


AN ABSTRACT OF THE THESIS OF

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Title EVALUATION OF METHODS OF PROGENY TESTING IN TALL
FESCUE SEED PRODUCTION (FESTUCA ARUNDINACEA,
SCHREB.)

Abstract approved 
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Seventeen parental clones were selected, from 9,000 plants, on the basis of self-sterility, seed and forage yield potential using phenotypic ratings, crude protein and chromogen content. The parental clones were divided into two populations based on date of maturity. Group I was intermediate in maturity and had nine parental clones, while group E was early maturing and had eight parental clones.

Six progeny testing methods (vegetative cuttings of parental clones, first generation selfed-seed (S_1 progeny), open-pollinated progeny, polycross progeny, seed from all possible single crosses, and selfed seed from the single-crosses or F_2 progeny) were compared using simple correlation coefficients between the progeny test and by comparing the rankings of the clones on the basis of

each progeny test. The actual polycross performance was compared with the theoretical polycross performance or average of all possible single crosses, to see if equal and random fertilization occurred in the actual polycross.

The results from the comparison of the six progeny testing methods indicated the vegetative cuttings of the parental clones and the single-cross progeny tests are the two most effective progeny testing methods when considering all four traits and both populations of plants.

The open pollinated and polycross progeny tests were generally undesirable, because frequently there was no significant difference among their progeny.

The S_1 progeny test was generally not desirable in group I; however, it appeared to be the most satisfactory test for seed yield when both populations of plants were considered.

The results illustrate why there are inconsistencies in the literature concerning the effectiveness of the progeny testing methods. The effectiveness of the six progeny tests varied, to some extent, from trait to trait and for the two populations. For all four traits there was much less agreement among the six progeny tests in group E than in group I.

In all four traits the F_2 generation showed a great inbreeding depression. The average of the single crosses was lower than the

parents for tiller number, plant height, and 100 seed weight, but equalled the parents in yield per plant. The S_1 progeny were usually approximately equal to the average of the single cross progeny. The open-pollinated and polycross progeny were generally the highest for all four traits.

The results from the comparison of the actual polycross with the theoretical polycross indicated that equal and random fertilization did not occur in the actual polycross. The more desirable clones appeared to contribute the majority of the pollen, since the actual polycross performance was usually greater than the theoretical polycross performance.

EVALUATION OF METHODS OF PROGENY TESTING
IN TALL FESCUE SEED PRODUCTION
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by

JOHNNY RAY THOMAS

A THESIS

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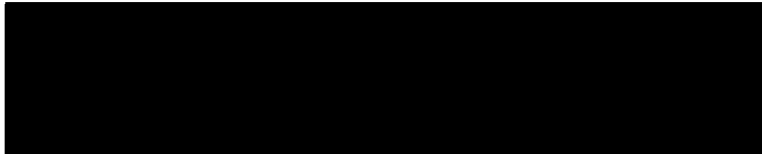
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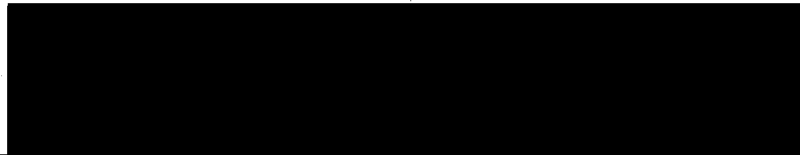
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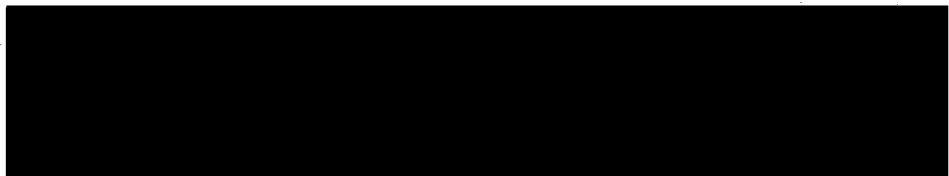


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EVALUATION OF METHODS OF PROGENY TESTING
IN TALL FESCUE SEED PRODUCTION
(FESTUCA ARUNDINACEA, SCHREB.)

INTRODUCTION

Tall fescue (Festuca arundinacea, Schreb.) is an important forage and seed crop in the United States and Oregon. The average production of tall fescue seed in the United States from 1957 to 1963 was almost 32 million pounds. Oregon produced 13 percent of this total or about 4.2 million pounds of clean seed and ranks number one in tall fescue seed production per acre.

The improvement of forage crops by breeding is an important task and its importance increases as more emphasis is placed on grassland farming. There are many problems which face the forage breeder, one of which is the selection of parental plants that will produce high yielding varieties, whether the varieties are synthetics or hybrids. Progeny tests have proved to be an effective method of selecting parental lines, but there are many types of progeny tests which may be used. The data concerning different methods of progeny testing have been inconsistent and more work is needed to aid the forage breeder in choosing the most efficient method of progeny testing.

The primary objectives of this study were (1) to compare the

polycross (PX), open-pollinated (OP), single-cross (SX), selfed (S_1 and F_2), and vegetative methods of progeny testing for two groups of tall fescue and (2) to compare the actual polycross performance with the theoretical polycross, or average of all possible single crosses. Two populations were used to permit comparison of the results from one population with the results from the second population. The characters studied were tiller number, total plant height (cms.), average seed yield per plant (gms.), and 100 seed weight (gms.).

LITERATURE REVIEW

Some of the methods of progeny testing have distinct advantages in cost and labor requirements; therefore, if all of the methods were equally effective, the final choice of a method could be based on cost and convenience. It seems desirable to review the literature concerning the advantages and disadvantages of the different progeny testing methods first and then to review the results obtained by using the different methods of progeny testing.

The use of inbred progenies for evaluation of forage crop clones has been suggested (7, p. 87; 13, p. 484). Several disadvantages arise since most of the forage crops are normally cross-pollinated and many species are highly self-sterile. Schaepman (21, p. 106-109) lists two disadvantages of using inbred lines; (1) the small amount of seed that is often produced with many of the forage crop species when they are self-pollinated, and (2) the characters associated with productivity are often difficult to evaluate in inbred material. Hansen, Myers, and Garber (7, p. 84) concluded that it was difficult to isolate a sufficient number of inbred orchardgrass lines to make a program feasible, due to the high self-sterility of orchardgrass.

The diallel analysis is generally considered a good method of progeny testing since both general and specific combining ability

can be obtained. Wit (30, p. 95) and Schaepman (21, p. 106-109) noted the diallel analysis is a laborious and expensive method, especially when a large number of crosses are involved. Wit also concluded the small quantities of seed obtained sometimes limits the number of progenies of individual plants; therefore, it may be difficult to test all the characters one would like to test.

The open-pollinated progeny test has a distinct advantage because it is the cheapest and easiest method to use (17, p. 24). A serious disadvantage of the open-pollinated progeny test is that there may be differential pollen effects for the various mother clones (30, p. 95-102). Wit (30, p. 95-102) has shown that 40 percent of the pollen comes from the two adjacent clones and 74 percent of the pollen comes from the three neighboring clones on each side of the mother clones, when perennial ryegrass is space planted. This indicates that open-pollinated progeny may be unreliable indicators of the breeding potential of mother clones, since the pollen source will differ from clone to clone.

Schaepman (21, p. 106-109) listed three advantages for the polycross progeny test; (1) polycross progeny gives an indication of general combining ability, which is more important than specific combining ability for the production of synthetics, (2) the polycross is an easy way to harvest seed for a reliable genotypic evaluation of mother clones; and (3) with the polycross the breeder obtains

seed in a similar way to what actually happens in the normal multiplication of seed. He also noted the polycross test is difficult to apply with a large number of clones and a preparatory selection should take place before the polycross test is used. Wit (30, p. 95) concluded the polycross method offsets the disadvantages of the diallel and the open-pollinated progeny test. He studied polycross progeny in perennial ryegrass and found no differential pollen effects; whereas, different pollen effects were noted among open-pollinated progeny.

Despite the advantages of certain progeny testing methods, the true value of a progeny testing method is in the effectiveness of selecting the genotypes which can be combined, in specific crosses or synthetics, to produce high yielding varieties. The results obtained, using different methods of progeny testing, have been inconsistent for different forage crop species and even for different populations of the same species.

Hansen, Myers, and Garber (7, p. 87) worked with fourth generation inbred lines of orchardgrass and found that the general combining ability of the I_4 lines was not materially different from their parental clones. They suggested using inbred lines to find good combiners and thus increase the productivity and uniformity of synthetic strains. Kalton, Smit, and Leffel (13, p. 484) found that certain differences among parental clones are reflected in

first generation selfed-progeny. This work in orchardgrass indicated that inbred lines may be a reliable progeny testing method. Smith (23, p. 338) concluded that selection among inbred plants was relatively more effective than selection among open-pollinated individuals.

