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1. Further studies on the inheritance of cob-rachis diameter.

The initial experiment conducted with cobs alone, as reported in last year's MNL, was repeated in part in 1968 to include tassel measurements together with those of the cob. This has led to the characterization of the two recessive genes involved in the thick cob of Iowa 5125 in terms of tassel morphology. One of the recessives results in high condensation in the tassel branches followed by reduced branching while the other recessive produces profuse tassel branching. An interaction between these two genes in the double recessive condition produces the thick cob and normal tassel of 5125.

Another genetic system produces thick cob in the northern flint derived races. This involves a third recessive gene which operates independently of the high "condensation--ramosa" system. It is suspected that the derived southern dents, like the Corn Belt dents, have acquired a combination of these two systems which would require the homozygous recessive condition at the three major loci concerned.

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2. Cytogenetic correspondence of corn chromosome 9 and its Tripsacum homeolog.

The assemblage of loci on a Tripsacum chromosome (no. 7 or 8, see item 8) is closely similar to that on corn chromosome 9. Of the 8 loci tested with markers yg_2, c_1, sh_1, bz_1, $wx:gl_{15}$, bk_2, bm_4, all are common to the two homeologs. Many other loci are probably also common between these chromosomes because the Tripsacum chromosome may substitute for its homeolog in the corn genome. Pachytene analyses of addition disomics (2n = 20 + 2) have shown that this Tripsacum chromosome has a total length of 34.0 microns with an arm ratio of 4.0:1.0. Its long arm is terminated by a large knob. Both in its length and arm ratio, this chromosome differs from chromosome 9 of corn which is about 43.0 microns long and has an arm ratio of 1.8:1.0.

Corn-Tripsacum crossovers have been obtained with some regularity (ca 1%) involving yg_2 on the short arm and bk_2 and bm_4 on the long arm of corn 9. Recombinants for the five other loci in the interstitial region of corn 9 have not been observed so far.

Because of preferential pairing at pachytene of the concerned corn and Tripsacum homologs observed in the addition disomics, it is not known yet whether the gene sequence or their relative distances are the same in the two chromosomes. The differences in their lengths and arm ratios could mean differences in both. Heterozygous substitution stocks (2n = 20) carrying all 8 dominants are under study and may provide this information.

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3. "Overdominance" between corn and Tripsacum alleles at the Bz locus.

When the dominant Bz gene borne on Tripsacum chromosome 7 or 8 (see item 8) is combined as a heterozygous substitution with its recessive allele bz on corn chromosome 9, the aleurone coloration is a deeper purple than when the Tripsacum chromosome is present as a homozygous substitution. The genotypes and phenotypes of kernels (aleurones) borne on a self-pollinated ear heterozygous for this corn-Tripsacum substitution are as follows:-

Genotype*	Phenotype Color	Ratio
$Bz^T/Bz^T/Bz^T$	pale purple	1
$Bz^T/Bz^T/bz$ }	dark purple	2
$bz/bz/Bz^T$ }		
$bz/bz/bz$	bronze	1

*Both the corn and Tripsacum chromosomes were dominant C. The presence of the Tripsacum allele is shown as Bz^T.

If this were a single allelic interaction, it would be overdominance. An alternate explanation could be the presence of a recessive modifier on the Tripsacum chromosome.

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