There is still a possibility that the differences are due to modifying genes linked with the loci in question rather than to the loci themselves. This possibility now seems somewhat remote since increasing isogenicity has served to differentiate the components instead of increasing the similarity between them as would be expected if they were actually identical.

As pointed out previously, a difference in the two components of the Tu locus suggests that (a) the wild locus was Tu or (b) that there were two wild loci, $tu^{h-d}$ and $tu^{h-1}$ which through unequal crossing over sometime during domestication were brought together to produce the present Tu locus. The fact that all early prehistoric corn so far studied is similar to half tunicate rather than to full tunicate favors the latter possibility.

Crosses were made in 1961 between plants heterozygous for the two components. In 1962 plants heterozygous for both (+-/-+, a modified trans form in which the two +'s represent different "wild" loci) were backcrossed to tu tu. A backcross population is now being grown in Florida to determine whether the Tu locus can be resynthesized by restoring its separate components to their original positions on the same chromosome.

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3. Combining extracted chromosomes with tripsacoid effects - its bearing on convergent improvement.

In last year's News Letter I reported the results of intercrossing lines of A158 which had been modified by incorporating into them chromosomes with tripsacoid effects extracted from varieties of maize from the countries of Latin America. During the past summer highly tripsacoid segregates from $F_2$ populations of such crosses were grown for the purpose of establishing new lines of A158 carrying extracted chromosomes from both parental lines. In virtually all lines some plants were completely barren, producing no ears - in some lines virtually all plants were barren. This confirms the conclusion reached last year that there is a limit to the amount of tripsacoid germplasm which can be introduced in a homozygous state into an inbred strain.

These results have an important bearing on the method of convergent improvement in maize which assumes that inbred strains and their single crosses can be improved by backcrossing an $F_1$ hybrid to each of its parental lines followed by selfing. If heterosis is due in some instances to blocks of genes originally from teosinte or Tripsacum then convergent improvement will not in such cases be successful because these blocks of genes tend to have deleterious effects when homozygous.

A survey of the published data on convergent improvement shows that results are, as expected, conflicting and the method has been unsuccessful more often than not. The data showing lack of improvement are of particular interest here. Of 54 single crosses of second cycle recovered lines of B2 and K4 tested by Sprague et al. (1959) not a single one was equal in yield to the original single cross. Of 40 single crosses involving recovered lines of Wf9 and 38-11 tested by Lonnquist (1960) not one was equal in yield to the original single cross.

When blocks of teosinte or Tripsacum genes are involved in heterosis convergent improvement is obviously not a valid test to distinguish between dominance, overdominance, and epistasis as the principal factor in heterosis. Practiced for a sufficient number of cycles on inbred strains carrying blocks of teosinte or Tripsacum genes, convergent "improvement" will almost certainly lead to eventual extinction of the lines.

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## 4. Linkage relations of the gene for pointed kernels.

An indication previously reported (MNL No. 35) that pointed kernels, characteristic of certain varieties of popcorn, may be a simple Mendelian character exhibiting incomplete dominance and having its locus on chromosome 4 has been substantially confirmed by additional data obtained in 1962. $F_2$ populations of crosses of round and pointed kernels segregated as follows:

| | 279A | 279B | 660 Su su | 660 su su | Total |
|---|---|---|---|---|---|
| Pointed | 45 | 36 | 104 | 18 | 203 |
| Intermediate | 96 | 86 | 177 | 56 | 415 |
| Round | 31 | 32 | 66 | 36 | 165 |
| | 172 | 154 | 347 | 110 | 783 |

The data fit a 1:2:1 ratio with reasonable closeness and in this respect differ from those of Hayes and East, 1915, which indicate that two factors are involved in the inheritance of pointed kernel shape. The consistent deficiency of round genotypes is probably due to the effect of the fourth chromosome Ga factor carried by the pointed-kernel stock. Evidence of linkage with Su, another chromosome 4 gene, is furnished by the data from family 660 in which 19 percent of the ears originating from starchy seeds were round kerneled compared to 31 percent among those originating from sugary seeds.