Carnahan et al. (2, p. 515), studied seedling vigor and fall growth habit in alfalfa and suggested that either polycross or inbred progeny could be used early in the program to accumulate favorable additive factors and suggested the use of single-crosses later to find specific combining ability. Tysdal and Crandell (26, p. 300-306), working in alfalfa, found inbred lines to be as effective as polycross progeny for evaluation of clones, but they suggested using polycross progeny to save labor and to get more seed produced.

Several workers have suggested all possible single-crosses or a diallel analysis for progeny testing; however, most of these workers suggest other methods of testing for a preliminary selection. Frandsen (5, p. 308) concluded that the diallel analysis will give the most uniform and significant progeny test, but he suggested use of a polycross for a preliminary selection to lower the number of clones. Oldemeyer and Hansen (20, p. 162) suggested using single-crosses for the final evaluation but polycross progeny and an evaluation of parental clones for a preliminary selection.

Theurer and Elling (25, p. 248), on the other hand, found very little association between the average of synthetics and the rank of the corresponding single-crosses, when studying persistence in alfalfa.

Hawk and Wilsie (8, p. 113-118) found 20-35 percent of the variability in open-pollinated progeny yields of bromegrass could be attributed to differences in the yielding ability in clones. All of the correlation coefficients for yield of their open-pollinated progeny versus parents were significant at the one percent level. They concluded that, in general, high yielding clones produced high yielding open-pollinated progeny. Knowles (16, p. 18) reported open-pollinated progeny appear to be a convenient and reasonable reliable type of progeny for identification of superior plants of bromegrass. He also reported that superior first generation synthetics have been formed on the basis of open-pollinated progeny test. In other studies Knowles (15, p. 284 and 298) concluded that open-pollinated progeny may be better than polycross progeny for evaluation of combining ability. It was Knowles opinion that there is no need to go to extra work to set up a polycross nursery since open-pollinated progeny testing is reliable. McDonald, Kalton and Weiss (17, p. 23) found a high correlation between parents and first-generation selfed-progeny for all the characters which they measured in bromegrass. The correlations were generally of low

predictive value. Nielson and Smith (19, p. 93), working in timothy, found selection from an open-pollinated population to be equally effective and more economical than inbreeding and selection during the initial stages of the breeding program. Frandsen (5, p. 308), on the other hand, concluded that the results obtained from open-pollinated progeny test are insignificant because of the varying male parents.

Several workers have concluded that polycross progeny are a reliable method of evaluating the parental plants. Tysdal and Crandall (26, p. 300-306) compared polycross progeny with the average single-cross progeny, in alfalfa, and found that with both methods they would select the same clones; therefore, they concluded that polycross performance was dependable. The value of the polycross method was demonstrated further when they showed that the clones with a high polycross performance also produced the best synthetics. Frandsen (5, p. 308) concluded that the polycross method is a simple method of comparing offspring of a large number of parents on a uniform basis. Graumann (6, p. 314-318) reported that the polycross progeny test was a worth-while method of breeding. He also concluded that the polycross method was particularly better than the diallel analysis with species which have floral habits unadapted for large scale controlled crossing by the bagging method. Davis (3, p. 574) found that polycross progeny

yields could be used to predict yields of synthetics, in alfalfa, while clonal performance could not be used for prediction. Wit (30, p. 102), working with perennial ryegrass, concluded polycross progeny are more reliable than open-pollinated progeny. Hittle (9, p. 523) concluded that ten or more replications are needed to minimize differential pollen effects in a polycross nursery.

Some workers have found evidence to support selection from parental clones. Theurer and Elling (25, p. 248) studied winter hardiness and bacterial wilt resistance in alfalfa. They concluded that the breeder can rank the clones and select the best material to utilize in preparing the best synthetics. Knowles (16, p. 17) worked with bromegrass and found that clonal performance could be used to select for creeping habit. Oldemeyer and Hansen (20, p. 161-162) concluded that parental performance and polycross performance could be utilized for the major part of the selection.

McDonald, Kalton and Weiss (17, p. 23) found that clonal performance in bromegrass did not provide a good indication of breeding behavior as measured by progeny test. Davis (3, p. 574) worked with alfalfa and found that yields of synthetics could not be predicted from clonal performance, although polycross performance could be utilized for prediction.

The work reviewed thus far has shown certain methods to be more effective than other progeny testing methods, but some work

has shown that different progeny testing methods are equal in effectiveness. Theurer and Elling (24, p. 52) found a highly significant correlation coefficient of 0.82 between single-cross progeny and first generation selfed-progeny. This indicates that both methods should rank the offspring similarly for wilt resistance. Murphy (18, p. 326) used orchardgrass, smooth brome grass, and red fescue in a comparison of polycross, selfed, and vegetative progeny. He found that all three methods could be used to isolate plants with high yield potential. Johnson (11, p. 333) in a review of forage breeding methods concluded that polycross, open-pollinated and single-cross progeny all appear equally valid for evaluating cross-pollinated diploid species. Johnson and Hoover (12, p. 596-597) worked with sweetclover and found a highly significant correlation between selfed, polycross and open-pollinated progeny. This indicates the three methods would give similar results. They suggested using both selfed and open-pollinated progeny when choosing parental plants to be used in synthetics. Knowles (15, p. 287-296) worked with crested wheatgrass (both the standard and fairway types) and inbred fairway types. He found good agreement between single-cross averages and open-pollinated progeny. Buckner (1, p. 180) found that inbred and polycross progenies of well grazed parental clones were also grazed consistently better than the other selections in grazing trials. This indicated a close relationship

between the parental clones, inbred progenies and the polycross progenies. Weiss, Taylor and Johnson (27, p. 601) calculated correlations between clones, single crosses and open-pollinated progeny. They found low and non-significant correlations for forage yield, although correlations for some of the other characters were high enough to be of predictive value. Davis (3, p. 357) found that both first generation selfed-progeny and polycross progeny could be used to estimate the prepotency of alfalfa clones in a breeding program. Wilsie and Skory (29, p. 792) found a significant correlation between first generation selfed-progeny and open-pollinated progeny, which indicates the two methods would give similar results.

Echeverri (4, p. 88-89) compared single cross, open-pollinated, first generation selfed and polycross progeny. The four methods did not show complete agreement in their ability to determine general combining ability of tall fescue clones. However, all the methods were equally effective in selecting the best combiner and would, in general, permit one to roughly separate at least two categories--good and poor. He suggested utilizing open-pollinated progeny for preliminary selections, then using polycross, selfed, or diallel analysis when the number of clones are reduced.

The literature indicates the inconsistencies that have been found with different methods of progeny testing. It should be noted

that only Buckner (1, p. 180) and Echeverri (4, p. 88-89) have compared progeny testing methods in tall fescue.

MATERIALS AND METHODS

Source of Material

The progeny testing nursery consisted of two groups of tall fescue; (1) an early maturing group identified as group E, and (2) an intermediate maturing group identified as group I. The eight parental clones of group E and the nine parental clones of group I were selected from 9,000 spaced plants. The 17 parental clones were selected for self-sterility, seed and forage yield potential based on phenotypic ratings, nutritive value on the basis of crude protein and chromogen content, and for time of maturity. Tables 1 and 2 identify the parental clones used in the progeny testing nursery for groups E and I respectively.

The single-cross seed (SX) was obtained by vegetatively propagating the parental clones and establishing 28 and 36 single-cross plots for E and I respectively. Each plot consisted of two rows, eight propagules per row with six inches between propagules. Panicles of plants from adjacent rows were bagged together in 3" x 5" x 17" parchment bags before anthesis to provide single-cross seed.

The open-pollinated seed (OP) came from unbagged panicles of the parental clones and first generation selfed-seed (S_1) came from panicles of the parental clones, bagged before anthesis. The

Table 1. Identification of the early maturing parental clones used in group E of the progeny testing nursery.

Culture	Flowering Date-May ¹	Chromogen ²	% Crude Protein ²	Grams Seed Yield ³	Appearance Forage ⁴	% Self-Fertility ⁵	Origin
<u>Early Maturity (5-14 to 5-20)</u>							
304	20	140	9.89	2.57	3, 3, 3	9.7	Goar
314	14	121	8.65	1.76	4, 4, 4	7.0	Goar
315	19	130	10.34	2.62	3, 3, 3	6.4	Goar
339	18	115	8.42	3.40	5, 5, 5	12.0	S-170
340	16	123	9.43	2.96	4, 5, 5	2.9	S-170
342	16	140	9.55	3.49	5, 4, 4	5.2	S-170
351	20	125	8.15	3.83	6, 5, 5	8.3	S-170
352	20	138	8.73	3.93	6, 4, 7	7.4	S-170

1. 1957-58 average.

