

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  $^3\text{H}$  uptake profiles may provide strong evidence on which to differentiate between a B chromosome and the distal segment in the long arm of K10.

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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 ( $\pm .04\text{mm.}$ ) 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

centromeres and standardized by dividing the distance between any two chromosomes by the greatest distance between two chromosomes in the cell. The output is expressed by the computer as a frequency histogram for the distances between each, any and every chromosome pair. The distributions of distances between each possible chromosome pair were compared to a theoretical distribution. For a description of the statistical considerations, see Feldman (1966) (Feldman, *et al.*, P.N.A.S. 56: 1192-1199, 1966). The theoretical distribution curve has a mean value of 0.453 where  $x$  can vary between 0 and 1. The Kolmogorov-Smirnov One-Sample or Two-Sample test of goodness of fit was used to compare the observed distributions with the theoretical distributions. We required at least 20% of the frequency class intervals in the histogram to show a deviation beyond the 95% level before the observed curve was considered significantly different from the theoretical curve.

In Table 1 are summarized the data from the distribution of distances among all 10 homologous pairs of chromosomes.

Table 1  
Mean distance between homologues. (N=50).

Treatment	Chromosome									
	1	2	3	4	5	6	7	8	9	10
8-hydroxy-quinoline 3 Hrs.	.420	.331*	.406	.479	.421	.448	.481	.473	.418	.417
Cold (5°C) for 24 Hrs.	.501	.373*	.375*	.346*	.449	.436	.346*	.357*	.343*	.412

\*Significant association beyond 95% limit.

Non-homologous associations between all four chromosomes of 3, 7 (.376) and 9, 4 (.351) have been noted in the cold treatment but not in the 8-hydroxyquinoline treatment. Where distribution means of distances between chromosomes, whether homologous or non-homologous, approached the theoretical

mean of .453, the shape of the distribution closely approximated that of the theoretical distribution.

In tests of the association of homologous chromosomes 6 in cells from both treatments, we found, as did Miles, that the mean distance between homologues did not differ significantly from the expected .453. The distribution distance mean (.417, .412) for chromosome 10 also did not deviate significantly from the theoretical curve. However, it appears that other homologous chromosome pairs are associated at metaphase in Seneca-60 and that the degree of this association is affected by the treatment used to arrest spindle development for the accumulation of metaphase spreads.

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1. Organization of the pigmenting and paramutagenic determinants of the R-stippled gene in maize.

The R-stippled ( $\underline{R}^{st}$ ) gene in maize is unstable in aleurone pigmentation and mutates in the germ line to a fully colored form, self-colored ( $\underline{R}^{sc}$ ). In mutation to  $\underline{R}^{sc}$  the potential of  $\underline{R}^{st}$  to reduce heritably the pigmenting action of sensitive alleles in heterozygotes (paramutation) may be fully retained, quantitatively reduced, or lost. The basis for the coincident alteration in paramutagenicity with  $\underline{R}^{st}$  to  $\underline{R}^{sc}$  mutation and the topographical arrangement of the components of R-stippled were the main objects of investigation.

Major reductions in paramutagenicity among  $\underline{R}^{sc}$  mutants from  $\underline{R}^{st}\underline{R}^{st}$ ,  $\underline{R}^{st}\underline{R}^{nj}$ , and  $\underline{R}^{st}\underline{R}^{nj:st}$  combinations were found in the class of mutants that arose in conjunction with recombination. Reductions among the noncrossover mutants were small. When exchange in the R region was suppressed by a closely linked heterochromatic knob, or precluded in the case of  $\underline{R}^{st}$  hemizygotes, the reductions were minor and infrequent. The association between recombinant origin of the  $\underline{R}^{sc}$  mutants and major