Enzyme was detected in normal dent and the mutants ae, bt_1, bt_2, du, fl_1, o_2, sh_1, sh_2, su_1, su_2 and wx. Results of analyses of kernels at 16, 20, 24 and 28 days after pollination and at maturity (air dry) indicated that activity increased from 16 to 24 days and then began to drop. Very little activity was detected in dry kernels.

The enzyme may play an important role in starch synthesis even though it is a degradative enzyme. Possibly, the enzyme degrades the long molecules formed by ADPG- and/or UDPG-transferase to form more acceptors for glucose transfer, thereby increasing the efficiency of the transferases. The enzyme was not demonstrated to synthesize higher polymers. It was concluded that the enzyme is an alpha-amylase because it cleaved the glucosidic linkages of amylose and cleaved beyond the branch points of beta-limit glycogen to produce small molecular weight oligosaccharides. The other characteristics of the enzyme are similar to alpha-amylases. This is the first time that alpha-amylase has been characterized in developing maize endosperm.

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1. Modification of Anderson's method for transferring genes via translocations.

Anderson's method (see Brookhaven Symposia in Biology No. 9 pp. 30, 31) involves three main steps as follows: Finding a translocation with a breakpoint close to the locus of the gene to be transferred, backcrossing the translocation into the inbred to be improved, and backcrossing the desirable gene into the inbred that temporarily carries the translocation. Two complete backcrossing programs are necessary to obtain the recovered inbred that contains the desired trait, a normal chromosome complement, and a minimum amount of foreign chromosome.

With the advent of an increasing proportion of single cross commercial hybrids, it might be advantageous to permanently place the translocation into the converted inbred along with the desired trait. This would reduce the number of backcross programs from two to one per line.

The main points of the modified scheme might be summarized as follows: Cross the suitable translocation (one with a breakpoint near the desired gene) to the stock carrying the desirable gene; then make the appropriate backcross in order that both the translocation and the desirable gene are segregating; identify and maintain crossover plants that link the desirable gene to the breakpoints of the translocation. Once the desirable gene translocation stock has been made, it may be used as a source for backcross programs to inbred lines; selection may be for the desirable gene and/or semi-sterility due to the translocation.

The modified scheme differs from Anderson's method and standard (without translocations) backcross methods in that converted inbreds must be used with other converted inbreds carrying the same translocation to avoid semi-sterility in the farmer's field. Consequently the modification's use is less cumbersome for single cross hybrids than where more inbreds are used per hybrid.

The modified translocation scheme differs from backcross programs without translocations in other ways: As in Anderson's method the suitable translocation stock must be found that has its breakpoints in close proximity to the location of the desired gene and in addition crossover plants that link the trait to the breakpoints must be produced. Semisterility may be used for selection in lieu of the trait in unfavorable environments (disease resistance in absence of disease for example), and fewer testcrosses (to insure the gene's presence) are necessary when a recessive trait is involved. Extra generations of backcrossing will be necessary (to obtain a minimum amount of foreign chromosome) in order to compensate for the reduction of crossing over near the desired gene due to the presence of the translocation. One less generation will be required at the end of the backcrossing program for a dominant trait because plants homozygous for the trait can be discerned from those heterozygous since the former will have normal and the latter semisterile pollen and ovules.

The following Mankato 1964 backcross data illustrate the method of obtaining the desired stocks that link breakpoints of translocations with Ht (a dominant gene that reduces sporulation of Helminthosporium turcicum leaf blight in corn):

Trans.	breakpoint	ht S	ht N	Ht S*	Ht N	% C.O.
2-6d	2L.41	146	37	30	155	18.2
2-4L	2L.59	184	10	21	153	8.4
2-4b	2L.81	144	21	36	179	15.0

*Crossover class linking Ht and the translocation.

These data indicate that Ht is located cytologically near the middle of the long arm of chromosome two. More translocation stocks were obtained with breakpoints in this general area. The 1966 Mankato backcross data follow:

Trans.	breakpoint	Ht S*	Ht N	% C.O.
2-10 (8219)	2L.50	3	133	2.2
1-2d	2L.56	9	154	5.5
2-6 (9002)	2L.57	36	108	25.0
2-8 (051-15)	2L.62	21	105	16.7
2-3d	2L.67	19	97	16.4

*Crossover class linking Ht and the translocation.

The Ht S class for 2-10 (8219) or the progeny from it that also link Ht and the breakpoints would be a desirable source to initiate a

backcrossing program for Ht.

The data for 2-6 (9002) appear to be somewhat out of line with the other stocks; this may be due to sampling error or faulty cytological determination of breakpoints.

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2. A second modification of Anderson's method.

A similar, but somewhat different modification of Anderson's method has been used to move $\underline{Rf}_1$ into genotypes of $\underline{rf}_1$ constitution. Selection of a close linkage between a translocation and the desired gene is made, as in the above scheme, but the intention is to break the linkage after sufficient backcrossing has been done. This will require selfing and testcrossing large numbers of individuals at the end of the backcrossing series, in order to pick up the infrequent recombinations of normal chromosomes with desired gene. In this respect the scheme is more cumbersome than the first one, but it does give one a recovered line with normal chromosomes, should one desire this.

Translocation 3-9c has about 3% recombinations with $\underline{Rf}_1$. The recombination of T3-9c and $\underline{Rf}_1$ was identified and has been placed in three inbred lines, by continual backcrossing (in normal cytoplasm) with selection (by examination of pollen and ears) for semi-sterility. Two plants per inbred were selected in each generation. At BC^4, testcrosses revealed that all plants tested still had the desired linkage of T3-9c and $\underline{Rf}_1$. At BC^7 an attempt was made to identify and self (with testcrossing) large numbers of normal-chromosome backcross plants in one of the lines ($WF9^7$), hoping that some 3% of the normal-chromosome plants would have $\underline{Rf}_1$. Due to hot weather at pollinating time nearly all BC^7 plants were partially sterile and it was not possible to classify their tassels for presence vs. absence of semi-sterility (presence of 3-9c in heterozygous condition). A few random selfs and testcrosses were made successfully, however, all going back to two semi-sterile BC^6 plants. One of the two BC^6 plants whose BC^7 progeny was tested proved still to have $\underline{Rf}_1$ linked with T3-9c (genotype $\frac{T\ \ \underline{Rf}_1}{N\ \ \underline{rf}_1}$). The other plant appeared to have an undesired recombinant, having $\underline{rf}_1$ linked to T3-9c (genotype $\frac{T\ \ \underline{rf}_1}{N\ \ \underline{rf}_1}$).

Further attempts will be made to identify desired recombinants.

This scheme also is being used to "cure" inbreds of partial restoration. T3-9c with $\underline{rf}_1$ is being transferred to plants of partial restorer genotype ($\underline{Rf}_1^P$) with the intention of selecting recombinants with normal chromosomes and $\underline{rf}_1$ genotype at the end of the backcrossing period. This method obviates the need for testcrossing backcross plants, to distinguish those of $\underline{Rf}_1^P\ \underline{rf}_1$ genotype from those of $\underline{Rf}_1^P\ \underline{Rf}_1$ genotype.

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