2. Clippings made 7-10 through 7-24-57 at similar maturity stages.

3. 5 panicle samples, 1955.

4. Phenotypic rating 1-7, made early intermediate and late in summer; 7 is most desirable.

5. Comparison of open vs. self-pollinated seed set.

Table 2. Identification of the intermediate maturing parental clones used in group I of the progeny testing nursery.

Culture	Flowering Date-May ¹	Chromogen ²	% Crude Protein ²	Grams Seed Yield ³	Appearance Forage ⁴	% Self- Fertility ⁵	Origin
<u>Intermediate Maturity (5-21 to 5-25)</u>							
296	24	132	10.52	3.53	5, 4, 5	15.5	Alta
298	22	132	10.05	3.44	5, 4, 6	2.1	Alta
299	22	162	9.98	4.42	4, 3, 5	9.5	Alta
311	23	151	8.70	3.35	6, 3, 5	5.5	K-31
329	23	135	9.05	3.00	4, 4, 4	4.6	K-31
359	24	127	10.30	3.04	4, 4, 4	7.6	Mo. #1
366	25	147	11.49	2.60	4, 4, 5	5.6	Mo. #2
368	22	125	8.99	4.04	5, 4, 7	7.4	Mo. #3
374	23	138	8.76	2.18	5, 3, 4	7.5	Mo. #3

1. 1957-58 average.

2. Clippings made 7-10 through 7-24-57 at similar maturity stages.

3. 5 panicle samples, 1955.

4. Phenotypic rating 1-7, made early, intermediate and late in summer; 7 is most desirable.

5. Comparison of open vs. self-pollinated seed set.

selfed seed from the single-crosses (F_2 seed) was obtained by bagging panicles of the single-cross plants before anthesis. Each F_2 was made up of equal amounts of seed from five F_1 plants of the single-cross. Some crosses did not produce seed on five plants, so these F_2 's were not included in the nursery.

The polycross (PX) seed of group E was obtained from an isolated polycross nursery of the eight parental clones, which consisted of ten replications in a randomized block design. The polycross seed of I was taken from a similar isolated polycross nursery made up of the nine intermediate maturing parental clones.

The SX, OP, PX, S_1 , and F_2 seeds were planted in trays filled with perlite, watered, and held at 38° F for five days to break dormancy. After germination the seedlings were transplanted to 2" x 2" x 3" plant bands and held in the greenhouse until they were planted in the field. Vegetative cuttings of the parent plants and seedlings of the check variety, Alta, were also established in plant bands.

Establishment

The seedlings and cuttings were transplanted to the Hyslop Agronomy Farm, Corvallis, Oregon, in the fall of 1962. Group I was transplanted October 2, and group E was transplanted October 6, 1962. Any missing or dead plants were replaced October 25

and November 7, 1962. The nursery was a randomized block design with four replications. There were 17 ranges and 45 rows (three feet between rows) per range, each row represented an entry with ten plants per row spaced one foot apart. Two orchardgrass plants were planted at the end of each row to separate ranges and to offset border effects. Extra tall fescue plants were taken from the greenhouse and used for border rows around the field. A total of 4,040 plants were used in group I and 3,280 in group E, excluding border plants.

Measurements

Tiller Number: The tillers of all the plants in the nursery were counted in June 1963.

Total Plant Height: The height of each plant was measured from the ground level to the average height of the tallest panicles, in centimeters. Two meter sticks were fastened together to make measuring easier. The plant heights were measured June 19 and 20, 1963.

Seed Yield Per Plant: The panicles of the ten plants per row were cut with a hand sickle and threshed in a plot thresher. The seeds were then cleaned with a clipper cleaner and weighed.

One-hundred Seed Weight: One-hundred seeds were counted and weighed to the nearest ten-thousandth of a gram.

Statistical Analysis

A functional analysis of variance was used to test for significance among groups, within groups, and among entries within generations. Duncan's multiple range test was used to compare the performance of each group with the other groups, for all four variables.

Simple correlation coefficients were calculated to compare the six progeny testing methods, for the four variables in both populations. In the correlation of the parental clones, S_1 , OP and PX progeny with the SX and F_2 progeny, the average value of the two clones involved in the SX or F_2 was used. This can be illustrated as follows; to correlate the parental clones with the SX progeny, the average of parent 296 and parent 298 was correlated with SX-296 x 298, the average of parent 298 and 299 was correlated with SX-298 x 299, etc. for all the single-crosses. To correlate the S_1 and SX progeny, the average of S_1 296 and S_1 298 was correlated with SX-296 x 298 and the average of S_1 298 and S_1 299 was correlated with SX-298 x 299, etc. for all the single-cross combinations. The same procedure was used to correlate the OP and PX progeny with the SX progeny and to correlate the parental clones, S_1 , OP, and PX progeny with the F_2 progeny. These correlations enable one to see how closely the six progeny testing methods are associated.

The clones were ranked, on the basis of each method of progeny testing, for each character and these rankings were compared to see how similarly the six methods ranked the clones. These rankings were made on actual performance of the clones without any statistical analysis, thus the clones ranked first and last may not be statistically different in all cases.

In the comparison of the actual and theoretical PX performance, the theoretical PX performance was calculated by averaging together all the single-crosses in which each clone was involved. The average of all possible single-crosses, theoretical PX, should equal the actual PX if equal and random fertilization occurs in the PX nursery.

RESULTS AND DISCUSSION

Before discussing the results, it should be pointed out that this experiment was designed to permit a comparison of the six progeny testing methods, rather than to determine the method which gives the best evaluation of the parental materials. In this experiment the best method will be considered the one which gives similar rankings with the other methods and is also the most convenient and economical. To determine the best progeny testing method one would need to select plants based on each progeny test to produce synthetics and see which test would lead to the best varieties. The amount of agreement between the progeny testing methods should vary for the different characters because of different gene actions controlling the characters. The OP and PX test should agree with the SX test for traits which are controlled primarily by additive gene systems; however one would not expect the OP and PX test to agree with the SX test on traits controlled primarily by non-additive gene systems.

Tiller Number

In both group I and group E, there was a significant difference at the .01 level among groups, within groups and among entries within the generations, with the one exception of the OP

generation in group E, which was not significant as shown in Table 3. In group I, the OP and PX progeny had the most tillers per plant, 43.9 and 44.9 respectively, while the parents and S_1 were next with 32.5 and 30.2 respectively. The single-crosses had 27.5 tillers per plant while the F_2 plants had only 14.0 tillers (Appendix Table 1). The parents, OP progeny, and PX progeny had the most tillers in group E, with 38.0, 38.2 and 40.1 respectively, while the S_1 progeny had 33.1 tillers, the single-crosses 24.1 tillers and the F_2 progeny had 14.8 tillers per plant, see Appendix Table 2.

The simple correlation coefficients among progeny testing methods in group I, Table 4, show that the parental performance is correlated with the OP progeny ($r = .68$), SX progeny ($r = .53$) and F_2 progeny ($r = .41$). This indicates that the parental performance should give similar results to the OP, SX, and F_2 progeny test. The S_1 progeny performance is correlated with the OP progeny ($r = .80$), PX progeny ($r = .69$), and SX progeny ($r = .56$). The SX progeny ($r = .67$) and F_2 progeny ($r = .40$) are correlated with the OP progeny performance.

When the three clones with the most tillers are selected on the basis of parental performance, OP progeny, SX progeny and F_2 progeny, clone 299 is in the top three by all four methods, clone 366 is in the top three by three of the methods, but it is fourth by the average of the single-crosses, and clone 374 is in

Table 3. Table of mean squares and levels of significance for tiller number in groups I and E of tall fescue, 1963.

Source of Variation	Group I		Group E	
	d. f.	Mean Square and Significance	d. f.	Mean Square and Significance
Replications	3	1,323.68**	3	296.49**
Treatments	99	626.25**	80	454.28**
Among groups	5	8,446.67**	5	5,610.97**
Within groups	94	210.28**	75	110.50**
Among parents	8	325.59**	7	424.25**
Among S ₁	8	464.88**	7	118.42**
Among OP	8	275.79**	7	38.01
Among PX	8	114.67**	7	97.19**
Among SX	35	242.29**	27	65.97**
Among F ₂	27	68.08**	20	88.09**
Error	297	33.29	240	18.57

** Significant at the 1% level.

Table 4. Simple correlation coefficients between six progeny testing methods for tiller number in tall fescue, group I, 1963.

	n ¹				
	9	9	9	36	28
	S ₁	OP	PX	SX	F ₂
Parental	.31	.68*	-.01	.53**	.41*
S ₁	—	.80*	.69*	.56**	.30
OP	—	—	.62	.67**	.40*
PX	—	—	—	.11	.22
SX	—	—	—	—	.27

¹ Number of paired observations.

