

3. Preferential pairing in standard-commercial inbred line trisomic
3 hybrids.

Preferential pairing was studied in eleven different standard-inbred line hybrids. The results are given in Table 4. Individual plants from all of the eleven types of hybrids showed aberrant ratios which are

Table 4
Gene segregation in standard-commercial inbred
line trisomic 3 hybrids

| Inbred line | Type of ratio ¹ | No. of plants tested | No. of gametes tested | No. of <u>A</u> gametes | % <u>A</u> | Inter-action χ^2 | χ^2 (1 <u>A</u> :2 <u>a</u>) |
|-------------|----------------------------|----------------------|-----------------------|-------------------------|------------|-----------------------|------------------------------------|
| M 14 | (+) | 10 | 11,280 | 3,882 | 34.42 | 8.67 | 5.94* |
| K 55 | (n) | 3 | 3,815 | 1,285 | 33.68 | 0.01 | 0.23 |
| | (+) | 3 | 5,141 | 1,965 | 38.22 | 4.29 | 55.14** |
| N 6 | (n) | 5 | 5,028 | 1,668 | 33.17 | 5.76 | 0.06 |
| | (+) | 1 | 1,086 | 404 | 37.20 | -- | 7.30** |
| CI 21E | (n) | 7 | 5,045 | 1,668 | 33.06 | 5.26 | 0.17 |
| | (-) | 3 | 2,206 | 532 | 24.12 | 1.52 | 83.28** |
| C 103 | (n) | 3 | 3,453 | 1,154 | 33.42 | 0.14 | 0.93 |
| | (+) | 1 | 775 | 326 | 42.00 | -- | 26.88** |
| | (-) | 1 | 1,431 | 435 | 30.40 | -- | 5.55 |
| CI 7 | (n) | 2 | 2,721 | 890 | 32.71 | 0.03 | 0.48 |
| | (-) | 4 | 5,629 | 1,580 | 28.07 | 15.08** | 70.05** |
| K 6 | (n) | 3 | 3,207 | 1,036 | 32.30 | 1.56 | 1.53 |
| | (-) | 2 | 2,664 | 614 | 26.64 | 0.47 | 126.82** |
| Kys | (n) | 2 | 1,304 | 458 | 35.12 | 0.03 | 1.83 |
| | (-) | 33 | 36,249 | 10,608 | 29.26 | 41.23 | 270.05** |
| B 41 | (-) | 5 | 6,188 | 1,535 | 24.81 | 18.45** | 202.70 |
| 38-11 | (-) | 10 | 8,473 | 1,985 | 23.43 | 47.41** | 373.89** |
| Hy | (n) | 1 | 709 | 213 | 30.04 | -- | 3.36 |
| | (-) | 7 | 6,338 | 1,241 | 19.58 | 65.06** | 539.79** |

¹
+ > 33%
- < 33%
n = 33%

indicative of preferential pairing. Gross chromosomal structural differences are not present between the chromosomes 3 of the inbred lines and the standard, so the results are probably caused by cryptic structural

rearrangements (small inversions, deletions, and duplications and genetic differences as the result of the differential introgression of Tripsacum via teosinte and spontaneous mutation). Despite the fact that the pollen parent used to form the test trisomics was an inbred line and therefore presumably possessed only one kind of chromosome 3, the data indicate that they were not always homogeneous. In the cases of K 55, CI 21E, CI 7, and K 6 there seems to be a 1 to 1 segregation for normal and aberrant ratios. One explanation is that the parental plants were not homozygous for a structurally similar chromosome 3.* The inbred lines of maize are known to be unstable phenotypically. A preferential pairing test may be very sensitive in detecting small differences.

Another explanation is that there may be a very strong environmental interaction. Anything, for example, temperature, which would change the frequency of trivalent formation would modify the expression of preferential pairing. The influence of the environment will be determined this summer by the use of split planting dates and by serial pollinations. Different planting dates will cause the pollen to be formed under different circumstances. By using the same plant for crosses every day during its pollen shedding period, environmental influences can be assessed. The pollen shed on one day may have formed during a cool period, and that shed on the next day during a warm period.

In general, the data are more homogeneous than those found when trisomic standard-exotic hybrids were used. Note interaction chi squares. The amount of preferential pairing observed is of a similar magnitude. In the cases of Hy and 38-11 it is as strong as that observed when In 3a or In 3b was used. This finding is relevant to the problem of the synthesis of an artificial allotetraploid. At first, it was thought necessary to use inversions; after the results with exotic races the program envisaged collecting all sorts of chromosomes with cryptic structural differences from all parts of the world. Now, it appears to be possible to use native adapted commercial inbred lines. In simple terms, many small structural differences from different inbred lines will be converged together by a breeding system employing recurrent selection for

*Possibly resulting from unequal crossing over in tandem duplications which may be very common in maize; see next note.

preferential pairing. Progress toward allotetraploidy will be monitored by observing the quadrivalent frequency and modifications of gene segregation. The exact details of the breeding system remain to be worked out.

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4. X-ray induced duplications from translocations between homologous chromosomes.

Translocations between the same arms of homologous chromosomes lead to the formation of a chromosome with an interstitial deletion and a chromosome with a tandem duplication, if the breakpoints are not identical. If it is assumed that the chromosomes in the interphase nucleus in somatic tissue are arranged at random, then the expected frequency of this event would be very low. Translocations between opposite arms of homologous chromosomes form pseudo-isochromosomes. The frequency of pseudo-isochromosomes has been found by Koo to be $1/4 (n-1)$ times the frequency of translocations between non-homologues, where n equals the haploid chromosome number. However, if there is a tendency for homologous chromosomes to be in a semi-paired state in the interphase nucleus as numerous investigators now believe, then we would expect the frequency of tandem duplication production to be higher than that of pseudo-isochromosomes. The probability of two broken ends uniting to form a new structural rearrangement is a function of the distance between them. A chromosome arm may be just as far away from the opposite arm of its homologue as it is from the arms of non-homologues, but may be much nearer the homologous arm of its homologue, than to any other arm.

The method used to detect tandem duplications has been presented in previous reports. In brief, they are detected by aberrant ratios from plants in the X_2 generation which come about by crossing over in one of the duplicated segments. Kernels which were heterozygous for 10 different markers were given 10,000 r in two different trials. The constitution of these kernels was Kys (with all dominant genes) over Mangelsdorf's tester (bm₂, lg₁, a₁, su, pr, y, gl₁, j, wx, and g). Only the lg, su, y, gl, wx, and g loci were followed. The plants grown from the irradiated seed were crossed to Kys to form the X_2 generation. There were 1169 X_2 plants which were crossed to Mangelsdorf's tester or to a