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I am submitting herewith a thesis written by Mark J. Sellmann entitled "Culling Soybean Crosses in Early Generations Based on Yield Tests of Bulks in Microplots." I have examined the final copy of this thesis for form and content and recommend that it be accepted in partial fulfillment of the requirements for the degree of Master of Science, with a major in Plant and Soil Science.

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ABSTRACT

Because of genetic heterogeneity and a limited seed supply, selection for yield in soybeans is not initiated until the F_5-F_7 generations. This study was conducted to (i) compare effectiveness of standard 6 m plot size with 3 and 1.5 m plots for yield testing of early generation bulks and (ii) determine if the superior crosses could be identified on the basis of tests of this type in early generations. This study was conducted at three locations in Tennessee. An incomplete block design was used with plot size as the main- and cross or line as the sub-plot effect. Single row plots 6, 3, and 1.5 m with a .91 m row spacing and seeding rate of 32 seed m^{-1} were used. The F_2 and F_4 cross bulks were evaluated and advanced without selection in 1987, the F_3 and F_5 bulks in 1988. Parentage of these crosses was all group V maturity with the exception of two which were of group IV. Sixteen lines were also utilized as benchmarks at each location. There were two, four, and eight replications of the 6 m, 3m and 1.5 m plots, respectively. By increasing the number of replications as plot size decreased, the harvested linear footage of row was kept constant. The 6 m plots were harvested in four 1 m subplots, the 3 m plots in two 1 m subplots, and the 1.5 m plots in one 1 m subplot. The patterns of the ranks of the breeding lines were similar in all plot sizes, suggesting no difference in relative yield performance when tested in different size micro-plots. This implies that all three plot sizes provided equal opportunity to discriminate the highest yielding from lowest

yielding lines. The CV values generally decreased as plot size increased. Based on the ranks of the five crosses from all data combined over generations, plot size, and locations, the top 3 crosses could have been identified in the F_2 generation and two of the top 3 crosses would have been identified from the F_3 and F_5 tests of bulks. It appears that early generation yield testing of individual cross bulks is a feasible way to eliminate crosses with the least potential.

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PART I

INTRODUCTION

In most soybean breeding programs, visual description plays an important part in the evaluation process of phenotypes so that large populations can be reduced in size and facilitate making precise measurements can be made on selected lines (22). Testing early generations for quantitative characteristics has positive and negative aspects from the genetic perspective. There are several ways that the culling of F_3 lines can be of fault (22): (i) Most crops do not produce sufficient seed to permit replication of trials so that mini-plots can rarely be replicated. (ii) Mini-plots result in a high variability due to design errors as a result of the difficulty of adapting the plot size to the variation in soil fertility and plant competition. (iii) Using several standard varieties can provide some insight into genotype X year interaction. (iv) The genotype X year interaction is difficult to estimate. Some indications could be provided by the behavior of standard varieties.

Weber (21) found that response to early generation selection for yield in soybeans to be less effective than in later generations. However, he did state that if the model is correct, the response to selection in early generations is large enough to justify selection. McGinnis and Shebeski (12) found that there is no significant correlation between F_2 plant and F_3 line yield in wheat. From their data they suggested that selecting plants in the F_2 with a reasonable level of tillering is just as effective as selecting those with more plentiful tillering as far as the F_3 is concerned. Finding that control genotypes were consistently outyielded by selected genotypes

indicated that selection had actually increased the frequency of the higher yielding genotypes.

Geiger (7) noted that heterosis and inbreeding depression play an important role in early selection for yield. Characters with high heritability require less intensive testing and display closer genotypic correlations between early and late generations than those with low heritability. Thus, the higher the heritability of the trait, the more effective is early selection (7). Since plants in early generations are heterozygous, the breeder may take advantage of the variation and reduce the number of initial entries needed. However, Geiger stated that the number of plants needed would increase if the traits were negatively correlated, if more traits were included, or if higher selection intensities were being applied. He concluded that in a multitrait situation, no rational alternative to selection in successive stages exists and early testing for yield can be recommended only in the last stage of the procedure.

In self-fertilized crop species the pedigree method (or modifications) of breeding predominates; therefore procedures of improving the selection efficiency of this method have their merit. Selection for a character of low heritability, such as yield, is only likely to be effective in early generations if sufficient replication is available and an efficient selection system exists (16). There are two advantages of rapid generation advancement techniques over the pedigree system. They save time in varietal development by enabling homozygous material to be available for large scale yield testing and stock multiplication at an earlier date (4). Also, more efficient

selection is possible in advanced generations because of the greater contribution of additive effects to the variation and the low within family genetic segregation. This allows better discrimination between genotypes within any one generation of field testing and a better response to selection across generations (4).

Knott (9) tried to increase the efficiency of breeding for yield in wheat by reducing environmental variability in the F_2 generation. He regressed the yield of F_3 lines on the yield of their F_2 parents three ways: i) F_3 seed weight expressed as a percentage of the replicate mean yield, ii) F_3 seed weight expressed as a percentage of the average yield of the two closest checks, and iii) F_3 seed weight expressed as a percentage of the moving average of the nearest seven hybrid plots, ignoring the checks, but including the plot in question. He stated that normally the moving average was calculated from the plot in question and the nearest three on each side. In poor selections, for every 1 g increase in yield of the parent F_2 plant, the F_3 line increased in yield by approximately 2%. For good selections though, there was about a 1 percent increase in the F_3 yields for each 1 g increase in F_2 yields. The yield of F_2 plants taken at random showed no significant relation to the yields of their F_3 offspring. This was somewhat surprising because it was assumed that there would be greater genetic variability among the F_2 plants than within either the good or poor classes and thus result in a higher regression value (9). Apparently, the environmental effects were so large that any genetic effects were obscured. Of the three methods of expressing the data, expressing the plot yields as a percentage of a moving average or as a percentage

of an adjacent check resulted in a significant reduction in the error mean square. Similarly, McGinnis and Shebeski (12) reported that the progeny of selected and random F_2 wheat plants did not differ in yield and there was no correlation between F_2 and F_3 yields. However, their F_3 yields were based on unreplicated plots.

Thorne (17) tested the association of yields of F_3- and F_5-derived soybean lines. Correlation coefficients for average yield over locations were calculated for each F_3-, F_5-derived line set. In a variety development program there is concern only for the best lines, thus the highest yielding F_5- derived lines in each test were considered. Thorne recommended that a 2 or 3 replicate single row trial could be grown from seed obtained from spaced F_3 plants so that selection could be based on preliminary yield information in conjunction with visual selection criteria. This was based on a standard plot size.

Garland and Fehr (6) compared the effectiveness of selection for yield, height, maturity, lodging, and phenotypic score among soybean lines in hill plots and row plots, in random and non-random designs. They stated that the primary advantage of hill plots are the larger number of lines that can be tested and the reduction in number of years required for cultivar development or recurrent selection by eliminating the need for a generation of seed increase. They also stated that the use of hill plots for soybeans should be for the first evaluation of random lines from segregating populations. The use of a non-random arrangement of entries for replicated tests would be dependent on their effectiveness for selection compared to conventional randomized

designs. It is most likely, because of biasness, that they would not be as effective as randomized designs. Garland and Fehr used conventional analyses of variance and covariance in which lines, years, and locations were considered random effects. Variance component estimates for yield were similar for the random rows and hills. Experimental error for yield was twice as large for the hill plots as for the row plots. Inferior yields per unit area in hills rather than in rows was due to wide spacing among hill plots. Correlations of line performance among plot arrangements were positive and highly significant for all traits. The coefficients of variation for yield in hill plots were nearly double that of the rows (6).

Voigt and Weber (19) concluded from their results that soybean selections from early generation F_4 testing were superior in yield to those selected from bulk and pedigree method. Boerma and Cooper (2), used four soybean crosses to test the effectiveness of early generation yield selection of F_2- derived lines using combined generation means. The coefficient of variation for yield from F_3 to F_5 lines decreased, suggesting that the variation of yield among lines selected each generation by early generation yield testing procedures was less than for the populations which they were selected from. Across all locations tested, purelines separated by pedigree selection and single seed descent methods were usually the same or higher in yield than heterogeneous lines selected in the F_3, F_4 and F_5 generations.

Parent-offspring regression is often used for estimating heritability of quantitative characters. According to Simmonds (15), in parent-offspring regression, if progeny have some resemblance to

their parents, then the progeny mean will tend to split toward a general mean. If parents and progeny were exactly the same, the regression would have a slope of unity. Simmonds concluded that close parent-offspring regression, otherwise known as high regression, implies a large genetic effect and a small environmental effect. He demonstrated that the regression coefficient, b, estimates the narrow sense heritability, V_A/V_P, if the parental values are means of both parents; if simply one parent is identified, then $b = 1/2(V_A/V_P)$.

Martin and Wilcox (11) calculated heritability of pod height, seed size, and yield in soybeans. Narrow sense heritability was estimated by regression of the F_3 progeny means on F_2 parental values. They found that the regression coefficients for the lowest pod height and seed size within each cross were similar, and at the same time higher than the values for seed yield.

Vogel et al. (18) performed experiments with indiangrass [Sorghastrum nutans (L.) Nash] to determine heritability estimates for plant height, leaf color, erectness, leafiness, and vigor. Heritability estimates were obtained using parent-offspring regression and variance components from the analyses of variance of half-sib families. They found that the effect of years was significant for height and vigor among progeny. The genotype X year interaction was significant for vigor of the parents. All the other year and genotype X year effects were nonsignificant. From these results they determined that there are significant genetic differences among indiangrass plants for height, leaf color, erectness, leafiness, and vigor. Also, on a phenotypic mean basis, broad sense heritability estimates determined by

the parental clones were only slightly higher than narrow sense heritability estimated from half-sib progenies. Their overall results indicated that most of the genetic variation within populations for these traits is additive.

Warner (20) suggested there are three main categories for estimating the degree of heritability. These include parent-offspring regression, variance components from an analysis of variance, and an approximation of non-heritable variance from genetically uniform populations to estimate total genetic variance. However, as he also mentioned, none of these methods is acceptable when one considers a population such as an F_2 population and asks, "To what extent is selection likely to be effective?" He stated that the usefulness of estimates of heritability as a practical tool of the plant breeder depends on many factors. First, the estimates of heritability provide information on the relevant practicality of selection. High heritability in the F_2 indicates that effective selection on an individual plant basis is possible. The usefulness of heritability also depends on the effort and expense needed to gain such information. Also, there is a need of at least several hundred F_2 individuals and the same number of backcrosses to reduce the sampling error to a reasonable level. The merit of theses estimates is dependent on the accumulation of similar data over a wide range of crosses and environments.

Narrow sense heritability estimates were computed by regression of the F_3 family mean on the F_2 plant measurement for a particular character (8). They also used the 'b' estimate of the narrow sense of heritability as it was presented by Frey and Horner (5). This method

tended to eliminate the environmental effects of different years which may increase or decrease the performance of the progenies relative to that of the parent. Actually it establishes a heritability ceiling of 100%, which is a contrast to the conventional regression method which has a ceiling for each experiment and can exceed 100% (5).

Bartley and Weber (1) considered heritable variance in soybeans to be divided into three parts. These included i) additive genetic variance, ii) dominance variance, and iii) epistatic variance. The purpose of their study was to estimate heritability in the narrow sense of four agronomic characteristics in the F_2 and F_3 generations from their relations with their respective F_3 and F_4 generations using three soybean crosses. Frequency distributions for seed yields of F_2 plants and F_1 means were determined and plotted. Also, F_1 and parental maturity dates were recorded. They did make an attempt to compare variation among means of F_3 families with variation between F_4 lines within F_3 families by their respective components of variance. The performances of F_2 or F_3 plants were determined by correlation coefficients. Regression of the F_3 progeny on F_2 plants has been shown to provide an estimate of heritability in the F_2, and likewise with the F_4 on F_3 (1). With dominance, the parent-offspring regressions overestimated the heritability. In populations with large genetic variability between family means, selection against extremes in maturity was expected to reduce variability within families as compared to that among families. Interactions of nonallelic genes and genotype-environment were assumed to be zero and their effect on the regression coefficients was unknown. Briggs and Shebeski (3) found that broad

sense heritabilities for the F_5 generation did support their thesis that selection between F_3 derived lines would be a practical plant breeding procedure for several breadmaking parameters in spring wheat.