* Significant at the 5% level.

** Significant at the 1% level.

Table 5. Comparison of the rankings of the actual tiller number counts of tall fescue clones for group I by six progeny testing methods, 1963.

Clonal Identification	Parental Clones	S ₁	OP	PX	Average of SX	Average of F ₂
296	9	4	6	3	8	8
298	5	1	4	1	4	1
299	2	2	1	4	1	3
311	4	9	9	7	6	7
329	8	6	5	1	3	5
359	7	8	8	6	7	4
366	1	3	2	2	4	2
368	6	7	7	8	5	5
374	3	5	3	5	2	6

Rankings 1-9, with 1 indicating most tillers and 9 the least tillers.

the top three in three of the four methods; however it is sixth in the F_2 performance. This indicates that the clonal performance can be used effectively in place of the OP, SX, and F_2 progeny test for selecting clonal lines with the highest tiller number in group I. The PX and S_1 progeny test rank the clones similarly (Table 5), since both methods indicate that clones 298 and 366 are high in tiller number and clones 311, 359, and 368 are the three lowest clones in tiller number. It should be noted; however, that the range of the PX progeny is only 43 percent of the S_1 progeny. This is one limitation of the PX method which Davis (3, p. 575) has pointed out.

The value of clone 299, which ranked in the top three for all of the six methods except the PX test (Table 5) is also indicated by the fact that it was involved in three of the top five single-crosses and three of the top five F_2 lines. Clone 366 which was ranked in the top three for all methods except the average of the single-crosses was involved in two of the top five single-crosses and two of the top five F_2 crosses.

The simple correlation coefficients for tiller number in group E as shown in Table 6 show that only the PX and F_2 lines ($r = .47$), and the SX and F_2 lines ($r = .73$) are correlated. None of the other progeny testing methods are significantly correlated.

When the clones are ranked by the different progeny testing methods in Table 7, it can be seen that there are no clones which

Table 6. Simple correlation coefficients between six progeny testing methods for tiller number in tall fescue, group E, 1963.

	n ¹				
	8 S ₁	8 OP	8 PX	28 SX	21 F ₂
Parental	.47	.41	.33	.04	.11
S ₁	_____	.54	-.20	.33	.19
OP	_____	_____	-.19	-.05	-.12
PX	_____	_____	_____	.17	.47*
SX	_____	_____	_____	_____	.73**

¹ Number of paired observations.

* Significant at the 5% level.

** Significant at the 1% level.

Table 7. Comparison of the rankings of the actual tiller number counts of tall fescue clones for group E by six progeny testing methods, 1963.

Identification	Parental				Average of SX	Average of F ₂
	Clones	S ₁	OP	PX		
304	7	8	6	3	8	8
314	5	5	1	2	3	2
315	8	6	7	8	5	6
339	6	2	5	5	1	3
340	3	4	3	7	7	4
342	2	3	4	4	6	5
351	4	7	8	1	2	1
352	1	1	2	6	4	7

Rankings 1 -8, with 1 indicating most tillers and 8 the least tillers.

ranked consistently high for all progeny testing methods, with the possible exception of clone 314. Clone 314 is ranked in the top three in the OP, PX, SX, and F_2 progeny test, but it is fifth in the S_1 progeny test and fifth in the clonal performance. Clones 339, 351, and 352 each rank in the top three for tiller number in three of the progeny test but rank from fourth to eighth in the other progeny test. The only two progeny testing methods which give very similar results are the single-cross performance and the F_2 performance, which were significantly correlated ($r = .73$). In both of these methods clones 314, 339 and 351 rank in the top three for tiller number and clone 304 has the least number of tillers (Table 7).

The OP progeny test would not be suitable for group E since there was no significant difference among OP progeny in the analysis of variance (Table 3). The range for tiller number among OP progeny was 9.5, whereas it was 31.6 among the parental clones, 18.5 among the S_1 progeny and 14.6 among the PX progeny. The range of the S_1 progeny was less than would be expected on the basis of Davis's work (3, p. 575) in which he expected the range of the S_1 progeny to equal the parental range.

The two populations of plants, group I and group E, gave different results concerning the effectiveness of the progeny test for tiller number. Group I indicates that the clonal performance,

OP progeny, SX progeny, and F_2 progeny would be equally effective; therefore, it would be advantageous to use either clonal performance or OP progeny test since these two methods are the most convenient. The results of group I also indicate the S_1 progeny and PX progeny will give similar results; therefore, it would be more convenient to use the PX test except the range of the variation in the PX progeny is only 43 percent of the S_1 range. The results from group E indicate that only the single-crosses and the F_2 performance will give similar results, which means there is no need to use F_2 progeny test since the single-crosses will give the same results and are much easier to use. Since only two of the six progeny testing methods give similar results in group E, it is difficult to say which of the progeny testing methods are most reliable, unless synthetic varieties are made on the basis of each test to determine which progeny test would give the best evaluation of the plant materials.

Plant Height

There was a significant difference at the .01 level among groups, within groups, and among entries within generations in group I and in group E with the exceptions of the OP and PX generations in group E, which were not significant (Table 8). In group I, the OP progeny (144.0 cms.) and the PX progeny (145.3 cms.)

Table 8. Table of mean squares and levels of significance for plant height in tall fescue, 1963, for both group I and group E.

Source of Variation	Group I		Group E	
	d.f.	Mean Square and Significance	d.f.	Mean Square and Significance
Replications	3	739.94**	3	256.71**
Treatments	99	915.52**	80	647.12**
Among groups	5	12,414.95**	5	6,985.72**
Within groups	94	303.85**	75	224.55**
Among parents	8	940.51**	7	1,015.08**
Among S ₁	8	212.68**	7	398.34**
Among OP	8	111.80**	7	58.08
Among PX	8	130.51**	7	11.96
Among SX	35	187.78**	27	104.27**
Among F ₂	27	400.96**	20	182.08**
Error	297	32.03	240	30.20

** Significant at the 1% level.

were the tallest, with the parents (139.0 cms.), the single-crosses (137.8 cms.), and the S_1 progeny (133.3 cms.) second in height. The F_2 progeny were the shortest (112.2 cms.), as shown in Appendix Table 1. In group E, the OP progeny (144.6 cms.) and the PX progeny (147.3 cms.) were the tallest while the parents (137.5 cms.) and the SX progeny (138.9 cms.) were intermediate in height. The S_1 progeny (131.0 cms.) were shorter than the parents and the F_2 progeny (117.7 cms.) showed the greatest inbreeding depression, Appendix Table 2.

The simple correlation coefficients for group I (Table 9) indicate the clonal performance, OP progeny, PX progeny and SX progeny should all give similar results. The correlation coefficients between these progeny testing methods were all significant and varied from .58 to .88. The significant correlations of .40 between OP progeny and F_2 progeny and .42 between SX progeny and F_2 progeny indicates that these methods should also give similar results.

The results of the rankings of the clones by each progeny testing method (Table 10) give the same results as the correlation coefficients. Clones 311, 329, and 359 would be selected as the three tallest clones by the clonal performance, OP progeny, PX progeny, SX progeny and the F_2 progeny. The S_1 progeny test differs from the other five test in selecting the three tallest clones.

Table 9. Simple correlation coefficients between six progeny testing methods for plant height in tall fescue, group I, 1963.

	n ¹				
	9	9	9	36	28
	S ₁	OP	PX	SX	F ₂
Parental	-.17	.88**	.86**	.60**	.36
S ₁	—	.00	.12	-.06	-.26
OP	—	—	.72*	.71**	.40*
PX	—	—	—	.58**	.21
SX	—	—	—	—	.42*

¹ Number of paired observations.

* Significant at the 5% level.

** Significant at the 1% level.

Table 10. Comparison of the rankings of plant height, in cms., of tall fescue clones for group I by six progeny testing methods, 1963.

Clonal Identification	Parental Clones	S ₁	OP	PX	Average of SX	Average of F ₂
296	6	1	7	4	9	9
298	9	2	8	8	6	6
299	8	7	9	7	7	7
311	2	8	3	1	1	3
329	3	3	2	2	3	2
359	1	5	1	3	2	1
366	7	9	6	9	8	4
368	4	6	5	5	4	5
374	5	4	4	6	5	8

Rankings 1-9, with 1 indicating the tallest plants and 9 the shortest plants.

The S_1 test ranked clone 311 as one of the shortest clones although it ranked in the tallest three in the other five methods (Table 10).

