

AN EVALUATION OF EARLY GENERATION SELECTION
PROCEDURES IN TRITICUM AESTIVUM L.

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ABSTRACT

A study was conducted to examine the effectiveness of selection on a single plant basis in F₂ and on an unreplicated line basis in F₃ for yielding ability. The effectiveness of selection for yielding ability in F₂ was determined by comparing the performance of the F₃ lines that were derived from single F₂ plants that had been selected on a visual basis for vigor and general appearance with first, the population mean, and second, F₃ lines that were derived from single F₂ plants taken at random from plants producing more than 750 seeds. In this study neither random selection of well tillered plants nor plants selected for agronomic superiority were better on the average than the population mean. The effectiveness of selection among unreplicated F₃ lines was determined by examining the inter-generation relationships between the yield of selected F₃ lines and the mean yield of their related F₄ bulks and F₅ families. When the yields were expressed as a percentage of the adjacent control plots a significant positive correlation (0.59, 0.56) and regression (0.39, 0.39) existed between the F₃ lines and F₄ bulk means, and between the F₃ lines and the F₅ family means. The highest yielding F₄ bulks and F₅ families originated from F₃ lines which

expressed high yield relative to the yield of their adjacent control plot. From F3 lines which expressed exceptional yielding ability F5 families were established, and remnant F3 seed of these selected F3 lines was used to establish F4 families which were grown simultaneously with the F5 families. Both the mean yield of the F4 families and mean yield of F5 families were significantly larger than the mean of the F3 nursery. The regression (0.34, 0.12) and correlation (0.20, -0.10) between F3 line values and F4 family means, and between F3 line values and F5 family means were non-significant because, in part, the number of F3 lines sampled was very small and the range of the F3 yield spectrum sampled was very narrow. But, the regression (0.98) and correlation (0.90) between the F4 family means and F5 family means were highly significant.

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INTRODUCTION

Plant breeding has been practised for many centuries, and it is generally considered that the beginnings of settled agriculture coincided with man's discovery that, by selection, he could domesticate certain of the wild plant species that then existed. Since then man has consciously sought to domesticate additional species, to synthesize new species, and to improve upon those he had already domesticated.

The foundation of modern plant breeding stems from the discovery, by Mendel, of the principles upon which the improvement of crops and animals is based. Mendel revealed that by hybridization he could release genetic variability, that this variability followed certain mathematical laws, and that, by selection of certain variants he could perpetuate their characteristics. Although Mendel's discoveries were initially neglected, the principles he evolved were later utilized by plant breeders to considerable advantage, which is testified by the present marked improvement in crop productivity, quality characteristics, and adaptability.

The principles involved are first, the creation of genetic variability; and secondly, the selection from

within the segregating populations for segregates which possess desirable heritable advantages. Initially crop species were improved markedly by using these genetic principles. In recent decades, however, the rate of improvement among established crops has been meagre. Hamilton (21) has pointed out that in the last twenty years in Western Canada we have not produced a variety with a higher yield potential than Thatcher. Various reasons for this have been proposed, one of which is the inefficiency of breeding methods to identify within early segregating populations those individuals which have the potential to transmit their desirable characteristics to their progeny [Hamilton (21)].

The purpose of this study was to investigate the efficiency and methodology of early generation selection procedures for yield improvement in wheat.

LITERATURE REVIEW

Selection is a powerful tool which is capable of modifying the genetic structure of a population. The principles of selection are: (1) some individuals are favoured in reproduction at the expense of others, (2) the mode of action is through heritable differences, and (3) selection only affects the variation already present in the population (47).

Most wheat breeding has been concerned with "qualitative character incorporation" and/or "selection for quantitative characters" e.g. yield and quality. To attain these goals the breeder first mates genetically different parents to create genetic variability, and secondly selects segregates which fulfill the specified goal. However, the discernable variation in the population is the result of both a heritable and non-heritable cause, i.e. a genetic and an environmental cause. For selection to be effective the breeder must be able to identify those "ideal" types whose variation, in part, is heritable. That is, he must be able to discriminate between the heritable and non-heritable components of variation.

1. Inheritance of Yield in Wheat

Chromosome substitution analysis by Kuspira and

Unrau (26) has provided evidence that each pair of chromosomes carry genes affecting yield. In addition, Haggag (20) has shown that the F3 mean yeild can be shifted in either direction depending upon which of the parents is backcrossed to the F1. The parent that contributes a greater number of desirable genes shifts the mean forward, and vice-versa for the other parent. This evidence indicates that yield is a complex quantitative character.

Among the properties of a metric character heritability is of prime importance to the breeder. Falconer (16) defines heritability as the ratio of additive genetic variance to phenotypic variance. The additive portion is capable of being fixed. The plant breeder's interest in heritability stems from his having to use the phenotypic value of the character as a guide in selecting individuals for further breeding purposes. The breeding value of the individual, however, can only be established by determining the mean value of its progeny. According to Falconer (16), "if the breeder chooses individuals to be parents according to their phenotypic values, his success in changing the characteristics of the population can be predicted only from a knowledge of the degree of correspondence between phenotypic values and breeding values.

Heritability estimates can be calculated in several different ways:

$$(1) \quad h^2 = \frac{V_a}{V_p}$$

where h^2 is the heritability value
 V_a is the additive variance component
 V_p is the phenotypic variance.

$$(2) \quad h^2 = b_{op}$$

where b_{op} is the regression of the off-spring on the parent.

Frey and Horner (18) proposed the standard units method to calculate the heritability of a character to avoid any scaling effect because of genotype x environment interaction. "Standard unit heritabilities are obtained by calculating the regressions on data coded in terms of standard deviation units . . . identical to correlation coefficients on the original data."

Heritability estimates are of limited value because they are a property not only of a character but also of the population and of the environment in which the population has been grown. Consequently, calculated values for the heritability of a given trait have meaning only for a particular population which has been grown under a particular set of conditions. This has consequences in a practical breeding program when successive generations must be grown in different years at different sites. Thus the individuals selected one year can not accurately predict the performance of the progeny grown the following year under a different set of conditions. Frey and Horner (18) reported

that under stress conditions, the phenotypic variance generally increases more rapidly than the genotypic variance; consequently, heritability estimates would likely be underestimated. Likewise genotype x environment interactions will affect heritability estimates. Falconer (16) postulated a relationship between heritability and reproductive fitness where he states "the characters with the lowest heritabilities are those most closely connected with reproductive fitness." Therefore, the problems in the study of yield and its response to selection are complex.

Briggs (13) has made an extensive report on the literature pertaining to the inheritance of yield in wheat, and notes that there have been two general approaches to studying its inheritance:

- (1) the study of yield as a "final" character and estimates of its heritability,

- (2) the resolution of yield into its components, along with heritability estimates of each of the components, estimates of the correlation between these components, and appraisal of their value as guides to select for higher yielding segregates.

Reports on the resolution of yield into its components are at variance. Rosenquist (39), Shebeski (40), and McNeal (35) found positive correlation between the yield components that they investigated. On the other hand Sprague (42), Fonseca et al (17), Johnson et al (25), and Reddi et al (38) obtained negative correlations between

such yield components. Consequently, selection for a higher expression of some single yield component need not necessarily result in higher yield per plant.

Heritability values for yield components as calculated by the regression of F3 on F2 were found by McNeal (35) to be, "so low that selection for these characters in the F2 generation is of doubtful value." Reddi et al (38) computed heritability estimates by regressing F4 means on F3 means for the yield components, tillers per plant, spike length, and kernel weight. The estimates were all low (0.20 to 0.48).

Heritability estimates of yield as a "final" character have been conducted by numerous workers. A number of the estimates reported have been low [McNeal (35), Davies et al (15), and Stuber et al (44)]. But, Baker et al (8) have demonstrated that the heritability estimates can be improved if the method of estimation takes into consideration the components of variance relating to genotype x environment interactions. They used the single seed descent method to propagate 50 random F2 plants until virtual homozygosity was reached. Yield heritability was estimated in the F7 and F8 generations using six combinations of numbers of replications, numbers of locations, and numbers of years. The heritability estimates increased as the numbers of replications, locations, and years sampled increased. Shebeski (41) has suggested that

many of the low heritability estimates reflect the procedures used in that inadequate provisions have been made to measure or to minimize the effects of soil heterogeneity and inter-line competition, and to use adequate sample sizes to prevent gross sampling errors.

All the evidence supports the premise that yield is inherited in wheat. However, the plant breeder's problem still remains that of identifying the higher yielding segregates. Because there simply is not enough seed available to conduct tests replicated in space and time, the best genotypes in the early generations can not be identified by conventional yield tests.

2. Early Generation Selection

Those wheat breeders who have defined the goal of their program as the production of higher yielding varieties, generally, proceed by one of the three following methods: (1) selection for defect deficient genotypes, (2) selection of genotypes which respond to an intensive management system, and (3) screen out those genotypes which have a higher yield potential [Briggs (13)]. The literature reviewed here will consider only the third approach.

The opportunity for selecting genotypes which have a particular gene combination capable of yielding more is limited by the prepotency of the parents and the size of population which can be handled in the early generations.

The size of population that can be handled is critical in the F₂ and F₃. If the plants selected in each generation do not possess the desirable genes affecting yield in either the homozygous or heterozygous condition, then this combination of genes is not recoverable in subsequent generations. Hence, in each generation the breeder must work with a large enough population to ensure that the best combination of genes present for yield in the F₂ generation are not lost because of sampling pressures. Moreover, it is imperative that the critical genotype or genotypes be identified in each generation.