Shannon et al. (14), measured soybean yield, maturity, lodging, height, and seed weight in hill plots. They found that yield increased consistently as distance between hills increased. Competitive effects between genotypes for maturity, height, lodging, and seed size were nonsignificant. Maximum differences in yield occurred at spacings from 65 to 76 cm when each isoline was bordered by itself. This implied that single hill plots should be spaced 65-76 cm to evaluate different genotypes for yield in pure stands.

Schutz and Bernard (13) found that good estimates of genotype X year and genotype X location interactions are necessary in evaluating the efficiency of a testing program and determining the optimum distribution of locations and years. Their investigations involved soybean strains from the Uniform Preliminary Tests, and they concluded that the variances among strains and the genotype X location interactions were less than would be expected from a random set of lines.

LeClerg et al. (10) noted that under conditions of high locational and seasonal variability it is often difficult to discriminate between varieties when averaged over all locations. To overcome this, they suggested using more replications at each location, more refined plot technique, and additional test sites as well as grouping the locations on the basis of their average response and their variability of response. Another problem they pointed out was the high year-by-year

variability at some locations. Again, grouping years may be helpful where detailed weather information is available. By analyzing the weather for years in which the tests were conducted and comparing them with the longterm average, permits a measure of how much the particular sample of years deviated from the population of years.

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PART II

LITERATURE REVIEW

According to Fehr (2), the objective of early generation yield testing is to estimate the genetic potential of an individual or population at an early phase of inbreeding. This should eliminate the populations that do not deserve attention for future inbreeding and selection. Early generation yield tests of bulk populations in self pollinated crops has been suggested as one way of eliminating inferior crosses (16, 18). By identifying the "best prospective" populations, one can improve efficiency by concentrating on selection and testing of only those cross combinations which have the highest probability of producing superior progeny and discarding those which have the lowest probability. The goal of early generation yield testing is to distinguish desirable heterogeneous populations of lines from which exceptional homozygous individuals can be selected (18). There are reports in the literature where the highest yielding crosses based on F_2 generation tests did not consistently provide the highest yielding progeny (1, 7, 8, 16, 18). On the other hand, Harrington (5) found that heterosis of six wheat crosses measured in bulk F_2 replicated yield trials indicated yielding abilities of segregates from these crosses. Varietal differences in the contribution of yield potency to crosses were apparent. In one wheat cross, Harrington (5) found that classification of several hundred single F_2 plants correctly predicted the value of the cross as to earliness, height, stem rust reaction, and seed characters. In replicated yield studies of bulk populations of six crosses in barley, Immer (6) found that there were substantial differences in cross mean yields among crosses in F_2, F_3 and F_4 bulk generation tests.

A limited seed supply is often a problem for replicated yield testing of early generation material. Small plots provide a way to circumvent this problem if reliable results can be obtained (4, 11, 15). With small plots, testing of a larger number of crosses in a given space compared to large plots is possible.

The width and length of row plots can affect the precision of comparisons among genotypes (18). In breeding programs where many varieties must be compared, it is desirable to cut down the amount of land required for estimating the performance of each (11, 15). Reducing the plot sizes may accomplish this, provided that the number of replications needed to achieve a given degree of precision does not increase a great deal. Small plots are necessary if the amount of seed is limited for each plant, family or population. This could be due to several reasons, but one most likely is that the seed came from a single plant. Even when there is enough seed, the length of a plot is rarely longer than 6 m (18). Wilcox et al. (18) pointed out that the length of plots is usually determined by the number of rows included. One disadvantage of using small plots may be the equipment used to plant and harvest. Seed spacing at planting and endtrimming at harvest were judged to be critical factors. Obviously, with a smaller population to work with, environmental variance will be more of a factor. Tattersfield and Mentz (15) found that the performance of some varieties in a micro-plot trial differed considerably from their performance in an advanced standard plot trial.

The main advantages in using hill plots, according to Garland and Fehr (4), are the reduction in number of years required to develop a

cultivar or for recurrent selection by eliminating the need for a generation of seed increase and the large numbers of lines that can be tested.

Ross and Miller (11) performed comparisons of hill plot and conventional yield tests with oats [Avena sativa] and spring barley [Hordeum vulgare]. They reported that yield levels differed significantly among methods seven out of nine times for both crops. Variability in hill tests was consistently higher than in any of the other methods.

Fischer and Kertesz (3) tested how well wheat yields measured in microplots predicted yielding ability as measured with the large plots. Phenotypic correlation coefficients were calculated using genotype means. The microplot yield was highly correlated with large plot yield, but only accounted for 46 percent of the variation between the genotypes. Much of the residual was thought to be related to the highly significant genotype X plot type interaction. They concluded that the land saved by the microplots would not justify the loss in accuracy in detecting yield differences.

The objectives of this study were to a) compare the similarities of results from 6, 3, and 1.5 m plots for testing yield of early generation bulks and b) determine if the high yielding crosses can be identified from yield tests of bulks of individual crosses in early generations.

PART III

MATERIALS AND METHODS

Experiments were conducted at the Knoxville Plant Sciences Field Laboratory (KPSFL), the Highland Rim Experiment Station (HRES), and Ames Plantation (Ames) in 1987 and 1988 utilizing an incomplete block design with plot size as the main effect and soybean cross or line as the subplot effect. These locations were utilized because they represent diverse edaphic and climatic conditions of Tennessee. A representative field diagram of an experimental layout is shown in Fig. A1 in the Appendix. Of these three locations, Knoxville was the only one that had irrigation. In 1987 this included two 1 inch applications with a 12 hours between them at flowering stage, and in 1988 this included one 1 inch application at flowering stage.

Single row plots of 6, 3, and 1.5 m in length were evaluated in this study. Spacing between rows was 91 cm. The seed were sown at a rate of 32 m^{-1}. At each location there were two replications of the 6 m plots, four replications of the 3 m plots, and eight replications of the 1.5 m plots. Different randomizations were used for each plot size at each location each year. The 6 m plots were harvested in four 1 m subplots, the 3 m plots in two 1 m subplots, and the 1.5 m plots in one 1 m subplot. Thus, the total harvested row length was the same for each plot size even though there was an unequal number of replications for each plot size. At each location there were 8 subplots of each entry in each plot size. For purposes of the study reported herein, the four and two subplots of each 6 and 3 m plot sizes, respectively were summed together and treated as one unit.

Bulks of five different crosses were evaluated in this study. The crosses were: 'TN 5-85' x 'TN 4-86', TN82-94 x TN83-6, 'TN 5-85' x V74-

315, 'Hutcheson' x TN83-65, TN85-55 x TN85-42. Bulked seed of the F_2 (3 locations) and F_4 generations (1 location) of each cross were evaluated in 1987. The F_3 and F_5 generations were evaluated at all three locations in 1988. Each cross was advanced without selection, as each generation was a heterogeneous group of plants. In addition to the crosses, there were 16 breeding lines included in this study. The 16 lines had been extensively tested for yield in two previous studies (9, 17). Eight lines were chosen on the basis of high yield and eight lines were chosen on the basis of lower yields. The lines served as "benchmarks" for determining the value of the different size micro-plots for discriminating the highest yielding from the lowest yielding lines. Therefore, each season there were twenty-six entries entered (Table 1). Due to a limited quantity of F_4 seed of each cross in 1987, the F_4 generation bulks were only tested at the Knoxville location. The values of the crosses were then computed and compared. Only the generations grown in the same season were compared with one another; therefore the F_2's were compared with the F_4's and the F_3's with the F_5's.

Data were analyzed via the Statistical Analysis Systems (SAS) software program (12, 13). The 6 m plot size was used as the "standard" by which results from the 3 m and 1.5 m plot sizes were compared. Determining if one plot type was better than another was based on the relative magnitude of error variance, coefficient of variation, and standard error of the difference between two means. The coefficient of variation (14), compared the variability of one plot population with the variability of another population. This value is

Table 1. Entries, generation and pedigrees of the germplasm used in this study.

Entry	Generation	Pedigree of Cross or Line	Cross Number
$F_2$87-1	F_2	'TN 5-85' x 'TN 4-86'	1
$F_2$87-2	F_2	TN82-94 x TN83-6	2
$F_2$87-3	F_2	'TN 5-85' x V74-315	3
$F_2$87-4	F_2	'Hutcheson' x TN83-65	4
$F_2$87-5	F_2	TN85-55 x TN85-42	5
$F_3$88-1	F_3	'TN 5-85' x 'TN 4-86'	1
$F_3$88-2	F_3	TN82-94 x TN83-6	2
$F_3$88-3	F_3	'TN 5-85' x V74-315	3
$F_3$88-4	F_3	'Hutcheson' x TN83-65	4
$F_3$88-5	F_3	TN85-55 x TN85-42	5
$F_4$87-1	F_4	'TN 5-85' x 'TN 4-86'	1
$F_4$87-2	F_4	TN82-94 x TN83-6	2
$F_4$87-3	F_4	'TN 5-85' x V74-315	3
$F_4$87-4	F_4	'Hutcheson' x TN83-65	4
$F_4$87-5	F_4	TN85-55 x TN85-42	5
$F_5$88-1	F_5	'TN 5-85' x 'TN 4-86'	1
$F_5$88-2	F_5	TN82-94 x TN83-6	2
$F_5$88-3	F_5	'TN 5-85' x V74-315	3
$F_5$88-4	F_5	'Hutcheson' x TN83-65	4
$F_5$88-5	F_5	TN85-55 x TN85-42	5
TN82-192 [H]	F_{11}	'Bedford' x 'Mitchell'	
TN82-32 [H]	F_{11}	J74-40 x 'Douglas'	
TN82-184 [H]	F_{11}	D74-8819 x TS72-824	
TN82-129 [H]	F_{11}	'Forrest' x 'Miles'	
TN82-84 [L]	F_{11}	D74-8819 x 'Columbus'	
TN82-294 [L]	F_{11}	'Forrest' x (K1018 x L73-977)	
TN82-76 [L]	F_{11}	D74-8819 x TS72-824	
TN82-74 [L]	F_{11}	J74-45 x SRF350	
TN82-265 [H]	F_{11}	'Essex' x ('Bay' x N73-520)	
TN82-264 [H]	F_{11}	'Essex' x ('Bay' x N73-520)	
TN82-268 [H]	F_{11}	'Essex' x ('Bay' x N73-520)	
TN82-262 [H]	F_{11}	'Essex' x ('Bay' x N73-520)	
TN82-259 [L]	F_{11}	J74-40 x TS72-824	
TN82-277 [L]	F_{11}	'Centennial' x J74-45	
TN82-250 [L]	F_{11}	J74-45 x TS72-824	
TN82-260 [L]	F_{11}	J74-40 x TS72-824	

[H] High yielding benchmark line
[L] Low yielding benchmark line

the square root of the error mean square of each plot size divided by the overall test mean. After analyzing the data at the three different locations, the data for all locations were combined and analyzed.

Means were calculated by plot size, location, and combined locations for the benchmark entries, $F_2 + F_4$, $F_3 + F_5$, F_2 individually, F_3 individually, F_4 individually, and F_5 individually. The model for individual locations included replication and entry and these were determined to be significant or nonsignificant. Mean square for errors, and coefficient of variation were also calculated. For combined locations the model included location, replication within location, and location X genotype interaction.

Mean separations were used to check whether mean yields of the populations were significantly different. Mean yield rankings in all plot sizes and locations were also used to determine if a population would rank the same from one generation to the next and with their rankings based on all data combined.

Spearman's coefficients of rank correlation (SCRC) were used to determine the relative consistency of ranks of crosses in different generations as well as the consistency of ranks of the crosses in different plot sizes.

The correlations were calculated between ranks of crosses in different generations within location, plot size, and year to test the consistency of rank of successive generations. For example, the ranks of the crosses in the F_2 generation, were correlated with the cross ranks based on the F_3, F_4 and the F_5 generation yield values summed together (F_2 excluded). Therefore, the F_2 yield did not contribute any

bias to the correlation. The same procedure was followed to calculate the rank correlations for F_3 with F_3 excluded and F_5 with F_5 excluded. The rankings were also tested across all locations and across all plot sizes, and across all locations and generations. They were also tested within locations and across plot sizes.

In order to test the hypothesis that plot size has no effect on selection of early generations, we then used SCRC and tested the yield ranks within location and across generations. Also, yield ranks of individual plot sizes were tested across locations with the overall yield rankings.