The simple correlation coefficients of group E (Table 11) indicate that there is less agreement between the progeny testing methods of group E than there was in group I. The correlation coefficients between the S_1 progeny, OP progeny and SX progeny are all significant which indicates that these three methods give similar results. The clonal performance and single-cross performance ($r = .39$), and the SX performance and F_2 performance ($r = .68$) should give comparable results.

The results of the rankings of the clones by each progeny testing method (Table 12) show that the S_1 , OP and SX progeny test are in fair agreement since all three methods indicate clone 352 is one of the two tallest clones and clone 339 is the shortest clone. It would appear that the clonal performance could be used in place of the S_1 progeny test since both methods indicate clones 342, 351, and 352 are the tallest and 304, 315, and 339 are the shortest clones. There is not real good agreement in the ranking of the clones by any of the methods other than the clonal performance and S_1 progeny.

The OP and PX progeny test would be unsatisfactory for plant height in group E since there was no significant difference among the progeny in these two generations (Table 8). The range of the

Table 11. Simple correlation coefficients between six progeny testing methods for plant height in tall fescue, group E, 1963.

	n ¹				
	8	8	8	28	21
	S ₁	OP	PX	SX	F ₂
Parental	.60	.45	.68	.39*	.35
S ₁	—	.74*	.00	.59**	.33
OP	—	—	-.02	.49**	.11
PX	—	—	—	-.04	.14
SX	—	—	—	—	.68**

¹ Number of paired observations.

* Significant at the 5% level.

** Significant at the 1% level.

Table 12. Comparison of the rankings of plant height, in cms., of tall fescue clones for group E by six progeny testing methods, 1963.

Clonal Identification	Parental Clones	S ₁	OP	PX	Average of SX	Average of F ₂
304	6	7	3	3	6	5
314	5	5	2	4	3	2
315	8	6	6	7	7	6
339	7	8	8	2	8	7
340	4	4	7	4	5	4
342	1	3	4	1	4	3
351	2	2	5	5	1	1
352	3	1	1	6	2	8

Rankings 1-8, with 1 indicating the tallest plants and 8 the shortest plants.

OP progeny and PX progeny was 12.4 and 6.2 respectively, while the parental clones and the S_1 progeny had a range of 47.6 and 33.2 respectively.

In comparing the results of the two populations for plant height, we find there are differences in the effectiveness of the progeny testing methods in group I and E. In group I the clonal performance, OP progeny, PX progeny, SX progeny and F_2 progeny would all be equally effective as progeny test, and the S_1 test would be unsatisfactory. In group E the clonal performance and S_1 progeny give the most similar rankings, while the OP and PX progeny test are unsatisfactory since there was no significant difference among the progeny of these two generations. It appears that the clonal performance would be as effective as any of the other five methods in both group I and group E, for plant height.

Seed Yield

There was a significant difference at the .01 level among groups, within groups, and among all generations except the F_2 generation, which was significant at the .05 level (Table 13) in group I. In group E there was a significant difference at the .01 level among groups, within groups and among all generations except the OP generation which was not significant (Table 13). In both groups, the parental clones, OP, and PX progeny had the

Table 13. Table of mean squares and levels of significance for seed yield, in tall fescue, for groups I and E, 1963.

Source of Variation	Group I		Group E	
	d. f.	Mean Square and Significance	d. f.	Mean Square and Significance
Replications	3	300.14**	3	77.70**
Treatments	99	225.43**	80	312.28**
Among groups	5	3,193.96**	5	3,652.09**
Within groups	94	67.53**	75	89.63**
Among parents	8	62.48**	7	422.18**
Among S ₁	8	207.58**	7	171.14**
Among OP	8	55.65**	7	18.74
Among PX	8	43.87**	7	44.19**
Among SX	35	77.74**	27	56.81**
Among F ₂	27	24.83*	20	29.72**
Error	297	14.47	240	10.76

* Significant at the 5% level.

** Significant at the 1% level.

highest yields, while the S_1 and SX progeny were second and the F_2 progeny showed a considerable inbreeding depression and were the lowest yielding group of plants (Appendix Tables 1 and 2).

The simple correlation coefficients, for group I seed yield (Table 14), indicate that the SX progeny are significantly correlated with the clonal performance, S_1 , OP and PX progeny test (r varies from .36 to .55). The S_1 progeny test is also correlated with the OP and PX progeny test (r = .73 and .68 respectively). The OP and F_2 progeny test were highly correlated (r = .82 with n = .28).

The rankings of the clones, for seed yield in Table 15, indicate that there is fair agreement between several of the progeny testing methods. The clonal performance, S_1 , OP and F_2 progeny test each rank clones 298 and 299 as two of the three highest seed yielders. The PX and SX progeny test each rank one of the above two clones in the top three seed yielders. The failure of the PX and SX test to rank both clones (298 and 299) high indicates that these two test may be less effective than the other progeny test. This is especially true of the PX progeny test which ranked clone 299 fourth, yet this clone ranked first in four of the six test and second in the S_1 test. The clonal performance would be a little less effective than the S_1 , OP and F_2 progeny test since it ranked clone 311 as the second highest seed yielder, yet the other five

Table 14: Simple correlation coefficients between six progeny testing methods for seed yield, in tall fescue, for group I, 1963.

	n ¹				
	9	9	9	36	28
	S ₁	OP	PX	SX	F ₂
Parental	.29	.45	.12	.48**	.24
S ₁	—	.73*	.68*	.55**	.16
OP	—	—	.48	.47**	.82**
PX	—	—	—	.36*	-.05
SX	—	—	—	—	.31

¹ Number of paired observations.

* Significant at the 5% level.

** Significant at the 1% level.

Table 15: Comparison of the rankings of nine clones for seed yield in group I, in tall fescue, by six progeny testing methods, 1963.

Clonal Identification	Parental Clones	S ₁	OP	PX	Average of SX	Average of F ₂
296	8	5	2	1	5	8
298	3	1	3	3	4	2
299	1	2	1	4	1	1
311	2	9	9	8	6	7
329	7	3	8	2	3	6
359	9	8	6	7	7	3
366	5	7	5	9	6	4
368	4	6	7	5	2	5
374	6	4	4	6	2	8

Ranking 1-9, with 1 indicating the highest seed yield and 9 the lowest seed yield.

progeny test ranked clone 311 as one of the two lowest yielding clones. Since the S_1 progeny test ranked the clones similar to several methods and had the greatest range among its progeny, it would appear to be the most desirable progeny test for yield, in group I. However, the OP and F_2 progeny test would also be satisfactory.

The simple correlation coefficients, for group E seed yield in Table 16, indicate that only the SX and F_2 progeny test ($r = .44$) are associated. This is quite different from the results for group I (Table 14) since seven of the fifteen correlations were significant in group I.

Although the SX and F_2 progeny test are significantly correlated, the two progeny tests do not rank the clones similarly (Table 17). However, both methods rank clone 351 as the highest yielder. When one looks at the average rank for all six progeny tests, it appears that clones 340, 351, and 352 are the highest seed yielders. The S_1 progeny test would be most desirable since it is the only test to rank all three of these clones as the highest three seed yielders. The clonal performance, OP, PX, and F_2 progeny test each rank two of the above three clones in the top three seed yielders. The OP progeny test would not be desirable since there was no significant difference among the OP progeny for seed yield in group E (Table 13). Due to the large range among the clonal and S_1 progeny and the similar rankings of these methods

Table 16. Simple correlation coefficients between six progeny testing methods for seed yield in tall fescue, for group E, 1963.

	n ¹				
	8	8	8	28	21
	S ₁	OP	PX	SX	F ₂
Parental	.56	-.03	.60	-.02	.08
S ₁	—	.59	.24	.18	.06
OP	—	—	-.55	.25	-.23
PX	—	—	—	.18	.24
SX	—	—	—	—	.44*

¹ Number of paired observations.

* Significant at the 5% level.

Table 17. Comparison of the ranking of eight clones for seed yield in group E, in tall fescue, by six progeny testing methods, 1963.

Clonal Identification	Parental Clones	S ₁	OP	PX	Average of SX	Average of F ₂	Average Rank
304	5	7	5	4	6	8	5.8
314	7	8	5	7	8	3	6.3
315	8	4	2	8	2	6	5.0
339	6	6	7	2	3	4	4.7
340	3	2	3	6	4	2	3.3
342	2	5	4	5	7	5	4.7
351	4	3	6	1	1	1	2.7
352	1	1	1	3	5	7	3.0

Ranking 1-8, with 1 indicating the highest seed yield and 8 the lowest seed yield.

with each other, it seems that these two methods would be the most desirable progeny test for seed yield in group E.

