

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.

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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

endosperm lines of corn, it is possible that a mutation involving just the endosperm portion of the complex of one of the twelve known white-albino loci may have given rise to white endosperm lines of corn that are non-allelic to y_1 . To search for such genes, 591 white endosperm accessions were obtained from the plant introduction station at Ames; these were grown along with two white endosperm mutants obtained from Mr. Kermicle and three from Dr. Bianchi, giving a total of 596 lines. An attempt was made to self pollinate two plants from each of these lines and at the same time outcross them to known y_1y_1 stocks. Any plant that was white endosperm because of a mutation of some locus other than y_1 should give yellow seeds in this outcross. Outcross tests were successful for 539 of the unknowns. Table 1 summarizes the results for the crosses where something other than white seeds was observed in the outcrosses.

Table 1

Class	Results			Source of accession
	Outcross to y_1 tester	Self pollination	Number of plants tested	
1	segregating yellow	segregating for recessive white	18	
2	segregating yellow	segregating for dominant white	7	
3	segregating yellow	homozygous white	2	1 Ethiopia 1 U. S. S. R.
4	homozygous yellow	homozygous very pale yellow*	8	2 Turkey 1 Ethiopia 1 New York State 2 Washington State 1 (Mutant furnished by Mr. Kermicle, Wisc., 2 tests made)
5	homozygous yellow	segregating very pale yellow*	3	2 Ethiopia 1 Paraguay
6	homozygous very pale yellow*	homozygous white	1	
7	heterozygous very pale yellow *	homozygous white	16	
8	homozygous very pale yellow *	segregating very pale yellow *	8	

Table 1, continued

Class	Results			Source of accession
	Outcross to Y_1 tester	Self Pollination	Number of plants tested	
9	heterozygous very pale yellow*	segregating very pale yellow*	12	
10	homozygous very pale yellow*	no test	2	
11	heterozygous yellow	red pericarp	2	
12	homozygous yellow	homozygous yellow	6	

*There is extremely little yellow pigment in the seeds classified as very pale yellow in this report. Such very pale yellow seeds have been frequently observed on ears that are otherwise $y_1y_1y_1$ and they are probably due to modifier genes. The amount of pigment is considerably less than that found in seeds of the $Y_1y_1y_1$ genotype. In selecting y_1 testers for these crosses, only pure white seeds were planted. However, because of a shortage of good y_1y_1 stocks, some white seeds were selected for use from ears that were segregating for very pale yellow seeds.

Class one probably represents cases where heterofertilization had resulted in white seeds being planted that carried Y_1y_1 embryos. Plants of class two were heterozygous for a dominant white gene. Class three could represent cases where the unknown was $Y_1y_1 y_x y_x$. The plants of classes four and five could represent instances where the unknowns were $Y_1Y_1 y_x y_x$. The presences of a slight tinge of yellow in the outcross seeds (very pale yellow) may or may not be significant since y_1 in some backgrounds also is very pale yellow. (See footnote to Table 1.) Classes 6-10 represent crosses where very pale yellow seeds are present. Endosperm color of the selfed plants of class 11 could not be determined with certainty because of the presence of red pericarp color. Class 12 consists of instances where there was some doubt as to whether the seeds of the accessions planted were white. In all these cases the planted seeds had considerable yellow pigment but compared to other seeds on the ear they were definitely pale.

The 13 plants from classes 3, 4 and 5 are the ones most likely to be carrying a new white endosperm gene and these will be tested further. The significance of very pale yellow seeds in some plants from classes 6-10 will be investigated further although there is very little likelihood that a major white endosperm gene is involved.

If on further testing, some of the promising lines do turn out to

possess a new white endosperm gene, these will then be tested against our white-albino mutants to determine if any of these loci are involved.

Donald S. Robertson

2. Chlorophyll, carotene and xanthophyll production in pastel-8549, pastel-4889 and pastel-8686 grown at high and low temperatures.

Chlorophyll, carotene and xanthophyll levels were determined for the following white endosperm-pastel (pale green) mutants and their F_1 's with available albino alleles after growing under a light intensity of 1400 foot candles and at temperatures of 22° C and 37° C.

Mutant	Chromosome
pastel-8549	6 (y_1 allele)
pastel-4889	7
vp_9 (albino allele) / pastel-4889	
pastel-8686	3
w_3 (albino allele) / pastel-8686	

Homozygous pastel and F_1 's with albino alleles are possible for the latter two loci. The pollen parents for the F_1 's were selfed and served as the source of the homozygous pastels. For each mutant and F_1 tested, seed was separated on the basis of endosperm color into normal (yellow) and mutant (white) classes and a sample of each was planted in rows in sand and grown under the above conditions of light and temperature. Plants were grown for 7 days at 37° C and 13 days at 22° C before harvesting. The methods of extracting the pigments and determining concentrations are described by Robertson and Anderson (Temperature sensitive alleles of the y_1 locus in maize. Jour. of Hered. 52:53-60. 1961). The pigment concentrations for each mutant are given in Table 1 and the percentage of pigments in the mutant as compared to that in the normal siblings at the two temperatures is given in Table 2.

Table 1. Chlorophyll, carotene and xanthophyll levels for normal and pastel seedlings. (mg/gfw is milligrams per gram fresh weight.)

Mutant	temp. °C.	Normal			Mutant		
		chlorophyll mg/gfw	carotene mg/gfw	xanthophyll mg/gfw	chlorophyll mg/gfw	carotene mg/gfw	xantho. mg/gfw
pas-8549	37	2.373	.0777	.0621	.329	.0517	.0140
	22	2.551	.0531	.0702	1.737	.0489	.0453
pas-4889	37	2.708	.0755	.0731	1.189	.0391	.0243
	22	2.746	.0573	.0746	.536	.0129	.0297
vp_9 F_1 / pas-4889	37	2.568	.0873	.0586	.429	.0121	.0254
	22	2.575	.0809	.0960	.203	.0082	.0147
pas-8686	37	2.860	.0787	.0407	1.704	.0483	.0589
	22	2.477	.0658	.0407	.275	.0052	.0183
w_3 F_1 / pas-8686	37	2.411	.0903	.0670	.550	.0128	.0306
	22	3.546	.1105	.0780	.100	.0024	.0100