# Sterility Studies With $M_3$ Oat Lines

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## INTRODUCTION

Mutagen treatment induces varying degrees of pollen sterility in crop plants. Caldecott *et al.* (*1*)[2] and Konzak (*3*) have indicated that, as a result of sterility, field hybridization can be a source of error for mutation studies. On the other hand, Krull and Frey (*4*) showed that natural crossing among oat plants derived from irradiated seeds was practically nonexistent when the plants were grown in the greenhouse.

This study was conducted to estimate the sterility in $M_3$ oat lines attributable to mutagen treatment which might influence the genetic variability present in mutagen-derived populations.

## MATERIALS AND METHODS

Seed lots of Clintland 60 variety of oats were given four mutagen treatments, ethyl-methanesulphonate (EMS), $P_{32}$, thermal neutrons, and a combination of EMS + $P_{32}$, and flowers of the same variety were treated with EMS. Seed were used without any treatment to serve as a check.

The $M_1$ generation of each mutagen population was grown in a separate greenhouse room at Ames, Iowa, to exclude the opportunity for interpopulation crossing. The $M_2$ generation was planted in the field as progeny rows 12 feet long and space planted with a maximum of 10 seeds. The rows were spaced 3 feet apart to permit cultivation and reduce the opportunity for interprogeny crossing. Ranges of rows were separated by alleys 5 feet wide.

When the $M_2$ plants were mature, 150 progeny rows were randomly selected in each treatment for use in an experiment designed to estimate the magnitude of genetic variability induced by different mutagen treatments. Four randomly selected plants were harvested from each of the selected progeny rows, and seed from each harvested plant were threshed into an envelope labeled with the appropriate pedigree.

Each of the 6 treatments was represented by 150 families, and each family consisted of 2 lines selected randomly from the 4 $M_2$ plants harvested. Lines from $M_2$ plants which produced fewer than 75 seeds had to be discarded, because this number of seeds was needed for the experiment.

The experiment was arranged in a split-split-plot design with three replicates. The main plots in each replicate consisted of the mutagen

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[2] Italic numbers in parentheses refer to Literature Cited, p. 68.

treatments, the subplots consisted of the families, and the sub-subplots were lines within families.

A plot was a hill planted with 25 seeds, and the hills were spaced 1 foot apart in perpendicular direction. As a precautionary measure the experiment was sprayed with a fungicide (active ingredients—Nabam and zinc sulfate) to prevent a rust epiphytotic which might confound the expression of genetic potential for the agronomic characters heading date, plant height, and weight per 100 seeds.

TABLE 1.—*Mean squares from the analysis of variance for fertility percentage in mutagen-derived and check populations of oat lines*

| Source of variation | Degrees of freedom | Mean squares |
|---|---|---|
| Total | 449 | |
| Replications | 2 | 56.62 |
| Populations | 5 | 65.23 |
| Error (a) | 10 | 33.98 |
| Lines within populations | 144 | 13.60**[1] |
| Error (b) | 288 | 5.23 |

[1] Significant at 1 percent level.

TABLE 2.—*Means, ranges, standard errors, and coefficients of variability of fertility percentages of mutagen-derived and check populations of oat lines*

| Mutagen | Mean | Range | Standard error | C.V. |
|---|---|---|---|---|
| Check | 89.3 | 84.7–93.5 | 0.41 | 2.3 |
| EMS seed treatment | 87.8 | 83.4–93.5 | .40 | 2.3 |
| $P_{32}$ | 90.4 | 85.2–94.3 | .41 | 2.3 |
| EMS + $P_{32}$ | 89.8 | 84.8–93.8 | .43 | 2.4 |
| Thermal neutrons | 88.7 | 85.4–91.7 | .38 | 2.1 |
| EMS flower treatment | 89.6 | 85.0–94.1 | .47 | 2.7 |

Twenty-five lines were selected at random for this study from each treatment grown in the variation-induction experiment. Two panicles were randomly selected from each plot of the selected lines, and the numbers of sterile and fertile florets were counted on each panicle. Fertility was determined as the ratio of total number of seeds to total number of florets.