In group I, the S_1 , OP and F_2 progeny test would each be satisfactory; however, the S_1 progeny test would be most desirable due to the larger range among its progeny. In group E, the clonal performance and S_1 progeny appear to be equally satisfactory. Since the S_1 progeny test was satisfactory in both groups it would be the recommended progeny test for seed yield.

Seed Weight

In group I, there was a significant difference at the .01 level within groups and among entries within generations, and there was a significant difference at the .05 level among groups (Table 18). There was a significant difference at the .01 level among groups, within groups and among all generations except the OP and PX which were not significant in group E (Table 18). In group I, the parental clones, OP and SX progeny had the heaviest 100 seed weights, while the S_1 , PX and F_2 progeny had the lightest 100 seed weights (Appendix Table 1). In group E, the parental clones, OP, PX and SX progeny had the heaviest 100 seed weights and the S_1 and F_2 progeny had the lightest 100 seed weights (Appendix Table 2).

The simple correlation coefficients in Table 19 for 100 seed weight in group I, show that all of the correlations between the

Table 18. Table of mean squares and levels of significance for 100 seed weight, in tall fescue for groups I and E, 1963.

Source of Variation	Group I		Group E	
	d. f.	Mean Square and Significance	d. f.	Mean Square and Significance
Replications	3	.00003	3	.00167**
Treatments	99	.00377**	80	.00207**
Among groups	5	.01032*	5	.00950**
Within groups	94	.00342**	75	.00157**
Among parents	8	.01121**	7	.00386**
Among S ₁	8	.00511**	7	.00233**
Among OP	8	.00290**	7	.00027
Among PX	8	.00184**	7	.00057
Among SX	35	.00304**	27	.00122**
Among F ₂	27	.00173**	20	.00179**
Error	297	.00053	240	.00042

* Significant at the 5% level.

** Significant at the 1% level.

clonal performance, S_1 , OP, SX and F_2 progeny are significant (r varies from .41 to .88) while none of the correlations for the PX progeny are significant. This indicates that all of the progeny test except the PX progeny test should give similar results.

The rankings of the clones by each progeny test (Table 20) show that the clonal performance, S_1 , OP, SX and F_2 progeny give the clones very similar rankings. Each of these five methods would be equally satisfactory in grouping clones 296, 298, 299 and 329 into the high 100 seed weight class. The methods also agree since they also rank clones 311, 359, and 374 as having low 100 seed weights. The PX progeny test would appear to be unsatisfactory for 100 seed weight in group I since the clones are ranked in a different order by this test.

The simple correlation coefficients for 100 seed weight in group E (Table 21) show that the clonal performance and S_1 progeny ($r = .75$) and the S_1 and F_2 progeny ($r = .55$) are significantly correlated. The clonal performance is negatively correlated with the OP progeny. This indicates the clonal performance and OP progeny should rank the clones differently.

The rankings of the clones, by each progeny testing method (Table 22) indicates the clonal performance, S_1 , SX and F_2 progeny are equally effective in selecting clones 340 and 351 as the two clones with the heaviest 100 seed weights. The OP and PX progeny

Table 19. Simple correlation coefficients between six progeny testing methods for 100 seed weight, in tall fescue, for group I, 1963.

	n ¹				
	9	9	9	36	28
	S ₁	OP	PX	SX	F ₂
Parental	.84**	.85**	.30	.42*	.41*
S ₁	—	.87**	.10	.84**	.59**
OP	—	—	.24	.88**	.73**
PX	—	—	—	.18	-.04
SX	—	—	—	—	.51**

¹ Number of paired observations.

* Significant at the 5% level.

** Significant at the 1% level.

Table 20. Comparison of the rankings of nine clones for 100 seed weight in group I, in tall fescue, by six progeny testing methods, 1963.

Clonal Identification	Parental Clones	S ₁	OP	PX	Average of SX	Average of F ₂
296	3	1	1	6	1	1
298	1	2	2	1	2	2
299	4	4	3	7	3	3
311	5	8	9	5	9	9
329	2	3	4	8	4	4
359	8	9	7	3	8	7
366	7	6	6	9	6	5
368	6	7	5	2	5	6
374	9	5	8	4	7	8

Rankings 1-9, with 1 indicating the heaviest 100 seed weight and 9 the lightest 100 seed weight.

Table 21. Simple correlation coefficients between six progeny testing methods for 100 seed weight, in tall fescue, for group E, 1963.

	n ¹				
	8	8	8	28	21
	S ₁	OP	PX	SX	F ₂
Parental	.75*	-.85**	.04	.37	.42
S ₁	—	.23	.25	.37	.55**
OP	—	—	.32	.00	-.10
PX	—	—	—	.37	.39
SX	—	—	—	—	.40

¹ Number of paired observations.

* Significant at the 5% level.

** Significant at the 1% level.

Table 22. Comparison of the rankings of eight clones for 100 seed weight in group E, in tall fescue, by six progeny testing methods, 1963.

Clonal Identification	Parental Clones	S ₁	OP	PX	Average of SX	Average of F ₂
304	5	5	7	3	6	4
314	8	8	2	2	3	6
315	7	4	1	5	4	3
339	3	6	5	8	7	7
340	1	2	8	6	1	1
342	6	7	4	7	5	5
351	2	1	3	1	2	2
352	4	3	6	4	8	8

Rankings 1-8, with 1 indicating the heaviest 100 seed weight and 8 the lightest.

test are not effective in ranking these two clones high in 100 seed weight. The OP and PX progeny test are both unsatisfactory since there is no significant difference among their progeny (Table 18).

The results, from the two populations for 100 seed weight, indicate the clonal performance, S_1 , SX and F_2 progeny test are equally satisfactory. The OP progeny test is satisfactory for group I, but is not satisfactory for group E. The PX progeny test is not satisfactory in either group. Since the clonal performance is an effective and convenient progeny testing method, it would be the most desirable progeny test for 100 seed weight.

There were some differences in the effectiveness of the six progeny testing methods for each trait and for each population. In group I, the clonal performance, OP progeny test, and F_2 progeny test generally gave similar results for all four traits; therefore, the clonal performance would be effective with one exception. For seed yield, clone 311 ranked second by clonal performance, but clone 311 ranked lowest or next to lowest in seed yield by the other five progeny testing methods. The S_1 progeny test was not satisfactory, in group I, for tiller number and plant height, but was the most effective test for seed yield since it ranked the clones similar to the other methods and had the greatest range. The single-cross progeny test, in group I, was effective for tiller number, plant height, and 100 seed weight, but not seed yield. In general the

polycross progeny test was the least desirable test in group I, although it could be used effectively for plant height.

In group E there was much less agreement between the six methods of progeny testing than in group I. In general the clonal performance and S_1 progeny test were the most desirable test. Since they ranked the clones similarly, the clonal performance would be the most desired progeny test in group E. The OP progeny test would be unsatisfactory because there was no significant difference among the OP progeny for all four traits. The PX progeny test is also unsatisfactory in group E, since there was no significant difference among the PX progeny in two of the four measured traits, plant height and 100 seed weight.

One would expect a greater range in group I since there is no significant difference in the OP and PX progeny in group E while there is in group I. However, 100 seed weight is the only one of the four traits in which the range of group I exceeds the range of group E. In the other three traits the range of group E equalled or exceeded the range of group I and in seed yield the range of group E was 2.3 times greater than the range of group I, yet there was no significant difference in the OP progeny test for yield in group E.

The fairly consistent agreement of the clonal performance with the other methods of progeny testing in both populations indicates that vegetative cuttings may be a sufficient progeny test in

tall fescue. Due to the nonsignificance among the OP and PX progeny these two tests are generally not satisfactory.

The methods used in this study allow one to make all possible comparisons between the six progeny testing methods. However, to determine which test gives the most reliable evaluation of the materials, one would need to make synthetic varieties on the basis of each progeny test and see which progeny test leads to the development of the "best" varieties.

Comparison of the Actual and Theoretical Polycross Progeny

The values for the actual and theoretical PX progeny for the four variables (Tables 23 and 24) show that the actual and theoretical polycross progeny are not similar for most variables. For group I, the theoretical PX progeny had only 60 percent as many tillers and the yield was only 66.7 percent as much as the actual PX progeny. Group E results were very similar since the theoretical PX progeny were 60.1 percent and 60.2 percent of the actual PX progeny, for tiller number and yield respectively.

The differences between the actual and theoretical PX progeny were less for the other two variables. In group I, the theoretical PX progeny was 94.8 percent and 110.0 percent of the actual PX progeny, for plant height and 100 seed weight respectively (Table 23). One-hundred seed weight was the only trait in which the

theoretical PX was greater than the actual PX (110.0 percent). The results from group E are similar to the results of group I since the theoretical PX was 94.3 percent and 101.7 percent of the actual PX for plant height and 100 seed weight respectively. One-hundred seed weight is the only trait which is greater for the theoretical PX than the actual PX (101.7 percent as shown in Table 24).