Aksel and Johnson (2) have presented a method to calculate "the expected proportions of homozygous and heterozygous individuals, in both genotypic and phenotypic expressions, for any number of different loci and any given generation." Utilizing this approach Shebeski (41) has prepared tables to show the percentages of plants having all the more desirable genes in either a homozygous or heterozygous condition in successive generations of a cross for the n factors entering a cross. For a cross differing by 25 genes for yield 7.53×10^{-2} % of the F₂ plants have all the 25 desirable genes, whereas the percentages decrease to 7.89×10^{-4} in F₃ and 5.66×10^{-5} in F₄. The consequences of delaying selection, therefore, become obvious when we consider the size of population required to have the chance occurrence of a single plant

possessing the 25 desirable genes; that is in the F₂, 1 in 1330 plants has the 25 desirable genes, in F₃, 1 in 126,743 and in F₄, 1 in 1,766,784. Hence the frequency of occurrence of the best genotype is the highest in the F₂. But the problem of identifying the best single plant in F₂ still remains. The problem of identifying the best genotype on a single plant basis in F₂ is magnified by: (1) heterosis, (2) environmental effects, and (3) genotype x environment interactions [Allard (1), MacKey (30)].

The difficulty in isolating superior yielding segregates in the F₂ has been reiterated by Allard (1), Bell (10), and MacKey (30). On the other hand McGinnis and Shebeski (33) contend that selection in F₂ has been ineffective due to inadequate nursery designs in which little effort is put to minimize or correct for genetic and environmental variation. Working with a hard red spring wheat cross, they were able to improve the general yield capacity of the population by selecting on a visual basis for what they believed "to be the high yielding genotypes with superior agronomic characters."

3. Design of Plots in a Selection Nursery

Screening a population for a quantitative character has resulted in the development of various plot designs. Moreover increased research costs and the need to test large populations have forced plant breeders to seek

ways to improve selection efficiency. One possible way is through more precise knowledge of optimum sample and/or plot size.

Bonnett and Bever (11) have described a miniature plot technique for growing wheat and oats in headhills. They have advocated its use not only for the growing of selections at the beginning of a breeding cycle but also as a means of purifying an old variety and to obtain estimates on qualitative characters such as disease reaction.

Supporting evidence for the work of Bonnett and Bever has been supplied by several other investigators. Working with soybeans (Glycine max (L.) Merr.), Torrie (46) compared the use of hills and rodrow plots to evaluate soybeans. He found that the use of hills does not provide the information available from standard yield tests. To obtain comparable experimental precision for yield, the required numbers of replications for rows and hills were 4 and 9, respectively.

Jellum et al (22), working with oats, found some encouraging evidence to advocate the use of head hills as a supplementary tool to select for yield in early generations. The coefficients of variability for hills and rodrows repeated over years and locations were 18% and 10%, respectively. Phenotypic correlations between yields from hill and rodrow tests were significant in 15 of 24 cases.

Frey (19) completed an intensive investigation into

the utility of hill plots in oat research. For such agronomic characters as grain yield, plant height, and heading date measured on the same varieties, the genetic correlations between hills and rodrows were 0.98, 0.96 and 0.96, respectively. The coefficient of variation for a character was similar regardless of whether the plants were growing in a hill or a rodrow. This was the case for such characteristics as plant height, weight per volume, spikelets per panicle, panicles per plant and weight per 100 seeds. But the coefficient of variation for grain yield ranged from 2 to 5 times larger for hills than rodrows.

Recently Jensen and Robson (24) devised miniature plots for cereal testing. The linear hill plot was 30.5 cm. long. They claimed that this miniature plot provides approximately the same competitive pressures of population dynamics found in rodrows. However, 2.4 replicates are needed to give precision equal to one replicate of a single rodrow.

Consequently, head hills and linear head plots do have value in a breeding program as a plot design used to purify a mixture of types, which possess distinct morphological features, or to score qualitative characters. But, miniature plots are of dubious value as a plot design to handle a quantitative character because: (1) there is not a consistent significant correlation between yields from headhills and rodrows, (2) the coefficient of variation for

yield is always greater from hills than rodrows, and (3) at least twice as many replications are required for head hills as for rodrows. Therefore, if a large number of F3's are to be tested, time, labor, and cost to prepare, to organize, and to sow replicated miniature plots would be prohibitive.

As early as 1918 Wiancko et al (48) reported that the minimum size for small grain plots should be 1/80 to 1/20 acre which is an impossible plot size in the early generations. From 1910 to 1920 many workers, using correlation coefficients, studied the degree of relationship between rodrows and field plots. Klages (27) found that some correlations were small but positive and high enough to give confidence in the rodrow method. Hence the rodrow plot design was adopted as a method to evaluate an F3 line since sufficient seed can be obtained to establish a rodrow plot.

Arny (3,4) and McClland (31,32) have done extensive investigation into the effect of alleys. They separately concluded that the effect of border rows on the interpretation of results was: (1) to increase the yields of plots as compared to plots where these border rows were eliminated, (2) to alter the rank of a variety or seeding rate in relation to the discard-point derived for a particular test. However, the removal of border rows did not necessarily reduce the probable errors.

Love and Craig (28) studied competition between

adjacent rows of different varieties and to see whether the effects of competition introduced a serious source of error in yield testing. They concluded that varieties ranked similarly when yields were estimated from all rows or from only the centre rows of a multi-row plot design.

Adjacent row competition in wheat was studied by Jensen and Federer (23). Rodrow plots were spaced one foot apart. The yields of taller wheats were enhanced while the yields of shorter wheats were depressed because of the competitive effects associated with height. They concluded that the observed effects preclude the use of single rows either as checks or selection plots because the error is sometimes greater than the real difference which exists between two wheats.

In order to overcome the various weaknesses of a rodrow plot design, Shebeski (41) advocates the use of a 2 foot spacing between adjacent 3-rodrow plots to reduce interplot competition. By planting and harvesting a 3-rodrow plot he has increased the sample size of a particular genotype (the number of individuals measured to obtain an estimate of a particular character, in this case yield). The increased sample size affords a more accurate estimate of the yield potential of each genotype being evaluated. However the wide inter-plot spacing, used by Shebeski may have introduced another source of variability in the form of a genotype x alley-effect interaction.

Brown and Weibel (14), using a two foot spacing between plots, obtained a significant interaction of this type for yield in two out of four replicated winter wheat and spring oat tests. The entire 3-rodrow plot, suggested by Shebeski (41) is harvested. Consequently the genotype x alley-affect may be of considerable importance in determining the yield of the plot. Selection of the highest yielding plots would tend to result in the selection of lines with a high tillering capacity. But, the varieties that have been grown widely in Western Canada have been characterized by a reasonable tillering capacity. Therefore, genotype x alley-effect interaction might not be a detrimental source of variability in Western Canadian selection nurseries.

4. Use of Systematic Control Plots

In order for selection to be effective the plant breeder must be able to discriminate between heritable and non-heritable variation. The phenotypic expression of a character, such as yield, can be represented as:

$$A = u + a + e + ae$$

where A is the phenotypic expression of the character,
u is the general population mean,
a is the genotypic effect,
e is the experimental error,
ae is the interaction effect.

Consequently the effectiveness of selection in a particular experiment is contingent upon the control of (e) and (ae) [Allard (1)].

Historically, control plots were introduced to provide a measure of the experimental error and thereby increase the rate of genetic advance under selection. Yates (49) criticized the use of randomized control plots in a randomized block design on the basis that such control plots furnish information only about the fertility of the adjacent area wherever they occur. If a control plot falls at the edge of a block, it is just as good an indicator of the fertility of plots in its neighborhood belonging to the next block, as it is of the block in which it falls. Consequently, Yates (49) advocated the use of systematic control plots to obtain a measure of fertility of adjacent plots. Soil fertility fluctuations can be corrected by: (1) subtracting the yield of the systematic control plots from the yield of the breeding plot, (2) calculating the yield of the breeding plot as a percentage of the systematic control plot, and (3) using the systematic control plot as a covariate. The analysis of covariance is the most accurate as it prevents overcorrection: "by this procedure the danger of overcorrection for the fertility measures, which will almost certainly occur if straight differences are taken, will be avoided, and only that weight will be attached to the fertility measures which is justified by

the results of the particular experiment under consideration [Yates (49)].

Melton and Finkner (36), working with alfalfa, studied the relative efficiency of systematically arranged control plots to randomized complete blocks and two lattice designs. The analysis of covariance utilizing systematic control plots resulted in increased efficiencies from 38% to 528%.

Baker and McKenzie (5) and Baker (6) have taken a critical attitude towards the reliability of control plots to measure soil fertility variation. They have pointed out that the use of systematic controls is not expected to be of any value unless Smith's coefficient of soil heterogeneity (the regression of the logarithm of the variances for plots of different sizes on the logarithm of their areas) is less than 0.5. Baker has stated that a correlation coefficient of at least 0.5 must exist between the fertility of a breeding plot and its adjacent control plot before systematic control plots are more efficient than conventional designs. Student (45) indicated that "the greater the contiguity of two plots in a field, the more alike they would be expected to be in yield." Yates (49) also supported this view but did not present data to demonstrate the degree of correspondence between contiguous plots. Briggs and Shebeski (12) investigated the degree of correlation between contiguous plots, that were sown to

one variety, as the distance increased. The correlation between yields of plots located at 2.7m (9 ft.) was 0.63, 0.87 and 0.88 for three different nurseries. As the distance increased the degree of correlation rapidly decreased to non-significance.

