Assuming gametophyte factors are not responsible for the aberrant ratios, all the trisomes with an exotic chromosome exhibited preferential pairing to a statistically significant degree, except in the case of the Gourdseed trisome. The possibility that gametophyte factors on chromosome 3 may be influencing the data can be checked using the disomic sibs of the trisomes. The disomic sibs should give a 1:1 ratio if gametophyte factors are absent. This has been found to be the case in Gourdseed, Papago, and Zapaluta chica.

This preferential pairing is believed to be indicative of structural dissimilarity between standard and exotic chromosomes. The nature of these structural differences is unknown. They may be small inversions, interpolations of heterochromatin or teosinte chromosome segments, or perhaps many very small structural differences on the level of magnitude of a gene. Crosses of standard-exotic hybrids and the standard trisomes will be made in the greenhouse this winter. The progeny will be examined for the degree of preferential pairing. In this way it should be possible to determine something about the structural differences.

It is noteworthy that the Gourdseed trisome did not exhibit a significant degree of preferential pairing. The standard is closely related to corn belt maize. Gourdseed (or a variety related to it) is believed to be one of the progenitors of corn belt maize. The exotic strain which exhibited the most preferential pairing, Avati tupi, is from Paraguay and is probably the least related to the corn belt maize strains.

G. G. Doyle

2. The synthesis of an artificial allotetraploid corn strain.

An allotetraploid corn strain would breed true for chromosome number and thus aneuploidy which is responsible for much of the sterility in tetraploid lines could be eliminated. Also an allotetraploid would be a true breeding single cross hybrid and any genetic constitution which is favorable for tetraploid fertility could be stabilized.

There are three methods by which an allotetraploid strain of corn can be produced. A corn genome must be modified by chromosome structural changes so that it loses most of its pairing affinity with the standard corn genome. In previous issues of the News Letter (32, 33, and 34) the writer presented data on the reduction in pairing affinity resulting from one inversion, In 3a. It was found that in tetraploids with the constitution of In 3a/In 3a/N 3/N 3 structurally homologous chromosomes were paired 77% of the time. In trisomes heterozygous for In 3a the corresponding frequency was 75%. If pairing were at random these values would be only 33.3%. If a chromosome contained several inversions it is probable that the pairing affinity would be very greatly reduced. Recent work by Grell with triploid Drosophila indicates that this is true. The first method is therefore to produce chromosomes containing many inversions by crossing inversion stocks. The writer has acquired 65 different inversions from various sources and has made crosses of combinable inversions. Unfortunately most of the inversions are overlapping and therefore not combinable. Extensive irradiation work is being carried on in an attempt to increase the supply of inversions.

The second method approaches the problem of developing multi-inverted chromosomes by the irradiation of material which already has one inversion in the hope of inducing a second one on the same chromosome. Last summer pollen from In 3a/In 3a plants was given 1000 r and was placed on silks of trisome 3 plants with constitution of $\underline{a_1}/\underline{a_1}/\underline{a_1}$. If no new inversion was induced then the frequency of $\underline{A_1}$ (from the In 3a stock) in the backcross progeny of the trisome used as the pollen parent should be about 22%. If another inversion has been induced in chromosome 3 then this frequency should be less. The modified In 3a chromosome will be subjected to further irradiation to obtain a third inversion and so forth. Eventually a new chromosome 3 will be produced which will have very little pairing affinity for the standard chromosome 3. If this procedure works satisfactorily it will be done with the other chromosomes.

The third method is suggested by the results obtained with the exotic trisomes. While none of the exotic chromosomes exhibited enough differential pairing affinity to be used in an allotetraploid, it should be possible to find recombinant chromosomes in the progeny of hybrids of exotic strains which will exhibit more preferential pairing than either of the parents. For example a hybrid of Zapaluta chica and Papago flour corn will be crossed with the standard trisome 3. Recombinant chromosomes should show transgressive segregation for pairing affinity if these two strains have different structural rearrangements. Other hybrids will be used.

G. G. Doyle

3. <u>Numerical non-disjunction in tetraploid corn.</u>

Numerical non-disjunction is the 3 to 1 separation of four homologous chromosomes of a tetraploid at the first division of meiosis. This event results in aneuploidy in the offspring of a eutetraploid.

The frequency of numerical non-disjunction can be determined for a particular chromosome by crossing a quadriplex (<u>AAAA</u>) with a nulliplex (<u>aaaa</u>), and then progeny test the offspring. If numerical non-disjunction has not occurred the result is a plant with the constitution of <u>AAaa</u> which will give a testcross ratio of about 5:1. The products of numerical non-disjunction will be triplex and simplex (usually <u>AAAaa</u> and <u>Aaa</u>) which give testcross ratios of about 12:1 and 1:1, respectively. All these ratios can be easily distinguished. The frequency of numerical non-disjunction has been determined for two chromosomes, 2 and 9, using the $\underline{Lg_1}$ and <u>Wx</u> loci, respectively. The initial crosses of quadriplex by nulliplex were made by D. L. Shaver.

Table 2. The frequency of numerical non-disjunction

Cross	Triplexes	Number of Duplexes	Simplexes	% Numerical Non-disjunction
4n lg X 4n Lg	2	83	1	3.5
4n Lg X 4n lg	5	239	9	5.5
4n wx X 4n Wx	4	332	1	1.5
4n Wx X 4n wx	2	93	5	7.0

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