The theoretical PX progeny were usually lower than the actual PX progeny. This indicates that there might be some differential fertilization in the actual PX nursery, in favor of the more desirable clones. In the theoretical PX, there was equal fertilization because each clone was crossed with each other clone under parchment bags.

The simple correlation coefficients between the theoretical and actual PX progeny for the four variables (Table 25) show that the two groups of progeny are not associated for any of the four variables except plant height in group I.

The data indicates that the theoretical PX progeny performance is generally lower than the actual PX performance. This suggests differential fertilization in favor of the more desirable clones. The two groups of the progeny are not associated in seven of the eight cases. This indicates the theoretical and actual PX did not give similar results in most cases.

Table 23. Table of means for actual and theoretical polycross progeny for four variables in tall fescue, group I, 1963.

Clonal Identification	Tiller Number		Plant Height cms.		Yield Per Plant gms.		100 Seed Weight gms.	
	Actual PX	Theo. PX	Actual PX	Theo. PX	Actual PX	Theo. PX	Actual PX	Theo. PX
296	48.1	20.2	147.4	132.5	25.5	12.2	.2197	.2811
298	50.6	28.6	138.3	135.9	23.6	14.0	.2755	.2680
299	46.1	34.1	142.2	134.1	23.4	19.2	.2148	.2599
311	36.8	22.9	153.2	143.4	19.0	12.1	.2237	.2293
329	50.6	29.7	152.0	140.8	23.9	15.4	.2122	.2580
359	42.5	21.0	150.7	141.2	19.1	11.4	.2293	.2338
366	50.0	28.6	138.1	132.7	14.9	12.1	.2032	.2428
368	36.4	28.4	143.4	139.7	22.2	15.6	.2454	.2506
374	45.2	31.3	142.8	139.6	20.0	15.6	.2292	.2359
Average	45.1	27.2	145.3	137.8	21.3	14.2	.2281	.2510
<u>Theoretical</u> Actual	x 100	60.3%		94.8%		66.7		110.0%

Table 24. Table of means for actual and theoretical polycross progeny for four variables in tall fescue, group E, 1963.

Clonal Identification	Tiller Number		Plant Height cms.		Yield Per Plant gms.		100 Seed Weight gms.	
	Actual	Theo.	Actual	Theo.	Actual	Theo.	Actual	Theo.
	PX	PX	PX	PX	PX	PX	PX	PX
304	42.1	21.3	147.7	138.5	26.7	15.0	.3122	.3022
314	45.4	25.0	147.6	140.4	23.3	14.1	.3141	.3156
315	31.9	23.7	144.0	137.9	21.2	16.7	.3012	.3089
339	39.9	26.4	148.0	134.0	26.9	16.4	.2838	.3009
340	34.7	22.8	147.6	138.7	25.3	16.2	.3008	.3237
342	40.9	22.9	150.2	139.1	25.6	14.7	.2974	.3058
351	46.5	25.4	147.1	141.5	32.6	17.3	.3228	.3213
352	39.8	24.9	146.3	140.8	26.8	15.6	.3048	.2992
Average	40.1	24.1	147.3	138.9	26.1	15.7	.3046	.3097
<u>Theoretical</u> Actual	x 100	60.1%		94.3%		60.2%		101.7%

Table 25. Table of ¹ simple correlation coefficients between the actual and theoretical polycross progeny for four variables in tall fescue, groups I and E, 1963.

² n	Population	Tiller Number	Plant Height cms.	Seed Yield Per Plant gms.	100 Seed Weight gms.
9	Group I	.26	.68*	.43	.20
8	Group E	.28	-.06	.40	.38

¹ Actual polycross progeny are from an isolated polycross nursery. Theoretical polycross progeny are calculated by averaging the performance of all possible single crosses for each parent.

² Number of paired observations.

* Significant at the 5% level.

SUMMARY AND CONCLUSIONS

Seventeen parental clones were selected, from 9000 plants, on the basis of self-sterility, seed and forage yield potential, crude protein and chromogen content. The parental clones were divided into two populations based on date of maturity. Group I was intermediate in maturity and had nine parental clones, while group E was early maturing and had eight parental clones.

Vegetative cuttings of the parental clones, first generation selfed-seed (S_1), open-pollinated seed (OP), polycross seed (PX), single-cross seed (SX), and selfed seed from the single-crosses (F_2 seed) were planted in the field in a randomized block design with four replications. Each entry consisted of ten plants in a nine foot row and the rows were three feet apart. During the summer of 1963 data were collected on tiller number, plant height cms., seed yield per plant gms., and 100 seed weight gms.

Simple correlation coefficients were calculated between the six progeny testing methods to determine the association of the methods, for each trait. The progeny testing methods were also compared by ranking the clones, by each of the progeny testing methods, and comparing the rankings for each trait. The actual polycross performance was compared with the theoretical polycross performance (average of all possible single crosses) by

calculating simple correlation coefficients between the two methods and comparing the mean performance of the two progeny groups.

In this experiment six progeny testing methods were compared with the objective of determining which test give similar results. The results from the comparison of the six progeny testing methods indicated the vegetative cuttings of the parental clones and the single-cross progeny tests, in general, are the two most effective progeny testing methods when considering all four traits and both populations of plants.

The open pollinated and polycross progeny tests were generally undesirable, because frequently there was no significant difference among their progeny. The S_1 progeny test was generally not desirable in group I; however, it appeared to be the most satisfactory test for seed yield, when considering both populations of plants.

The results illustrate why there are inconsistencies in the literature concerning the effectiveness of the progeny testing methods. The effectiveness of the six progeny test varied, to some extent, from trait to trait and from population to population. For all four traits there was much less agreement among the six progeny test in group E than in group I. In group I, 33 of the 60 correlations between progeny tests were significant while only 11 of the 60 correlations were significant in group E.

In all four traits the F_2 generation showed a great inbreeding depression. The F_2 plants were much shorter, had less tillers, a lower yield and lighter seeds than any other group of plants. The single-crosses were lower than the parents for tiller number, plant height and 100 seed weight, but equalled the parents in yield per plant. The OP and PX generations were generally the highest for all four traits. The parents usually equalled the OP and PX plants or were slightly lower. The S_1 plants were intermediate and approximately equal to the single cross plants.

The results from the comparison of the actual polycross with the theoretical polycross indicated that some differential fertilization occurred in the actual polycross, in favor of the desirable clones, since the theoretical polycross performance for most of the traits was lower than the actual polycross performance. The actual and theoretical polycross performance were not associated in seven of the eight cases.

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APPENDIX

Appendix Table 1. Table of means and standard errors of the mean (\bar{y}) for tiller number, total plant height (cms.), seed yield (gms.) and one-hundred seed weight (gms.), group I, tall fescue seed phase, 1963.

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
Parents				
2960	19.9	136.1	16.2	.2927
2980	30.9	110.2	20.1	.3444
2990	42.5	126.1	27.0	.2893
3110	32.2	156.0	24.0	.2244
3290	21.4	153.8	17.0	.3247
3590	28.5	157.6	14.6	.2137
3660	45.4	135.2	17.6	.2192
3680	30.4	139.0	19.2	.2228
3740	41.4	137.0	17.3	.2078
Average	32.5	139.0	19.2	.2599
S ₁ Progeny				
2961	29.8	143.2	14.0	.2998
2981	46.6	140.4	25.6	.2716
2991	44.5	126.4	21.6	.2438
3111	13.4	125.5	3.5	.2006
3291	29.2	139.7	15.3	.2703
3591	19.0	133.6	5.8	.1992
3661	34.4	124.0	7.2	.2173
3681	25.2	128.8	12.4	.2114
3741	29.5	137.9	14.2	.2252
Average	30.2	133.3	13.3	.2377

Appendix Table 1. (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
OP Progeny				
2962	40.9	139.5	24.7	.2812
2982	46.9	137.8	24.1	.2781
2992	54.3	137.4	29.0	.2666
3112	31.2	147.8	17.8	.2081
3292	41.5	149.6	18.4	.2560
3592	35.8	151.9	19.2	.2272
3662	53.9	141.7	19.9	.2338
3682	38.4	143.7	18.9	.2401
3742	51.8	146.9	22.2	.2135
Average	43.9	144.0	21.6	.2450
PX Progeny				
2963	48.1	147.4	25.5	.2197
2983	50.6	138.3	23.6	.2755
2993	46.1	142.2	23.4	.2148
3113	36.8	153.2	19.0	.2237
3293	50.6	152.0	23.9	.2122
3593	42.5	150.7	19.1	.2293
3663	50.0	138.1	14.9	.2032
3683	36.4	143.4	22.2	.2454
3743	45.2	142.8	20.0	.2292
Average	44.9	145.3	21.3	.2281