Haggag (20) claimed that the use of adjacent control plots will check against environmental variability due to location. He went further without experimental data to state that "interactions (ae) may exist but should be small". Briggs (13) admitted the possible confounding effect of the interactions in the results obtained from his experiments on early generation yield and quality evaluation. Whereas Baker (9) has calculated the interaction components of variance and has found them to be sizable except the genotype x year interaction (1969).

The statistical advantage in the use of systematic controls over simply increasing the replications in a randomized design is dubious. The efficiency of randomized designs would be expected to increase markedly if the area used for systematic controls were instead used for additional replications. However, doubling the number of replications requires twice the amount of seed for each entry and the seed of some of these entries would be in short supply, especially in early generation progeny tests.

EXPERIMENTS CONDUCTED AND THE RESULTS OBTAINED

The hybrid material used in this study was derived from two crosses made in the summer of 1966--(CT244 x Tizanos Pintos Precos) x Manitou and (Sonora 64 x Tizanos Pintos Precos) x Manitou. Three experiments were conducted; the objectives of the three experiments were:

- (1) to determine if the yield potential of a single F2 plant can be evaluated visually,
- (2) to determine if the yield potential of F2 progeny, an F3 line, can be evaluated directly by a yield test, and
- (3) to compare the performance of F4 and F5 families with the yield performance of their F3 progenitors.

The objectives stated necessitated that three different experiments be conducted even though these experiments are related. To avoid any confusion that could arise from the range of terminology used and the different generations compared in different years, it has been decided, for convenience, to present each experiment separately.

EXPERIMENT I

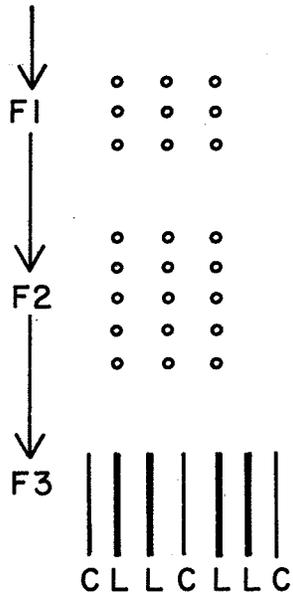
The object of the first experiment was to determine if the yield potential of an F2 single plant can be assessed visually. The performance of the F3 lines relative to the population mean provided evidence for the accuracy of visual assessment of F2 single plants.

Materials and Methods

The sequence followed in handling the generations has been illustrated in Figure 1. In the winter of 1966-67 the F1 plants were planted in Mexico, and in the following spring the F2 generation was planted at the University of Manitoba. Plants were spaced 18 inches apart within rows. The rows were laid out in pairs and planted 36 inches apart, with 18 inches between the rows of any one pair. The lay-out of the F2 nursery is illustrated in Figure 2.

Three plant breeders examined the spaced F2 plants in the nursery immediately prior to harvest. They selected 278 plants out of 10,000 on the basis of plant appearance and general vigor which, in their opinion, would produce high yielding progeny lines. In addition, all F2 plants yielding in excess of 750 seeds (the number of seeds required to sow a 3-row plot) were identified. From this group 118 were taken at random and will be referred to as the "upper random sample". A bulk that would represent

Crosses Made



- U of M, 1966. The crosses were made.
- Mexico 1966-67. The F1's were grown as individual plants .
- U of M 1967. The F2's were grown individually.
- Visual selection of F2 single plants
- Random selection of those plants that produced enough seed to sow a 3-row plot .
- U of M 1968
- Each F3 line (L) derived from a single F2 plant and was compared to a contiguous bulk control plot (C).

FIGURE 1. The Sequence followed in Experiment I to determine the efficiency of single plant selection.

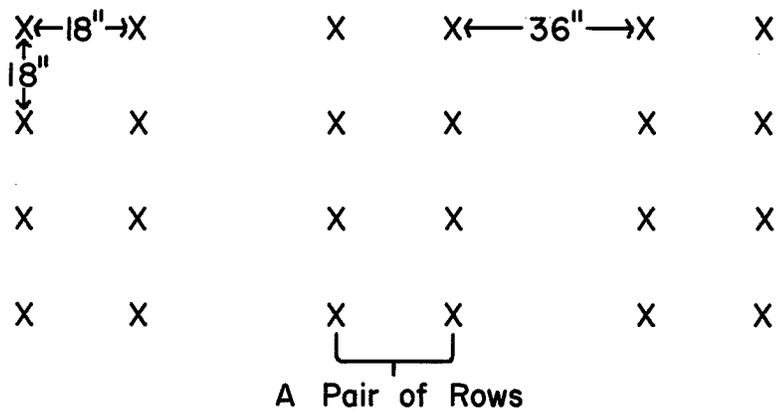


FIGURE 2. Lay-out of the F2 single plant nursery.

the population and the yield of which could be considered to estimate the population mean was constituted by taking one head from every F2 plant in the nursery.

The selected F2 plants were threshed individually using a single plant threshing machine. The seed produced by each plant was weighed to the nearest gram.

The F2 progeny test consisting of 396 F3 lines was conducted at the University of Manitoba during the summer of 1968. The nursery was organized in the manner described by Briggs and Shebeski (12) and has been shown in Figure 3. Each plot consisted of three rows, 6 inches apart and 18 1/2 feet long. A space of 2 feet separated plots in order to minimize inter-plot competition. A set of systematic control plots were included by sowing every third plot to bulk seed, which was constituted by compositing the seed from one head of every F2 plant in the nursery. Thus each F3 line could be compared directly with its own contiguous bulk control.

At harvest the plots were trimmed to 16 1/2 feet. Because of excessive lodging, the whole nursery was harvested by hand rather than by a mechanical harvester. The heads from each plot were cut with a sickle and collected into cotton bags prior to threshing with a "Vogel" thresher. The yield of each plot was recorded in grams, and expressed in both this form and as a percent of its adjacent control.

The means and standard errors were calculated for

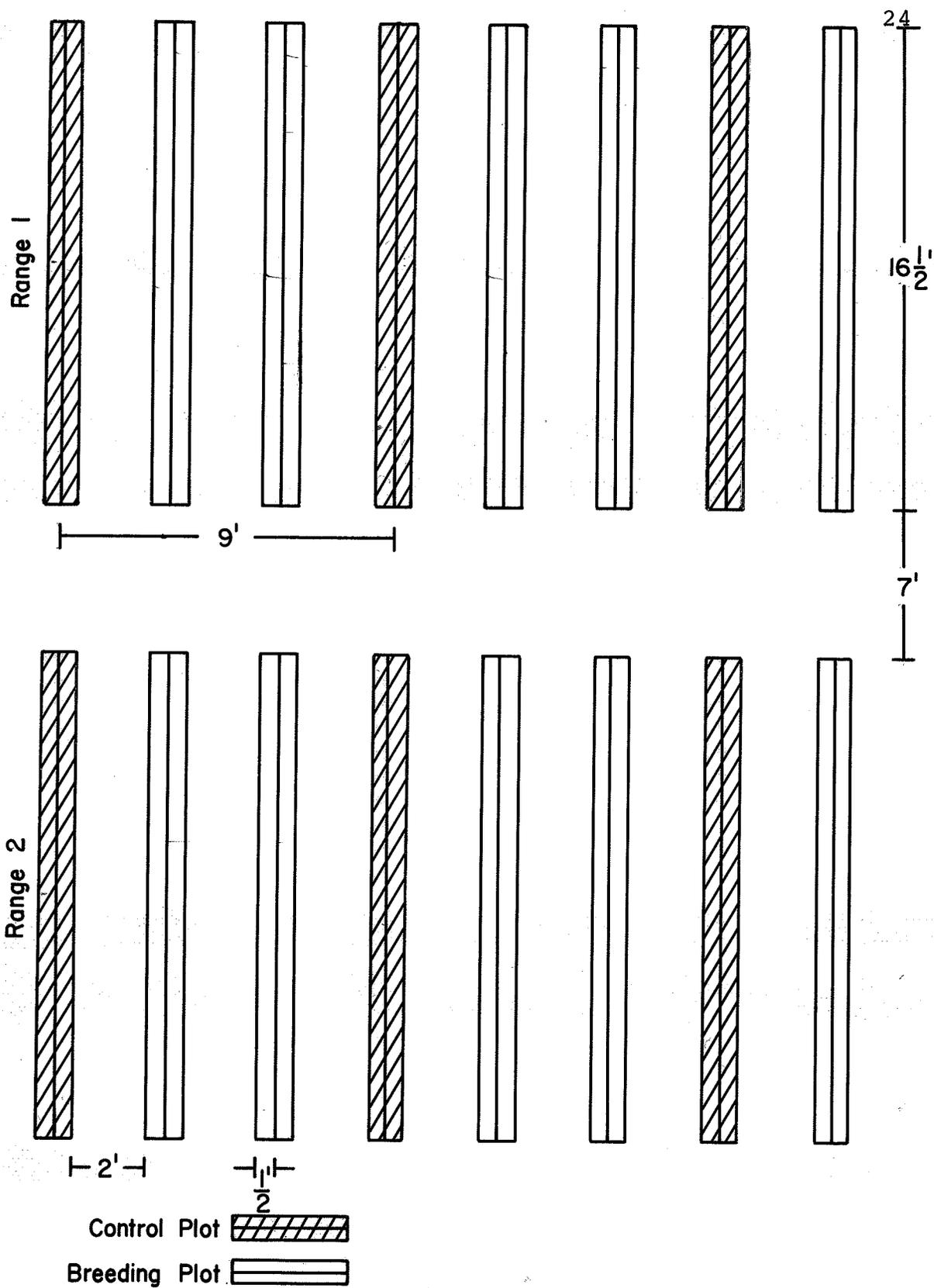


FIGURE 3. Diagrammatic arrangement of a portion of the nursery at harvest time. Only two of the six ranges are illustrated.

the F2 single plant yield, the yield of the F3 lines, and the yield of the bulk control plots. The bulk control plots were replicated 237 times and their mean value and standard error were considered as parameters describing the population. Pearson's correlation coefficient was calculated between: (1) the visually selected F2 plants and their progenies, and (2) the upper "randomly" selected F2 plants and their progenies. A t-test of a difference between treatment means was performed on the F2 single plant yield, and also, on the F3 mean yields.

