from the population in a few generations, but the supply is being constantly replenished by errors in the meiosis of eutetraploids. Additional data on numerical non-disjunction are presented in Table 4.

Table 4

Numerical non-disjunction in tetraploid maize

Cross	Number of plants with the genotypes of:				
	2(Ash) 2(aSh)	3(Ash) 2(aSh)	2(Ash) 3(aSh)	2(Ash) 1(aSh)	1(Ash) 2(aSh)
4(aSh) X 4(Ash)	219	3	6	6	1
4(Ash) X 4(aSh)	62	2	3	1	0
Total	281	5	9	7	1

Progeny tests were made on 303 plants from a cross of 4(aSh) X 4(Ash) or the reciprocal. It may be seen from Table 2 that each of the five expected genotypes gives very characteristic ratios and may be readily distinguished. All ears with fewer than 100 kernels were discarded.

There were 14 plants (4.53%) which resulted from trisomic gametes and 8 (2.59%) which were from monosomic gametes. If this difference is valid, it probably is due to the fact that hypoploid zygotes are less viable than hyperploid ones. It would appear also that aneuploid gametes function more frequently on the female side than they do on the male. There were 14 cases of aneuploidy attributible to the female and only 8 in the case of the male. Additional data are required to settle some of these points.

G. G. Doyle

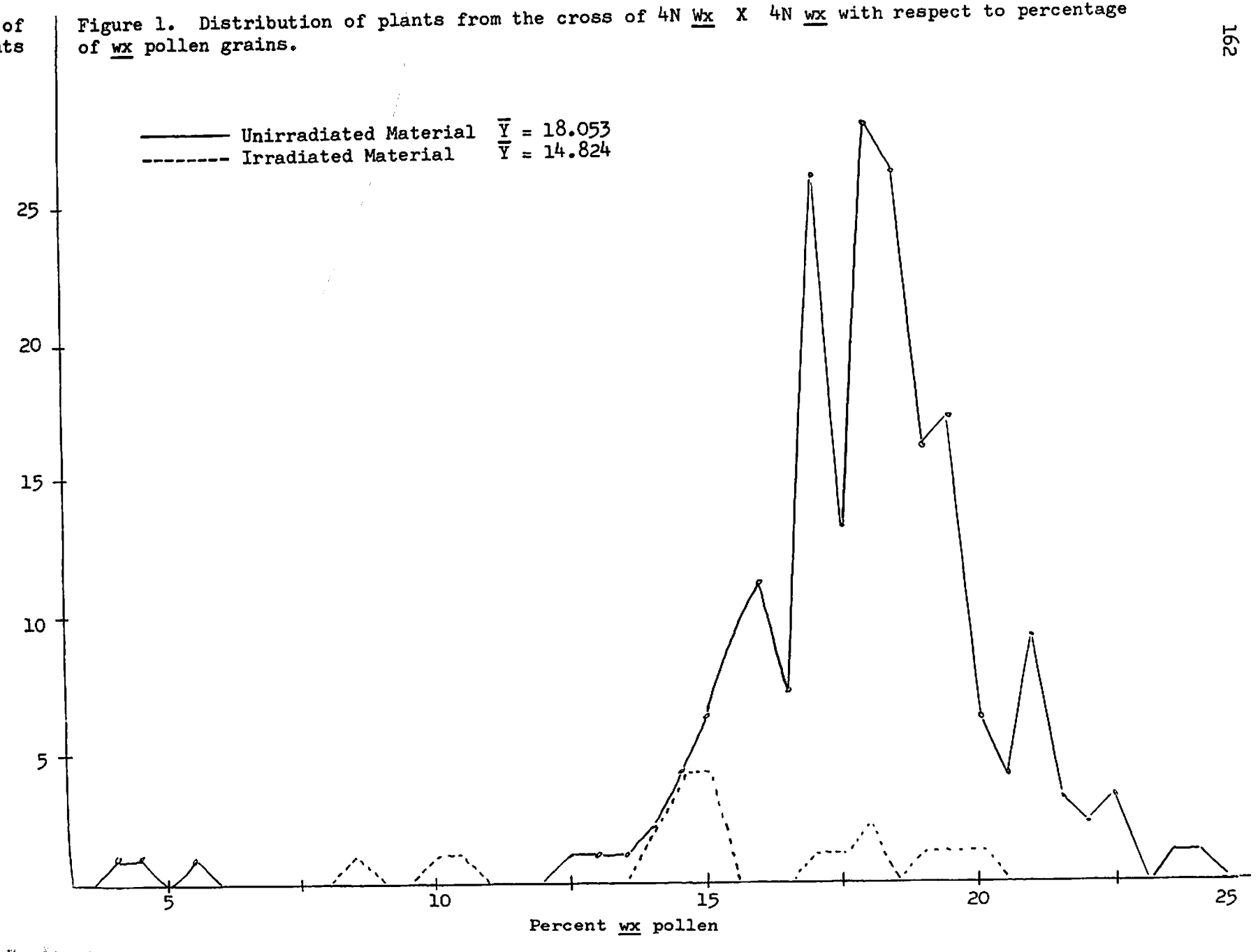
5. The synthesis of artificial allotetraploid maize.

An artificial allotetraploid maize would be true breeding for chromosome number and the partial sterility resulting from aneuploidy could be eliminated. In addition, it would be a true breeding hybrid.

Since maize is not closely related to any other species (with the exception of teosinte), it is necessary to create a "new species" of maize in order to produce an allotetraploid. This is theoretically possible to do in two ways. A maize genome must be produced which has very little pairing affinity with the standard genome. Structural rearrangements of the chromosomes have been shown to produce a decrease in pairing affinity. Therefore, 21 inbred lines of maize have been irradiated for seven generations with an accumulated dose of 35,000 r. Also, a tetraploid line (a selection from Alexander's Synthetic B) has been likewise irradiated for five generations with an accumulated dose of 25,000 r.

Alternatively, we can take advantage of the fact that maize is a widely spread species which has a great number of races. These races have been shown by preferential pairing studies in trisomic 3 racial hybrids to be quite variable in their chromosome structure. It is possible, by a system of recurrent selection to be described later, to concentrate these small structural differences in a few lines and then to cross them with the standard genome. There is a question as to whether these small structural differences, which modify pairing affinity on the trisomic level, will also do so on the tetraploid level. Consequently, a 4n wx stock was crossed with seventy-eight different 4n Wx plants. These plants were a heterogeneous mixture of various marker stocks derived from various sources and newly synthesized tetraploids. They were not homozygous and cannot be characterized as to origin. They probably represent only a small fraction of the variability in chromosome structure to be found among the races of maize. Tassel samples from three plants in each of the progenies of the seventy-eight crosses were taken and preserved in 70% alcohol with a dash of formalin. Pollen from anthers of 6 florets was stained with I-KI solution and between 600 and 700 pollen grains were counted. The results are given in Figure 1. A total of 198 tassel samples was examined and found to be of the desired constitution (Wx/Wx/wx/wx); a number of others were found to be simplex-- either Wx/wx/wx (from numerical non-disjunction) or Wx/wx/wx/wx (from unsuspected Wx/Wx/Wx/wx triplexes in the "4n Wx" parents). These tassel samples were discarded. Also three tassel samples gave very low

Figure 1. Distribution of plants from the cross of 4N Wx X 4N wx with respect to percentage of wx pollen grains.



percentages of wx; these plants were probably pentasomics (Wx/Wx/Wx/wx/wx) which arose from numerical non-disjunction. They are shown at the left side of the graph, but the data from them are not included in computing the mean.

The distribution appears to be trimodal. A total of 136,694 pollen grains was counted, of which 18.053% were wx. There were seventeen plants which had significantly higher percentages of wx pollen and fifteen plants where the percentage was significantly lower. This is believed to be indicative of the presence of structural dissimilarity in regard to chromosome 9. The deviations above the mean frequency have been observed in analogous experiments with trisomes. It is believed that structural differences affect the patterns of multivalent disjunction in a yet unexplained manner.

Likewise, 20 tassel samples were taken from the progenies of nine crosses between tetraploid wx and the tetraploid Wx strain which had been subjected to irradiation for several generations. A total of 14,706 pollen grains was counted and 14.82% were wx. Thirteen out of 22 plants showed a significantly lower percentage of wx pollen.

These results indicate that there is a wealth of naturally occurring structural differences which affect pairing affinity at the tetraploid level and also that they can be readily produced by irradiation. Consequently, a breeding program designed to concentrate these differences in a single genome would have something to work with and would have a good chance of success.

Any breeding system in tetraploids must take into account that there are no good inbred lines available and that only a small fraction of the available germ plasm has been introduced into the tetraploid level. Consequently, we must work with material which is equivalent to open-pollinated varieties and allow for the introduction of new material into the breeding system as it becomes available.

The proposed method is to create a pool composed of samples from all the tetraploid strains available to which will be added new strains as they are produced. The gene ameiotic (am) is being introduced into a wide variety of exotic races and into irradiated and unirradiated

Corn Belt inbred lines. When a diploid plant homozygous for am is crossed by a tetraploid pollen parent, a few tetraploid kernels are formed. All possible crosses and selfs will be made in this pool and kept separate. Every year plants from this pool will be self-fertilized and used as the male parents in crosses with tetraploids which are homozygous for one or more of the markers: bz_2, lg_1, a_1, su_1, pr, y_1, gl_1, v_{16}, wx, and g_1. There is one marker for each of the 10 chromosomes. Ideally, all these markers would be in the same strain. Since some of the traits interfere with expression of other traits (a_1 with bz_2 for example), two or three strains will be used. These strains will be made as closely related as possible and will arbitrarily be called the standard. In the following year the hybrids will be testcrossed onto the standard multiple recessives and a value called the allosyndetic index will be computed. The allosyndetic index is the sum of the percentages of all 10 recessive segregants. It has a theoretical maximum of 214 and a minimum of 0. The maximum occurs when all genes are segregating as in random chromatid assortment. The minimum would be found in a true breeding allotetraploid. Strains which have a high allosyndetic index will be discarded from the pool, and those with low indices will be retained and crossed with each other in an effort to concentrate the structural differences responsible. Several strains which have high allosyndetic indices will be maintained outside the pool to provide the eventual breeding partners with the modified strains.

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

This experiment has been described in great detail in previous reports. Translocations between the same arms of homologous chromosomes form a chromosome with an interstitial deletion and a chromosome with a tandem duplication. The probability of this occurrence is rather low in relation to the frequency of translocations between nonhomologous chromosomes. For a particular gene to be included in the tandem duplication the probability is $1/4(n-1)(1/2n)(1/2)T$, where n is the haploid number of chromosomes and T is the frequency of translocations between