

It is hypothesized that a deoxyribonucleotide which forms a complex with the DNA via a specific agent is responsible for the peculiar base composition. The synthesis of the atypical DNA from Black Mexican Sweet Corn appears to depend on the stage of kernel development and probably coincides with the time of pigment development. The abnormal base ratios reported previously are presumably not related to heterochromatin content.

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1. A new striate mutant on chromosome 10.

A new mutant type was isolated which has longitudinal white stripes that parallel the leaf venation from early seedling stage onward. This mutant arose in M_2 segregating material from the combined chemical mutagen treatment of ethyl methanesulfonate followed by diethyl sulfate to the seed of a multiple marker stock used in mutation experiments. This character is recessive and very similar to Waseca stripe (sr_2) in chromosome 10 which was described by Joachim and Burnham (1953) MNL 27:66. Classification is good in the seedling and mature plant stage and pollen and ears are produced on most plants.

Intercrosses were made with homozygous recessive $sr_2 sr_2$ stocks obtained from Dr. R. A. Brink. There were no striate individuals among 193 F_1 plants from eight crossed ears.

The mutant was crossed to a waxy marked chromosome-nine translocation series involving all chromosomes and F_2 waxy seeds were screened. All F_2 populations showed normal 3:1 segregation except those involving the wx 9-10b interchange (9S.13, 10S.40) in which the following data were collected in ten families. Waxy seeds gave 349 normal : 12 striate plants. These data indicate that the mutant is located close to the interchange point on the short arm of chromosome 10, whereas the Waseca stripe (sr_2) gene has been placed distal to R on the long arm of chromosome 10. The symbol, sr_3 , has been assigned tentatively to this new mutant.

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2. A compact plant gene located on chromosome 1.

This mutant was given to this station by Allan Caspar of the Blandy Experimental Farms. The mutant produces seedlings which have very wide and

somewhat blunted leaves which are wider than normal siblings. The mature compact plant develops to at least three feet in height, or to nearly 50 per cent of the height of normal siblings; the internode number is the same, but the average internode length is two inches shorter than in the normal siblings. The shortened internode length is evident throughout the mutant plant and is not confined to those internodes below the ear node. The mutant plants have enlarged stalks. The ear is reduced in size and the tassel is compacted, but pollen is shed abundantly and ears are produced on most plants.

Intercrosses were made with thick-tassel-dwarf (ttd) in chromosome 5, Hy-rd and ct obtained from Dr. O. E. Nelson, none of which gave a positive allele test. Phenotypically the mutant appeared not to be similar to d₁ or d₂ in chromosome 3, or br₁ in chromosome 1.

The mutant was crossed to a waxy marked chromosome-nine translocation series involving all chromosomes and F₂ waxy seeds were screened. All F₂ populations showed normal 3:1 segregation except those involving the wx 1-9c (1S.48, 9L.22) and wx 1-9⁴⁹⁹⁵ (1L.19, 9S.20) interchanges in which the following data were collected. Waxy seeds from 4 families involving the cross with wx 1-9c gave 57 normal : 7 compact plants, and waxy seeds from 3 families involving the cross with wx 1-9⁴⁹⁹⁵ gave 74 normal : 14 compact plants. These data gave indications of linkage only with chromosome 1. This mutant is tentatively designated codw.

Dwarfs such as midget 8043, tiny 8446, dwarf 4963 and others have been associated with chromosome 1, but the codw phenotype is not similar. A test of allelism with br₁ has not been made. Its position in relation to the known markers on this chromosome is at present uncertain.

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1. Frequency of R^{st} to self colored (R^{sc}) aleurone mutations.

Early in the studies of paramutation at the R locus it was observed that Rst mutated to R^{sc}, and the frequency of such mutations has been reported by several investigators. The results from recent tests, together with some previously reported, are brought together in Table 1. The frequencies shown are the number of verified R^{sc} mutations over the number of stippled gametes tested. Where verification of self colored kernels was not accomplished the number of stippled gametes tested was proportionately reduced. The number of kernels scored was determined by actual counts or estimated from the weight of a sample of 500 to 1000 kernels from each family.

Certain of the allelic combinations have been tested more than once, and the number of tests and pooled frequency are shown in Table 1. Prior to pooling, the limits of expectation were calculated for each test and in