Results and Discussion

The mean yield per selected F2 plant, for their respective progeny and for the control plots representing the population mean is presented in Table I. Table II presents the t-values for the difference between the treatment means.

The mean weight of seed produced by the visually selected F2 plants was significantly higher than the mean of the "upper randomly" selected F2 plants. The mean grams per line for the F3 lines derived from the visually selected F2 plants was not significantly different from the population mean. The mean percent of control for the F3 lines derived from the visually selected F2 plants was significantly less than the population mean. The mean yield of the F3 lines derived from the visually selected

TABLE I

MEAN YIELD OF F2 SINGLE PLANTS, F3 LINES AND F3 BULK CONTROL PLOTS
AND THE CORRELATION COEFFICIENT BETWEEN F2 AND F3 YIELD

	n	F2 gms/plant	F3 Line Yield		Pearson's Correlation Coefficient (F2-F3)
			gms/plot	% of control	
Visual Selection	278	51.24±0.60	1357.3±14.2	96.53±1.01	0.034
Upper Random Selection	118	48.39±0.92	1402.5±20.6	98.38±1.55	-0.086
Bulk Control Plots ⁺	237		1391.1±11.1	100.00	

⁺One head from every F2 plant in the nursery was composited to provide F3 seed which was used to establish control plots in the F3 nursery. These bulk control plots were replicated 237 times.

TABLE II

CALCULATED t-TEST VALUES OF DIFFERENCE BETWEEN
THE MEAN VALUES FOR VISUAL SELECTION, RANDOM
SELECTION, AND THE POPULATION MEAN

	F2	F3 Yield	
	gms/plant	gms/plot	% of control
Visual Selection v.s. Population Mean		-1.889	-3.410**
Upper Random Selection v.s. Population Mean		0.490	-1.05
Visual Selection v.s. Upper Random Selection	2.661**	-1.782	-1.006

* Significant at the 5% level.

** Significant at the 1% level.

F2 plants was statistically equal to the F3 lines derived from the "upper randomly selected" F2 plants.

Neither selection method gave rise to progenies whose mean yield exceeded the mean of the population. The visually selected F2 single plants did not produce progenies that yielded more than the mean of the progenies derived from the "upper randomly selected" F2 plants.

As would be expected, therefore, the correlation coefficient between the yield of visually selected F2 plants and their progenies was non-significant. Similarly the F2-F3 correlation for the "upper randomly selected" set was non-significant.

In this study selection at random among those F2 plants which have produced enough seed to establish a 3-row plot was equivalent to, if not more effective than visual selection. It is therefore concluded that visual selection of single F2 plants is of doubtful value and could, in fact, be inferior to random selection. This conclusion agrees with some investigators (1,10), but disagrees with a recent investigation (33).

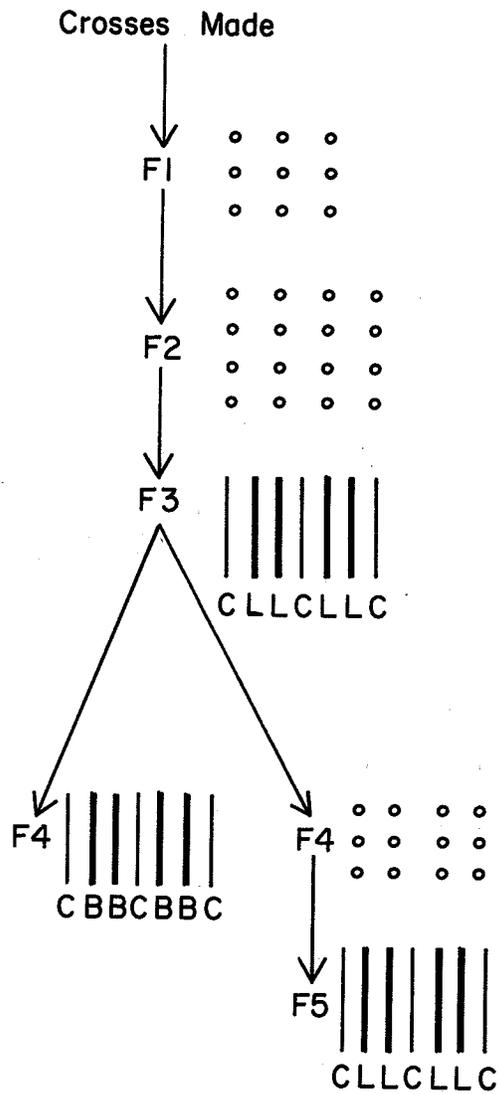
EXPERIMENT II

Concurrent with the experiment designed to assess the efficiency of single plant selection for yield on the F2 level, Experiment II was conducted to obtain information about the relationship between the yield of an F3 line and the mean performance of its related F4 bulk and F5 family.

Materials and Methods

The materials utilized in this study were handled in the sequence presented in Figure 4. Individual F3 lines were grown in 1968 and each was compared with a contiguous bulk control that represented the mean of the population, as described in Experiment I. Seventeen out of 528 F3 lines representing the low (inferior), middle (average), and high (superior) areas of the yield spectrum were selected for evaluation in a replicated F4 bulk yield test. In addition, nineteen of the F3 lines representing the upper 30% of the yield distribution were selected and advanced through the F4 generation in Mexico during the winter of 1968-69 in order to provide families of F5 lines whose mean yields could be compared with the yields of their F3 progenitors.

The same nursery design and organization was followed as in Experiment I for the F1, F2, and F3 generations.



- U of M 1966 The crosses were made.
- Mexico 1966-67 The F1's were grown as individual plants.
- U of M 1967 The F2's were grown singly.
- U of M 1968
- Each F3 line (L) derived from a single F2 plant and was compared to a contiguous bulk control plot (C).
- U of M 1969
- Each F4 bulk entry (B), a random sample of seed from an F3 line, was replicated and compared to a control (C).
- Mexico 1968-69
- A random sample of seed from selected F3 lines was grown singly.
- U of M 1969
- Each F5 line (L) derived from an F4 single plant and was compared to an adjacent control (C).
- All of the F5 lines that were derived from the same F3 line constitute an F5 family.

FIGURE 4. The sequence followed to determine the effectiveness of selection on an unreplicated F3 line basis.

F4 Bulk Test

All of the F3 lines selected for the F4 bulk test were derived from the cross (Sonora 64 x Tizanos Pintos Precos) x Manitou.

Seventeen F3 lines that were advanced to a replicated F4 bulk test were selected on the basis of their yielding ability relative to their respective contiguous bulk control plots. By this criterion seven F3 lines of superior, five of inferior, and five of average performance were included in the F4 bulk test. A random sample of seed from the F3 bulk control plots was composited to represent the population, called POPAVE (population average), and was also included in the F4 bulk test. The yield of POPAVE would, therefore, represent the population mean in F4. In addition two entries from an F8 yield test in 1968 (953A and 1151C) and two commercial varieties (Manitou and Pitic 62) were also included.

The twenty-two entries were replicated six times in a completely randomized design with Manitou grown in every third plot as a systematic control.

The yield of the twenty two bulk test entries were recorded in grams per plot. An analysis of covariance was performed. A t-test of a difference between the category means inferior, average, and superior was conducted in the F3 and F4 generations. The relationship between F3 values and related F4 bulk means was determined by Spearman's rank

correlation and simple regression.

F5 Family Test

Seed from 78 out of 528 F3 lines was sent to Mexico to be advanced through the F4 generation over the winter of 1968-69. The F3 lines that were selected had to satisfy at least one of the following criteria:

(1) plot yield greater than 1600 grams, greater than 120% of adjacent control, and agronomically equal or better than Manitou (the best commercial variety in Western Canada at the time).

(2) plot yield greater than 130% of adjacent control

(3) plot yield greater than 1700 grams

(4) plot yield greater than 1550 grams and plant height less than 39 inches.

The seventy-eight F3 lines thus selected represented approximately the upper 30% of the F3 population. A random sample of 240, F4 seeds of each selected F3 lines was space-planted in Mexico. From these a sample of twenty to forty single plants of the best agronomic type was selected for progeny testing at the University of Manitoba during the summer of 1969. Each F5 line grown was, therefore, the progeny of an F4 single plant, and all of the F5 lines that derived from the same F3 line were considered an F5 family. However, only nineteen of the original seventy-eight families

were selected for testing in F5 because a number of them arose from F3 lines expressing poor bread-making quality, and because others failed to flower due to their daylength sensitivity.

The design and organization of the F4 bulk test and F5 family test was the same as for the F3 progeny nursery, except that Manitou was grown in every third plot as a systematic control. Both tests were harvested and threshed by the same procedure as in the previous year.