Heritability was estimated by parent-offspring regression for F_2:F_4 (Knoxville only) and F_3:F_5. In addition, heritability was estimated in each generation, plot size, and location using the variance components calculated via the maximum likelihood method in SAS Varcomp (12). This procedure was used because it gave a more conservative estimate of the variance components.

PART IV

RESULTS AND DISCUSSION

I. Comparisons Among Plot Sizes

In general, the patterns of ranks of the benchmarks based on yield were similar for the different plot sizes at each location and in both years (Table 2). The 1.5 m plots were as effective as either the 6 m or 3 m plots for the purpose of discriminating among the high yielding versus low yielding benchmark lines. The number of the eight high benchmark lines which ranked in the top 8 at each location each year ranged from 5-7 for the 1.5 m plot size and 4-6 for the 3 and 6 m plot sizes (Table 2). The plot size/location combinations which gave the poorest ranking (4 of 8) of the benchmarks were the 3 and 6 m plots at Ames in 1987 and the 3 m plots at Ames in 1988. When summarized over locations by plot size, 6 of the 8 high benchmarks ranked in the top 8 in 1.5 m plots, and 5-6 in the top 8 in 3 or 6 m plots. Based on the results obtained with the benchmarks, it appears that reliable results were obtained with all of the plot size arrangements. Combining information across locations within a given plot size did not improve appreciably the effectiveness of the plot size (Table 2).

Supporting evidence was obtained using the overall yield ranks of the five crosses in the 1.5, 3, and 6 m plot sizes. The data were combined for each cross across all generations and locations in order to determine the best ranking of the crosses. The best cross was No. 4 which had the highest rank in all three plot sizes (Table 3). The lowest yielding cross was No. 3 which had the poorest (fifth) ranking in the 1.5 and 3 m plot sizes and fourth in the 6 m plot size (Table 3). Based on the overall ranking of the crosses, cross No. 3 and

Table 2. The number of "high" yielding benchmarks that ranked in the top 8 at each location and all locations combined in the 1.5, 3, and 6 m plot sizes for 1987 and 1988.

	1987			1988		
	Plot size (m)					
Location	1.5	3	6	1.5	3	6
	number					
Ames	6	4	4	5	4	5
Highland Rim	6	5	6	7	6	6
Knoxville	6	6	6	5	6	6
Combined	6	6	5	6	5	5

Table 3. Overall yield ranks of the five crosses in 1.5, 3, and 6 m plot sizes combined across generations and locations.

Cross No.	Plot size (m)			All Data Combined
	1.5	3	6	
	rank†			
1	2	4	5	4
2	3	3	2	2
3	5	5	4	5
4	1	1	1	1
5	4	2	3	3

† 1=best, 5=worst

possibly No. 1 would have been candidates for culling. Crosses 2, 3 and 4 were very consistent in rank in the 3 different size plots. The biggest discrepancy in rank was for crosses 1 and 5 in the 1.5 m compared to the 3 and 6 m plots. Cross 1 ranked high and cross 5 ranked poor in the 1.5 m plots; whereas the reverse was true in the 3 and 6 m plots (Table 3).

Ranks of the five crosses with generations combined were plotted for each plot size at each location (Fig. 1). There are noticeable patterns in the shape of the lines of each cross in the 6, 3, and 1.5 m plots. As an example, cross No. 5 has a V-shape in all plot sizes, and No. 4 has an inverted V-shape. Cross 1 is the only one that did not have a consistent pattern in all three plot sizes, but it does have a characteristic V-shape in the 3 and 1.5 m plots. These patterns suggest that the crosses performed similar across locations whether they were tested in a 1.5, 3, or 6 m plots.

Comparisons were made among plot sizes for the crosses evaluated in the F_2 generation at each individual location and plot size (Fig. 2). Once again there were comparable trends from the 6 to 3 to 1.5 m plot size. Crosses No. 2, 3, 4, and 5 had consistent patterns across all three plot sizes. Cross No. 1 followed a similar pattern as in the Fig. 1, whereby only the 3 and 1.5 m plots resulted in similar patterns. This suggests that even in the F_2 generation, there was a pattern in the rank of the yields of the crosses. The crosses were ranked based on their F_3 bulk yields for the same plot size-location combinations (Fig.3). The patterns of crosses No. 3, 4, and 5 are consistent throughout the 6, 3, and 1.5 m plots. The pattern of cross

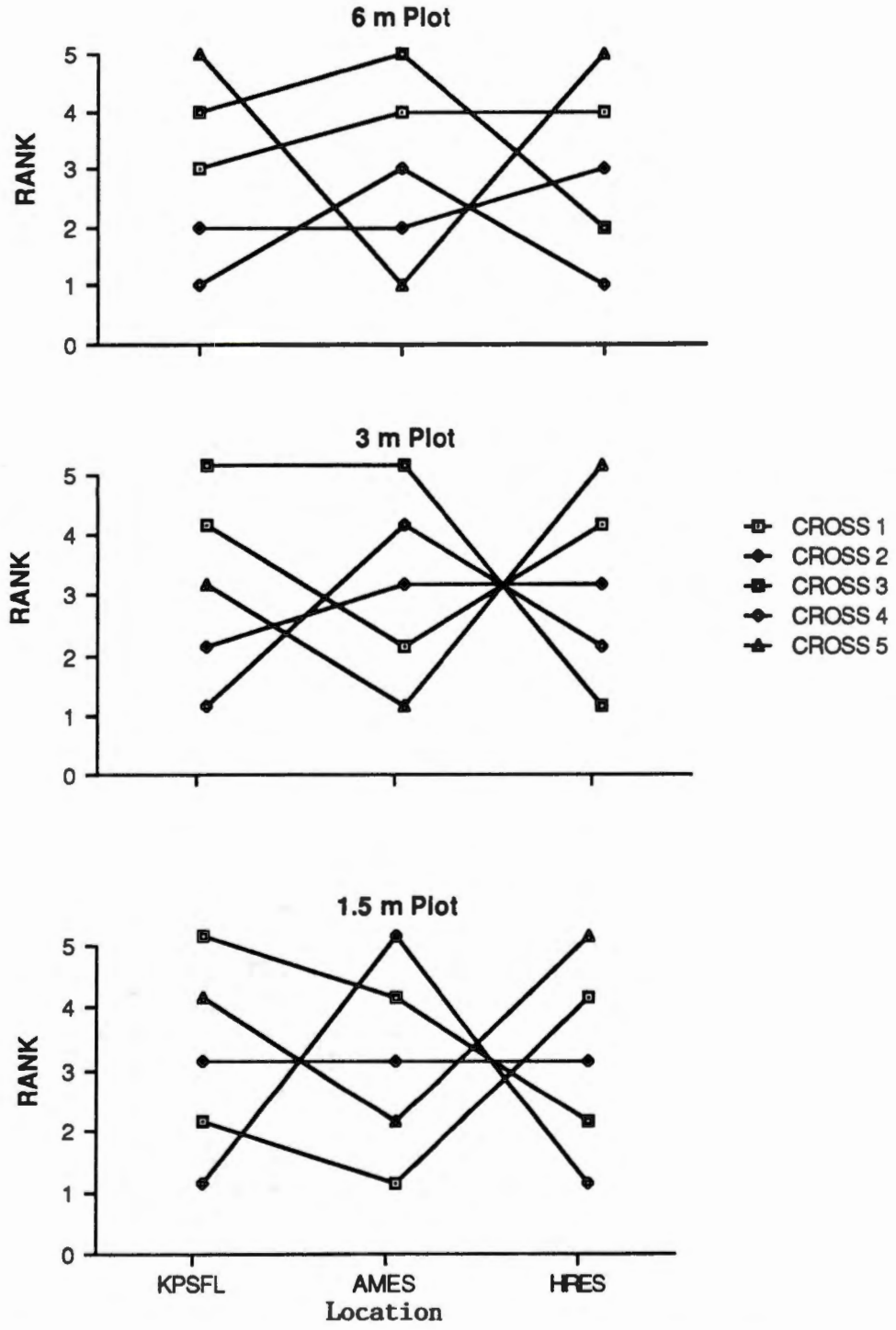


Fig. 1. Ranks of the five crosses (generations combined) at the Knoxville (KPSFL), Ames, and Highland Rim (HRES) locations in all three plot sizes.

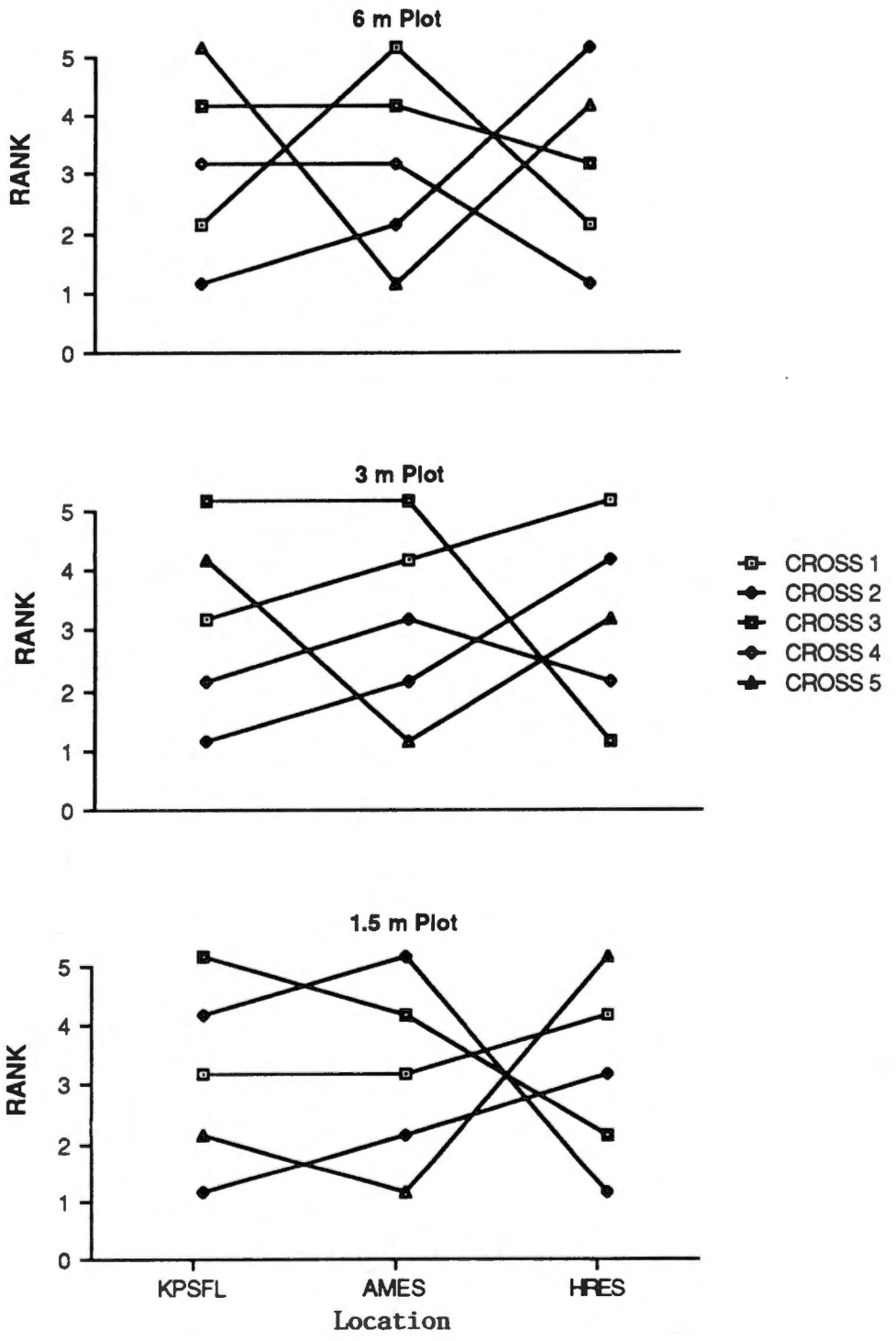


Fig. 2. Ranks of the five crosses in the F2 generation at Knoxville (KPSFL), Ames, and Highland Rim (HRES) in all three plot sizes.

