1. A-B interchanges as a method of screening for new mutants in specific segments.

The use of A-B interchanges in assigning the linkage group of a previously isolated recessive factor makes it possible to obtain information in the F_1 generation. Where large numbers of unplaced mutant factors are available and the problem is that of assigning these to their respective linkage groups the conventional use of A-B translocations should prove a great advantage over the older method. Considered from the point of view of maize genetics as a whole the placement of such large numbers of factors more or less at random on the chromosome maps is a highly desirable enterprise since it stands to benefit all maize geneticists in the long run. However experimental studies often place a premium on several marker genes in a particular linkage group, in a single arm or even in a restricted region of a particular arm of a chromosome. Considering the current status of chromosome maps in maize that aspect of a problem which poses these requirements often must either be dropped or postponed until our present "shot-gun" method yields the desired markers. The numerous stocks of reciprocal translocations which are now available may be the solution to this problem in some cases but have the disadvantage that the phenotype of this kind of marker is manifest only in the mature plant; moreover the associated effects on crossing over and gametophyte viability are disadvantages in numerous studies. Some method is required which will enhance the frequency with which plants carrying new mutant genes may be recognized and which will at the same time screen for mutants which have a favorable location in terms of the requirements of specific studies.

The A-B interchanges should prove to be ideal testers for this purpose. According to the method proposed here a pollen parent carrying a selected reciprocal A-B interchange is crossed, not with plants carrying a previously selected mutant character whose linkage placement is sought, but with normal plants. Since, following non-disjunction in the second microspore division of the pollen parent, the great majority of immediate offspring (embryos or endosperms) are deficient for the acentric portion of the A-chromosome which is translocated to the B chromosomes, any mutations which occur in the corresponding segment in the normal plant, which are incorporated in functional megaspores and which finally come to reside in hypoploid complements should be immediately expressed and identified. Thus each F_1 hypoploid, plant or endosperm tests a single gamete of the normal plant for mutation of previously unidentified genes lying in the specified segment. In contrast, by the present method of obtaining new mutants, an entire F_2 progeny is required to test single gametes. The method proposed here has the same advantage as that enjoyed in studies dealing with the isolation of visible mutations carried in the X-chromosome of Drosophila males, the latter being from the standpoint of most of the sex-chromosome material, haplo-X.

In addition to the expected greater efficiency in the recognition of newly arising mutants this method is expected to have the following advantages: (1) Depending on the particular A-B interchange employed a variety of A-chromosome segments may be screened for mutation; (2) In the case of hypoploid mutant embryos the deficient complement is not expected to transmit through the gametophyte and since the mutant gene is carried on a normal chromosome the progeny of the selfed, mutant hypoploid should be composed entirely of plants which are homozygous for the mutant factor and have an entirely normal complement of chromosomes; (3) The incorporation of desired gene combinations or structural modifications into the background of the new mutant stocks need not await the discovery of a desired new mutant factor. Stocks with the desired combinations may be utilized directly as the egg parent in the cross with the interchanged tester parent.

The degree of application of the proposed method would be a function of the variety of A-B interchanges available. While stocks involving such interchanges for almost half of the 20 chromosome arms in maize are now available studies involving the remaining arms would not be aided by this method. Moreover, the technique does not lend itself to the isolation of mutants lying in close proximity to their respective centromeres. A further disadvantage which applies to the isolation of seedling mutants by this

method lies in the fact that the hypoploid plant is often less vigorous than the normal plant.

We are at present studying the feasibility of this method and are utilizing several A-B interchanges and analyzing mutations in both the embryo and endosperm. A recent search for mutants among the seedling progenies of crosses of normal plants with a plant carrying the T B-3a interchange gave encouraging results. At the present time it is not possible to state the frequency of mutant embryos among these progenies since the analysis is not complete and moreover there is always the tendency to select as possible cases the plant, with slight as well as striking deviations from normal. However, there were included among selected cases a number of striking virescent, albino, glossy, pale-green and luteus plants. In a number of families there occurred several individuals with the same striking singular phenotype. These are expected in the event that mutations in the egg parents occur early enough to be included in a number of megasporocytes.

In a cooperative program among maize genetecists aimed at finding and mapping new mutant genes previous methods would require that the various cooperators exchange stocks carrying the newly-isolated recessive factors which would then be crossed with numbers of tester stocks to facilitate the placement of the mutant factors. If the method discussed here proves feasible it would not require this exchange and incidentally save considerable bookkeeping. Each cooperator would be responsible for the current mapping of a single arm of chromosome and would cross to screen for and deal with only those mutants occurring in that arm or chromosome.