The yield of each F5 line was recorded in grams per line and also expressed as a percent of the adjacent control. An analysis of variance was performed on the yield data from the F5 families. The inter-generation relationships between F3 values and related F5 family means and between F4 bulk means and related F5 family means were measured by Spearman's rank correlation and simple regression.

Results and Discussion

Performance of the F3 Lines

A frequency distribution of yield, expressed in grams per plot, of the 528 F3 lines and the 237 bulk control plots is drawn in Figure 5. The yield of the F3 lines ranged from 640 to 2164 grams per plot. A smaller range of 936 to 1815 grams was expressed by the bulk control plots. A histogram of the F3 lines' yield calculated as a percent of adjacent control is presented in Figure 6. After correcting the

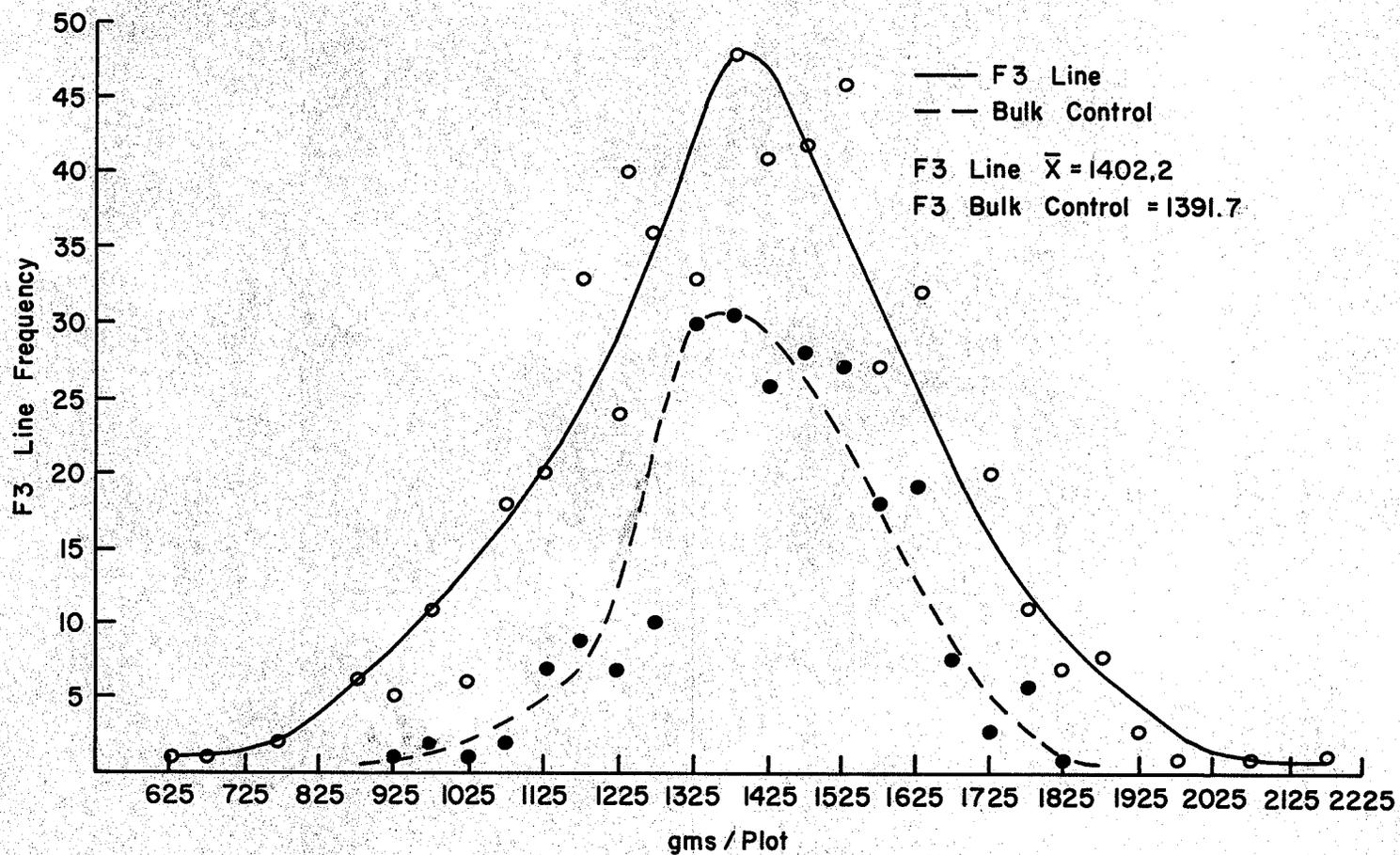


FIGURE 5. Frequency distribution of the yield of F3 lines and the bulk controls.

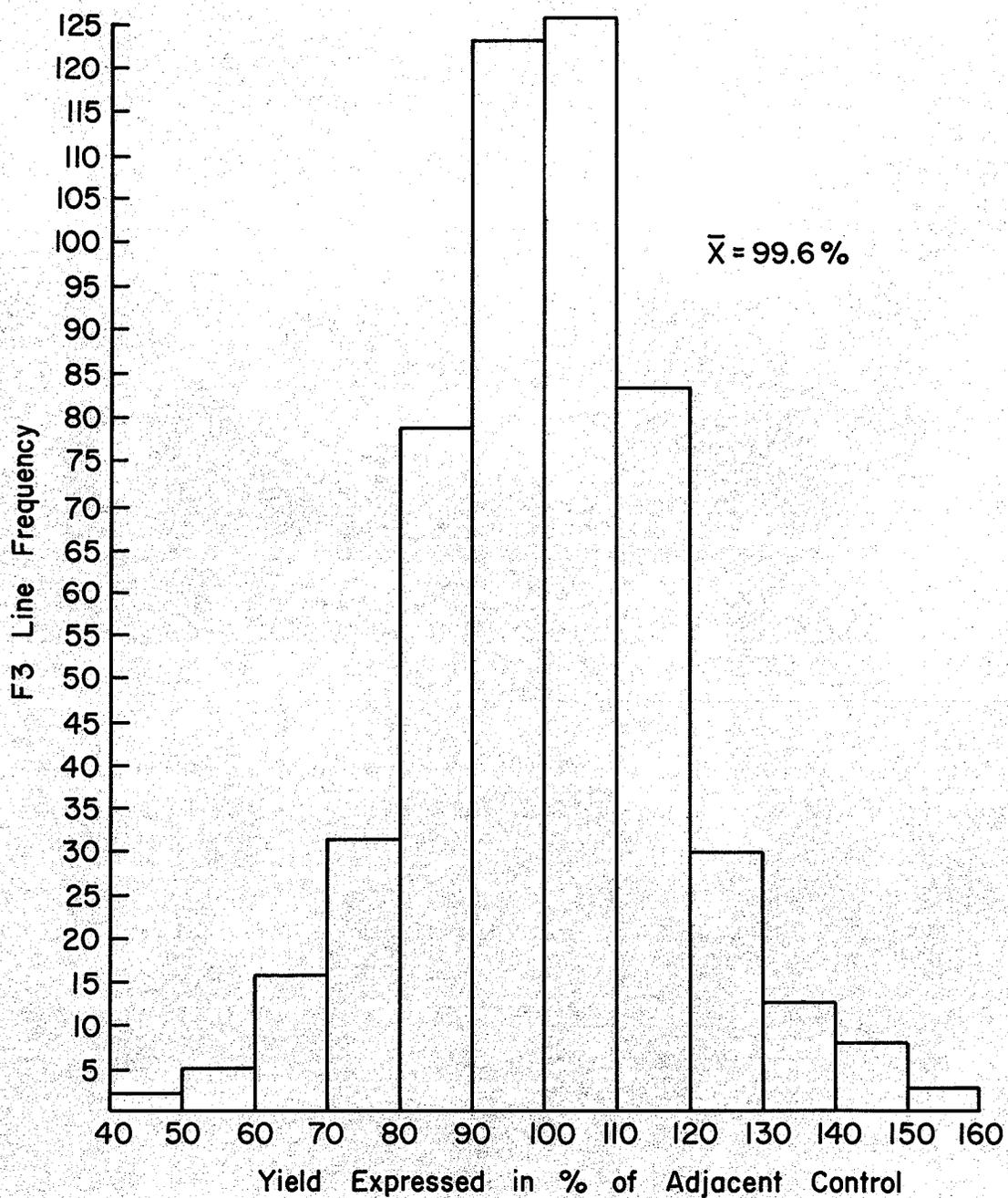


FIGURE 6. Frequency distribution of the yield of the F3 lines.

yield of individual F3 lines by using the yield of the contiguous bulk control plots as a fertility index, it was found that they varied from 41% to 154.5% of their respective control with a mean of 99.6%.

F4 Bulk Test

Table III presents the yield of each F3 line from which the entries were selected, and the mean yield of their respective F4 bulks. The entries have been arranged in accordance with the criterion of their selection.

The F4 bulk test entries were analyzed as a completely randomized analysis of covariance, and a highly significant F-value indicated differences among the entries (Table IV). Table V presents the t-values for the difference between the category means in both the F3 and F4 generation. The mean yield of each of the categories in F3 differed significantly. The F4 mean of the "inferior" category was significantly less than the mean of the other categories. Likewise the F4 mean of the "average" category was significantly less than the mean of the "superior" category and the mean of the "varieties". The mean yield of the "varieties" and "superior" categories did not differ significantly.