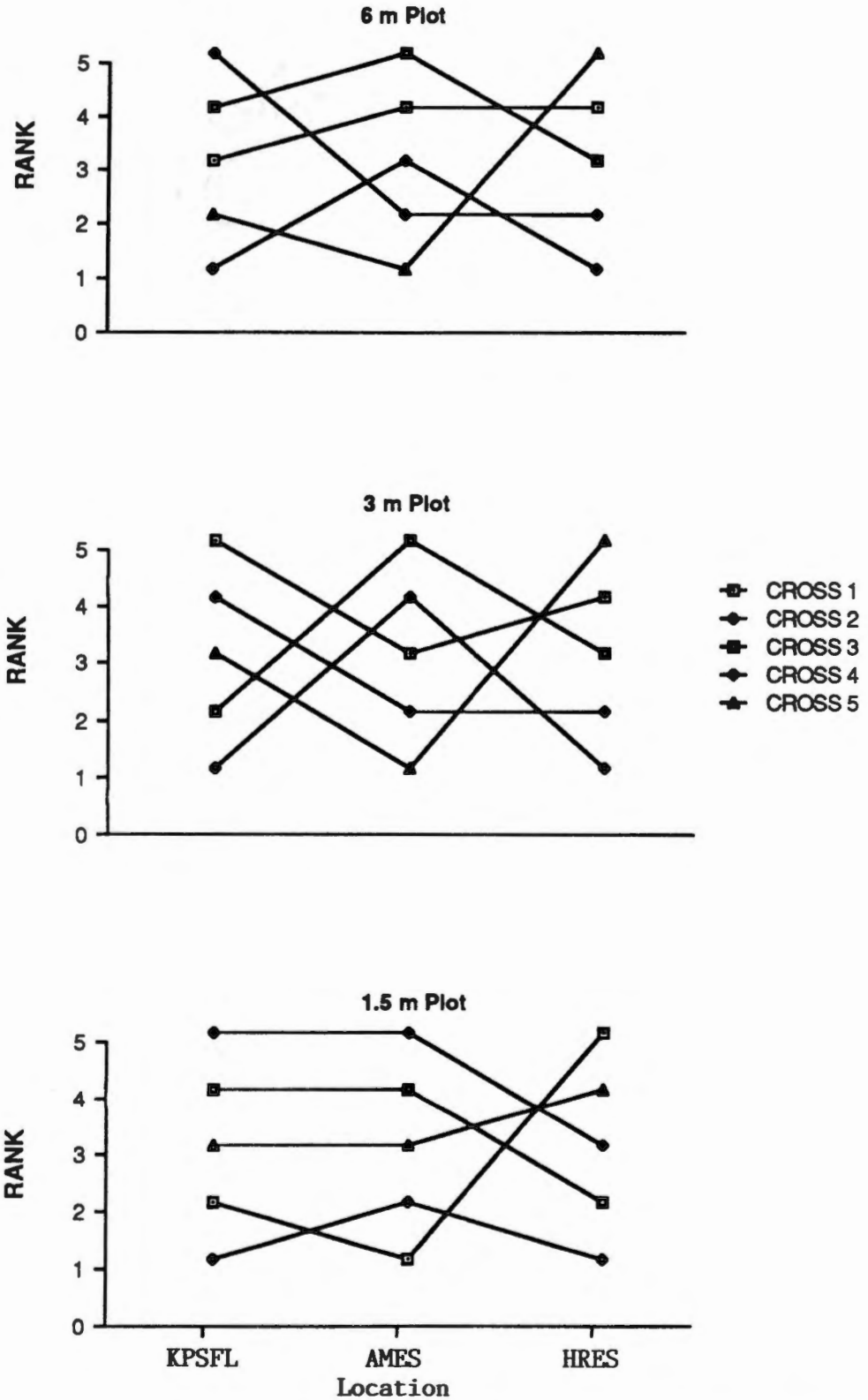


Fig. 3. Ranks of the five crosses in the F3 generation at Knoxville (KPSFL), Ames, and Highland Rim (HRES) in all three plot sizes.

1 and 2 were not as consistent for all three plot sizes. In the F_5 generation, crosses 3, 4, and 5 maintained patterns similar to those in the F_2 and F_3 generations (Fig. 4). Again, crosses No. 1 and 2, had inconsistent patterns. From this information there seems to be little if any change in the performance of the crosses when comparing the 6, 3 and 1.5 m plot sizes in the F_5 generation. Across all three generations, the patterns were maintained, indicating that crosses will perform the same whether in 6, 3 or 1.5 m plots in any generation.

The coefficients of variation (CV) were determined at each location for each generation and plot size (Fig. 5). Across all locations and at each individual location, as plot size increased the CV's decreased, with the exception the F_2 generation at the Ames location in which all three were similar (Fig. 5). The CV's at Knoxville and Highland Rim were similar, but Ames did have the lowest CV's. At each location, as generations were advanced, CV's increased for all plot sizes except the 6 m plots. In the 6 m plots CV's were similar in magnitude in the F_2 and F_5 generations, but decreased in the F_3. In general, CV's decreased as plot size increased, there was more variation in the smaller plots than in the large plots.

The standard errors (SE) of difference between two means were determined for each plot size at each location. In general, there was little or no difference in the SE as plot size changed at Ames and Highland Rim, but at Knoxville the SE's did decrease as the plot size increased (Fig. 6). At each individual location, the SE of the F_3 and F_5 was considerably higher than the F_2 generation. Based on the SE's, larger differences between cross means would have been required in

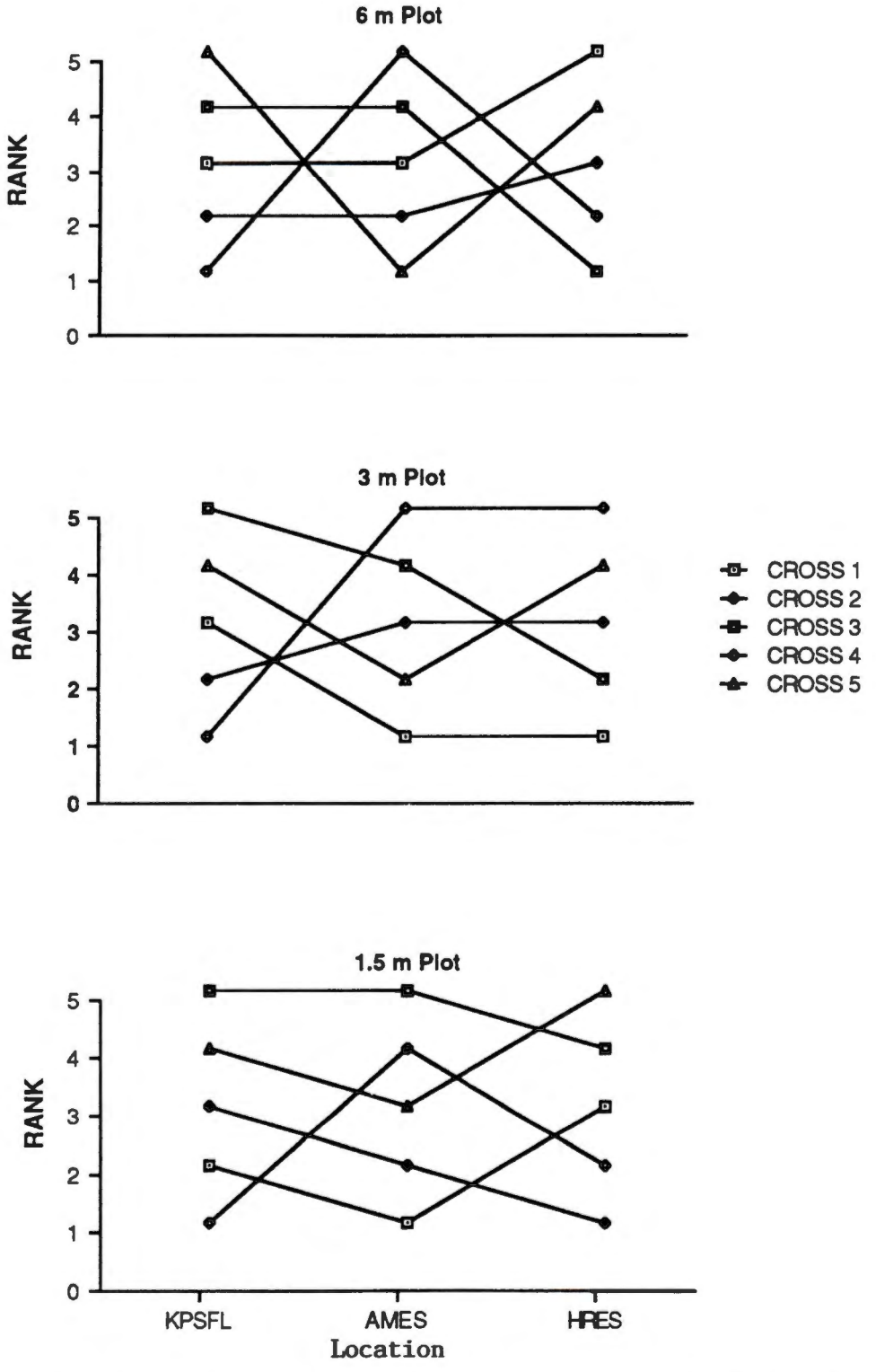


Fig. 4. Ranks of the five crosses in the F5 generation at Knoxville (KPSFL), Ames, and Highland Rim (HRES) in all three plot sizes.

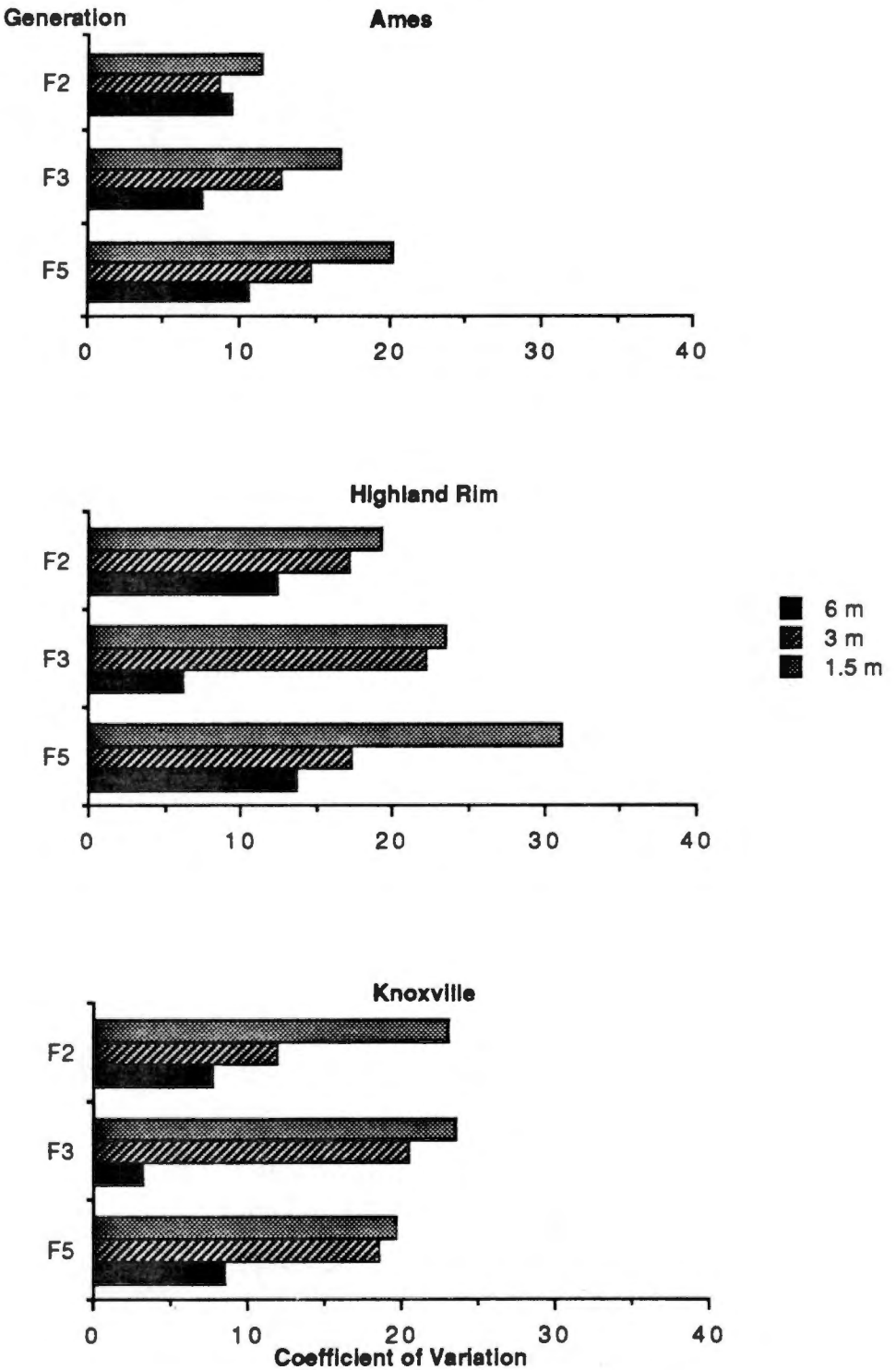


Fig. 5. Coefficients of variation in the 1.5, 3, and 6 m plots in the F2, F3, and F5 generations at three locations.

