

AN ABSTRACT OF THE THESIS OF

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Title: THE HERITABILITY OF AGRONOMIC CHARACTERISTICS  
IN TALL FESCUE (FESTUCA ARUNDINACEA SCHREB.)

Abstract approved: Signature redacted for privacy.  
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Three genotypes of tall fescue (Festuca arundinacea Schreb.) cultivar Fawn and four genotypes from the cultivar Fortune were used as parents to form 15 of a possible 21 single crosses to study the heritability of certain agronomic characteristics. The Fawn variety is considered to be tall in growth habit, vigorous and early in anthesis. The Fortune variety represents germ plasm with a shorter growth habit, less vigor and later anthesis. Crossing was accomplished by mutual pollination in the greenhouse during February 1972.

A greenhouse experiment was started in June 1972 using the 15 single crosses in a randomized block with three replications. Plants were supplied with one half strength of a modified Hougland's solution twice weekly until August 3 followed with an application of the same nutrient solution every two weeks until they were taken to

the field for establishment. Greenhouse data were collected on July 7, August 4 and September 11.

These data indicated that the variation among single crosses for tiller numbers and dry weight were greater as the plant grew older. Nutrient stress affected dry matter yield by reducing the variation and mean performance of the single crosses. Differences among single crosses for shoot length, tiller number, and plant spread were still quite evident under the stress conditions.

Shoot length showed significant general combining ability (GCA) with non significant specific combining ability effects (SCA) on July 7 and September 11. GCA effects for tiller numbers were evident on August 4 and September 11. Both GCA and SCA effects were significant for plant spread on September 11. GCA for dry weight were significant only on July 7. Based on the diallel analysis, additive gene action was primarily responsible for shoot length, tiller numbers and dry weight. Both additive and non additive gene action influenced plant spread.

The field establishment included the 15 single crosses from greenhouse experiments and the seven parent clones, established in a randomized block design with three replications. From the diallel analysis, it was observed that the GCA:SCA mean square for the characters measured were: plant height (19:1), plant spread (2.1:1), anthesis date (3.2:1), panicle number (1.4:1), panicle length (12:1),

number of primary pedicels per panicle (7.4:1), five panicle seed weight (0.2:1), seed yield per plant (0.4:1) and 100 seed weight (15.1:1).

This indicated that additive gene action was of major importance in the expression of plant height, number of primary pedicels and 100 seed weight. Non additive gene action was contributed substantially more to the expression of five panicles seed weight and seed yield. Both additive and non additive gene action contributed to plant spread and anthesis. Inferences about gene action for panicle numbers and panicle length were not as evident. This is because of the low GCA:SCA ratio, a barely significant GCA for panicle number, and no significant GCA or SCA for panicle length.

Single cross progeny were superior to mid parent for plant height (9.27 percent), plant spread (20.33 percent), anthesis (20.90 percent, which suggested earlier anthesis than mid parent), panicle number (36.69 percent), and panicle length (11.44 percent). No apparent superiority of single cross progeny over their corresponding mid parent for number of primary pedicels and 100 seed weight was observed.

Of all single crosses, only Fawn x Fortune crosses were inferior to mid parents for five panicle seed weight (65.93 percent) and seed yield (60.22 percent). The Fawn x Fortune performance for both of these characters (0.4062 and 1.23 g per plant,

respectively) was low. The diverse parentage of these crosses may have resulted in irregular meiotic behavior in the  $F_1$  which in turn may have caused inviable gametes to be formed. This sterility would result in the low seed yields observed. This is a problem that should be cytologically investigated.

Crosses between diverse germ plasm (Fawn x Fortune crosses) did result, however, in heterosis for all characteristics except number of primary pedicels and 100 seed weight. But Fortune x Fortune crosses, for certain characters such as plant height, plant spread, panicle numbers, panicle length, exhibited even more heterosis. No heterosis was observed in the Fawn x Fawn crosses.

Medium to high heritability estimates were observed for 100 seed weight, plant spread, anthesis date, panicle number and panicle length, while medium to low heritability were observed for panicle length. Low heritable value was evident for plant height, number of primary pedicels, five panicle seed weight and seed yield. Heritability estimates were based on parent progeny relationships involving all single crosses and mid parents.

The relationships among various plant characteristics and seed yield was studied. Five panicle seed weight and panicle numbers were significantly correlated with seed yield. However there was a non-significant association of panicle length with seed yield and number of primary pedicels with seed yield.

These relationships suggest that higher yielding genotypes may be identified by observing only few panicles per plants. The panicle characteristics examined in this study (other than seed weight) were of little value in identifying high seed yield genotypes, but panicle seed weight was positively related to plant yield.

The Heritability of Agronomic Characteristics in  
Tall Fescue (Festuca arundinacea Schreb.)

by

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# THE HERITABILITY OF AGRONOMIC CHARACTERISTICS IN TALL FESCUE (FESTUCA ARUNDINACEA, SCHREB.)