Appendix Table. 1 (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
SX Progeny				
366x368	36.7	132.0	15.4	.2306
366x374	29.9	134.6	11.4	.2205
368x374	33.7	141.5	17.5	.2185
311x329	19.9	139.4	11.0	.2217
311x359	15.5	152.5	9.0	.2231
311x366	19.3	133.3	8.1	.2238
299x359	30.6	137.4	19.7	.2338
299x329	39.2	135.7	20.5	.2629
299x311	29.2	139.2	12.6	.2290
359x374	19.0	141.0	8.4	.2121
359x368	23.3	145.4	12.9	.2499
359x366	18.1	129.3	6.5	.2157
299x366	38.8	127.6	18.5	.2544
299x368	31.8	131.5	19.0	.2710
299x374	44.2	139.6	27.4	.2312
311x368	23.2	150.6	14.8	.2312
311x374	34.2	148.2	15.7	.2048
329x359	29.7	152.2	14.5	.2531
296x366	23.4	132.4	12.6	.2752
296x359	14.8	134.2	10.0	.2649
296x329	20.1	129.8	12.3	.2842
329x374	34.7	141.2	17.0	.2549
329x368	27.6	146.2	14.3	.2461
329x366	30.4	143.0	15.4	.2636
298x299	34.3	131.9	19.4	.2808

Appendix Table 1. (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
SX Progeny (continued)				
298x311	21.9	144.1	13.4	.2548
298x359	17.3	137.8	9.9	.2177
298x329	36.3	138.8	17.8	.2774
298x366	32.6	129.4	8.6	.2588
298x368	33.6	138.8	19.5	.2759
296x368	17.4	131.3	11.8	.2819
296x374	21.6	133.7	13.0	.2731
298x374	33.0	137.3	14.5	.2718
296x311	19.9	139.8	12.0	.2461
296x299	24.6	129.6	16.8	.3160
296x298	20.0	129.0	8.7	.3072
Average	27.2	137.8	14.2	.2510
F ₂ Progeny				
366x368	13.4	113.0	2.8	.2251
366x374	13.1	113.4	2.1	.2121
368x374	14.1	112.5	4.4	.2223
311x329	13.6	117.4	4.0	.2219
311x359	9.6	116.2	1.5	.2123
311x366	13.8	111.8	3.9	.2348
299x359	22.8	122.6	13.0	.2587
299x329	10.6	97.6	2.2	.2511
299x311	15.4	108.9	3.6	.1958
359x374	18.7	106.0	3.1	.1721

Appendix Table 1. (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
F ₂ Progeny (continued)				
359x368	11.2	111.8	4.2	.2113
359x366	12.5	113.1	2.0	.2159
299x366	18.1	111.8	7.0	.2430
299x368	18.3	123.6	6.1	.2325
299x374	13.0	98.7	3.6	.2267
311x374	12.6	122.2	2.2	.2046
329x359	13.0	131.5	2.9	.2121
296x366	14.4	109.6	5.5	.2309
296x359	9.9	114.2	2.7	.2357
296x329	8.2	100.7	2.1	.2538
329x374	13.2	123.2	3.1	.2215
329x368	11.3	110.6	1.8	.2348
329x366	26.2	129.4	7.8	.2435
298x299	17.5	106.4	5.4	.2488
298x359	16.3	117.6	6.7	.2647
296x374	8.0	83.6	1.4	.2403
298x374	15.0	108.5	2.4	.2156
296x299	9.4	105.5	2.2	.2560
Average	14.0	112.2	3.9	.2285
Grand mean	26.9	130.1	12.8	.2389
s \bar{y}	2.88	2.83	1.90	.012

Appendix Table 2. Table of means and standard errors of the mean (\bar{s}_y) for tiller number, total plant height (cms.), seed yield (gms.) and one-hundred seed weight (gms.), group E, tall fescue seed phase, 1963.

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
Parents				
3040	31.6	138.5	26.2	.3048
3140	36.0	141.2	15.2	.2761
3150	18.8	103.3	7.6	.2768
3390	35.6	126.0	20.8	.3146
3400	43.0	142.0	31.6	.3657
3420	49.9	150.9	36.1	.2807
3510	38.5	149.4	30.4	.3325
3520	50.4	148.6	36.3	.3118
Average	38.0	137.5	25.5	.3079
S_1 Progeny				
3041	23.0	124.4	9.4	.2800
3141	32.5	132.3	5.2	.2582
3151	31.5	126.8	14.7	.2980
3391	36.9	112.0	11.8	.2768
3401	34.1	133.5	18.4	.3193
3421	35.4	136.6	13.8	.2646
3511	29.8	137.0	16.2	.3221
3521	41.5	145.2	27.2	.3036
Average	33.1	131.0	14.6	.2903

Appendix Table 2. (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
OP Progeny				
3042	36.8	146.6	23.3	.2948
3142	41.6	147.0	23.3	.3068
3152	36.7	143.2	27.0	.3120
3392	37.8	138.1	21.4	.2956
3402	39.8	141.5	24.6	.2855
3422	39.6	146.0	24.1	.2976
3512	32.1	143.6	21.8	.3026
3522	41.2	150.5	27.4	.2950
Average	38.2	144.6	24.1	.2987
PX Progeny				
3043	42.1	147.7	26.7	.3122
3143	45.4	147.6	23.3	.3141
3153	31.9	144.0	21.2	.3012
3393	39.9	148.0	26.9	.2838
3403	34.7	147.6	25.3	.3008
3423	40.9	150.2	25.6	.2974
3513	46.5	147.1	32.6	.3228
3523	39.8	146.3	26.8	.3048
Average	40.1	147.3	26.1	.3046

Appendix Table 2. (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
SX Progeny				
339x342	23.4	135.2	14.0	.2960
339x340	22.0	128.1	12.6	.3254
304x314	18.9	137.4	9.8	.2959
304x315	16.9	130.6	8.9	.2945
315x352	22.5	141.1	15.3	.2863
339x351	23.2	131.1	13.8	.2980
339x352	24.6	131.4	12.9	.2701
315x351	26.3	140.6	21.6	.3388
304x339	27.0	141.9	19.4	.2939
304x340	21.8	141.5	18.1	.3114
315x342	21.0	141.8	14.0	.2928
304x342	15.9	133.2	10.4	.3156
340x351	22.9	139.8	15.6	.3229
315x340	26.5	143.2	22.5	.3251
304x342	18.6	136.3	13.8	.2939
304x351	24.2	142.0	19.0	.3178
315x339	32.2	132.9	23.8	.3137
340x352	24.8	140.3	17.4	.3264
342x351	25.3	142.8	17.8	.3382
314x352	23.0	141.0	11.9	.3104
304x352	21.9	140.0	15.7	.3079
314x315	20.4	135.0	10.6	.3110
314x351	27.6	145.3	15.8	.3228
342x352	29.2	143.0	18.0	.2830

Appendix Table 2. (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
SX Progeny (continued)				
351x352	28.1	149.2	17.8	.3106
314x342	27.1	141.6	15.2	.3209
314x339	32.6	137.6	18.0	.3093
314x340	25.8	145.1	17.2	.3392
Average	24.1	138.9	15.7	.3097
F ₂ Progeny				
339x342	16.5	119.5	5.0	.2619
304x314	9.6	114.6	2.2	.2899
304x315	9.5	110.6	2.4	.2976
315x352	10.5	120.0	6.1	.2832
339x351	19.1	115.3	5.2	.2824
339x352	11.0	102.9	2.0	.2397
304x339	15.6	115.9	4.3	.2439
304x340	11.5	112.9	3.7	.2908
315x342	9.8	121.0	2.8	.2870
304x342	10.3	109.2	3.3	.2963
340x351	17.3	129.2	10.6	.3368
315x340	16.2	116.6	7.5	.2990
304x342	9.8	117.8	3.7	.2862
304x351	14.2	127.4	4.4	.2845
315x339	17.3	112.1	5.4	.2830
342x351	14.3	119.7	6.0	.2712
314x352	17.6	117.2	4.3	.2545

Appendix Table 2. (continued)

Clonal Identification	Tiller Number	Total Plant Height	Seed Yield	100 Seed Weight
F ₂ Progeny (continued)				
314x315	12.3	114.1	2.0	.2687
314x351	26.8	131.6	12.5	.2921
314x342	19.4	122.3	6.0	.2697
314x339	22.2	121.6	7.7	.2711
Average	14.8	117.7	5.1	.2804
Grand mean	26.4	132.0	15.5	.2946
s \bar{y}	2.16	2.75	1.64	.010