Considering the altered stearic acid percentages in monosomic 8 embryos and the great differences exhibited by the monosomic 2 fatty acid profiles, it is clear that altering the gene dosage in certain chromosomes has profound effects on fatty acid levels. Thus, monosomic analysis has proven to be a valuable system in locating genes that express dosage effects controlling a biochemical pathway.

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Michael J. Plewa
David F. Weber

2. A monosomic mapping method.*

Recently, massive numbers of chemically induced maize mutants have been isolated. For this reason, it is desirable that the most efficient possible method be utilized in mapping these mutants. To this end, I would like to propose a new method of mapping certain classes of mutants to given chromosomes utilizing monosomics of Zea mays generated by the r-Xl deficiency. This method requires only one tester strain and two crosses.

The r-Xl deficiency is an X-ray induced deficiency of the r locus which was originally obtained by L. J. Stadler. Satyanarayana (unpublished) noted that gametes carrying the r-Xl deficiency included large numbers of monosomics and trisomics. He generously provided the deficiency to our laboratory where it has been studied for several years. Some of the characteristics of the system are:

1. The deficiency is only female transmissible.
2. We have isolated three or more cytologically and genetically confirmed cases of monosomy for nine of the ten maize

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chromosomes. One plant of the remaining type (monosomic 5) was found which by genetic analysis was monosomic for chromosome 5, but no cytological confirmation was possible. Thus, monosomics are produced for most, possibly all of the ten maize chromosomes.

3. Most of the monosomic types are sufficiently vigorous that successful crosses can be made. Monosomics 4, 6, 7, and 10 shed abundant pollen, and monosomics 3 and 8 shed sufficient pollen that crosses can be made with some difficulty. Monosomics 2, 3, 4, 6, 7, 8, and 10 can readily be utilized in crosses as female parents. Monosomics 1 and 9 can usually not be used in crosses but the one presumptive monosomic 5 plant was a good male and female parent. However, monosomic 9 plants can be readily recognized by a distinctive narrow leaf and conical plant shape. Thus, monosomics for most of the ten maize chromosomes can be used in crosses or recognized by distinctive phenotypes.
4. The nondisjunctive event is post-meiotic; thus there is noncorrespondence between embryo and endosperm markers.
5. Most monosomic types are generated with a frequency greater than 1% in the r-X1-carrying gametes.

If r-X1-carrying plants are crossed as females by plants with an unplaced recessive mutation that is expressed in the sporophyte, monosomics for the chromosome carrying the mutation would express the recessive sporophyte mutation. This is because the chromosome carrying the recessive was contributed by the male parent and no homolog was contributed by the female. If one identifies the monosomic chromosome, one identifies the chromosome on which that gene is located. However, identification of a monosomic chromosome at pachytene is difficult because the univalent chromosome usually folds back and pairs with itself, obscuring its morphological characteristics. Identification of chromosomes in root-tip preparations is also extremely difficult. Thus, cytological identification of the monosomic chromosome is impractical in most cases.

However, if the r-Xl-carrying female parent in the above cross also carries a known recessive mutation on each of the ten maize chromosomes and the male parent carries the corresponding dominant alleles, the monosomic chromosome can easily be identified genetically. All diploid plants produced by this cross would be heterozygous for the ten recessives carried by the female parent and would give a 1:1 ratio for all genes in a backcross to the female parent. However, in a monosomic plant, the monosomic chromosome is contributed by the male parent and carries only the dominant allele. Since the only viable gametes produced by a monosomic are haploid, in a backcross one would obtain only dominants for the gene on the monosomic chromosome and a 1:1 ratio for genes on the other chromosomes.

We are developing a line for use in the genetic approach outlined above. For this purpose, we are introducing the r-Xl deficiency into Mangelsdorf's Multiple Chromosome Tester ($\underline{bm}_2$; $\underline{lg}_1$; $\underline{a}_1$; $\underline{su}_1$; $\underline{pr}$; $\underline{y}_1$; $\underline{gl}_1$; $\underline{j}_1$; $\underline{wx}$; $\underline{g}_1$).

To illustrate the use of this system, let us assume that a new recessive mutation (m) that is expressed in the sporophyte is found, and this mutation is located on chromosome 7. The cross to be made and the expected progeny are shown below (for the sake of simplicity, the r-Xl deficiency on chromosome 10 is not illustrated):

Chromosome number	Female parent	Male parent	2N progeny	Progeny expressing m phenotype (monosomic 7)
1	bm/bm	Bm/Bm	Bm/bm	Bm/bm
2	lg/lg	Lg/Lg	Lg/lg	Lg/lg
3	a/a	A/A	A/a	A/a
4	su/su	Su/Su	Su/su	Su/su
5	pr/pr	Pr/Pr	Pr/pr	Pr/pr
6	y/y	Y/Y	Y/y	Y/y
7	gl M/gl M	Gl m/Gl m	Gl m/gl M	Gl m/--
8	j/j	J/J	J/j	J/j
9	wx/wx	Wx/Wx	Wx/wx	Wx/wx
10	g/g	G/G	G/g	G/g

The only plants expressing the mutant phenotype (m) in the F_1 would be plants monosomic for the chromosome carrying the gene, m. When this plant is backcrossed to Mangelsdorf's Multiple Chromosome Tester, all genes in Mangelsdorf's tester would be segregating 1:1 except gl, and all progeny would be Gl. Thus, the unplaced gene is located on chromosome 7.

Although monosomic 9 plants cannot be used in crosses, the gene use to mark monosomic 9 plants (wx) is expressed in the pollen itself; thus if a pollen sample were collected from the plant and stained with IKI, monosomic 9 plants could be readily recognized because all pollen would stain darkly.

The advantages of this system over others currently in use are:

1. All genes on an entire chromosome are uncovered simultaneously in a monosomic plant.
2. A single tester strain is needed to make the analysis; thus a single cross and a single testcross would be needed to locate a gene to a specific chromosome.

Disadvantages of this system are:

1. Only sporophyte-expressed, recessive mutations can be mapped in this way.
2. Two generations are necessary, whereas a single generation is sufficient with TB translocations.
3. Monosomics are produced with a relatively low frequency; thus relatively large populations would be necessary from the initial cross.

I believe that the proposed system will be extremely useful in mapping certain classes of mutations.

David F. Weber

INDIANA UNIVERSITY
Bloomington, Indiana
Department of Plant Sciences

1. On the quaternary structure of the temperature-sensitive mutant Adh_1^{S-1108}.

Plants homozygous for the EMS induced, temperature-sensitive, alcohol dehydrogenase allele, Adh_1^{S-1108}, show a reduced level of enzyme activity, equal to about ten percent of that in sib plants which are homozygous for a fully active, normal allele. Recent studies have revealed