## INTRODUCTION

Tall fescue (Festuca arundinacea Schreb.) is a vigorous and highly competitive grass plant which can be grown in many different climatic areas. It is used as a multipurpose crop; being grown for pasture, hay, soil conservation and turfgrass purposes.

Several tall fescue cultivars, Fawn, Alta, Goar and Kenmont are grown in Oregon for forage and seed production. Fawn is considered to be superior in seed and forage yield to other cultivars, especially in the Willamette Valley (Frakes and Beeson, 1968).

In 1967, Fortune, a unique germplasm source of tall fescue, was released by Oregon State University. This cultivar possesses turfgrass characteristics such as short height, narrower leaves, dark green color and the ability to tolerate frequent clipping. Fortune also exhibits a certain amount of the spreading habit of growth, a rare characteristic in tall fescues.

The diverse morphological characteristics of Fortune versus other tall fescues are of interest to the plant breeder. The genetic variation created by crosses between the two types would provide an opportunity to examine the genetics of agronomic characteristics in this important species. Quantitative characters result from both additive and non additive gene action. The effects due to additive

gene action are expected to remain fixed from generation to generation, whereas non additive genetic influences may not remain fixed following selection. However, by careful selection, the breeder may be able to utilize heterosis in early generations of synthesis.

The objectives of this study were:

1. To estimate gene action for plant height, plant spread, anthesis date, panicle number, panicle length, number of primary pedicels, five panicle seed weight, 100 seed weight and seed yield per plant.
2. To study the inheritance of forage regrowth in the greenhouse, among single crosses between Fawn and Fortune clones in relation to physiological age and nutrient supply.
3. To examine the relationship among agronomic characteristics and their effects on seed yield.
4. To determine the expression of heterosis and the heritability value by mid parent-offspring relationships.

## LITERATURE REVIEW

### Heritability

Heritability has been defined as the degree of transmittability from parent to progenies. In a broad sense it is expressed as a ratio of genetic variance to phenotypic variance. In a narrow sense, it is the ratio of additive genetic variance to phenotypic variance. The greater the environmental influence, in relation to genetic influence, the more difficult it is to expect improvement from selection. On the other hand, if the environmental variance is small in relation to genetic variance for those characteristics of interest, selection will be effective (Briggs and Knowles, 1967).

Lush (1940) and Kneebone (1958) indicated that heritability estimates aid the breeder in planning efficient breeding programs. Heritability estimates have been used extensively by many authors in the past three decades. These estimates fall into three main categories (Werner, 1952):

1. Variance components from the analysis of variance
2. Parent-offspring regression for narrow sense heritability estimates
3. Approximation of environmental variance from a genetically uniform population



### Diallel Analysis

Griffing (1956) proposed four methods for the analysis of diallel crosses. The most commonly used method, assuming no genotypic reciprocal effects employs one set of  $P_1$ 's or  $\frac{P(P-1)}{2}$  combinations; where P is equal to the number of parental clones involved in the diallel.

Dickinson et al. (1956) proposed a generalized method of analysis for diallel crosses where either homozygous or heterozygous parents could be used.

Al Rawi and Kohel (1969) in diallel crosses involving nine parents in cotton (Gossypium hirsutum) found significant additive and dominance genetic variance for yield and earliness. Matzinger et al. (1971) used eight cultivars of burley tobacco (Nicotina tabacum) in a diallel cross to study yield, total alkaloids, number of leaves, leaf length, leaf width, plant height and plant lodging. There were significant general combining ability effects for all characteristics and significant specific combining ability effects for all except yield.

Yap and Harvey (1971), using all possible crosses (reciprocals included) among four commercial barley cultivars (Hordeum vulgare), observed significant general combining ability for grain yield, kernel weight, kernel heads, head/subplot, heading date, plant height and also significant specific combining ability in most traits except kernel

weight and heads/subplot. The major portion of the genetic variance for the traits measured was due, however, to variation in general combining ability. This suggested that additive gene action was the main contributor to genetic difference for these plant characteristics. Muehlbauer et al. (1971) in a three parent diallel cross in oats (Avena sativa), reciprocals included, found significant specific combining ability effects for plant height and tiller number but non significance general combining ability effects. This represented a case where non additive genetic variance was of more importance.

Rutger (1971) in a seven parent diallel cross with corn (Zea mays) observed significant general and specific combining effects for ear leaf characteristics and grain yield. In sweet corn, Rosenbrook (1971) in an eight inbred line diallel, found significant general combining ability but non significant specific combining ability of reducing sugar and water soluble polysaccharide content in the kernels, indicating a highly additive form of gene action influencing the accumulation of sucrose and water soluble polysaccharides.