The three significantly different yield categories in the F3 generation remained significantly different at the 1% level in the F4 and also maintained the same relative order. This indicated, therefore, that highly heritable

TABLE III

YIELD OF F3 PARENTAL LINES AND THE F4 BULK TEST
ENTRIES AND ANOVA TESTS OF SIGNIFICANCE FOR THE F4 DATA

Category	F3 Line	F3 Yield		F4 Yield
		(gms/line)	(% of control)	(gms/plot) 1/
Inferior	345x	883	57.1	735abcd
	349x	983	67.3	869abcd
	444y	866	60.8	1285abc
	512x	912	58.0	1073abcd
	513y	978	81.7	1226abc
Group Mean		924±19.71	65.0±4.06	1038±24.51
Average	311x	1418	101.0	1205abc
	335x	1391	99.5	1250abc
	413y	1645	101.1	1278abc
	420x	1492	97.5	1097abcd
	441y	1462	101.1	952abcd
	POPAVE	1505	100.0	1141abcd
Group Mean		1486±33.18	99.5±0.55	1154±20.75
Superior	401y	2164	131.2	1166abcd
	405y	1883	115.7	1136abcd
	432x	1886	142.7	1425a C
	434x	2083	128.0	1313 ab
	518y	1744	139.8	1322ab D
	532y	1777	152.1	1584A
	611y	1882	154.5	1272abc
Group Mean		1921±56.11	137.7±4.82	1317±19.41
Varieties	953A			1532 B
	1151C			1135abcd
	Pitic			1283ab
	Manitou			1225abc
Group Mean				1294±25.46

1/ LSD multiple range test ($P \leq 0.05$). Treatments in the upper case are significantly larger than those in the lower case, at the 95% confidence level.

TABLE IV

ANALYSIS OF COVARIANCE COMPLETELY RANDOMIZED DESIGN

Source of Variation	DF	XSS	XYSP	YSS	Red. due to Y adjusted			
					DF Regression	for X	MS	F
Treatments	21	1024172.25	-538362.37	4144159.00	21	4440442.00	21449.52	13.89**
Error	110	1890018.00	771515.50	1974916.00	109	314936.75	1659979.00	15229.16
Total	131	2914191.00	233153.13	6119075.00	130	18653.68	6100421.00	46926.31

**Significant at the 1% level.

TABLE V
 THE t-VALUES FOR THE DIFFERENCE BETWEEN
 THE BULK TEST CATEGORY MEANS

F3	Inferior	Average	
Average	-8.30**		
Superior	-9.97**	-6.72**	
F4	Inferior	Average	Superior
Average	-3.72**		
Superior	-9.21**	-5.68**	
Varieties	-7.36**	-4.20**	0.71

**Significant at the 1% level.

group differences could be detected in F3 which could be exploited in the F4 generation.

Within each category, however, the F4 bulks expressed considerable variation. But none of the F4 bulk entries from the categories "inferior" and "average" ranked among the four highest yielding entries.

The regression coefficient and Spearman's rank correlation coefficient between F3 values and related F4 bulk means are presented in Table VI. Significant regressions and rank correlations were found for yield, when both measured as grams per plot and expressed as a percent of adjacent control. Therefore, the yield performance of an F3 line was a good indicator of the likely performance of an F4 bulk derived from it.

F5 Family Test

Table VII presents the yield data, expressed both in grams per plot and percent of control, for the nineteen F5 families and their parent F3 lines. Nine of the nineteen F5 families yielded more than 100% of the adjacent control. Each of these nine families were derived from F3 lines that yielded at least 120% of their adjacent control. Of the ten families that yielded less than 100% of control seven of them were heavily infected with stem rust. The grand mean of the nineteen F5 families was 102.0% of Manitou control plots. When the F5 families which expressed susceptibility

TABLE VI

INTER-GENERATION RELATIONSHIPS BETWEEN F3 VALUES AND F4 BULK MEANS, AND F3 VALUES AND F5 FAMILY MEANS, AND F4 BULK MEANS AND F5 FAMILY MEANS FOR THE TWO YIELD VARIABLES AS MEASURED BY SPEARMAN'S RANK CORRELATION AND SIMPLE REGRESSION

	n	Grams per Plot		% of Control	
		Rank r	b value	Rank r	b value
1968 F3 to 1969 F4	18	0.55*	0.22*	0.59**	0.39**
1968 F3 to 1969 F5	19	0.05	0.04	0.56*	0.39*
1969 F4 to 1969 F5	7	0.82*	0.72*		

* Significant at the 5% level.

** Significant at the 1% level.

TABLE VII

YIELD MEASURED IN GRAMS PER PLOT AND CALCULATED AS A
PERCENT OF CONTROL FOR F3 LINES, F4 BULKS, AND F5 FAMILIES

F3 Sel- ections	Yield in Grams per Plot					Yield as % of Adjacent Control				
	F3 Line Value	F4 Bulk Mean	F5 Family			F3 Sel- ections	F3 Line Value	F5 Family		
			Mean	Max	Range			Mean	Max	Range
434x	2083	1313	1346	1690	653	611y	154.5	111.9	138	65
118x	1914		1332	1732	793	532y	152.1	121.5	152	75
432x	1886	1425	1337	1671	629	432x	142.7	110.0	150	70
405y	1883	1136	1075	1330	682	117x	139.6	106.6	152	64
611y	1882	1272	1286	1500	528	332x	132.4	117.7	153	59
417y	1837		1186	1540	528	434x	128.0	108.5	148	72
532y	1777	1584	1396	1706	611	229y	127.9	120.2	156	66
428x	1712		1112	1412	562	315y	133.7	112.4	146	50
117x	1683		1219	1435	635	118x	119.6	120.9	150	74
229y	1670		1470	1790	557	405y	115.7	83.0	109	63
315y	1648		1352	1765	725	428x	106.3	89.5	126	63
332x	1511		1368	1845	865	417y	103.3	98.5	135	89
401y ⁺	2164	1166	1082	1425	815	349y	145.6	95.6	141	75
518y ⁺	1744	1322	1172	1628	978	518y	139.8	98.9	147	97
431x ⁺	1668		1159	1490	702	401y	131.2	85.2	121	74
407x ⁺	1667		1190	1470	840	431x	121.0	89.7	112	67
503x ⁺	1621		975	1350	718	414y	116.3	97.1	122	56
414y ⁺	1572		1139	1438	678	503x	100.7	79.3	115	64
349y ⁺	1563		1096	1460	652	407x	96.3	91.6	133	66

⁺F5 families which were segregating for stem rust resistance. At least 38% of the lines within a family were heavily infected.

to stem rust were disregarded, the adjusted F5 mean became 108.4% of adjacent control. This was significantly different at the 1% level from the mean percent of control for the F3 lines (99.6%, Figure 6). Therefore, selection among unreplicated F3 lines that expressed high yield relative to the adjacent control has been effective in identifying F3 lines with a high yield potential.

When yield was measured in grams per plot both the rank correlation and the simple regression coefficients were non-significant (Table VI). But, when yield was expressed as a percent of an adjacent control, the rank correlation and regression were significant.

Out of the nineteen F5 families tested, seven derived from F3 lines whose progeny had also been included in the F4 bulk test (Table VII). The regression coefficient and the rank correlation coefficient between F5 family mean yield and F4 bulk mean yield measured in grams per plot were 0.72 and 0.82, respectively. Both of these coefficients were significant.

Because significant regression and rank correlations were obtained between F3 values and related F4 bulk means, and between F3 values and related F5 family means, it can be concluded that the yield potential of an F3 line was measured with a reasonable degree of accuracy and could be used to predict the yield performance in the subsequent F4 and F5 generations. Two features of the F3 progeny test which

improved the precision of the yield potential measurement were: (1) each genotype was represented by a large sample of seed (750 seeds per 3-rodrow plot), and (2) each genotype was compared to an adjacent control. This was taken to indicate that a large plot size has provided a more accurate estimate of a genotype's yield potential and that using contiguous control plots was effective in correcting for soil heterogeneity effects. Their use, in correcting the phenotypic yields of the test material, allows the breeder to discriminate among F3 lines on a more genetically sound basis. This advantage would be particularly valuable when, as in most practical programs, the problem is to distinguish between good and very good rather than over the range from good to bad.

Stem rust may be considered a non-random factor affecting yield which the selected F3 lines did not express, but some of the F5 families did due to segregation. The regression and correlation, therefore, were probably biased downwards by the inclusion of families infected with stem rust.

It can be concluded that selection among F3 lines has been effective in discriminating between differences that were heritable. While the performance of the progeny of a group of unreplicated F3 lines can be predicted in the F3, by a replicated F4 bulk test the performance of an individual F3-derived F5 family can be predicted in the F4.

