

UNIVERSITY OF ILLINOIS
 Urbana, Illinois
 Department of Agronomy

and

NORTH CAROLINA STATE COLLEGE
 Raleigh, North Carolina
 Department of Crop Science

1. Some estimates of double reduction in autotetraploid maize.

The coefficient of double reduction (α) was determined for eight loci in autotetraploid maize (Table 1). Alpha values were derived from duplex backcross data. Two estimates of alpha appear for each locus. The first is based upon the assumption of no numerical non-disjunction ($x = 0$) while the second alpha value is corrected for a numerical non-disjunction of 0.0258 per chromosome ($x = 0.0258$). The occurrence of numerical non-disjunction results in an over estimation of alpha; therefore, correction for numerical non-disjunction decreases the size of alpha.

Formulas for estimation of the parameter alpha and its standard error were derived by the log likelihood method. The formula for alpha and its standard error are:

$$\alpha = \frac{12z - x - 2}{4 - 3x},$$

and,

$$S_{\alpha} = \frac{12}{4 - 3x} \sqrt{\frac{z(1 - z)}{n}},$$

where z is the proportion of recessive phenotypes in the population, x is the frequency of numerical non-disjunction and n is the total number in the population.

Crude estimates of a gene's location with respect to the centromere can be ascertained from the magnitude of alpha. Genes in close proximity to the centromere have small alpha values while genes more distal to the centromere have larger alpha values. The alpha values for the a_1 and lg_1 loci are not significantly different from alpha values expected from random chromatid segregation. Since the genes, a_1 and lg_1 are known to be more than 50 map units from the centromere, these alpha values are in general agreement with the known location of the loci with respect to their centromeres. The loci, r , g_1 , ye_2 , su_1 and y_1 , have alpha values which are significantly different from those expected of random chromatid segregation, complete equational separation and chromosomal segregation. Alpha values of this magnitude are

expected of genes which are less than 50 units from the centromere but not completely linked to the centromere. Four of the five loci, r_1 , g_1 , su_1 and y_1 , have alpha values in agreement with their location with respect to the centromere. The fifth, yg_2 , has an alpha value which is too small, since yg_2 is known to be located more than 50 units from the centromere. The gene wx_1 has an alpha value which is not significantly different from that expected of chromosomal segregation. There is a difference of opinion as to the distance between the wx_1 locus and its centromere. It has been estimated by Anderson and Randolph to be between 2.0 and 3.6 units away from the centromere. The alpha value obtained for the wx_1 locus indicates very close linkage of the gene and its centromere. With one exception, therefore, the magnitude of alpha was reliable in giving a rough estimate of the gene's location with respect to the centromere.

Table 1 Alpha and its standard error when numerical non-disjunction is zero and 0.0258.

Locus	Standard error		Standard error	
	α		α	
	$x = 0$		$x = 0.0258$	
a_1	.1693	$\pm .0380$.1661	$\pm .0387$
r_1	.0526	$\pm .0153$.0471	$\pm .0156$
lg_1	.1066	$\pm .0201$.1021	$\pm .0204$
g_1	.0514	$\pm .0146$.04858	$\pm .0149$
yg_2	.0988	$\pm .0482$.0942	$\pm .0389$
wx_1	.0097	$\pm .0341$.0033	$\pm .0348$
su_1	.0478	$\pm .0080$.0422	$\pm .0082$
y_1	.0385	$\pm .0066$.0327	$\pm .0067$

C. S. Levings, III
D. E. Alexander