Frakes et al. (1961) used the diallel approach to show that natural height and longest stem measurement in alfalfa (Medicago sativa) responded to the effects of general combining ability whereas natural plant width and number of stems per plant were low in their response to general combining ability. These combining ability estimates were related to gene action estimates for the plant

characteristics measured.

The diallel analysis outlined by Griffing (1956) has been utilized for genetic studies in tall fescue. Caceres (1963) found significant general combining ability for maturity and selfed seed yield in tall fescue. Echeverri (1964) found significant general combining ability for height, maturity, culms per plant, open pollinated seed yield, selfed seed yield and forage yield. Frakes and Matheson (1973) found general combining ability was of more importance than specific combining ability for forage yield in tall fescue for several harvesting dates. However, the ratio of the mean square for general to specific combining ability varied from 25.6:1 to 2.9:1. The higher this ratio, the greater the contribution of additive gene action.

#### Parent-offspring Regression

Heritability estimates in the narrow sense may be of greater value than the broad sense estimates because they provide information about the additive gene action (Lush, 1940). Fisher (1918) proposed the use of regression coefficients between parents and offspring for narrow sense heritability estimates. Later, Lush (1948), Falconer (1960) and Mather (1965) extended the parent-offspring regression concept for estimating narrow sense heritability. They noted that in self-pollinated crops, the narrow sense heritability estimates,  $h^2 = b$ . In cross pollinated crops,  $h^2 = 2b$ , if offspring are regressed on maternal parent.

Frey and Horner (1957) proposed a modified method of the

parent-progeny regression for calculating heritability percentage. With this procedure, the original data of both dependent progeny and independent parent were coded in terms of their standard deviation units. This means that, the deviation of the value for each variable from its respective mean is expressed in terms of the standard deviation. The procedure was referred to as the "standard unit method" and identified as  $b'$  in contrast to the conventional regression method which was designated  $b$ . According to Frey (1957), the standard unit method for calculating heritability has two advantages over the conventional one. First, the ceiling of the heritability value is 100 percent. Second, the standard unit method tends to be better or equal in accuracy when compared to the conventional methods of predicting actual gain by their offspring.

Frey and Honner (1955) regressed  $F_5$  generations on  $F_4$  generations in barley and found low heritability estimates. These were believed to under-estimate the true heritability values.

Bartley and Weber (1952) in an effort to estimate narrow sense heritability of various soybean (Glycine max) characteristics, used  $F_1$ ,  $F_2$  and  $F_3$  and regressed the later generations on the earlier generations. Low heritability values were obtained for seed yield (10 to 44 percent) but higher heritability values were observed for plant height (49 to 63 percent). Johnson and Elbanna (1955) regressed  $S_1$  progeny on  $S_0$  parent plants in sweet clover (Melilotus officinalis)

and found high heritability value for growth habit.

Nielson and Kalton (1959) regressed  $S_1$  topcross progeny to  $S_0$  parents in bromegrass (Bromus inermis Leyss.) and found regression coefficients of 0.32, 0.38, 0.83 and 0.67 for seed yield, panicle number, fertility index and seed weight, respectively. By the regression of polycross progeny on maternal parents, Christie and Kalton (1960) found regression coefficients for seed weight, seed yield, bloom date, fertility index were 0.39, 0.39, 0.78 and 1.19, respectively.

In tall fescue, Thomas (1967) used several methods of parent-progeny regression to study the narrow sense heritability estimates for several characteristics. He suggested the term of "average heritability estimation" which he calculated from five methods of parent-progeny regression and the mean square estimates from the diallel analysis. The "average heritability estimation" for tiller number, seed number, seed weight and seed yield were 0.187, 0.371, 0.506, 0.193 for early maturing clones and 0.567, 0.417, 0.622 and 0.374 for intermediate maturing clones. The data suggested variation for the given traits among clones with different dates of maturity.

### Heterosis

Heterosis is a phenomenon in which the performance of the offspring differs from the mid parent. Heterosis is due primarily to dominance and epistatic effects which are more evident in

generation where heterozygosity is prevalent. A heterotic response is usually observed when the cross is from genetically diverse parent plants.

Meir (1973) made interspecific crosses between Crambe abyssinica and Crambe hispanica which differ in plant height, amount of pubescence and maturity and observed the mean of the  $F_1$  generation to exceed the high parent in yield, test weight, and oil content.

MacIlrath (1968) crossed common wheat (Triticum aestivum) cultivars of diverse origin and observed  $F_1$  yields to range from 45 to 141 percent greater than the better parent. Widner et al. (1973) established a diallel in durum wheat (Triticum durum) of ten parents representing a broad range of genetic diversity, and 17 hybrids displayed significant heterosis for grain yield. Some of the other hybrids in this diallel showed negative heterosis.

