

locus is suppressed. "I" is found at the A₁ and at the Pg locus. En is specific for the "I" component and the introduction of En results in mutability. In some cases, however, differing patterns of mutability are considered to be due to differences in "I". By crossing a single specific En to an array of independently derived a₁^{m(r)} alleles different expressions are observed. This indicates that the change must be in "I" and additional studies are being carried on to determine the nature of this change.

Thus, the final pattern is dependent on the particular En as well as the particular "I" and/or the interactions between them. This is unlike the mutable pericarp locus where pattern differences result from the varied number of tr-Mp present.

Peter A. Peterson

2. A dominant mutable.

Among a group of r mutants originating from standard R, there occurred a seedling mutable characterized by dark stripes on a virescent-like background. Outcrosses of this mutant to green plants of Dr. Brink's color converted W-22 strains (a strain which has not given rise to any seedling mutants in our cultures) yielded progeny, 1/2 of which were similar in expression to this same mutable. This type of mutable has not previously appeared among the numerous mutables studied in our cultures. It would seem, therefore, that this represents the origin of a dominant mutable allele.

Peter A. Peterson

3. Pales at the a₁ locus.

Pales, both stable and mutable, arise from certain a^m alleles. They arise from the same autonomous alleles that give rise to different pattern types in the presence of En. Stable pales are similar to a^{m(mr)} in that they do not respond to independent En. Neither do the mutable pales show any response to En. The individual isolates of the stable pales show a wide range of expression from those displaying only a slight amount of color to those possessing deep pale color.

Peter A. Peterson

4. Knob and centromere associations of non-homologous maize chromosomes at pachytene.

This report is an extension of previous studies on the non-homologous association of knobs and centromeres (S. R. Peterson, M.S. Thesis--Univ. of Ill.; Gurgel MGCNL 30 and 31):

These studies were undertaken with stocks possessing 8 and 12 knobs in the hemizygous condition and were derived from a standard genetic line and maize chapolote, respectively, crossed with Tama knobless flint. The table below shows that more knob association and more multiple association occur in the higher knobbed family than in the lower knobbed families.

Family	# of knobs	% of cells having knob association	% of associations which were of 3 or more knobs
848	2	4.99	----
844	8	43.14	5.15
862	12	100.00	50.64

Knob association appears to be related to knob size--larger knobs tend to associate more frequently than smaller knobs. This agrees with earlier reports of Longley, Peterson and Gurgel.

There is also a relationship between knob association and the distance of the knob to the end of the chromosome arm; those knobs farther from the end of the arm appear in association more frequently than those closer to the end of the chromosome arm. From multiple regression analysis however, it was determined that knob size is more influential in associations than is knob position.

More chromosomes appear in centromere association and more associations of 3 centromeres occur in the 12 knob family than the 8 knob family.

The frequency of centromere association in this material appears unrelated to chromosome length. This is inconsistent with the observations in the KYS material (Peterson and Gurgel).

Some knob association persisted from pachytene to metaphase I. This was verified from the observation that more associations were seen at the various stages in the 12 knob strain than in the cells containing 2 knobs which agrees with the analysis of association at pachytene. The 8 knob cells gave intermediate values at all stages except diakinesis where fewer bivalents were associated than were found in the 2 knob cells.

Sylvia E. Zvingilas

IOWA STATE UNIVERSITY
Ames, Iowa
Department of Genetics

1. Tests of white-seeded lines of corn of undetermined genotype for allelism with y_1 .

Results of suppressor and allele studies with the white-albino (white endosperm, albino seedlings) mutants have indicated that the genes involved might have a complex structure consisting of two portions, one responsible for carotenoid synthesis in the endosperm and the other controlling carotenoid production in the seedling. Studies with some of these mutants have indicated that the two parts of the complex can be modified independently by suppressor genes or mutation. (Maize Genetics Cooperation News Letter 34:69-70, 1960). The discovery of the y_1 alleles, pas_{8519} , and w_{mut} (white endosperm, pale green seedling) suggests that y_1 might be the result of a mutation at a white-albino locus involving just the endosperm element of the complex. If this is the origin of y_1 , the gene responsible for most of our white