB</u> upon the mutability of <u>a</u> remained unaltered. Because transpositions and losses of <u>Dt</u> were known to occur, a comparison of <u>Dt</u> stability at its standard location and at other positions was made by χ^2 analysis of <u>Dt:dt</u> ratios in backcrosses involving <u>Dt</u>, <u>Dt-TA</u>, and <u>Dt-TB</u>. Table 4 lists the χ^2 values for <u>Dt:dt</u> segregations when <u>Dt</u> was linked to <u>Yg2</u> of chromosome 9. The six ears of Table 3 and 4, nos.2, segregated 1026 <u>Dt</u> to 1066 <u>dt</u> kernels (χ^2 = 0.765, P = .4-.3), and the 16 ears of Tables 3 and 4, nos.4 segregated 2190 <u>Dt</u> to 2186 <u>dt</u> kernels (χ^2 = 0.003, P = 0.9-0.8). Both agree with the expected 1:1 ratio of Mendelian genes.

<u>Dt-TA</u> on chromosome 6 segregated in Mendelian fashion. Thirteen ears yielded 2838 <u>Dt</u> on 2791 <u>dt</u>kernels, with a χ^2 value of 0.127 (P = 0.8-0.7) (Tables

3 and 4, nos 1). The unlinked <u>Dt-TB</u> however, significantly deviated from the 1:1 ratio expected in a testcross. There were 1355 <u>Dt</u> and 1526 <u>dt</u> kernels found on eight ears (Tables 3 and 4, nos.4). The <u>Dt</u>-induced mutation rate was sufficiently high to make misclassification an unlikely cause of this deviation. Although seven of the eight ears did not have significant deviation from 1 <u>Dt</u>: 1 <u>dt</u>, the <u>dt</u> class was in excess in each instance producing the highly significant total deviation with a χ^2 value of 10.150 (P = 0.005-0.001). Upon transposition from chromosome 9 to a new location, <u>Dt-TB</u> had evidently undergone a change in stability.

Consistent with these apparent losses of <u>Dt-TB</u> was the small proportion of ears segregating 1:1 for <u>Dt-TB:dt</u> (from which the eight ears of Table 3, no.3 were taken). Only 10 of a total of 77 ears segregated <u>Dt-TB</u>, whereas 67 segregated 1:1 for <u>Dt</u> when there should have been equal numbers of each type. The low recovery was similar to that of the previous generation (see "Detection of transpositions"). Gametophyte factors cannot be invoked, however, because, in the later backcrosses, the <u>Dt</u>-containing plants were used as egg parents. It is more likely that losses of <u>Dt-TB</u> were occurring during the development of the sporophyte.

A further indication that "changes in state" were associated with the transposition of <u>Dt</u> was the frequent recovery of backcross ears segregating three and four <u>Dt</u>'s among <u>Dt-TB</u>, <u>Dt-TC</u>, <u>Dt-TD</u>, and <u>Dt-TF</u> families (see section discussing these transpositions). As mentioned before, however, secondary transpositions of the <u>Dt-T</u> and additional transpositions of <u>Dt</u> could not be distinguished in these instances.

Discussion

Transpositions

Were it not that the elements of other mutable systems in maize changed position in the chromosomes, there would have been no reason to suspect that <u>Dt</u> might move from its known position in the short arm of chromosome 9. <u>Dt</u> had been maintained for more than 30 years in genetic stocks and had been used in diverse linkage studies as a consistent marker of the terminus of that arm. In this respect, it resembled the typical gene. When sufficiently rigorous means of detection were employed, however, transpositions of <u>Dt</u> were readily isolated. <u>Dt</u> need not be confined to one location for it to effectively regulate <u>a</u> activity. No difference was observed in the response of <u>a</u> to <u>Dt</u> at any of its new locations, although such a change was commonly associated with transpositions of <u>Ac</u> (McClintock 1951). Selection of kernels with an increased number of <u>a</u> mutations as possible cases of transposition may have resulted in detection of <u>Dt-T</u>'s that affected <u>a</u> mutability in much the same manner as did <u>Dt</u>; thus, transposed <u>Dt</u>'s producing altered <u>a</u> responses may have been overlooked.

Six primary transpositions of <u>Dt</u> were isolated in the initial study. Although their effects on a mutability were the same, differences in the behavior of the <u>Dt-T</u>'s were obvious. <u>Dt-TA</u> showed 39 per cent recombination with <u>Y</u> of chromosome 6. <u>Dt2</u>, also on chromosome 6, was reported to have 26 per cent recombination with <u>Y</u> (Nuffer 1955). The difference in recombination values does not allow the conclusion that <u>Dt2</u> and <u>Dt-TA</u> are at distinct sites because the frequency of crossing over can vary considerably in dissimilar genetic backgrounds. Therefore, it is possible that <u>Dt-TA</u> and <u>Dt2</u> are allelic and that <u>Dt</u> transposes preferentially to certain sites on the chromosomes.