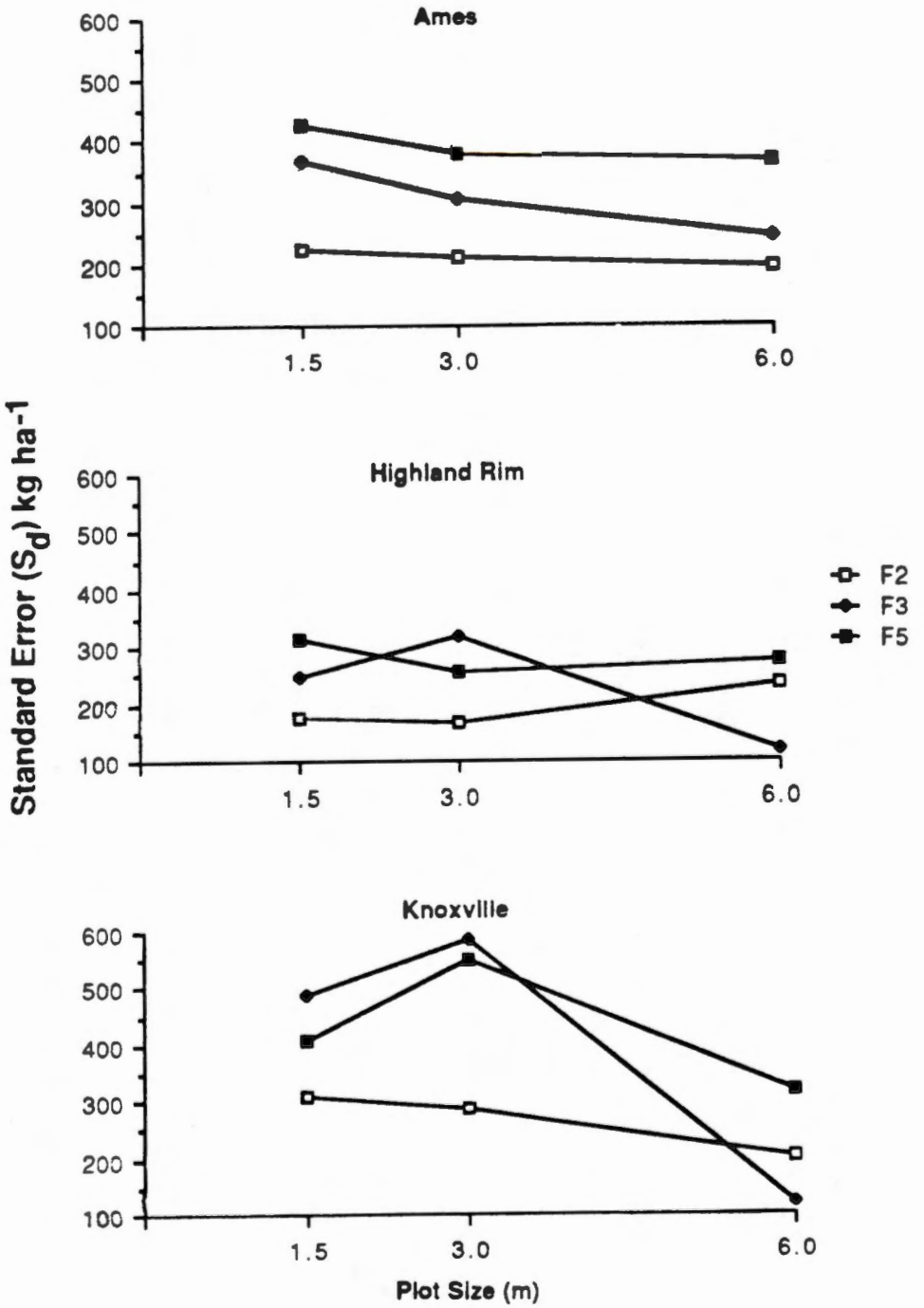


Fig. 6. Standard errors of difference between two means in the 1.5, 3, and 6 m plot sizes at each location.

order to be significantly different at Knoxville compared to Ames and Highland Rim.

II. Comparisons Among Generations Using Yields and Ranks of Cross Bulks

Based on the overall data, the top 3 ranking crosses were Nos. 2, 4, and 5 (Table 3). Using that ranking as the standard, it is possible to compare how effective the bulk tests would have been in discriminating the best crosses in each generation. Based on the yield evaluations, in the F_2 generation, the top 3 ranking crosses were Nos. 2, 4, and 5 (Fig. 7). Using only F_3 evaluations, the top 3 crosses would have been Nos. 3, 4, and 5 and using F_5 evaluations the top 3 were Nos. 1, 2, and 4 (Fig. 7). Consequently, the yield tests of these crosses in the F_2 generation gave the best match to the overall ranking.

Spearman's coefficients of rank correlation were determined within location and within plot size for all bulked crosses for each generation with itself excluded. In the 1.5 m plot size there were no significant correlations among the generations except in the F_2 and F_3 generations at Highland Rim. In the 3 m plot size there were no significant correlations except among the ranks of the F_3's at Ames and F_2 and F_3 at Highland Rim. One was negative ($r=-0.80$) and the other positive ($r=0.80$). In the 6 m plots there were no significant correlations of ranks among the generations except in the F_3 generation at Highland Rim (Table 4). One possible reason for the lack of

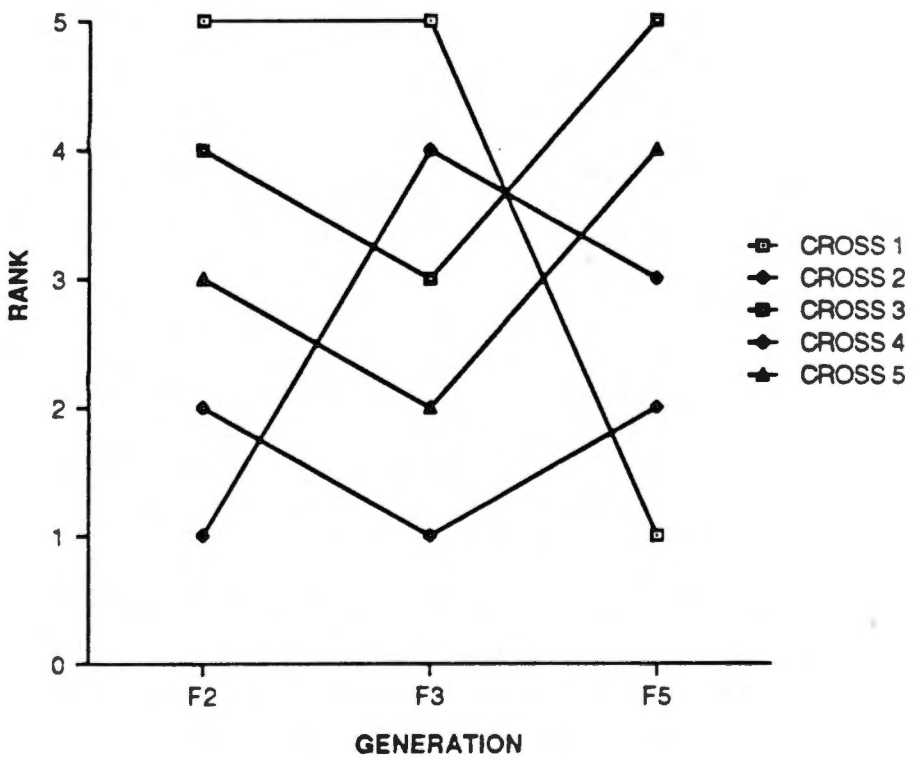


Fig. 7. Ranks of the five crosses in the F2, F3, and F5 generations (combined over plot sizes and locations).

Table 4. Spearman's coefficients of rank correlation[†] between cross performance in each generation and the remaining generations combined at each of the three locations and plot sizes.

	Plot Size (m)									Combined Locations and Plot Size
	1.5			3			6			
Generation	AMES	HRES	KPSFL	AMES	HRES	KPSFL	AMES	HRES	KPSFL	
F_2:F_2 excluded	.60 (.29)	1.00 (<.01)	.10 (.87)	.50 (.39)	-.50 (<.39)	.30 (.62)	-.10 (.87)	.50 (.39)	.30 (.62)	.23 (.12)
F_3:F_3 excluded	.30 (.62)	.80 (.10)	.40 (.51)	.80 (.10)	-.80 (.10)	.10 (.87)	.70 (.19)	.80 (.10)	.10 (.87)	.35 (.02)
F_4:F_4 excluded			.40 (.51)			.30 (.62)			.30 (.62)	.33 (.23)
F_5:F_5 excluded	.50 (.39)	.50 (.39)	.70 (.19)	.60 (.29)	.70 (.19)	.50 (.39)	-.10 (.87)	.20 (.75)	.60 (.29)	.47 (<.01)

[†] level of probability of a greater value shown inside parentheses

correlation is that there were only 15 observations used for computing each of these correlations.

Spearman's coefficients of rank correlation were then determined across all locations and plot sizes combined (Table 4). With the larger number of observations (n=45) the trend was for low positive associations but they were significant only with the F_3 and F_5 generations (r=0.35 and 0.47, respectively).

Mean yields for individual crosses averaged over all the locations in the F_2, generation ranged from 2154 kg ha^{-1} in 6 m plots to 2782 kg ha^{-1} in 1.5 m plots (Table 5). Mean yields for individual crosses in the F_3 generation ranged from 2869 (6 m) to 3742 (1.5 m) kg ha^{-1} and in the F_5 generation from 2979 (6 m) to 3731 (1.5 m) kg ha^{-1} (Table 5). For each cross in each generation and location, the yield levels decreased as the plot size increased (Figs. 8-10). This was expected due to harvesting a small vs. a larger plot area and then converting them to the same large unit land area (hectare). Mean yields in each cross at Ames and Highland Rim increased as generations advanced in each plot size (Figs. 8, and 9, respectively). However, at Knoxville, the yields of the F_4 generation in each cross were lower than the yields of the F_3 and F_5 generations (Fig. 10). A probable explanation for this is that the F_2 and F_4 generations were grown in 1987 and the F_3 and F_5 generations were grown in 1988 and the rainfall distribution during the reproductive stages of growth was better in 1988 than in 1987.

The heritabilities were determined by the variance component method (VCM) and by parent-offspring regression (POR). In general, the

Table 5. Mean yields (kg ha^{-1}) of the individual crosses in the F_2, F_3, and F_5 generations as determined across all locations combined in 1988-89.

	1987 (F2)			1988 (F3)			1988 (F5)			
	Plot Size (m)									Grand
Cross	1.5	3	6	1.5	3	6	1.5	3	6	Mean
1	2540 A†	2504 A	2237 A	3581 A	2889 A	2954 AB	3731 A	3584 A	2998 A	3002
2	2782 A	2698 A	2281 A	3291 A	3186 A	2926 B	3613 A	3222 A	3154 A	3017
3	2563 A	2541 A	2154 A	3545 A	3098 A	2869 B	3156 A	3062 A	2979 A	2885
4	2460 A	2687 A	2272 A	3742 A	3382 A	3166 A	3536 A	3452 A	3115 A	3090
5	2592 A	2687 A	2206 A	3533 A	3225 A	3018 AB	3260 A	3276 A	3114 A	2990

† means followed by a common letter within a plot size and generation are not significantly ($P<0.05$) different based on Duncan's Multiple Range Test.

