Caution also might be advisable in the use of new cytoplasms where fertility might be the result of heavy partial restoration rather than full restoration. A case in question could be the restoration of the S type cytoplasm. Even though some testcrosses appear to have a great amount of fertility, much of this fertility does have more of a semblance of heavy partial rather than actual full and positive restoration.

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1. Translocations generated by monosome X diploid crosses in Zea mays.*

It is well documented that certain regions of the genome are present in duplicate in maize as well as in other organisms. If a given monosomic chromosome bears a region which is also present on another chromosome, these two regions might occasionally pair in the monosome and recombination might take place between the duplicate regions. If this happens, reciprocal translocations would be found in the progeny of monosome X diploid crosses.

Plants confirmed to be monsomic for chromosomes 2, 4, 6, 7, 8, or 10 have been used successfully as males and monosomes 4, 6, 7, 8, and 10 as females in our cultures. Large numbers of progeny from crosses between specific monosomes and diploid inbreds are being analyzed for plants with about 50% ovule and pollen abortion. Three translocations have been cytologically confirmed from such crosses and 20 additional lines carrying transmissible semisterility have been isolated. Thus, translocations are obtained in the progeny of monosome X diploid crosses.

Through the use of a given monosome, a specific chromosome is tested against the entire genome for redundant segments; thus such segments can be determined chromosome by chromosome. If a specific translocation were repeatedly found this would indicate homology between two chromosome segments. However, if a random array of translocations is

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found between a monosomic chromosome and the rest of the genome, this might indicate that illegitimate recombination is taking place between nonhomologously synapsed segments.

David F. Weber

2. The relative concentrations of different fatty acids in monosomic Zea mays embryos as determined by gas liquid chromatography analysis.*

Monosomes generated by the r-x_1 deficiency are being used to detect genes that have a dosage effect on the relative concentrations of the different fatty acids of Z. mays embryos. By comparing a monosome with its diploid sibling it is possible to evaluate one versus two doses of every gene on a given chromosome at the same time. Using this experimental approach, we previously demonstrated that genes or gene complexes that alter the total lipid content of maize embryos are located on chromosomes 2, 6, and 10. No such genes were detected on chromosome 8 (Plewa, 1971; Plewa and Weber, 1971); thus monosomy per se does not alter lipid content. The present study will determine the effect of monosomy on the proportions of different fatty acids composing the extractable lipid fraction of maize embryos. This paper discusses the procedure of the study.

Experimental kernels were obtained from a cross between a W22 inbred line carrying the r-x_1 deficiency and inbred Mangelsdorf's Multiple Chromosome Tester (bm_2; lg_1; a_1; su_1; pr; y_1; gl_1; j_1; wx; g_1). A scutellum sample of approximately 1.5 mg adjacent to the embryonic axis was removed from each F_1 kernel (r/r-x_1). Each scutellum sample was placed in a separate vial, coded, and stored at -22°C. The corresponding kernels were planted. The monosomic plants were detected at the seedling stage by expression of appropriate genetic markers and confirmed by cytological analysis. The scutellum samples from the monosomes and their control diploid siblings were subsequently prepared for gas liquid chromatography (GLC) analysis of the lipid fraction. The fatty acid extraction and methylation followed a modification of procedure 1 as described by Jellum (1970). The samples were analyzed using a Hewlett-Packard model

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