

The environmental component was obtained from a large number of nonsegregating progenies (not related to Gobi, but with comparable average yield) in an adjacent field. The  $S_0$  estimate was obtained from a comparison of about 150 individual noninbred plants of the variety Gobi. The expected values are based on the assumption of additive gene action for yield (see Wright, Genetics 37: 312). Deviations from the expected values could be ascribed to nonadditive gene action. The limited numbers in this preliminary experiment must be borne in mind. It is felt that genotype-environment interaction is probably a major factor in causing these discrepancies, especially since the trial included plants varying greatly in yield. As soon as more information is available on the elimination of interaction by scaling, this type of experiment should definitely be subjected to appropriate scaling.

(e) Genotype-environment interaction.

This phenomenon is being studied with inbred and single cross material. Statistically significant differences in variability were found between different genetically nearhomogeneous progenies grown in the same field. A partitioning of variance into environmental, genetic, and interaction components was made, giving the estimates 259, 1120 and 312 respectively when differences between hybrids and inbreds were not taken into account. A correlation coefficient of  $-.69$  was found between mean ear weight and coefficient of variability. The mean C. V. of the inbreds was 57% as compared to 22% for the single crosses. When transformed into an antilog scale, differences in variability between progenies lacked significance and the mean C. V. of inbreds was 8% compared to 10% for the hybrids. Scaling, therefore, successfully reduced genotype-environment interaction or apparent "genetic homeostasis". More detailed results appear in "Proceedings of the First South African Genetic Congress, 1958".

In view of the extreme importance of interaction in interpreting experiments in quantitative genetics, more data is being collected at present and a greater variety of scales being tested.

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1. Gene order of  $y$ ,  $ms-si$ , and  $rg$  on chromosome 6.

Data from the cross  $y\ si \times rg\ Y\ Si/Rg\ y\ si$  are 907  $Y\ Si:23\ Y\ si:27\ y\ Si:110$   $y\ si$  which gives 2.5% recombination for the  $y-si$  region. Data from selfed ears of the triply heterozygous genotype give 2231  $Y\ Rg:983\ Y\ rg:1107\ y\ Rg:8\ y\ rg$  indicating  $9.0 \pm 1.5\%$  recombination for the  $y-rg$  region. Recovery of one  $rg\ Y\ Si/Rg\ Y\ Si$  genotype, one  $Rg\ y\ si/rg\ y\ si$

genotype and two  $Rg \underline{y} \underline{si}/Rg \underline{y} \underline{Si}$  genotypes clearly establish that  $\underline{y}$  is between  $\underline{rg}$  and  $\underline{si}$ . Experiments with  $\underline{po}$  and  $\underline{Pl}$  are in progress to determine orientation.

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## 2. The location of $\underline{y}$ on chromosome 6.

Linkage tests of  $\underline{y}\text{-su}_2/\underline{Y}\text{-Su}_2$  in homozygous translocation T6-10b (6L.17, 10L.14) showed 65  $\underline{Y}\text{-Su}_2:110 \underline{y}\text{-su}_2:118 \underline{y}\text{-Su}_2:59 \underline{Y}\text{-su}_2$  which gives 35.2% recombination and indicates the translocation point to be to the left of  $\underline{y}$  with  $\underline{y}$  on the long arm. Data presented by Patterson (1958 Newsletter p. 64) showed recombination between  $\underline{y}$  and  $R$  to be 18.8% in the homozygous translocation placing the break on 6 to the right of  $\underline{y}$ . These two sets of data are compatible only if the break on 6 is in the short arm as Burnham (Genetics, 1950) indicated. If the break on 6 is in fact in the short arm, the possibility of  $\underline{y}$  also being on the short arm is not ruled out.

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## 1. Intracistron recombination at the $\underline{Wx/wx}$ locus.

The dependence of the type of starch (amylopectin vs. amylopectin + amylose) produced in a microspore on the genotype at the  $\underline{Wx/wx}$  locus of the microspore itself and not the parental plant allows a test in maize for the occurrence of intracistron recombination. The barrier to the investigation of such a phenomenon in higher organisms is our inability to handle populations of sufficient size to detect the infrequent recombinants if such exist. In this system, however, the requisite numbers are easily available since a maize plant produces millions of microspores and since slides containing 50,000 or more microspores can be prepared and scored in twenty to twenty-five minutes.

If two independently occurring waxy mutants at the  $\underline{Wx/wx}$  locus represent changes at different mutational sites within the cistron and if recombination between such sites is a reality, it should be detectable in preparations from the pollen produced by the  $F_1$  between the mutant stocks. One of the products of recombination would be a reconstituted functional locus; in this case some amylose would be formed, and a microspore carrying such a locus would stain black with a KI,  $I_2$  stain in contrast to the brownish color typical of waxy microspores. Where in a cross between 2 waxy mutants the frequency of such black (normal)

7  $\underline{y}\text{-Si}:100$

si