EXPERIMENT III

Assuming that superior F2 genotypes for yield could be identified in the F3, and with remnant seed available from vigorous F2 plants that gave rise to very high yielding F3 lines, an experiment was designed:

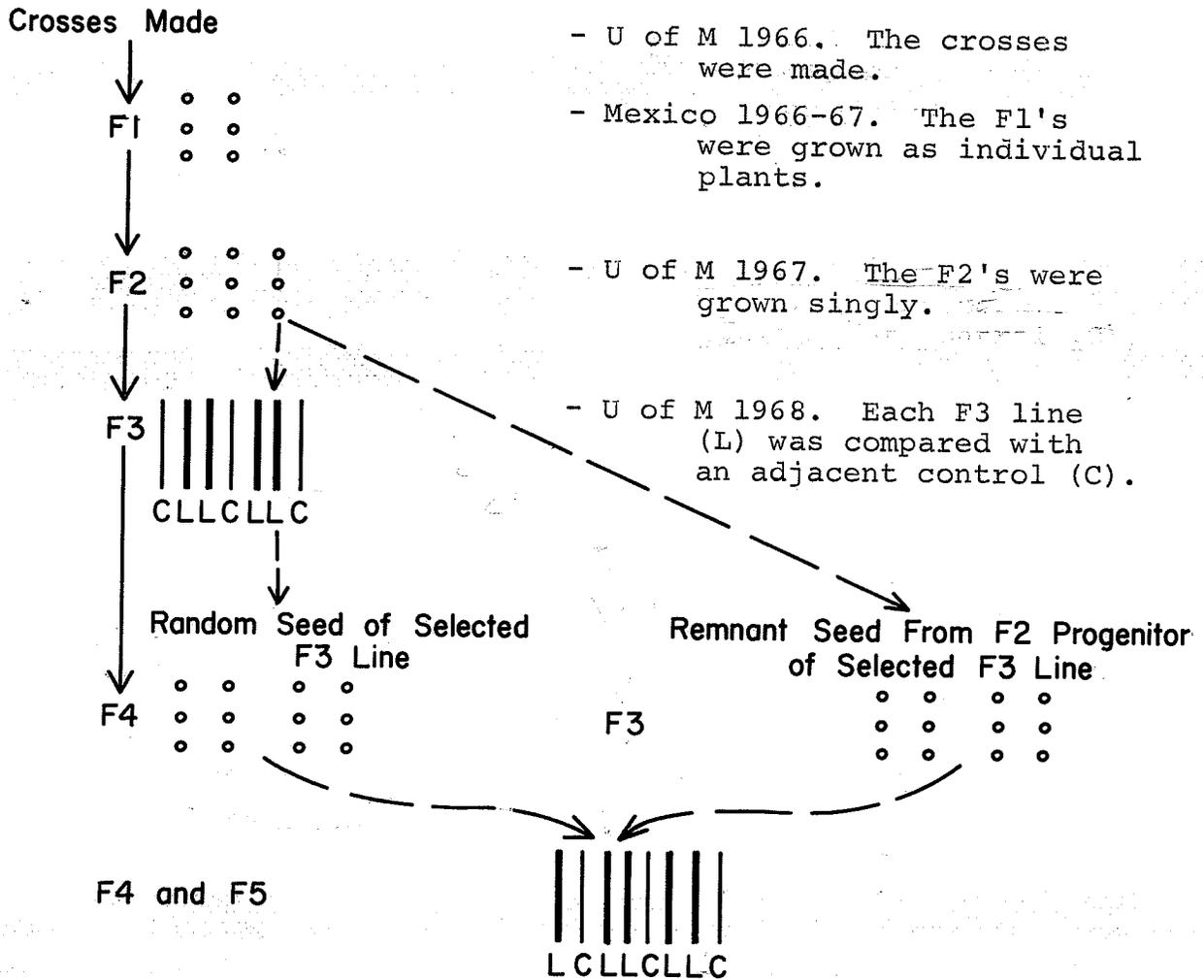
- (1) to compare the mean yield of the F4 and F5 lines with the mean of all the F3 lines, and
- (2) to determine by using correlation and regression analysis the relationships between the F3, F4, and F5 generations.

Materials and Methods

The segregating generations were handled as shown in Figure 7. The same nursery lay-out was followed as in Experiment I for the F1, F2, and F3 generations. F2 single plants which produced more than 750 seeds were put into an F3 progeny nursery during the summer of 1968 at the University of Manitoba, the remnant seed being held in reserve. The yield potential of each F3 hybrid line was measured by the method described in Experiment II.

F3 lines were considered to be of superior agronomic worth if they met all of the following criteria:

- (1) plot yield greater than 1600 grams,
- (2) plot yield greater than 120% of adjacent control, and
- (3) agronomically superior to Manitou.



- U of M 1966. The crosses were made.
- Mexico 1966-67. The F1's were grown as individual plants.
- U of M 1967. The F2's were grown singly.
- U of M 1968. Each F3 line (L) was compared with an adjacent control (C).

- Mexico 1968-69. A random sample of seed from the selected F3 lines and the remnant seed of the progenitors of the selected F3 lines were grown as individual plants.
- U of M 1969. F4 and F5 lines (L) which derived from F3 and F4 individual plants were randomized within one nursery and compared to adjacent control plots (C).

FIGURE 7. The sequence followed to establish and to compare F4 and F5 families grown simultaneously within one nursery.

Only seven F3 lines, representing 1.3% of the entire F3 nursery, satisfied all three criteria. From each of these seven F3 lines 240 seeds were space planted in Mexico during the winter of 1968-69. In addition 240 remnant seeds from the seven respective F2 plants were space planted in Mexico.

Because two of the seven families were photoperiod sensitive to the short days of the Mexican winter, selections were made within the remaining five families. A sample of sixteen to forty single plants of the best agronomic type from each of the five families in each of the two generations was selected for progeny testing at the University of Manitoba. This provided five groups of F4 and the corresponding five groups of F5 families for testing simultaneously during the summer of 1969.

The design and organization of the nursery plots was the same as in the previous year. The progeny lines (137, F4 lines and 144, F5 lines) were randomized within one nursery. The variety Manitou was grown in every third plot as a systematic control. The yield per line was recorded in grams and calculated as a percent of the adjacent Manitou control plot.

The mean, range, and variance for yield expressed as grams per line and as a percent of control were calculated for both the F4 and F5 families. A t-test of a difference between means was used to compare: (1) the mean

yield of the F3 lines to the mean of the F4 families, (2) the mean yield of the F3 lines to the mean of the F5 families, and (3) the mean yield of the F4 families to that of the F5 families. Simple regression and rank correlation were calculated between selected F3 line values and F4 and F5 family means and also between F4 family means and F5 family means.

Results and Discussion

Frequency distributions for the yield of the F4 and F5 lines expressed as a percent of control has been illustrated in Figures 8 and 9, respectively. The F-test, used to test the equality of the F4 and F5 variances resulted in a non-significant F-value of 1.23. The F4 mean percent of control was 104.0%, and the F5 mean percent of control was 103.9%. When an unpaired t-test of a difference was applied to the generation means, a non-significant t-value of 0.08 obtained. Consequently, the F4 and F5 yield distributions were considered similar.

Table VIII presents the mean, maximum, and range for the yield of the F4 and F5 families. The yield was expressed both as grams per line and as a percent of control. Each F5 family's mean yield, both in grams per line and as a percent of control, was equal to the mean yield of its related F4 family, with the exception of family 229y. In this case the mean F4 grams per line was significantly less.

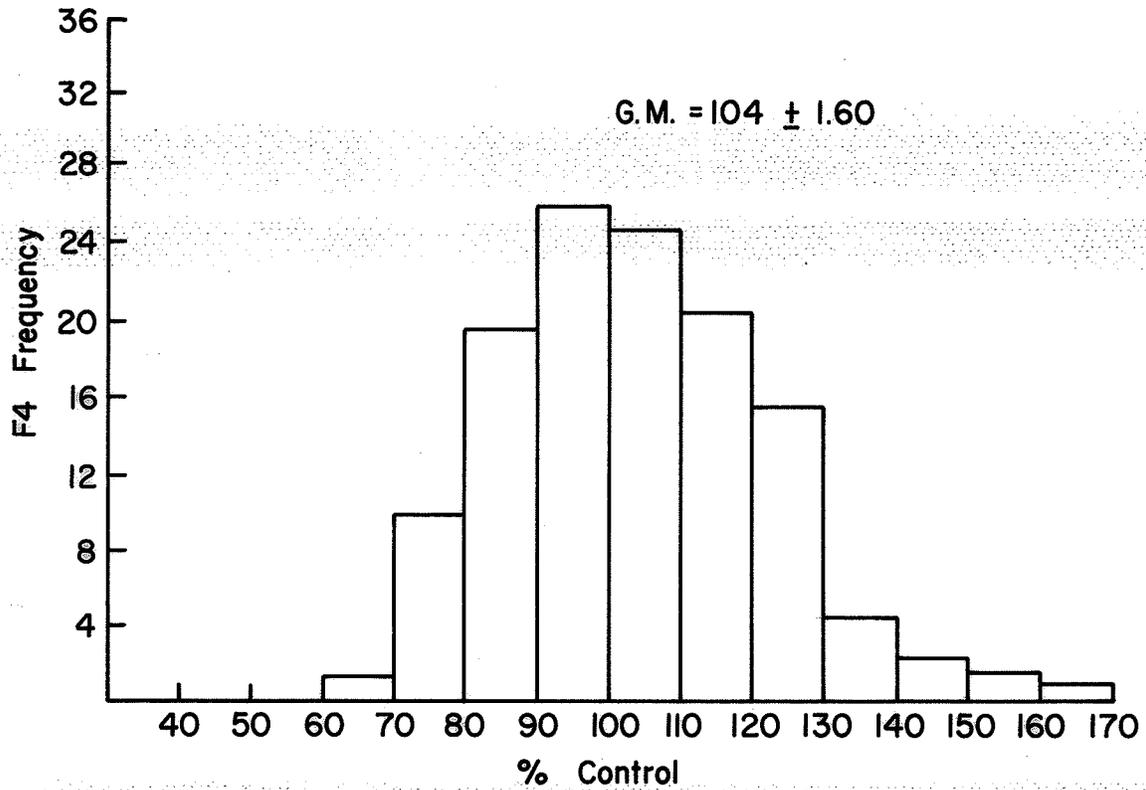


FIGURE 8. Yield distribution of F4 lines derived from superior F2 plants.

