3. EMS induced mutations of the Sh_1 locus.

Schwartz (Genetics 45:1419-1427, 1960) presented evidence to show that the Sh_1 gene controls the synthesis of a major protein component (designated as the Sh_1 protein) in the endosperm. This protein is completely lacking in the $sh_1/sh_1/sh_1$ material. We have obtained 16 new sh_1 mutants by ethyl methanesulfonate (EMS) treatment of Sh_1Wx seeds. The mutants were detected by crossing the treated material to a recessive sh_1wx tester. On the basis of electrophoretic and immunochemical analysis of 20 day old endosperm these mutants were grouped into the following four classes:

Class	Characterization of the sh_1 mutants		Number of mutants	Remarks
	Electrophoretic behavior on the starch gels	Immunochemical behavior in Ouchterlony plates		
I	No Sh_1 protein band.	CRM^-	9	similar to previously analyzed sh_1 mutants.
II	No Sh_1 band detectable by protein staining.	CRM^+ (very faint precipitation band)	1	probably indicates low concentration of Sh_1 protein.
III	Sh_1 protein band with altered migration rate.	CRM^+	2	one is faster and another is slower migrating in relation to Sh_1 protein band.
IV	Sh_1 protein band present (unaltered migration rate)	CRM^+	4	indistinguishable from wild type protein by these two criteria.

These results show that the Sh_1 protein has high specificity in activity since its function in kernel development can be eliminated by point mutations which cause little or no change in net charge or size (Classes III & IV). Although the Sh_1 protein in the Class IV mutants shows the wild type migration rate, it must differ in primary structure. A majority of amino acid replacements in a protein resulting from base changes would not alter the charge of the molecule and would remain

undetected by electrophoretic analysis. The presence of Class II and III type mutations offers strong support, along with the previously presented evidence, that this protein is specified by the Sh_1 gene, since qualitative and quantitative changes in the protein are associated with the appearance of the sh_1 phenotype.

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4. An effect of B chromosomes on crossing over in chromosome 5.

It was reported in last year's News Letter (p. 63) that B chromosomes might cause an increase in crossing over in the A_2-Bt_1-Pr region of chromosome 5. This work was followed up during the summer of 1968, when plants of two related families (536 and 537) which were heterozygous for $A_2 Bt_1 Pr$ were root-tipped and scored for B chromosomes, then transplanted to the field and backcrossed as females and as males to $a_2 bt_1 pr$ testers.

The results are shown below:-

Family no.	Used as:	No. of plants	No. of B's	No. of kernels	% Recombination			
					A-Bt	Bt-Pr	Total	% increase
537	♀	8	0	2897	5.9	15.9	21.8	-
		8	1	2797	6.9	18.1	25.0	15
		10	2	3197	8.8	21.7	30.5	40
536	♀	4	0	1529	8.2	23.0	31.2	-
		10	2	3493	9.6	22.3	31.9	2
		10	4	3527	10.7	25.3	36.0	15
537	♂	9	0	4560	11.3	26.8	38.1	-
		8	1	4505	15.1	31.8	46.9	23
		10	2	5814	17.7	34.6	52.3	37
536	♂	5	0	2764	13.4	26.0	39.4	-
		10	2	4812	18.1	35.8	53.9	37
		10	4	4829	23.6	37.6	61.2	55

The recombination values for the Bt_1-Pr region were obtained from the A_2 kernels only, since a_2 kernels lack color.

Although the data have not yet been statistically analyzed, both of the above families and the one mentioned last year showed increased