

No haploid plants appeared in the progeny, as judged by morphological traits, sterility and guard cell measurements. There were also no tetraploids. As expected, about 70% of the plants were either triploids or multiple trisomics, identified by high sterility, specific morphological properties, and characteristic ratios. The rest were diploids.

The mode of origin of diploids from such crosses can be traced by distribution of markers. Maternal diploids coming from unreduced eggs should be heterozygous at all the loci, whereas paternal diploids should be homozygous at all loci. Diploids originating from fertilization of a normal egg by haploid pollen from tetraploid male should have at least one dominant at each locus. Doubling of reduced egg or fusion of any two haploid nuclei in the embryo-sac without fertilization should result in plants homozygous at all loci. Plants arising from megaspore fusion without male contribution could also be detected by statistical distribution of markers. Diploids originated from either self- or outside contamination could easily be categorized by following through the distribution of different markers. Progeny tests revealed that the diploid exceptions in this experiment came only from contaminations and none of the other possibilities mentioned above could be realized. Also, no case of noncorrespondence between endosperm and embryo was noticed.

From this investigation it appears that the occurrence of haploids, diploids and tetraploids from diploid x tetraploid crosses is infrequent. Studies are being continued, employing a larger population and the reciprocal cross using diploids as the male.

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9. Symbol index to the Newsletters.

Copies of the Symbol Index to volumes 12 through 35, prepared as an Appendix to volume 36, are available and will be sent on request (Curtis Hall, University of Missouri, Columbia, Missouri). Notes on errors will be appreciated. One error that has been found may be indicative of others, though an attempt was made to avoid these: On page 42 under ws, 32:80 and 34:88 belong under ws₃.

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10. Mutable glossy-1.

A mutable glossy allelic to gl₁ (designated gl^m) has been found in an Ac-carrying line. Expression is excellent in sheaths of older plants; seedlings do not show clear sectors. As far as I am aware no mutability for the glossy character has been reported previously. Seed is available.

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