Moutray and Frakes (1973) examined the effects of genetic diversity on heterosis in tall fescue. The single cross progenies from crosses involving nine parental clones of diverse morphology anthesis date and origin exhibited heterosis for plant height, anthesis date, panicle number and fall vigor rating. However the single cross progeny were inferior to their parents in seed yield.

### Association among Certain Characteristics and Seed Yield

Forage yield and seed yield are complex characteristics resulting from the interaction of many variables. Selection for yield alone may not be successful, unless the breeder is aware of the role played by these associated variables.

Several agronomic traits which are associated with seed or forage yield have been reported in the literature.

Petr and Frey (1966) reported that oat grain yield was positively correlated with plant height, panicle length, number of spikelets/panicle and number of panicles per plant with correlation coefficient values of 0.66, 0.54, 0.59 and 0.71, respectively. Stuber (1966) determined the genetic correlation coefficients between yield and number of tillers in corn was similar to the same statistic for yield and plant height ( $r = 0.49$ ). Johnson et al. (1966) observed a highly significant correlation coefficient for plant height and grain yield in wheat. Yap (1971) showed that the number of head/subplot and kernel weight of barley were positively associated with grain yield.

Frakes, Davis and Patterson (1961) using the path-coefficient analysis found natural plant width of spaced plants had a direct effect on yield in alfalfa while stem number was indirect in its effect on forage yield. Busbice (1966) reported highly significant correlations between seed yield and profuse flowering and vegetative vigor in

alfalfa. Bray (1960) studied the variation between yield and creeping rootedness in alfalfa and found highly positive genetic correlations between creeping rootedness and yield at all times of the year.

Albrechtsen (1966) used the path-coefficient analysis to calculate the coefficient of determination ( $R^2$ ) for seed yield of birdsfoot trefoil (Lotus corniculatus) in relation to number of umbels setting seed, number of pods/umbel, seed size, and number of seeds/pod. The  $R^2$  values were 89 and 96 percent, respectively, for the phenotypic and genotypic determinations.

McDonald et al. (1952) reported significant associations for vigor, spread, panicle scores and height with seed yield of bromegrass. However the spreading habit was the most important character for seed yield. Caceres (1963) found a highly significant correlation coefficient between forage yield and plant height and also for forage yield and plant width in tall fescue. Thomas (1967) observed a relationship for tiller number and seed/head with yield but low correlations between weight/seed and yield in tall fescue.



## MATERIALS AND METHODS

### Greenhouse Study

#### Plant Material

Seven genotypes of tall fescue were identified from two groups of plants with diverse morphological characteristics. Three of the seven clones were from the tall and early anthesis date cultivar, "Fawn." The remaining four clones were from the short and late anthesis date line, "Fortune." (Table 1).

#### Greenhouse Establishment

The individual clones were vegetatively propagated on July 8, 1971 and transplanted to 10.79 x 10.79 cm<sup>2</sup> plastic pots with ten propagules used in each pot. This was done to obtain sufficient panicles for crossing purposes. The plants were grown in the greenhouse for three months and then were taken to a cold frame on October 9, exposing them to outside environmental conditions. On December 29, all plants were placed in a growth chamber, with a 3.33 °C temperature and eight hours per day of artificial light for seven days. After the exposure, the temperature of the growth chamber was changed to 15.56 °C and the photoperiod to 18 hours of light. On January 15, 1972 the plants were returned to the greenhouse where the temperature was 21.11 °C, and an 18 hour

Table 1. Identification of plant material, establishment date of parents, crossing date, and date of greenhouse and field establishment.

Groups	Identification	Date parents established	Crossing	Date entries established in greenhouse for field study	Field establishment
Fawn genotype					
01	01	7/8/71	-	6/13/72	9/15/72
02	02	"	-	"	"
03	03	"	-	"	"
Fortune genotype					
04	04	"	-	"	"
05	05	"	-	"	"
06	06	"	-	"	"
07	07	"	-	"	"
Fawn x Fawn crosses					
01 x 02	08	-	2/4-18/72	"	"
01 x 03	09	-	"	"	"
02 x 03	12	-	"	"	"
Fawn x Fortune crosses					
01 x 05	10	-	2/15-26/72	"	"
02 x 05	13	-	"	"	"
02 x 07	14	-	"	"	"
03 x 04	15	-	"	"	"
03 x 05	16	-	"	"	"
03 x 07	17	-	"	"	"
Fortune x Fortune crosses					
04 x 05	18	-	2/15-26/72	6/13/72	9/15/72
04 x 06	19	-	"	"	"
04 x 07	20	-	"	"	"
05 x 06	21	-	"	"	"
05 x 07	22	-	"	"	"
06 x 07	23	-	"	"	"

photoperiod was established. Since there were differences among clones for panicle emergence, the clones with early panicle emergence were placed outside the greenhouse so the cooler temperatures would delay floral development. When the panicles of later genotypes emerged, the early genotypes were returned to the greenhouse. This was done to facilitate hybridization by mutual pollination. All parental clones were crossed in every combination by bagging panicles of two plants together just prior to anthesis. Parchment bags measuring  $7.5 \times 12.5 \times 42.5 \text{ cm}^3$  were used to enclose the panicles. The bagging procedure was completed on February 26. All plants were harvested on the 30th and 31st of March. The seeds from each cross were carefully threshed and cleaned by hand.