## EXPERIMENTAL RESULTS AND DISCUSSION

The mean squares from the analysis of variance for fertility percentage in mutagen-derived and check populations are presented in table 1. There were no significant differences in fertility among the six populations. The mean fertility of the six populations ranged from 87.8 to 90.4 percent (table 2).

There were significant differences in fertility among lines within treatments, but the ranges and standard errors were similar for all populations, indicating that the mutagen-derived populations were similar to the check. The coefficients of variation within the populations ranged from 2.3 to 2.7, which indicates that the variabilities within the various populations were also homogeneous.

The frequency distribution for the fertility percentage of the check population (fig. 1) was typical of that for all populations. This shows that

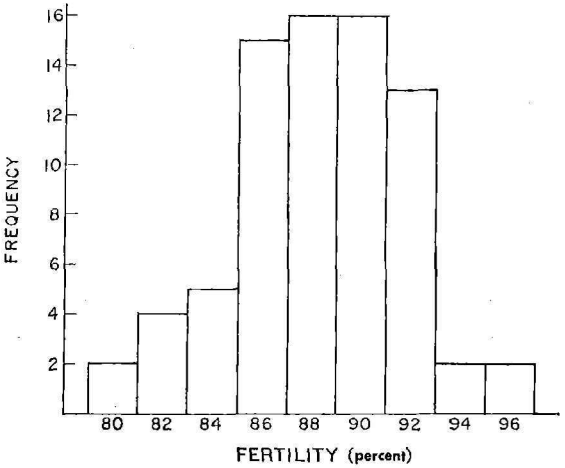


FIG. 1.—Frequency distribution for the fertility percentage of oat lines from the check population.

the variability for quantitative characters observed in the mutagen-derived populations was not caused by sterility induced by mutagens.

To minimize the opportunity for intrapopulation crossing, and consequently, the likelihood of this factor contributing significantly to the mutagen-induced variances, the $M_1$ generation of each mutagen population was grown in a separate greenhouse room.

Natural crossing between $M_2$ plants grown in the field could occur, especially if the plants displayed considerable sterility. However, its effect on the data collected from the $M_3$ generation experiment should be negligible for the following reasons: 1, Individual plants spaced at least 1 foot apart in rows 3 feet apart which would reduce the opportunity for natural crossing; 2, the minimum number of seeds required for the $M_3$ experiment was

75, and an $M_2$ plant, if highly sterile, would not produce that many seeds and would be discarded; and 3, the effects of 1 or 2 outcross seeds on the mean data for a given line would be diluted nearly out of existence because 75 seeds were used to test each $M_3$ line.

Sterility could also cause what would appear to be additional genetic variation by interferring with the balance that occurs between number of seeds borne on a panicle and seed weight. Frey (*2*) showed that when the number of spickelets on a panicle was reduced by cutting some off, the seeds in the remaining spickelets increased in weight. Sterility of some florets would be expected to have a similar effect. However, as shown herein, there were no significant differences in the mean-fertility percentages of the six populations.

With the precautions taken to minimize inter- and intra-population crossing in the $M_1$ generation, and the apparent lack of sterility in the $M_3$, it may be concluded that sterility did not contribute significantly to the genetic variability present in the mutagen-derived populations.

## SUMMARY

$M_3$-generation oat lines derived from populations treated with irradiation and chemical mutagens were studied to estimate the extent of sterility attributable to mutagen treatment. It was found that the fertility for all mutagen-derived populations was similar to the check, and that sterility did not contribute significantly to the genetic variability for the characters observed.

## RESUMEN

Se estudiaron poblaciones $M_3$ de avena tratadas con agentes mutagénicos químicos y mediante irradiación, a fin de determinar el porcentaje de esterilidad inducida por los agentes mutagénicos. Se encontró que la fertilidad de las poblaciones derivadas de la avena así tratada fue similar a la de las poblaciones derivadas de la avena sin tratar. Es evidente que de acuerdo con estas pruebas, la esterilidad inducida por los agentes mutagénicos y por la irradiación no produjo significativamente variaciones genéticas de los caracteres bajo estudio.

## LITERATURE CITED

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