Essentially all the transpositions of a regulatory element can be detected when a controlling elementregulatory element complex is initially present at the locus showing instability. Studies of such autonomously controlled loci have been made by Greenblatt (1968, 1974) of Modulator and by Peterson (1970a) of Enhancer. These regulatory elements were shown to transpose preferentially to sites on the same chromosome. Furthermore, there was a decided preference for positions close to the initial location of the elements. A significant proportion of the transpositions, however, did move to unlinked sites (35 % of transpositions of Modulator and 75 % of transpositions of Enhancer). The method of detection for <u>Dt</u> transpositions used here selected for transfer of Dt to unlinked locations; transposition to closely linked sites would have been overlooked. Therefore, no direct comparisons may be made in this regard.

Inasmuch as \underline{Y} is approximately 17 map units from \underline{rgd} ("ragged seedling"), which is at or near one end of the short arm of chromosome 6, <u>Dt-TA</u> must lie in the long arm distal to \underline{Y} and close to the locus of \underline{su}_2 ("sugary endosperm"). At this position, <u>Dt-TA</u> was

as stable as \underline{Dt} . χ^2 analysis of its segregation at either position in testcrosses revealed no significant deviation from 1:1.

Testcrosses of <u>Dt-TB</u> (unknown location), however, produced highly significant deviations from 1:1. A large excess of dt kernels was found. It is not known whether the excess was due to losses of Dt-TB activity or to actual physical deletions of the element. If the latter were responsible, an increased transposition rate of Dt-TB might be expected. Indeed, two secondary transpositions were found among siblings of the testcrossed plants showing irregular segregation of <u>Dt-TB</u>. The occurrence of secondary transpositions in plants with Dt-TC, Dt-TD, or Dt-TF suggested that limited instability may be common in some locations while Dt's on chromosomes 9 and 6 show greater stability. Differences in stability of <u>Dt</u> at different locations are similar to those found for the regulatory element of Supressor-mutator (Spm) by McClintock (1957). From a position near Wx on chromosome 9, Spm transposed in most plants, whereas, when it was located on chromosome 6 near Y, there was evidence for only one transposition in a total of 44 ears.

The first step of a <u>Dt</u> transposition would be its removal from the original chromosomal site. If it were then incorporated elsewhere in the complement, a transposition would have occurred. If, however, it were not incorporated elsewhere, a loss of <u>Dt</u> would be observed. Thus, the losses of <u>Dt</u> (activity) and the occurrence of transposed <u>Dt</u>'s are both likely to be consequences of its initial removal from the chromosome.

The discovery of \underline{Dt} at new locations, the correlation of the instability of one of these, \underline{Dt} -TB, with secondary transpositions, the high recovery rate of dt kernels in homozygous \underline{Dt} stocks, and the occurrence in the same progeny of transposed \underline{Dt} 's and of chromosomes 9 that lost \underline{Dt} all point to a causal relationship of transpositions of \underline{Dt} and its instability at the previous locations.

Significance of transpositions

The discovery of the regulation of one gene (\underline{a}) by another (\underline{Dt}) was an important contribution to the development of genetic theory (Rhoades 1936, 1938, 1941, 1945), for it demonstrated one means by which gene activity could be controlled. After resumption of <u>A</u> activity through the action of <u>Dt</u>, a stable and heritable A allele was present that thereafter seemed to be unaffected by <u>Dt</u>. By analogy with similar control of genes by <u>Ac-Ds</u>, it was postulated that a controlling element at the <u>A</u> locus suppressed the activity of the dominant allele and that <u>Dt</u> caused resumption of <u>A</u> activity by inducing loss of the controlling element from the chromosomal locus (McClintock 1956b). The responding element presumably transposes from a in a manner similar to transpositions of <u>Dt</u>.