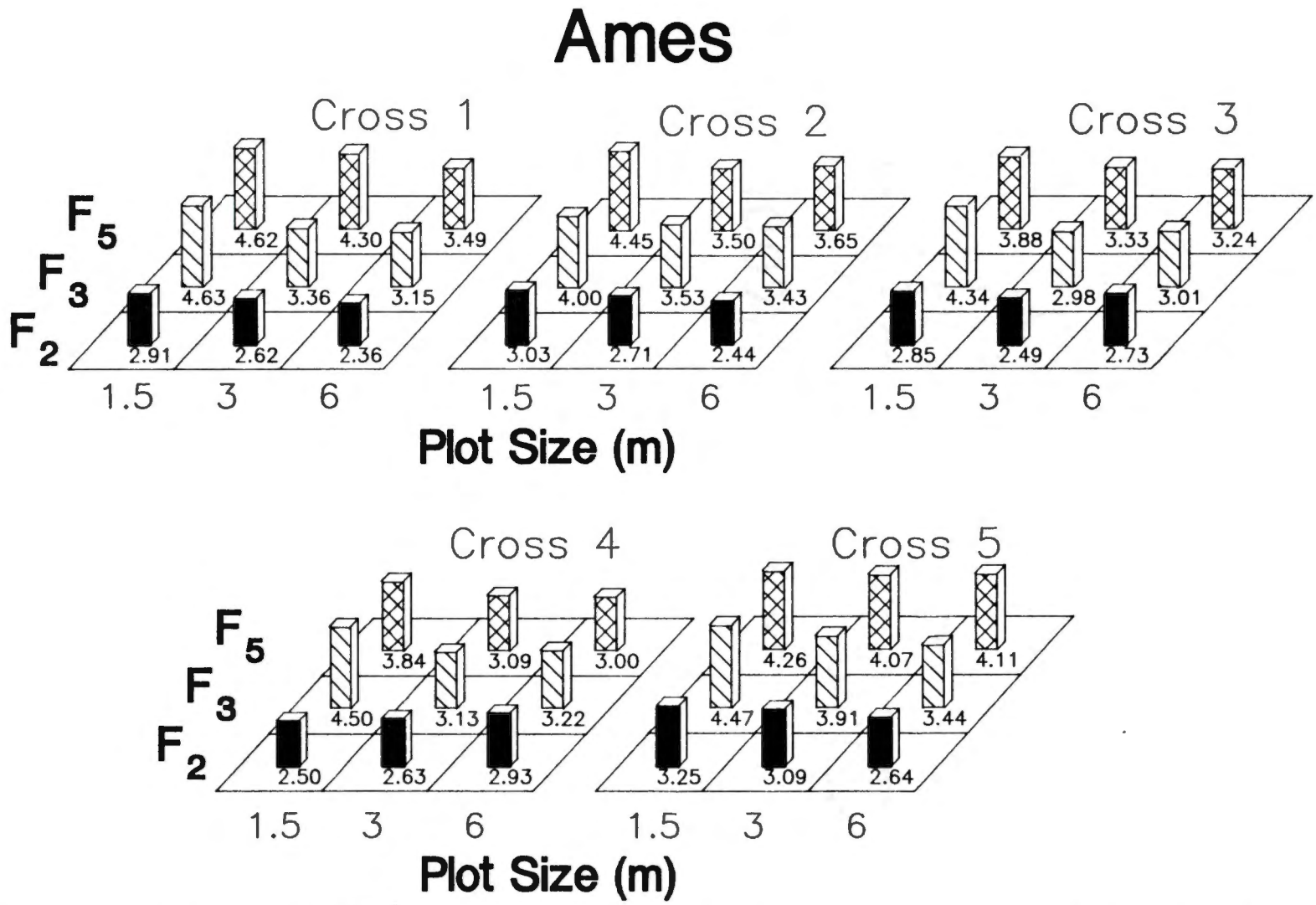


Fig. 8. Mean yields (mg ha^{-1}) of each cross in the F_2, F_3, and F_5 generations in each plot size at Ames (1987-1988).

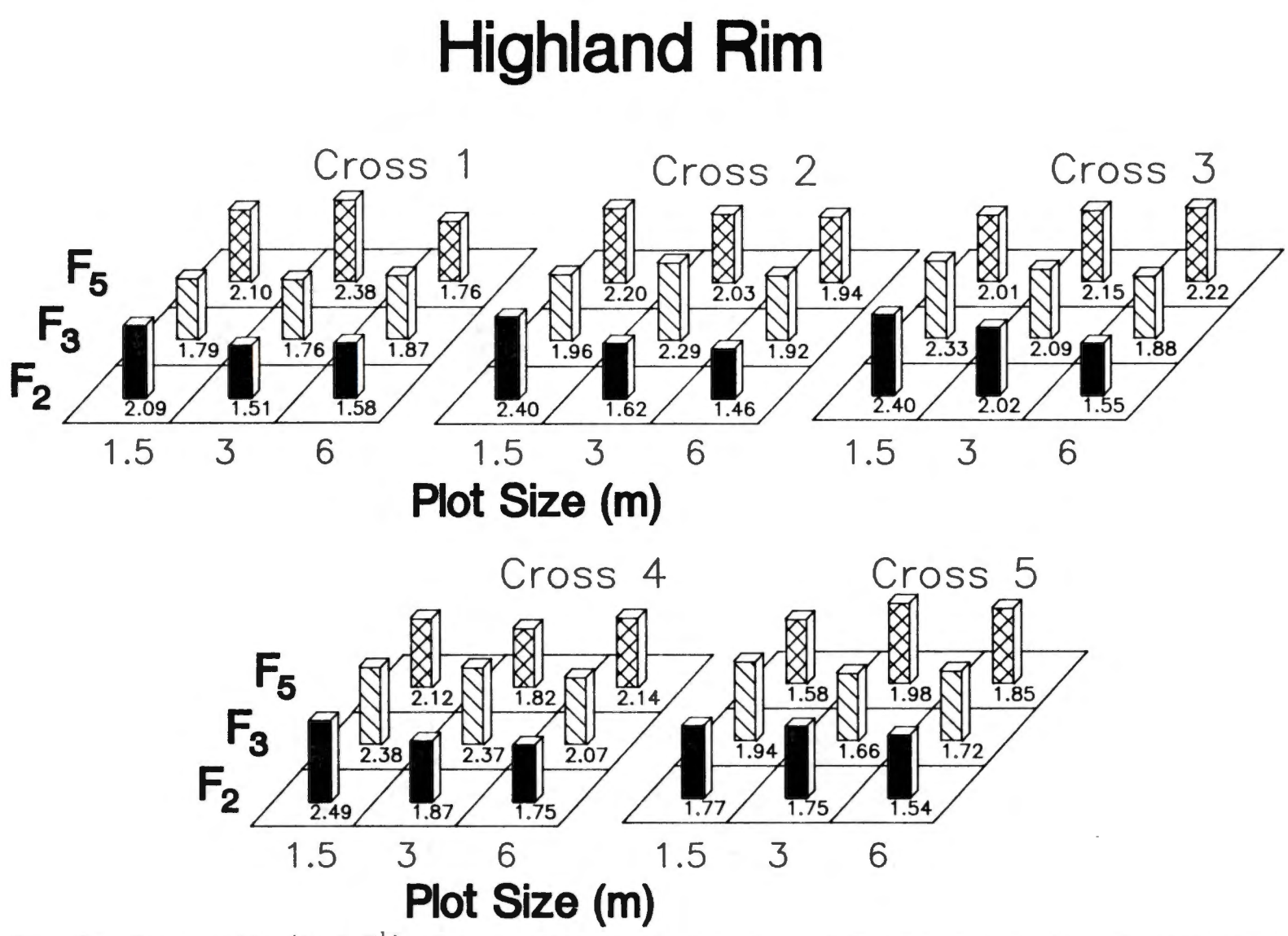


Fig. 9. Mean yields (Mg ha^{-1}) of each cross in the F_2, F_3, and F_5 generations in each plot size at Highland Rim (1987-1988).

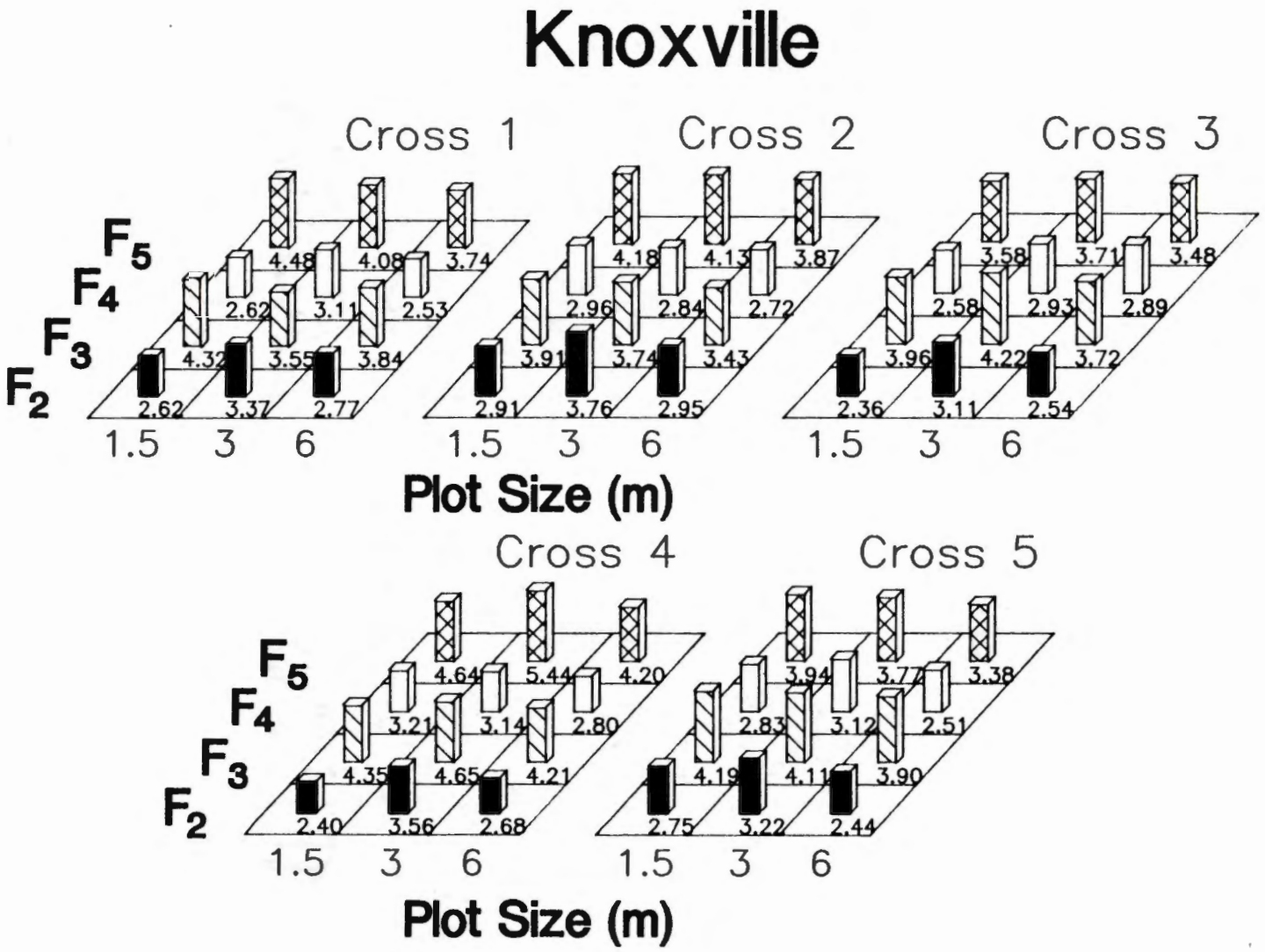


Fig. 10. Mean yields (Mg ha^{-1}) of each cross in the F_2, F_3, and F_5 generations in each plot size at Knoxville (1987-1988).

results were variable and inconsistent (Table 6). Heritabilities determined by the variance component method ranged from 0 to .77 in the F_2 generation, 0 to .58 in the F_3 generation, and 0 to .56 in the F_5 generation. Heritabilities determined through parent-offspring regression had ranges of .27 to 1.23 in the $F_2:_4$ and 0 to .88 in the $F_3:_5$ generations. There were greater genotypic differences expressed among crosses at Ames and Knoxville in comparison to Highland Rim. At Knoxville, heritability did increase as plot size increased in both VCM and POR. In some generation-location-plot size combinations, the genotypic variance among crosses was masked by environmental variation but it was not unique to any generation or plot size. True heritability cannot exceed 1.0, but regression has no limits, thus explaining why there was a value of 1.23 at Knoxville. This inconsistency is attributed to the fact that F_4 yields were greater than the F_2 yields.

