This form of analysis has facilitated the identification of some but not all of the A chromosome arms (chromosome arms were treated independently) suggesting at least limited autonomy of ^{3}H-TdR uptake within arms. The B chromosome, the distal segment (long arm) of abnormal 10 and the satellite on chromosome 6 could easily be identified as unique segments in the principal components analysis.

Some chromosome arms 'change' their replication behavior depending upon the experimental conditions. Notable in this regard were the short arm of chromosome 9 in the presence of a B chromosome, and the short arm of abnormal 10 compared to that of normal 10. A similar change was not detected in the proximal segment of the long arm of abnormal 10.

While B chromosomes in many other ways behave differently from the distal segment of the long arm of K10, it is interesting to note how one parallels the other with respect to replication of DNA. They both have similar and unique replication profiles and both respond similarly in a principal components analysis. Likewise, they both can influence the replication characteristics of other chromosome segments. In addition, they both exhibit similar effects on the synchrony of replication between homologous chromosomes (see following report).

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12. Analysis of synchrony of DNA replication between homologous chromosome segments in maize root-tips.

The question of homologue synchrony of DNA replication has not yet been resolved. Testing for this phenomenon by standard statistical methods is not feasible, since they require the restriction that one can distinguish between two homologous chromosomes. We present here a method by which synchrony may be analyzed statistically without the above constraint.

The data employed were silver grain counts described above (i.e., ^{3}H-TdR uptake over all homologous chromosome arms at hourly intervals of the S period, replicated in a number of cells).

The hypothesis of the synchrony of ^{3}H-TdR uptake between homologous chromosome arms was separated into two testable portions which could be approached by statistical methods, as follows:

1) For synchrony to exist, there must be a high degree of concordance between homologues in a population of cells. We would declare concordance in a pair of homologous chromosome segments to exist if both members are either labelled or unlabelled. Non-concordance would exist if one homologue was labelled, the other not labelled. A population exhibiting a significant degree of concordance may be detected using a X^2 test.

2) For synchrony to exist, there must also be little difference in the number of silver grains over each member of a homologous pair. The degree of asynchrony in this case may be tested using information theory. The specific test is an I-divergence test which tests the degree of pairwise divergence between members in a population of unordered paired observations.

The summary of the results of tests (1) and (2) is presented in Table 1 under four conditions of experimental input. Both tests were performed on populations represented by each of the 20 chromosome arms plus the satellite on chromosome 6 (21 chromosome segments) at hourly intervals throughout the S period.

Table 1

Summary of results of X^2 tests for concordance and I-divergence tests for disimilarity of ^{3}H-TdR uptake, between homologous chromosome segments

Genetic stock	Temp.	No. of tests performed	Percent of tests significant ($p \leq 0.05$)	
			(1) X^2-concordance	(2) I-divergence
3 tester + 1 B	18°C	315	36.8	51.4
K10/k10	18°C	252	38.1	62.3
3 tester	18°C	231	40.3	24.7
3 tester + 1 B	28°C	126	46.0	29.4

A higher proportion of tests of divergence between homologous segments was observed to be significant ($p \leq 0.05$) when the genome contained large segments of heterochromatin (B chromosome or K10). This proportion was greatly reduced by removing the extra heterochromatin, or by raising the temperature. While the proportion of significant tests of concordance was relatively low, it remained independent of the presence of extra heterochromatin.

While the tests themselves have been deemed valid, we are still assessing the objectivity of the test criteria in terms of the more general hypothesis of synchrony. We are extending our study to include specific translocation stocks as an experimental input to provide a further, more vigorous test of synchrony and autonomy of DNA replication.

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1. Effect of $\underline{M}^{st}$ on mutation of $\underline{R}^{st-f}$, a modified form of the $\underline{R}^{st}$ (Wisconsin) allele.

The effect of $\underline{M}^{st}$ (modifier of $\underline{R}^{st}$) on $\underline{R}^{st}$ to $\underline{R}^{sc}$ (self-colored) mutation in the aleurone is to increase the frequency of late occurring mutational events. Kernels with equal dosage of $\underline{R}^{st}$ appear much darker if they also carry $\underline{M}^{st}$ in the genome than if they don't. On the other hand, the frequency of corresponding colored aleurone and colored embryo kernels (a class which includes mutations of $\underline{R}^{st}$ to $\underline{R}^{sc}$ occurring from meiosis up to and including the second megagametophyte division) does not appear to be influenced by $\underline{M}^{st}$. Likewise, the available data do not show any effect of $\underline{M}^{st}$ on the frequency of kernels having non-corresponding aleurone and embryo phenotypes (a class representing mutations of $\underline{R}^{st}$ to $\underline{R}^{sc}$ at any of the three megagametophytic divisions). Therefore, the control of mutation of $\underline{R}^{st}$ to $\underline{R}^{sc}$ exerted by $\underline{M}^{st}$ appears to be limited to a specific tissue (the aleurone) and a specific time in the development of this tissue (late divisions).

Several derivatives of $\underline{R}^{st}$ showing a heritably modified aleurone phenotype have been isolated. One of these responds to $\underline{M}^{st}$ in an