were observed occurred in labelled cells and the results in general indicate that there is an increase in sensitivity with increasing fixation time, i.e., the cells in early S show a higher aberration yield than the cells in late S at the time of treatment. The aberration frequency at 20 hr. after MC treatment is higher than other treatments; these cells would have been in late G_1 or early S at the time of treatment.

MC-induced chromosomal aberrations among the 10 pairs of chromosomes showed an apparent non-random distribution. If the drug was acting randomly per unit of chromatin, then the distribution of breaks should be according to the length of the chromosomes. The relative lengths in percentage of the complement (long arm plus short arm using Chen's data, 1969) of metaphase chromosome are shown in Table 4. The observed versus expected values were tested by Chi-square and a highly significant value was obtained. We attempted to assign the location of each aberration not only to a specific arm, but in most cases to a segment within arms. While admittedly somewhat arbitrary, our distribution analysis suggests that the frequency of breaks in certain arm segments is higher than in other arm segments. Future work to identify the locations of heterochromatin or knobs on the chromosome may lead to the study of the relationship between breakage and heterochromatin in maize chromosomes. At this time we can report only that the greatest concentration of breaks induced by MC appears at the secondary constriction and centromeres.

M. S. Lin

11. <u>The identification of chromosome segments by their replication behavior using principal components analysis</u>.

Previously we described the DNA replication behavior of maize chromosomes using ^{3}H-TdR autoradiography in different genetic stocks and at two temperatures (MGCNL 44:195-198, 1970). Replication behavior was described by plotting the mean number of silver grains for each chromosome arm at hourly intervals of the S period (a 'replication profile'). The data have been extended to include a chromosome 3 tester stock containing one B chromosome. The experimental input now includes:

1) Chromosome 3 tester + one B chromosome (28°C)
2) Chromosome 3 tester + one B chromosome (18°C)
3) Chromosome 3 tester (18°C)
4) Heteromorphic abnormal 10 (18°C)

This study depends on two features: positive, unambiguous identification of metaphase chromosomes, and localization in the autoradiographs of the silver grains. Sampling appropriate to these studies was described in the earlier report.

The replication profiles of B chromosomes from the 18°C and 28°C experiments were not of the same configuration. At 28°C the S period was much shorter, and the B chromosome exhibited extensive ^{3}H-TdR uptake in the last half of the S period, although uptake did occur throughout the entire S period. At 18°C, the S period was longer, and the B chromosome demonstrated a constant rate of labelling throughout the S period, such that there was no peak in the profile. Its replication profile is thus, at 18°C, much like that of the distal segment on the long arm of abnormal chromosome 10 (MGCNL 44:195-198, 1970).

While it was possible to distinguish the profiles of either the heterochromatic segment on abnormal 10 or the B chromosome from the other chromosomes, it was difficult to identify most arms of the A chromosomes on the basis of replication profiles.

A principal components factor analysis (see Jancey this newsletter) was employed in a further attempt to characterize chromosome segments by their replication behavior. Within the data there exists for each chromosome arm a population of grain-count observations made at each hour (sample) of the S period. From such a population of grain counts a number of descriptive statistics or characters may be derived. Since a number of populations exist, a large number of characters may be accumulated to describe the replication behavior of each chromosome segment for the entire S period.

The analysis was carried out using grain count data standardized for the length of the chromosome arm concerned. Preliminary analyses demonstrated that the most useful characters were the mean, variance, g_1 (skewness), g_2 (kurtosis) at each hour of the S period, and the percentage increment or decrement in mean grain count between sampling intervals.

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).

G. R. Douglas

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: