Previously, Dempsey (1956 Maize News Letter) reported 50.1 and 48.8 percent waxy for simplex and 18.7 percent for duplex segregations. Levings (1963 Thesis, Illinois) reported about 17 percent waxy segregation for duplex and computed an alpha value of 0.0097 for duplex.

As the differences between the percentages expected for no double reduction and for maximum double reduction are not great, alpha values, and consequently map units from centromere, vary considerably for even small percentage changes. Hence, double reduction and alpha values determined in this way may be of little value in mapping the centromere.

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8. Bivalent pairing in autotetraploids.

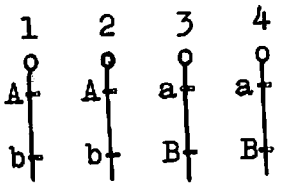
In autotetraploid maize and alfalfa, it is not known whether the bivalent pairing that occurs is preferential or at random. Consequently, a linkage method has been devised to determine which type of pairing actually occurs. Although single locus segregations are affected by the type of pairing, differences will be much greater where linkage is involved, and the linkage test is more discriminating.

Autotetraploid alfalfa produces mostly bivalents at meiosis, and the test was conceived for use on alfalfa. However, the principles also apply to putative allotetraploids such as 4n maize X 4n teosinte hybrids, and to lines of 4n maize which consistenly produce some bivalents. Many 4n maize lines observed at Minnesota produced two or more bivalents per cell, probably chromosome 10, and presumably the number will increase in time through 'diploidization'.

The technique in its simplest form requires:

1) two linked genes in a biduplex X binulliplex testcross,
2) phenotypic classification of progeny, and
3) chi-square tests of observed to expected segregations for random or preferential pairing.

The three possible modes of bivalent pairing for four 'homologous' chromosomes are given below. A biduplex repulsion genotype is illustrated.



Mode

I Homogenic preferential (Autosyndetic in alloploids) — 1 pairs with 2; 3 with 4

II Heterogenic preferential (allosyndetic in alloploids) — 1 " " 3; 2 " 4
1 " " 4; 2 " 3

III Random pairing - 1/3 homogenic + 2/3 heterogenic

With homogenic pairing, no phenotypic segregation is expected in the first testcross and it may be easily distinguished. With partial or complete heterogenic pairing, however, chi-square tests will be required to accurately distinguish it from random pairing.

Percentages of each phenotype expected from the bi-duplex X binulliplex testcross and the chi-square differences between random and heterogenic preferential pairing are listed below. Chi-square values are based on a population of 200.

COUPLING	50% recomb.			10% recomb.		
	Homo-genic	Random	Hetero-genic	Homo-genic	Random	Hetero-genic
A-B-	100	70.83	56.25	100	80.16	70.25
A-bb		12.50	18.75		3.17	4.75
aaB-		12.50	18.75		3.17	4.75
aabb		4.17	6.25		13.50	20.25
		$X^2 = 17.28$**			$X^2 = 9.41$*	
REPULSION						
A-B-	(same as above for coupling)			100	66.83	50.25
A-bb					16.50	24.75
aaB-					16.50	24.75
aabb					.17[1]	.25[1]
					$X^2 = 22.0$**	

[1]This class is very small and may be eliminated from the test.
**Probability exceeds the 1 percent level.
* " " " 5 " " .

Comparisons of the chi-square values for coupling and repulsion indicate that the difference in repulsion increases as the strength of linkage increases. Therefore, the test in repulsion should be the most useful, especially when it is necessary to distinguish frequencies of preferential pairing that are close to those expected for random pairing.

In a self-pollinating species, the same test could be carried out using F_2 genotypic classifications based on F_3 segregations.

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1. Viruses as agents for mutation and chromosome breakage.

The resemblance of the variegated phenotype produced by certain mutable systems in corn and the variegated symptoms produced by certain viruses in other plants suggests a possible relationship. Perhaps viruses are involved in the production of controlling elements or perhaps systems of mutability represent latent forms of infectious viruses. To test these possibilities a number of experiments have been conducted including one designed to determine whether particular viruses that infect corn can cause gene mutation or chromosome breakage. Evidence has already been presented by Sprague, McKinney and Greeley (1963) that corn plants infected with barley-stripe-mosaic have a higher frequency of loss of the dominant endosperm markers A Su and Pr than do healthy plants.

This experiment consisted of inoculating seedlings of an A^b ($\alpha\beta$) Sh, Dt stock with a virus and then using the pollen from infected and healthy plants, when they matured, to pollinate ears of the genotype a^m-sh, dt. In addition, some of the healthy and the infected pollen parents were treated with X-rays, either premeiotically or postmeiotically applied. The doses were 750r and 2000r respectively, and were given to provide broken chromosome ends for possible interaction with the virus and for comparison with virus results.