calculated values for G_1, yielding negative numbers, required further investigation. We considered three factors:

i) the labeling time (duration of pulse);

ii) misclassification of prophase and background label;

iii) the length of meristematic region of the root tip included in the study.

In an attempt to broaden the scope of this study, a second stock (a chromosome 9 tester) was added. Employing Chen's (1969) methods, two root tip lengths ("long" = 2.40 ± 0.08mm and "short" = 1.52 ± 0.02 mm) were studied at 25°C. All slides from each treatment were coded and scored blindly. The classification data are presented in Table 1 and the new interphase and mitosis estimates at 25°C are presented in Table 2.

The data revealed no differences in the nuclear cycle of the two stocks. Likewise, the data did not reveal major differences between root preparation techniques. The duration of mitosis and its components, and the S period, are unaltered from our earlier estimates (MGCN 43: 186-190, 1969). However, the calculations of G_1 and G_2 yielded new estimates. G_1 and G_2 were partitioned from the residual of the interphase minus S interval; it follows logically that a change in G_1 in one direction will alter G_2 in the opposite direction in so far as we employ the proportion method. Since G_1 and G_2 are derived values from the slopes of the curves, it is clear that the alterations we made in our protocol are responsible for the changes recorded (Table 2) for G_1 and G_2.

We have reduced our acceptable labeled cell from 4 x background to 2 x background. Coupled with a more critical classification of prophase, we feel that this modified protocol more accurately represents the nuclear cycle in maize root tips.

R. S. Verma

5. Chromosome replication profiles from maize root tips.

In MGCN 43: 190-192 (1969) we reported preliminary data from a study of the replication behavior of individual maize somatic chromosomes at 28°C in a chromosome 3 tester stock in which each cell contained one

B-chromosome. This experiment (98 cells) is complete with grain count data for each chromosome arm in each hour during the 7-12 hour period after the ^{3}H-thymidine pulse.

These data were processed as follows.

The mean grain counts per hour of the S period were determined for each chromosome arm. These data or their derivatives, namely the measure of activity in a chromosome segment during S, if plotted against the time intervals of S, are referred to below as a "replication profile." Thus far, we have recognized two kinds of profiles, the "uptake profile" which is a frequency histogram and the "increment profile" which is a plot of the change per unit time of label accumulation. Profiles have been constructed for each arm of all A-type chromosomes in the maize complement.

The profiles obtained from the above study (28°C) revealed little detail in most chromosome arms. The B-chromosome profile did indicate that extensive ^{3}H-thymidine uptake (DNA synthesis) occurs in the last half of the S period, although synthesis does occur during the entire S period. Thus, the uptake of tritium in the B-chromosome is clearly not confined to the S period as has been reported elsewhere.

The lack of detail in profiles at 28°C led us to reason that increased resolution might be obtained by lengthening the S period (by lowering the incubation temperature). Two experiments employing a temperature of 18°C have been completed: one using a chromosome 3 tester stock (164 cells), the other using a stock heteromorphic for abnormal chromosome 10 (300 cells). Experimental procedures were those outlined in MGCN 42: 175-178 (1968) and MGCN 43: 190-192 (1969). In addition, the length of the S period treated in the two experiments was 12 hours.

The profiles of all chromosome arms of the complement in both experiments showed a rapid increase in ^{3}H-thymidine uptake in early S, followed by a gradual decline in uptake toward the end of S. In all cases, there was a marked dip in the profiles at the end of the first one third of the S period. There was a remarkable similarity between profiles of the same chromosome arms in the two experiments.

We have recognized three types of uptake profiles:

1. Profiles in which, at each hour of the S period, the arm ratio

(L/s) is representative of the ratio of ^{3}H uptake (L/s). Chromosome 5 (arm ratio 1.1) is an exemplar chromosome.

2. Profiles in which the arm ratio does not predict the ratio of ^{3}H uptake (L/s) at each hour of the S period. Thus, during a specific interval, the short arm may be accumulating more ^{3}H than the long arm, observed as an intersection of the arm profiles. Chromosome 6 (arm ratio 2.25 less satellite) is an example of this type.
3. Profiles intermediate between types 1 and 2 above, in which there are no arm profile intersections although the areas under the curve (profile) are not representative of the arm lengths. Chromosome 9 (arm ratio 1.6) is an exemplar chromosome.

All A-type chromosomes of maize can be assigned to one of these three types of profile. In so far as ^{3}H uptake represents DNA synthesis, our data support the arguments that the synthesis is time and chromosome segment dependent.

We have examined K10 in addition to A and B chromosomes. Abnormal 10 has a large distal segment, which at mitotic metaphase is approximately equal in length to the long arm of normal chromosome 10; the long arm of K10 is approximately double the length of the long arm of N10. This segment of K10 has no demonstrable effect on the replication profile of the long arm segment proximal to it, since the profile of this region is identical to that of the normal chromosome 10. The profile of the K10 distal segment is different from the profiles of all the chromosome arms of the complement in that:

i) uptake occurs at a constant rate throughout S such that there is no peak in the profile;
ii) ^{3}H uptake at most hours of the S period was greater than that attained by a comparable length of A-type chromosome;
iii) uptake in the K10 segment continued at least one hour after all other arms had completed uptake.

Our data show that for the A-type chromosomes without exception the 18°C profile amplifies the 28°C profile, indicating but not proving that similar processes are involved in uptake at the two temperatures. While

we do not have profiles for the B chromosome (28°C) and the K10 segment (18°C) at the same temperature, it is interesting to note that they present quite dissimilar profiles. If the dissimilarity persists in tests at both temperatures, the ^{3}H uptake profiles may provide strong evidence on which to differentiate between a B chromosome and the distal segment in the long arm of K10.

G. R. Douglas

6. Somatic association as a general phenomenon in maize.

Miles (M.G.C.N.L. 42:77-79) studied the effect of the presence of 0, 1, or 2 abnormal chromosomes K10 on the somatic association of chromosomes 6. From that portion of her study in which K10 was absent, Miles concluded that "during mitotic metaphase in root tip cells the homologous chromosomes are not associated." By studying all possible 190 homologous and non-homologous associations of chromosomes in somatic cells of maize, we have attempted to test whether in fact somatic association is a real event in maize. To the best of our knowledge, this is the first study with plant or animal cells in which all possible chromosome combinations have been examined in a normal stock.

Root tips of the single cross hybrid 'Seneca-60' were treated with 8-hydroxyquinoline for 3 hrs. in one experiment and with cold (5°C) for 24 hrs. in a second experiment. Both treatments have been shown previously to arrest spindle fiber development and permit the accumulation of metaphases. Squash preparations were made following Chen's (1969) protocol. Cells were chosen and photographed which were flat, reasonably circular, and with all 20 chromosomes and their centromeres clearly visible. The chromosomes were projected to a final magnification of 30,000x and measured using a highly accurate ($\pm$ .04mm.) measuring device of our own design and construction. The chromosomes were objectively identified by a computer program that we have written specifically for maize. The program uses a hieristic reasoning sequence to identify the chromosomes from arm ratio and arm length measurements. No pairing of chromosomes for purposes of identification is involved. The distances between chromosomes were calculated from the x, y co-ordinates of the