The single cross seeds were placed in  $11.43 \times 11.43 \text{ cm}^2$  petri dishes with 50 seeds each. The petri dishes were filled with perlite with 0.2 percent potassium nitrate added as the moisture medium, and held for 6 days at  $3.33^\circ \text{C}$ . They were then placed in a germinator with alternating photoperiod-temperature combination of 16 hours of dark at  $15^\circ \text{C}$  and eight hours of light at  $25^\circ \text{C}$ . The germinated seedlings were transplanted into aluminum trays filled with perlite. Each seedling within the tray was in a  $6 \times 6 \times 6.3 \text{ cm}^3$  plastic block.

Fifteen of the possible 21 single crosses produced sufficient seedlings for use in this test. On June 13, 1972 the 15 single crosses were arranged in a randomized block design with three replications

and eight plants per entry per replication.

At the same time, the parental clones were propagated vegetatively and transplanted to a 10.79 x 10.79 cm<sup>2</sup> plastic pot with one propagule each. They were maintained separately from the group of 15 single crosses. These were used later in a field establishment.

#### Nutrient Supply

The single cross progenies and the parental clones were supplied with one half strength of modified Hougland's solution (Table 2) two times a week until August 3, 1972 after which they were supplied with the same nutrient concentration every two weeks until they were transplanted to the field.

#### Measurements

On July 7, 1972 the single cross progenies were lifted from the 6 x 6 x 6.3 cm<sup>3</sup> plastic blocks and the roots carefully washed with tap water. The shoots were clipped to five cm height and the forage was dried at 48.89° C for two days. The dry matter weights were determined on a torsion balance to the nearest milligram. The following measurements were also recorded.

1. Shoot length, measured from the base of the culm to the longest leaf (cm).
2. Root length, measured from the base of the culm to the longest

Table 2. Modified Hougland's nutrient solution (Leonard and Torrey, 1956).

Macronutrient	mg/l
$\text{Ca}(\text{NO}_3)_2 \cdot 4\text{H}_2\text{O}$	1180
$\text{KNO}_3$ (anhydrous)	505
$\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$	495
$\text{KH}_2\text{PO}_4$ (monobasic)	135.5
Fe EDTA (iron salt of ethylene diamine tetra acetic acid)	50
Micronutrient	
$\text{H}_3\text{BO}_3$	2.86
$\text{MnCl}_2 \cdot 4\text{H}_2\text{O}$	1.81
$\text{ZnCl}_2$	0.11
$\text{CuCl}_2 \cdot 2\text{H}_2\text{O}$	0.05
$(\text{NH}_4)\text{MoO}_4 \cdot 4\text{H}_2\text{O}$	0.028

- root branch (cm).
3. Shoot-root ratio (length measurements)
  4. Tiller number
  5. Forage dry matter (g)
  6. Plant spread (cm).

Data were recorded on the first five variables listed on July 7. On August 4 and September 11 data were recorded for shoot length (cm), tiller number, forage dry weight (g) and plant spread (cm).

#### Statistical Analysis

The eight observations per entry in each replication were averaged for the measured characteristics. The analysis of variance was used to test differences among groups, among parent genotypes and among the single crosses. The replication x treatment interaction was used as the error term in these analyses.

Of the seven parents involved in the crossing plan, a diallel was available from only four of the parents. This diallel analysis for a four parent diallel was used to examine combining ability effects. The replication x single cross interaction was used as the error term to test for significance of general (GCA) and specific combining ability (SCA).

## Field Study

### Field Establishment

The individual plants from the greenhouse study were transplanted to the Hyslop Agronomy Farms, Corvallis, Oregon on September 15, 1972. The nursery consisted of the seven parents and 15 single crosses. A randomized block design with eight plants per entry in each of three replications was used. The plants were established on 91.44 cm centers. Border plants were placed around the nursery

### Maintenance

During the early stages of transplanted development, the weeds were controlled by tillage between the rows, followed by hoeing around the plants. Once the transplants were well established, periodic hoeing was the only means of weed control used.

Fertilizer (16-20-0) was applied to the nursery at the rate of 89.69 kg/ha in late September 1972 and early April 1973.