Table 6. Heritabilities determined by the variance component method and by parent-offspring regression for the F_2, F_3, F_4 and F_5 generations in the 1.5, 3, and 6 m plot sizes at Ames, Highland Rim, and Knoxville.

Generation	1.5	3	6	1.5	3	6	1.5	3	6
	Ames			Highland Rim			Knoxville		
	Variance Component Method								
F2	.77	.72	0	.69	.37	0	.12	.35	.46
F3	0	.58	0	.47	.55	.14	0	0	.55
F4	-	-	-	-	-	-	0	0	0
F5	.24	.74	.56	0	.20	0	.41	.70	.46
	Parent-Offspring Regression								
F2:4	-	-	-	-	-	-	.27	.49	1.23
F3:5	.64	.42	.88	.03	.28	0	.21	.80	.86

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SUMMARY

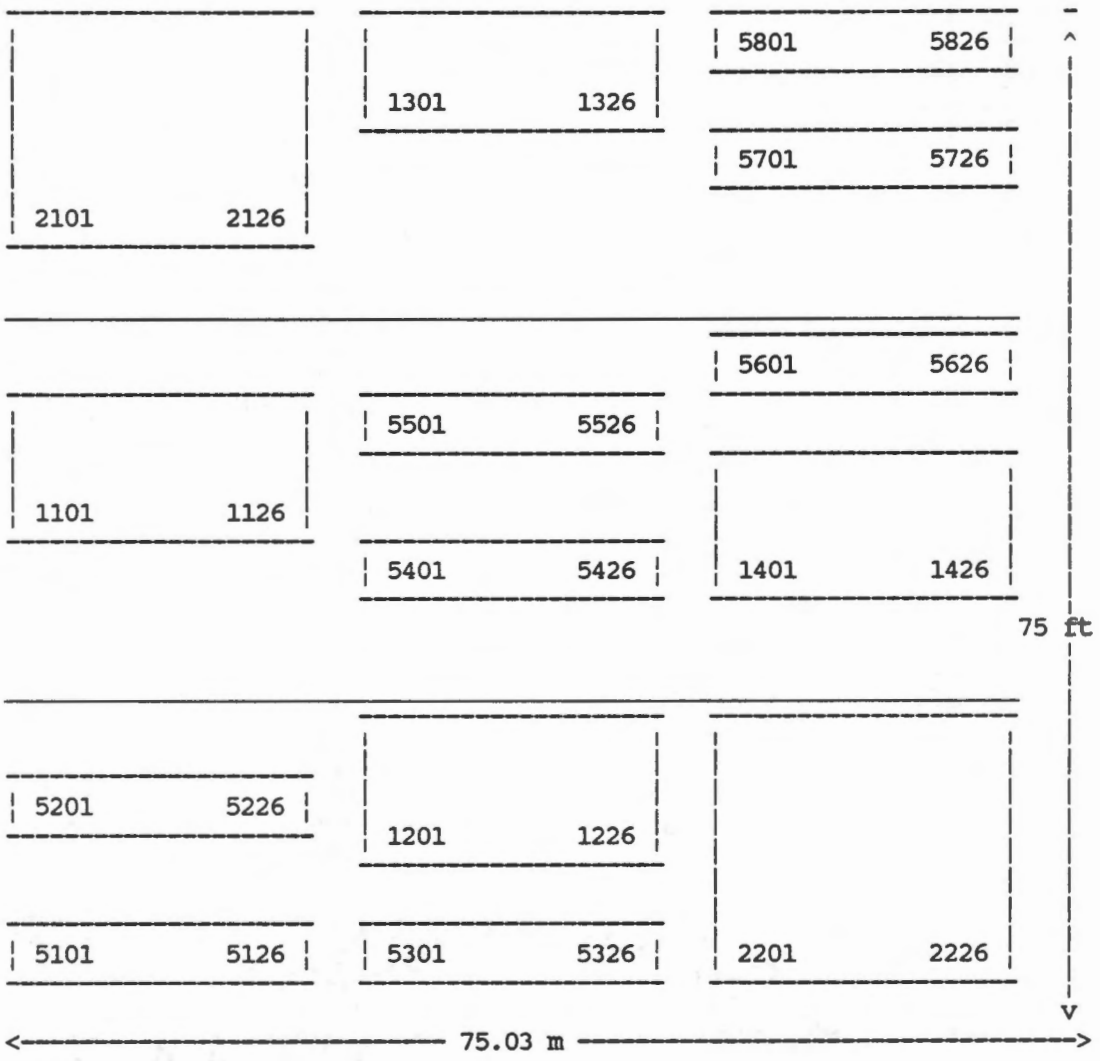
Most yield testing of soybeans strains is generally initiated in the F_5 to F_7 generations. By that time considerable resources and time have been expended on each cross being considered. If crosses with the least potential for superior genotypes can be identified and discarded in early stages, there can be a reduction in costs. However, one problem with early generation material, is having a low supply of seed. Using smaller plot sizes is a way to circumvent this problem.

In this study the benchmark lines performed similarly in the 1.5, 3, and 6 m plot sizes at each location and all locations combined. This suggests that the 1.5 and 3 m plot sizes provided comparable information to the 6 m plots. However, more time and effort were expended for planting and harvesting the smaller plots. The question remains as to whether the reduction in land and seed is offset by the increased labor required. If the replications for the 1.5 m plots could be reduced with no significant increase in CV or SE, then they would be of more practical use.

Using the standard errors of the difference between the means, there were few differences in the values associated with the different plot sizes at the Ames and Highland Rim locations. However, at the Knoxville location the trend was for the SE's to increase as the plot size decreased. The SE's for the different plot sizes were lower at Ames and Highland Rim compared to Knoxville. The heritability was variable, but at Knoxville it generally increased as plot size

increased based on estimates from both VCM and POR. Based on all information, the crosses were ranked from the best to the worst to serve as the "standard". In the F_2 generation, the top 3 ranking crosses were identical to the top 3 overall. In the F_3 and F_5 generations, two of the top 3 were the same as the top 3 overall. In a breeding program, a breeder will not want to eliminate many of the crosses at an early generation, because considerable planning and effort went into deciding the cross combinations to make. However, if one eliminates a small percentage (e.g. 5-10%) of the crosses via early generation yield testing, the efficiency of a breeding program could be increased.

APPENDIX



Plot Size: single rows, 6 m, 3 m, and 1.67 m. long, 91 cm row spacing
Field Dimensions: 75.03 m X 22.88 m
Example Key to Plot #:

1101 = 3 meter plot, 1st rep, entry 01 (randomized in each rep)
1201 = 3 meter plot, 2nd rep, entry 01 (randomized in each rep)
2201 = 6 meter plot, 2nd rep, entry 01 (randomized in each rep)
5301 = 1.7 meter plot, 3rd rep, entry 01 ("" "" "" "")

Fig. A1. Field map of the Knoxville location in 1987.

Table A1. Least square mean yields (Mg ha^{-1}) and ranks (R) of crosses in each generation and plot size at the Ames, Highland Rim and Knoxville locations, (1987-88).

1.5 m Plots

	AMES								HIGHLAND RIM								KNOXVILLE									
CROSS	F2		R	F3		R	F5		R	MEAN	F2		R	F3		R	F5		R	MEAN	F2		R	F3		R	F4		R	F5		R	MEAN	MEAN	R
1	2.91	AB†	3	4.63	A	1	4.62	A	1	4.05	2.09	AB	4	1.79	B	5	2.10	A	3	1.99	2.62	A	3	4.32	A	2	2.62	A	4	4.48	AB	2	3.51	3.19	2
2	3.03	AB	2	4.00	A	5	4.45	A	2	3.83	2.40	A	3	1.96	AB	3	2.20	A	1	2.19	2.91	A	1	3.91	A	5	2.96	A	2	4.18	AB	3	3.49	3.17	3
3	2.85	B	4	4.34	A	4	3.88	A	4	3.69	2.40	A	2	2.33	AB	2	2.01	A	4	2.25	2.36	A	5	3.96	A	4	2.58	A	5	3.58	B	5	3.12	3.02	5
4	2.50	C	5	4.50	A	2	3.84	A	5	3.61	2.49	A	1	2.38	A	1	2.12	A	2	2.33	2.40	A	4	4.35	A	1	3.21	A	1	4.64	A	1	3.65	3.20	1
5	3.25	A	1	4.47	A	3	4.26	A	3	3.99	1.77	B	5	1.94	AB	4	1.58	A	5	1.76	2.75	A	2	4.19	A	3	2.83	A	3	3.94	AB	4	3.42	3.06	4

3 m Plots

	AMES								HIGHLAND RIM								KNOXVILLE									
CROSS	F2		R	F3		R	F5		R	MEAN	F2		R	F3		R	F5		R	MEAN	F2		R	F3		R	F4		R	F5		R	MEAN	MEAN	R
1	2.62	B	4	3.36	AB	3	4.30	A	1	3.43	1.51	A	5	1.76	A	4	2.38	A	1	1.88	3.37	A	3	3.55	A	5	3.11	A	3	4.08	B	3	3.53	2.95	4
2	2.71	A	2	3.53	A	2	3.50	ABC	3	3.25	1.62	A	4	2.29	A	2	2.03	A	3	1.98	3.76	A	1	3.74	A	4	2.84	A	5	4.13	B	2	3.62	2.95	3
3	2.49	B	5	2.98	B	5	3.33	BC	4	2.93	2.02	A	1	2.09	A	3	2.15	A	2	2.09	3.11	A	5	4.22	A	2	2.93	A	4	3.71	B	5	3.49	2.84	5
4	2.63	B	3	3.13	B	4	3.09	C	5	2.95	1.87	A	2	2.37	A	1	1.82	A	5	2.02	3.56	A	2	4.65	A	1	3.14	A	1	5.44	A	1	4.20	3.06	1
5	3.09	A	1	3.91	A	1	4.07	AB	2	3.69	1.75	A	3	1.66	A	5	1.98	A	4	1.80	3.22	A	4	4.11	A	3	3.12	A	2	3.77	B	4	3.56	3.01	2

6 m Plots

	AMES								HIGHLAND RIM								KNOXVILLE									
CROSS	F2		R	F3		R	F5		R	MEAN	F2		R	F3		R	F5		R	MEAN	F2		R	F3		R	F4		R	F5		R	MEAN	MEAN	R
1	2.36	A	5	3.15	A	4	3.49	AB	3	3.00	1.58	A	2	1.87	B	4	1.76	A	5	1.74	2.77	A	2	3.84	B	3	2.53	A	4	3.74	A	3	3.22	2.65	5
2	2.44	A	2	3.43	A	2	3.65	AB	2	3.17	1.46	A	5	1.92	AB	2	1.94	A	3	1.77	2.95	A	1	3.43	C	5	2.72	A	3	3.87	A	2	3.24	2.73	2
3	2.73	A	4	3.01	A	5	3.24	AB	4	2.99	1.55	A	3	1.88	AB	3	2.22	A	1	1.88	2.54	A	4	3.72	BC	4	2.89	A	1	3.48	A	4	3.16	2.68	4
4	2.93	A	3	3.22	A	3	3.00	B	5	3.05	1.75	A	1	2.07	A	1	2.14	A	2	1.99	2.68	A	3	4.21	A	1	2.80	A	2	4.20	A	1	3.47	2.84	1
5	2.64	A	1	3.44	A	1	4.11	A	1	3.40	1.54	A	4	1.72	B	5	1.85	A	4	1.70	2.44	A	5	3.90	AB	2	2.51	A	5	3.38	A	5	3.06	2.72	3

† means followed by a common letter within a plot size, location, and generation are significantly ($P \leq 0.05$) different based on Duncan's Multiple Range Test.

Table A2. Mean yields (Mg ha^{-1}) and ranks (R) of all crosses at the Ames, Highland Rim (HRES), and Knoxville (KPSFL) locations.

