2. <u>A promising method of analyzing marked chromosome segments carrying genes for quantitative characters</u>.

Backcross-heterozygote testing involves using two parents with contrasting genetic factors, which make it possible to separate the homozygote from the heterozygote on the basis of endosperm characteristics. Past studies of quantitative gene action have generally involved the entire chromosome complement. A more accurate test might be obtained by studying only segments containing genes linked with the marker gene.

With yellow endosperm as the marker, an F_1 between a white and a yellow inbred was backcrossed to both parents. Seed homozygous and heterozygous for endosperm color may be separated in both backcrosses, giving the four classes in Table 1. The marked chromosome segments will be variable in size due to crossovers. However, with adequate sampling the marked segments should be equal in all classes.

Table 1. Types of Marked Segments and Possible Theoretical
Action of Genes on These Segments

| | | | Action of genes on the marked segments | | | | |
Class	Pedigree	Genotype of marked segment	R30(y) segment dominant	M14(Y) segment dominant	Heterosis for Y/y	Y interacting with R30 complement	y interacting with R30 complement
1	(M14XR30)R30	Y/y	1	1	1	1	1/3
2	(M14XR30)R30	y/y	1	0	0	0	1/3
3	(M14XR30)M14	Y/y	1	1	1	1/3	1
4	(M14XR30)M14	Y/Y	0	1	0	1/3	0

Classes 1 and 3 (Table 1) will be equal in regard to the marked segments, each having M14(Y) and R30(y) segments. Class 2 will be homozygous for the R30(y) segments and class 4 will be homozygous for the M14(Y) segments. The genotype of the remaining unmarked chromosomes on the average will be 3/4 R30 and 1/4 M14 when backcrossed to R30 and 1/4 R30 and 3/4 M14 when backcrossed to M14. In Table 1 this proportion of recurrent parent is assumed to have no differential effects independent of the marked segments. In actual tests this would not be true in many instances.

The actions of genes on the marked segments in Table 1 are theoretical. There also may be complicated interactions of the various types of gene actions, which would make it impossible to determine the gene actions concerned. However, there will be some instances in which the gene action is discernible.

Table 2. Performance of Single Cross Hybrid & Backcross-Heterozygotes*

| | | | Height | | Ear | Kernel | Ear |
Class	Pedigree	Genotype	Ear	Plant	length	row no.	weight

1	(M14XR30)R30	Y/y	29.6	68.9	8.56	7.56	17.5
2	(M14XR30)R30	y/Y	30.4	69.8	7.99	7.50	15.7
3	(M14XR30)M14	Y/y	30.2	70.6	8.20	8.34	14.8
4	(M14XR30)M14	Y/Y	26.4	66.6	8.30	8.09	13.9
	M14XR30		32.7	74.6	9.23	7.67	18.9
	L.S.D. 5%		1.8	1.4	.29	.37	1.6

*Four replications of 30 plants each.

Table 2 gives some actual data on such material. Classes 1, 2, and 3, possessing the R30(y) segment, exhibited greater plant and ear height than class 4 which has no R30(y) segment. This indicates the R30(y) segment carries genes dominant for greater plant and ear height, while the M14(y) segment carries recessive genes.

Classes 3 and 4 are of nearly equal ear length, despite the presence of R30(y) segment in class 3 and its absence in class 4. Therefore, the R30(y) segment does not appear to carry genes modifying ear length, or does not differ from the M14(Y) segment in such genes. The M14(Y) segment may carry dominant genes for ear length, but class 1 is longer eared than expected. These ear length data may fit the scheme in Table 1 in which genes on the M14(Y) segment are interacting with the unmarked R30 complement. This would account for the greater ear length in class 1 as it contains the M14(Y) segment and has a maximum amount of R30 complement.

The larger proportion of M14 complement present in classes 3 and 4 resulted in higher kernel row number than classes 1 and 2 which are made up largely of R30 complement. Since classes 1 and 2 are nearly equal in row number, the presence of the M14(Y) segment in class 1 had little effect on row number. If the superiority of class 3 over 4 is significant, it might indicate that the R30(y) segment was interacting with the M14 complement.

Presence of a larger proportion of R30 in classes 1 and 2 (backcrossed to R30) resulted in greater yield than classes 3 and 4 (backcrossed to M14). Class 1 significantly outyielded class 2, due, of course, to the presence of the M14(Y) segment in class 1. The presence of the R30(y) segment in class 3 did not differentially affect yield in contrast to class 4 in which the R30(y) segment is absent.

All the possibilities of the backcross-heterozygote testing outlined above have not been discussed in this brief note. However, on the basis of the limited data, the method does appear to offer some promise in determining the action of genes affecting quantitative characters.

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