### Measurements

Data were collected on the following characteristics:

1. Anthesis date (rating)
2. Panicle numbers

3. Plant height (cm)
4. Plant spread (cm)
5. Panicle length (cm)
6. Number of primary pedicels
7. Best five panicle seed weight (g)
8. Seed yield (g)
9. 100 seed weight (g)

The plants in the nursery were rated individually for anthesis on May 30, 1973. The rating values ranged from one to six where one represented the most advanced stage of anthesis and six represented no visible anthesis. Panicle number was also determined on the same day as the anthesis values.

Plant height was measured from the base of the culm to the tip of the inflorescence for each plant on June 13. Plant spread was the diameter of the plant measured at the culm base on June 14.

Individual plants were harvested separately for seed yield with a hand sickel during June 22 to July 8. Two bags were used for each plant. The first bag held the best five panicles and the remaining panicles were placed in a second bag. The panicle length and the number of primary pedicels were measured individually on each of the five panicles in the first bag. The length of panicle was measured from the lowest primary pedicel to the tip of the panicle. A primary pedicel is one that arises directly from a main rachis node.



The panicles were threshed in a head thresher, then further separated by the use of a rub-board to insure maximum separation of the filled florets. The seed then was cleaned with a clipper cleaner and a South Dakota blower. The cleaned seeds from the best five panicles was weighted to one hundredth of a gram on a Toledo scale. The seed from the second bag was weighed to one tenth of a gram on a Metler scale. Total seed weight was, then, calculated by adding the two measurements.

One hundred seeds from each plant were drawn at random and weighed to one ten thousandth of a gram on a chainomatic balance. In some samples 100 seeds were not available. If sufficient seed was not available, all weights were adjusted to a one hundred weight equivalent.

### Statistical Analysis

The analysis of variance was used to test for differences among groups, among the parent genotypes, and among the single crosses. The sampling error was used to test for significance of the various groups. The simple correlation coefficients between each of the nine variables were determined in all possible combinations for all entries. The multiple coefficient of determination and regression equation of seed yield as associated with best five panicles seed weight, 100 seed weight, panicle numbers, panicle length, primary pedicel

was computed.

A four-clone diallel analysis was used and the sampling error served to test for significance of general and specific combining ability.

To examine heterosis, the mid parent mean values were computed from the parental clone data and used to represent the treatments in the replication. Thus, the treatments were composed of seven parental clones, 15 single cross and 15 corresponding mid-parent values. The single degree of freedom approach was used to test for significant heterosis of specific crosses. In the heterosis phase of this study, the replication x treatment interaction was used as the error term.

## EXPERIMENTAL RESULTS

### Greenhouse Study

Treatment means for all characteristics measured in the greenhouse study are listed in Tables 6, 7 and 8.

#### Growth and Regrowth Potential

Shoot-root Ratio A significant mean square value for shoot-root ratio were observed among the 15 single crosses at the one percent level of probability. This significance was due to significant variation among the Fawn x Fortune crosses and significant differences among the hybrids as groups (Table 3). The means of shoot-root ratio for Fawn x Fawn, Fawn x Fortune and Fortune x Fortune crosses, considered as groups were 2.99 2.86 and 2.46 cm, respectively (Table 6). This showed that Fawn x Fawn crosses gave the highest shoot-root ratio while Fortune x Fortune crosses exhibited the smaller ratio. Neither of these groups, however, showed significant differences among crosses within groups. There were no differences in shoot-root ratio among the crosses involved in the diallel arrangement of treatments (Table 3).

Shoot Growth. The 15 single crosses were measured for shoot length on July 7, August 4 and September 11, 1972 and were significant on each date at the five or one percent probability level (Tables 3,

Table 3. Mean squares and levels of significances for shoot/root ratio, root length, shoot length, tiller numbers and dry weight for single crosses of tall fescue on the first harvest date, July 7, 1972.

Source of variation	d. f.	shoot/root ratio	Shoot length	Root length	Tiller numbers	Dry weight
Single crosses	14	0.47**	10.43**	1.18 <sup>ns</sup>	1.49*	0.0155**
Fawn x Fawn	2	0.21 <sup>ns</sup>	8.19 <sup>ns</sup>	-	2.83*	0.007 <sup>ns</sup>
Fawn x Fortune	5	0.62**	101.24**	-	1.44 <sup>ns</sup>	0.012**
Fortune x Fortune	5	0.16 <sup>ns</sup>	23.91 <sup>ns</sup>	-	0.61 <sup>ns</sup>	0.005 <sup>ns</sup>
Among groups	2	1.12**	241.95**	-	2.47*	0.06**
R x SC	28	0.11	12.89	1.27	0.59	0.003
<u>Diallel Analysis</u>						
Diallel crosses	5	0.4423 <sup>ns</sup>	88.23**	-	2.12 <sup>ns</sup>	0.016*
GCA	3	-	146.82**	-	-	0.025**
SCA	2	-	0.33 <sup>ns</sup>	-	-	0.0032 <sup>ns</sup>
R x DC	10	0.169	14.53	-	0.98	0.0029

\*, \*\* Significant at the five and one percent level, respectively

GCA General combining ability

SCA Specific combining ability

SC Single crosses

DC Diallel crosses

- Not calculated because of non significant differences among entries

<sup>ns</sup> Non significant differences

Table 4. Mean squares and levels of significances for shoot length, plant width, tiller numbers and dry weight for single crosses of tall fescue on the second harvest date, August 4, 1972.