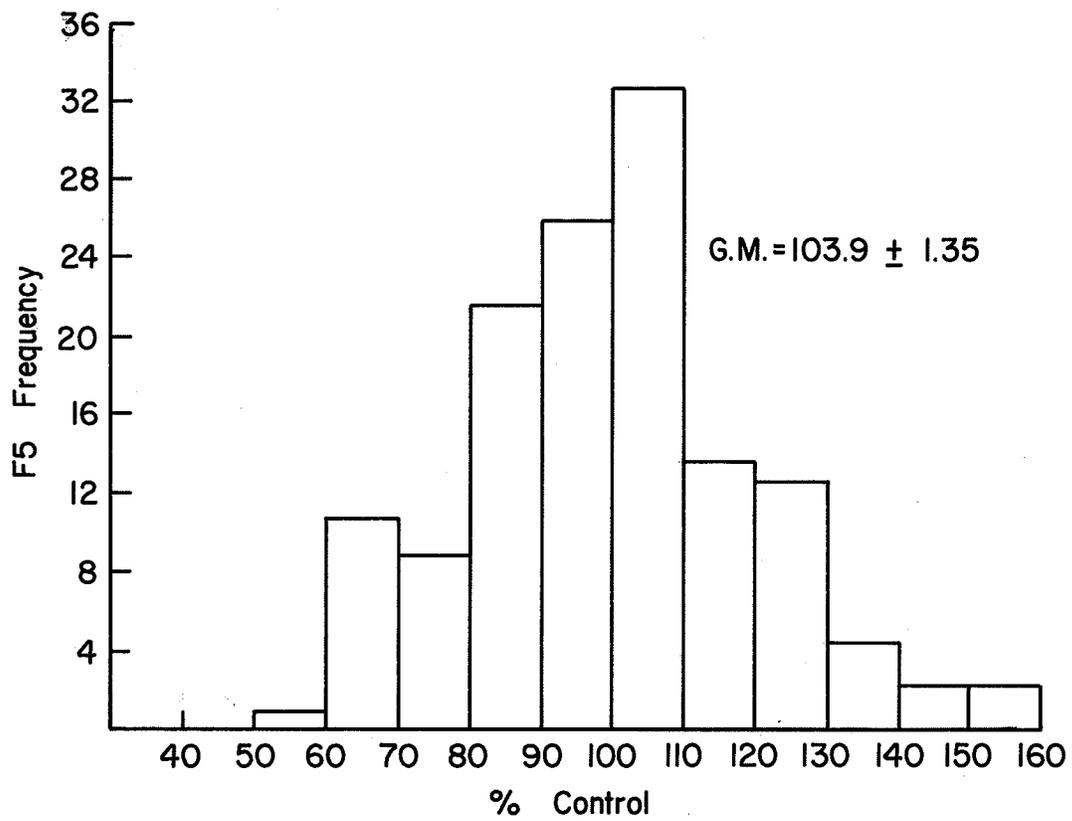


FIGURE 9. Yield distribution of F5 lines derived from the same superior F2 plants as those which gave rise to the F4 lines.

TABLE VIII

YIELD MEASURED IN GRAMS PER PLOT AND CALCULATED AS A
PERCENT OF CONTROL FOR THE F3 LINES, F4 AND F5 FAMILIES

Family	Gener- ation	n	Yield in Grams per Plot			Yield as a % of Adjacent Control		
			Mean	Max	Range	Mean	Max	Range
117x	F3	1	1683			139.6		
	F4	20	1290	1540	490	113.9	139	56
	F5	16	1219	1435	635	106.6	152	65
229y	F3	1	1670			127.9		
	F4	29	1336	1632	662	117.3	166	71
	F5	25	1470	1790	557	120.3	156	66
315y	F3	1	1648			122.7		
	F4	29	1345	1789	649	111.5	147	54
	F5	25	1352	1765	725	112.4	146	50
401y ⁺	F3	1	2164			131.2		
	F4	29	1078	1348	738	83.3	114	46
	F5	40	1082	1425	815	85.2	122	75
431x ⁺	F3	1	1668			121.0		
	F4	30	1160	1453	683	94.3	130	53
	F5	38	1159	1490	702	89.7	113	48

⁺F5 families which were segregating for stem rust resistance. At least 38% of the lines within a family were heavily infected.

than the F5 mean although its mean percent of control was equal. This exception lends supporting evidence to the use of systematic control plots to correct for micro-environmental fluctuations [Haggag (20) and Briggs (13)].

Three of the five families in both generations yielded more than 100% of adjacent control. The two families that yielded less than 100% of control were heavily infected with stem rust, and therefore, their yield performance can not be used meaningfully to assess the effectiveness of selecting unreplicated F3 lines.

Table IX presents the mean, standard error, and the comparisons between the adjusted yield of the F3, F4, and F5 generations. Although there was no significant difference between the F4 and F5 means, both the F4 and F5 mean yield, expressed as a percent of control, were significantly higher at the 1% level than the mean percent of control for all the F3 lines.

The inter-generation rank correlation and simple regression coefficients are presented in Table X. Both the regression and rank correlation between F4 family means and their related F5 family means were significant for yield, measured in grams per line and expressed as a percent of control. But, the F3-F4 and F3-F5 correlation and regression coefficients for yield were non-significant, which differs from the results obtained in Experiment II (cf. Table VI). The reasons for the lack of significant

TABLE IX
 THE MEAN, STANDARD ERROR, AND UNPAIRED t-TEST FOR THE
 ADJUSTED YIELD OF THE F3, F4, AND F5 LINES

	N	Mean	SE	Unpaired t-test (t-value)
1968 F3 lines	528	99.6%	± 1.01	(F3 v.s. F4) 6.17**
1969 F4 lines	75	114.2%	± 2.34	(F3 v.s. F5) 6.25**
1969 F5 lines	63	113.1%	± 2.01	(F4 v.s. F5) 0.35

** Significant at the 1% level.

TABLE X
 INTER-GENERATION RELATIONSHIPS FOR YIELD MEASURED BY
 SPEARMAN'S RANK CORRELATION AND SIMPLE REGRESSION

	N	Yield in Grams per Plot rank r	b	Yield as a % of Control rank r	b
1968 F3 to 1969 F5	5	-0.70	-0.42	0.20	0.34
1968 F3 to 1969 F5	5	-0.50	-0.45	-0.10	0.12
1969 F4 to 1969 F5	5	0.90*	1.16**	0.90*	0.98**

* Significant at the 5% level.

** Significant at the 1% level.

regressions and correlations between selected F3 values and F4 and F5 means in this experiment were : first, in Experiment II a larger range was sampled (the upper 30%) than in Experiment III (the F3 lines that were selected represented the top 1.3% of the population). The net result was that when a relatively large range of the F3 lines were selected, the environmental variability which was not controlled by control plots was relatively insignificant compared to the genetic differences among the F3 lines. But when a small range was correlated between generations grown in different years, the uncontrolled environmental variability had a magnified effect relative to the genetic differences among these F3 lines. Secondly, a genotype x year interaction may have affected the yield ranking of the selected F3 lines and the families derived from them. Thirdly, the F3 lines may have possessed different levels of heterozygosity and/or the effect of heterozygosity on yield expression may have been different among the F3 lines. This agrees with the work of Briggs (13).

By utilizing remnant seed of genetically superior F2 plants, one has effectively established an elite population containing a larger proportion of genetically superior lines. Because these families derived from F2 genotypes which presumably carried the best combination of desirable genes in either the homozygous or heterozygous condition,

these F2 genotypes are the only ones worth exploiting. By concentrating on these and growing larger populations of the better genotypic F2's one should have increased the probability of recovering high yielding genotypes with various combinations of other traits. This would give the breeder greater freedom to select for other traits, e.g., quality, maturity, height, awns, lodging resistance, disease resistance, without having to sacrifice a yield gain.

CONCLUSIONS

In Experiment I of this study the progeny test of selected single F2 plants provided evidence that neither random selection of well tillered plants nor visual selection of agronomically superior plants were capable of identifying F2 plants whose progenies yielded higher than the mean of the population. This conclusion concurs with the reports of Allard (1) and Bell (10), but differs from a recent work by McGinnis and Shebeski (33).

Significant positive regressions and correlations were obtained between selected F3 line values and F4 bulk means and F5 family means. Consequently the yielding capacity of an F3 line, if determined on the basis of a large plot adjacent to a control plot, provided an estimate of its performance in subsequent generations. These inter-generation relationships indicated that low yielding F3 lines do not on the average give rise to high yielding lines in the following segregating generations. Alternatively, high yielding F3 lines give rise to high yielding families in subsequent generations. The regression and correlation between F4 bulk means and F5 family means were highly significant; and therefore support the use of an F4 bulk test in a breeding program as suggested by Shebeski (41).

That is, those F3 lines which produced the highest yielding bulks also gave rise to the highest yielding F5 families. By harvesting and analyzing the F4 bulks first the breeder can identify that F5 family which will produce on the average the highest yielding lines.

The results of Experiment III confirm the findings of Briggs (13) that within the high yielding sector of F3 lines, yield correlation between the F3 and F4 or F5 generation is low. Therefore, in terms of practical plant breeding, the high yielding sector (1 to 2% of the F3 population) should be retained, and the best of these are then determined either by the bulk F4 test or by the means of F5 families.

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