Thus, a unique feature of Dt, the inferred element at <u>a</u>, and other regulatory and controlling elements, is their ability to physically leave a chromosomal position and reassociate elsewhere. In this respect, the elements resemble various bacterial plasmids, proviruses, or pieces of transposable inserted DNA (Jacob and Monod 1961; McClintock 1961; Smith-Keary and Dawson 1964). The most striking similarity transposition has been discussed. Although the exact location of the transposed <u>Dt</u>'s has not been determined in most instances, one situation was found in which four <u>Dt's</u> segregated independently of each other. <u>Dt</u> factors have been discovered on chromosome 6 (Dt2, Brazil) and chromosome 7 (Dt3, Peru) in two maize strains of 98 tested from Central and South America (Nuffer 1955) in addition to the original site on chromosome 9 (\underline{Dt}) (Rhoades 1945). Two of the \underline{Dt} 's may well have arisen as transpositions of the third, although evidence of such an event is lacking. An additional site of Dt in the chromosomal complement may have been discovered in this study; Dt-TA represents a transposition of <u>Dt</u> from chromosome 9 to a position on chromosome 6 close to or coincident with the locus of Dt2. The transpositions detected here, as well as those found in studies of other controlling elements (McClintock 1951, 1956a, b, 1964; Van Schaik and Brink 1959; Greenblatt and Brink 1962; Greenblatt 1966, 1968, 1974; Peterson 1970a) attest to the fact that attachment sites are not restricted to specific chromosomes. Likewise, in bacteria, the sex factor, the multiple drug resistance factor, and bacteriophage that perform generalized transduction are able to occupy many chromosomal sites (Driskell-Zamenhof 1964). On the other hand, most temperate bacteriophage attach at unique positions. The best studied temperate phage, λ , was shown to occupy a distinct position linked to the cistron controlling phosphogalactotransferase.

Peterson (1970b) presents a thorough discussion of possible microbial counterparts to maize controlling elements. On the basis of Nelson's (1968) placement of four independent insertions of controlling elements at distinct sites within the wx locus, Peterson suggested that controlling elements are foreign genetic material inserted without site specificity into a gene, consequently interfering with transcription or translation. As described by Peterson, there are adequate analogous situations in bacteria; e.g., the Mu-1 gene inserted at the gal and other loci in E. coli (Taylor 1963) and three different insertions of various size into the gal operon (Jordan et al. 1968). In each of these situations the insertion of genetic material (450 to 1800 nucleotide pairs in the latter reference) causes suppression of gene activity, which is restored upon the removal of that exact piece of DNA from the gene. This explanation is perhaps more appropriate, at least at present, than considering controlling elements and their regulatory properties analogous to temperate phage. There is no direct evidence to support the latter possibility; furthermore, controlling elements have not been observed to replicate independently of the chromosome, nor to cause gross changes in the physiological activity of the cells in which they exist.

The physical relationship between controlling elements and the chromosome is puzzling and was the subject of another report (Doerschug 1973). The chromatid and chromosome breaks associated with the origin or controlling elements during the bridge-breakage-fusion cycle (McClintock 1950; Bianchi et al. 1969; Doerschug 1973) and the chromatid breaks that are the result of activity of the element Ds argue that some recombination-like mechanism is responsible for their insertion and excision (Campbell 1969). That elimination of elements evidently occurs in somatic cells does not detract from such a mechanism because the enzymatic events involved in meiotic recombination occur throughout the life cycle; synapsis simply increases the probability that a recombinational event will occur between homologous regions of two chromosomes (Howell 1971). In view of this and the mapping of controlling elements within the wx locus (Nelson 1968), the integration of controlling elements into the chromosome rather than a lateral attachment is favored (Greenblatt 1968). The size of controlling elements

is unknown, although it has been argued (Peterson 1970b) that the fine structure analysis by Nelson (1968) shows no increase in recombinational distance when an element is inserted into the \underline{wx} locus, and that, consequently, elements must be short. A large insertion of a portion of chromosome 9, however, resulted in no increase in recombinational distance between markers on either side of the added piece (Rhoades 1968). Thus, I would be hesitant to relate the lack of greater recombinational distance to the small size of the element.

The importance of controlling element systems has yet to be evaluated fully. A system involving frequently transposing regulatory elements seems too variable to play a major role in gene regulation and differentiation. Yet, the transient regulation of structural genes may represent a state in the evolution of stable controlling systems. It may be advantageous for transposable elements (initially nonspecific) to exist in cells, enabling rapid development of regulatory systems. After initiation of control, whether or not the system stabilizes, would depend on the selective forces. Thus, instability may result from the modification of a stable regulatory element and may reflect a previous condition of that element or may be due to the initiation of control of a gene by an uncommitted element.

Most, if not all, of the mutable genes studied in maize have been unessential for plant development. Some argue that the behavior of elements controlling such genes may not be characteristic of regulators of genes necessary for cell and plant development. It is only because the mutable genes are unessential, however, that the control system could be tested genetically. That transposable elements can affect major genes was demonstrated by the fact that transpositions of <u>Ds</u> from a known location to new positions in the short arm of chromosome 9 often were associated with dominant lethality (McClintock 1956b).

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