Sources of variation	df	Shoot length	Plant spread	Tiller numbers	Dry weight
Single crosses	14	47.21 <sup>**</sup>	0.25 <sup>ns</sup>	13.35 <sup>**</sup>	0.0715 <sup>**</sup>
Fawn x Fawn	2	13.24 <sup>ns</sup>	-	16.215 <sup>**</sup>	0.025 <sup>*</sup>
Fawn x Fortune	5	77.04 <sup>**</sup>	-	22.14 <sup>**</sup>	0.018 <sup>*</sup>
Fortune x Fortune	5	46.02 <sup>*</sup>	-	6.53 <sup>ns</sup>	0.028 <sup>**</sup>
Among groups	2	9.59 <sup>ns</sup>	-	5.57 <sup>ns</sup>	0.36 <sup>**</sup>
R x SC	28	13.21	0.39	2.62	0.0059
<u>Diallel Analysis</u>					
Diallel crosses	5	42.83 <sup>ns</sup>	-	17.59 <sup>*</sup>	0.032 <sup>ns</sup>
GCA	3	-	-	27.39 <sup>**</sup>	-
SCA	2	-	-	2.89 <sup>ns</sup>	-
R x DC	10	17.59	-	3.74	0.019

\*,\*\* Significant at the five and one percent level, respectively

GCA General combining ability

SCA Specific combining ability

SC Single crosses

DC Diallel crosses

- Not calculated because of non significant differences among entries

ns Non significant differences

Table 5. Mean squares and levels of significances for shoot length, plant spread, tiller numbers, and dry weight for single crosses of tall fescue on the third harvest date, September 11, 1972.

Source of variation	d. f.	Shoot length	Plant spread	Tiller numbers	Dry weight
		*	**	**	
Single crosses	14	123.73	0.5793	21.01	0.0133
Fawn x Fawn	2	52.23	0.15	20.73	-
Fawn x Fortune	5	22.24	0.71	34.09	-
Fortune x Fortune	5	154.07	0.502	10.55	-
Among groups	2	373.07	0.89	14.77	-
R x SC	28	42.79	0.1925	4.29	0.0081
<u>Diallel Analysis</u>					
Diallel crosses	5	162.72	0.606	25.33	-
GCA	3	267.49	0.4332	40.67	-
SCA	2	5.58	0.865	2.32	-
R x DC	10	38.12	0.075	5.97	-

\*, \*\* Significant at the five and one percent level, respectively

GCA General combining ability

SCA Specific combining ability

SC Single crosses

DC Diallel crosses

- Not calculated because of non significant differences among entries

ns Non significant differences

Table 6. Means, standard errors of the mean ( $\overline{SX}$ ), and coefficients of variation (CV) for shoot/root ratio, shoot length (cm), root length (cm), tiller numbers and dry matter per pot (g) for single crosses of tall fescue on July 7, 1972.

Entries	Identification	Shoot/root ratio	Shoot length (cm)	Root length (cm)	Tiller number	Dry weight (g/pot)
08	Fawn x Fawn	2.92	35.18	11.20	3.88	0.224
09	"	3.28	38.24	11.98	4.58	0.288
12	"	2.77	35.64	12.99	5.80	0.322
Mean Fawn x Fawn group		2.99	36.35	12.06	4.75	0.278
10	Fawn x Fortune	3.51	40.18	11.62	4.50	0.318
13	"	2.76	28.28	12.56	5.33	0.208
14	"	2.16	24.19	11.56	5.67	0.133
15	"	2.77	35.70	13.20	4.84	0.237
16	"	3.15	36.11	12.01	3.88	0.211
17	"	2.79	32.26	11.89	4.13	0.173
Mean Fawn x Fortune group		2.86	32.79	12.14	4.73	0.213
18	Fortune x Fortune	2.53	27.81	11.23	4.17	0.146
19	"	2.41	29.08	12.20	4.67	0.186
20	"	2.50	28.05	11.53	3.63	0.132
21	"	2.85	32.25	11.76	4.09	0.185
22	"	2.21	23.99	11.07	4.34	0.114
23	"	2.25	25.83	11.61	3.46	0.086
Mean Fortune x Fortune group		2.46	27.84	11.57	4.06	0.142
Grand mean		2.72	31.52	11.89	4.46	0.198
$\overline{SX}$		0.19	2.07	0.65	0.44	0.032
CV		12.79'/.	11.39'/.	9.48'/. <sup>ns</sup>	17.22'/. <sup>ns</sup>	27.66'/. <sup>ns</sup>
LSD .05		0.55	6.00	1.88 <sup>ns</sup>	1.28	0.092
LSD .01		0.75	8.10	2.54 <sup>ns</sup>	1.73	0.124

ns = non significant value

Table 7. Means, standard errors of the mean ( $\bar{S}\bar{X}$ ) and coefficients of variation (CV) for shoot length, plant width, tiller numbers and dry weight per pot for single crosses of tall fescue on August 4, 1972.