CROSS	Ames	R	HRES	R	KPSFL	R	OVER ALL MEAN	R
			1.5 M					
TN5-85/TN4-86	4.05	1	1.99	4	3.51	2	3.19	2
TN82-94/TN83-6	3.83	3	2.19	3	3.49	3	3.17	3
TN5-85/V74-315	3.69	4	2.25	2	3.12	5	3.02	5
V78-184/TN83-65	3.61	5	2.33	1	3.65	1	3.20	1
TN85-55/TN85-42	3.99	2	1.76	5	3.42	4	3.06	4
			3 M					
TN5-85/TN4-86	3.43	2	1.88	4	3.53	4	2.95	4
TN82-94/TN83-6	3.25	3	1.98	3	3.62	2	2.95	3
TN5-85/V74-315	2.93	5	2.09	1	3.49	5	2.84	5
V78-184/TN83-65	2.95	4	2.02	2	4.20	1	3.06	1
TN85-55/TN85-42	3.69	1	1.80	5	3.56	3	3.01	2
			6 M					
TN5-85/TN4-86	3.00	4	1.74	4	3.22	3	2.65	5
TN82-94/TN83-6	3.17	2	1.77	3	3.24	2	2.73	2
TN5-85/V74-315	2.99	5	1.88	2	3.16	4	2.68	4
V78-184/TN83-65	3.05	3	1.99	1	3.47	1	2.84	1
TN85-55/TN85-42	3.40	1	1.70	5	3.06	5	2.72	3

Table A3. Standard errors of the difference (kg ha^{-1}) between the means within each generation and plot size at the three locations.

	AMES			Highland Rim			Knoxville		
Generation	1.5	3	6	1.5	3	5	1.5	3	5
F2	224.40	211.89	194.49	176.35	165.47	231.90	310.22	289.45	204.65
F3	228.98	257.25	254.61	345.54	317.11	346.20	430.51	481.54	334.58
F4							310.22	289.45	204.65
F5	228.98	257.25	254.61	345.54	317.11	346.20	430.51	481.54	334.58

Table A4. Summary of genotype and error mean squares from the analyses of variance of all genotypes and benchmarks only for each plot size at the Ames, Highland Rim (HRES), and Knoxville (KPSFL) locations in 1987.

Sources of Variation	ALL GENOTYPES				BENCHMARKS			
	DF 1.5	DF 3	DF 6		DF 1.5	DF 3	DF 6	
AMES								
Genotype	20 1198934**	20 547235**	20 165962*		15 1003029**	15 461564**	15 140020	
Error	29 124390	25 119530	23 61215		24 130731	20 119725	18 65094	
HRES								
Genotype	20 1255556**	20 243671**	20 78851		15 1140858**	15 173520*	15 61308	
Error	29 201435	25 84999	23 43262		24 205987	20 87523	18 41904	
KPSFL								
Genotype	20 986313**	20 525217	20 318349*		15 1045218**	15 563918	15 479852*	
Error	29 384933	25 483339	23 150276		24 370595	20 507464	18 200190	

*,** Significant at P<0.05 and 0.01, respectively based on the F test

Table A5. Summary of genotype and error mean squares from the analyses of variance of all genotypes and benchmarks only for each plot size at the Ames, Highland Rim (HRES), and Knoxville (KPSFL) locations in 1988.

Sources of Variation	ALL GENOTYPES						BENCHMARKS					
	DF	1.5	DF	3	DF	6	DF	1.5	DF	3	DF	6
AMES												
Genotype	25	2031063*	20	1016884*	20	436066*	15	2210553*	15	901497*	15	491584*
Error	29	477589	25	201116	23	119852	24	367798	20	175733	18	89494
HRES												
Genotype	25	303123	20	275923*	20	82270	15	210648	15	284844*	15	86869
Error	29	209723	25	132356	23	64825	24	174930	20	123397	18	59444
KPSFL												
Genotype	25	1562021*	20	1385644*	20	345358*	15	2089762*	15	1495671*	15	463981*
Error	29	741360	25	463760	23	111945	24	623665	20	391511	18	137796

*,** Significant at $P<0.05$ and 0.01, respectively based on the F test

Table A6. Summary of genotype and error mean squares from the analyses of variance at Ames, Highland Rim (HRES), and Knoxville (KPSFL) in the F_2, F_3, and F_5 generations for the 1.5, 3, and 6 m plot sizes.

Sources of Variation	F2						F3						F5					
	DF	1.5	DF	3	DF	6	DF	1.5	DF	3	DF	6	DF	1.5	DF	3	DF	6
AMES																		
Genotype	4	612202**	4	208638*	4	25789	4	458299	4	518950	4	66389	4	929349	4	1028191*	4	357727
Error	11	109499	7	54762	5	53777	11	538501	7	186555	5	60749	11	724386	7	289975	5	137056
HRES																		
Genotype	4	765277**	4	160236	4	22579	4	539983	4	397004	4	31301	4	480382	4	173166	4	76051
Error	11	188217	7	89796	5	37824	11	240581	7	202370	5	13694	11	389759	7	129550	5	74333
KPSFL																		
Genotype	4	441340	4	267055	4	78131	4	323644	4	738268	4	163069*	4	1445509	4	1984614*	4	215694
Error	11	359674	7	167559	5	41883	11	950770	7	685156	5	14800	11	669287	7	609926	5	101143

*,** Significant at P<0.05 and 0.01, respectively based on the F test

Table A7. Spearman's coefficients of rank correlation† within location and across generations (not including benchmarks).

Plot size (m)	Ames		Highland Rim		Knoxville		All Locations	
	3	6	3	6	3	6	3	6
1.5	.80 (.10)	.20 (.75)	.90 (.04)	1.00 (<.01)	.70 (.19)	.80 (.10)	.80 (<.01)	.67 (<.01)
3		.70 (.19)		.90 (.04)		.70 (.19)		.77 (<.01)

† level of probability of a larger value inside parentheses

Table A8. Spearman's coefficients of rank correlation† within location and across plot size for all crosses at Ames, Highland Rim, and Knoxville (1987-88).

Generation	AMES	HIGHLAND RIM	KNOXVILLE
F2:F2 excluded	.33	.56	.03
	(.23)	(.04)	(.91)
F3:F3 excluded	.60	.36	.20
	(.02)	(.19)	(.48)
F4:F4 excluded			.33
			(.23)
F5:F5 excluded	.33	.07	.60
	(.23)	(.80)	(.02)

† level of probability of a larger value inside parentheses

Table A9. Spearman's coefficients of rank correlation† across locations with the overall rankings (1987-1988).

Plot size (m)	
1.5:1.5 excluded	.28 (.05)
3:3 excluded	.23 (.11)
6:6 excluded	.20 (.16)

† level of probability of a larger value inside parentheses

Table A10. Benchmark line mean yields (kg ha^{-1}) in 1.5, 3, and 6 m plots at Ames, Highland Rim (HRES), and Knoxville (KPSFL), 1987 and 1988.

	Plot Size (m)									Grand
	1.5			3			6			
Line	Ames	HRES	KPSFL	Ames	HRES	KPSFL	Ames	HRES	KPSFL	Mean
					1987					
TN82-32H	2290 CD†	1630 D-F	2246 B-C	2098 C-E	1347 A-C	3193 AB	1719 CD	1315 AB	2622 AB	2051
TN82-74L	2066 C-E	1886 B-E	2133 B-D	1950 D-F	1546 AB	2679 AB	1918 A-D	1315 AB	2817 AB	2034
TN82-76L	2021 DE	1527 EF	2359 B-D	1899 EF	1411 A-C	2208 B	1784 CD	1078 B	2239 BC	1836
TN82-84L	1867 E	1521 EF	1976 CD	2021 C-F	1379 A-C	2434 B	1578 D	1302 AB	1807 BC	1765
TN82-129H	2451 BC	1925 B-E	2534 A-C	1957 D-F	1668 A	2823 AB	2111 A-D	1418 AB	2202 BC	2121
TN82-184H	2207 C-E	1751 C-E	2616 A-C	1514 F	1520 A-C	3212 AB	1854 B-D	1437 AB	2666 AB	2086
TN82-192H	2425 B-D	1732 C-E	2365 B-D	2419 A-E	1450 A-C	3218 AB	2008 A-D	1219 AB	2785 AB	2180
TN82-250L	2361 CD	1514 EF	2208 B-D	2431 A-E	1450 A-C	3306 AB	2072 A-D	1155 B	2559 AB	2117
TN82-259L	3028 A	1476 EF	2296 B-D	2534 A-D	1136 BC	2948 AB	2476 AB	1026 B	2534 AB	2162
TN82-260L	2277 CD	2162 BC	2748 AB	2472 A-E	1142 BC	2817 AB	1995 A-D	1424 AB	2697 AB	2193
TN82-262H	2932 A	2117 B-D	2817 AB	2310 A-E	1302 A-C	3030 AB	1963 A-D	1238 AB	2741 AB	2272
TN82-264H	2810 AB	2303 AB	2559 A-C	2483 A-E	1732 A	2835 AB	2412 AB	1713 A	2773 AB	2402
TN82-265H	2771 AB	2303 AB	3187 A	2566 A-C	1379 A-C	3105 AB	2496 A	1373 AB	3626 A	2534
TN82-268H	2945 A	2656 A	2754 AB	2752 A	1707 A	3789 A	2162 A-D	1456 AB	2873 AB	2566
TN82-277L	2464 BC	1264 F	2553 A-C	2662 AB	1033 C	2798 AB	2271 A-C	1065 B	2371 BC	2053
TN82-294L	2245 C-E	1700 C-F	1687 D	2014 C-F	1649 A	2641 AB	2104 A-D	1290 AB	1418 C	1861
					1988					
TN82-32H	3779 C-E†	2088 AB	4606 AB	3083 C-D	1950 AB	4201 A-C	3198 B-D	1894 AB	3935 A	3193
TN82-74L	2930 F	1829 AB	3482 CD	2581 D-F	1632 B	3634 B-E	2375 EF	1521 AB	3402 A-D	2598
TN82-76L	3191 EF	1742 B	3310 D	2285 F	1645 B	2694 E	2478 D-F	1491 B	2561 D	2377
TN82-84L	3367 D-F	1809 AB	3484 CD	2475 EF	1686 B	3430 C-E	2472 D-F	1619 AB	3027 B-D	2597
TN82-129H	3536 C-F	1946 AB	4259 A-C	2773 D-F	1789 B	4081 A-C	2520 C-F	1836 AB	4150 A	2988
TN82-184H	3808 C-E	1997 AB	5014 A	3030 C-E	2423 A	4841 A	3146 B-D	1929 AB	4000 A	3354
TN82-192H	3815 C-E	1948 AB	4212 A-C	3086 C-E	1706 B	3980 A-C	3115 B-D	1674 AB	3758 A-C	3033
TN82-250L	3715 C-E	1938 AB	4472 AB	3565 A-C	1704 B	3565 B-E	3081 B-E	1458 B	3558 A-C	3006
TN82-259L	4616 AB	1872 AB	4672 AB	3611 A-C	1917 AB	4291 A-C	3231 BC	1617 AB	4068 A	3322
TN82-260L	3961 B-D	2196 AB	4368 A-C	3164 B-E	1819 B	4530 AB	3147 B-D	2035 AB	3868 AB	3232
TN82-262H	4212 A-C	1967 AB	4653 AB	3224 B-D	2131 AB	4834 A	2958 B-F	1799 AB	3588 A-C	3263
TN82-264H	4146 A-C	2115 AB	4826 AB	3144 B-E	2187 AB	3860 A-D	3617 AB	2018 AB	4143 A	3340
TN82-265H	4800 A	2241 AB	4763 AB	3804 AB	2467 A	4218 A-C	3624 AB	2100 A	4111 A	3570
TN82-268H	3911 CD	2260 A	4220 A-C	2671 D-F	2155 AB	4302 A-C	3079 B-E	1989 AB	4092 A	3187
TN82-277L	4227 A-C	1787 AB	3935 B-D	3906 A	1964 AB	3636 B-E	4043 A	1916 AB	2941 CD	3151
TN82-294L	3038 F	1878 AB	4019 B-D	2739 D-F	1809 B	2900 DE	2291 F	1683 AB	3620 A-C	2664

† means followed by a common letter within a plot size, location, and year are significantly ($P \leq 0.05$) different based on Duncan's Multiple Range Test.

VITA

Mark Sellmann was born in Dover, New Jersey, and was raised in Randolph Township, New Jersey. In 1982 he graduated from Randolph High School and started college at Kansas State University in Manhattan, Kansas. He completed his Bachelor of Science degree in Agronomy in May, 1986. After a two month adventure in Alaska, he started working toward a Master of Science degree in August of 1986 in Plant and Soil Science at the University of Tennessee at Knoxville. Mark graduated in May, 1989 and accepted a position as an assistant plant breeder for Jacklin Seed Company in Post Falls, Idaho.