Entries	Identification	Shoot length (cm)	Plant spread (cm)	Tiller numbers	Dry weight (g/pot)
08	Fawn x Fawn	40.68	2.40	10.21	0.994
09	"	44.49	2.67	9.25	1.058
12	"	41.05	2.05	13.67	1.178
Mean Fawn x Fawn group		42.07	2.37	11.04	1.077
10	Fawn x Fortune	43.10	2.27	10.00	1.071
13	"	37.15	2.95	14.25	1.057
14	"	34.01	2.51	17.00	1.091
15	"	47.57	2.50	11.84	1.155
16	"	45.08	2.46	10.42	0.974
17	"	40.18	3.11	10.88	0.941
Mean Fawn x Fortune group		41.18	2.63	12.40	1.048
18	Fortune x Fortune	39.73	2.77	11.38	0.825
19	"	41.41	2.84	13.29	0.841
20	"	44.98	2.82	10.09	0.813
21	"	43.58	2.62	11.04	0.806
22	"	38.09	2.66	13.96	0.901
23	"	34.17	3.04	11.25	0.617
Mean Fortune x Fortune group		40.33	2.79	11.84	0.801
Grand mean		41.02	2.64	11.90	0.96
$\bar{S}\bar{X}$		2.10	0.36	0.93	0.044
CV		8.86%.	23.66%.	13.60%.	8.04%.
LSD <sub>.05</sub>		6.08	1.04	2.71	0.128
LSD <sub>.01</sub>		8.20	1.41	3.65	0.173



Table 8. Means, standard errors of the mean ( $\bar{S}\bar{X}$ ) and coefficients of variation (CV) for shoot length, plant width, tiller numbers and dry weight per pot for single crosses of tall fescue on September 7, 1972.

Entries	Identification	Shoot length (cm)	Plant spread (cm)	Tiller numbers	Dry weight (g/pot)
08	Fawn x Fawn	34.82	3.02	10.87	0.713
09	"	38.08	3.33	10.07	0.778
12	"	29.80	2.90	14.97	0.869
Mean Fawn x Fawn group		34.23	3.08	11.97	0.787
10	Fawn x Fortune	42.07	2.80	10.73	0.812
13	"	38.87	3.97	16.57	0.879
14	"	36.60	3.43	19.73	0.843
15	"	44.13	3.13	13.40	0.792
16	"	41.67	3.23	11.70	0.800
17	"	42.33	4.03	12.90	0.795
Mean Fawn x Fortune group		40.95	3.43	14.17	0.820
18	Fortune x Fortune	45.07	3.03	12.43	0.721
19	"	46.17	3.50	13.83	0.716
20	"	54.00	3.60	11.27	0.821
21	"	39.41	4.28	13.20	0.763
22	"	52.10	3.81	16.80	0.882
23	"	35.33	3.54	14.17	0.655
Mean Fortune x Fortune group		45.35	3.63	13.62	0.760
Grand mean		41.36	3.44	13.51	0.789
$\bar{S}\bar{X}$		3.78	0.25	1.20	0.052
CV		15.82%	12.75%	15.33%	11.41%
LSD <sub>.05</sub>		10.94	0.73	3.46	0.151
LSD <sub>.01</sub>		14.76	0.99	4.67	0.203

4, 5). On the first harvesting date, significant differences in shoot length among Fawn x Fortune crosses and among hybrids as groups were observed (Table 3). Fawn x Fawn crosses showed the highest mean performance (36.35 cm) followed by Fawn x Fortune crosses (32.79 cm) and Fortune x Fortune crosses (27.84 cm). Of the Fawn x Fortune crosses, treatment 10 showed the highest value (40.18 cm) while treatment 14 showed the lowest (24.19 cm) (Table 6).

Significant differences in shoot length among Fawn x Fortune and Fortune x Fortune crosses were observed on the second date of measurement (Table 4). Fawn x Fawn crosses again showed the highest mean performance (42.07 cm), followed by Fawn x Fortune (41.18 cm) and Fortune x Fortune (40.33 cm) (Table 7). However, the differences among the groups of hybrids were not significant. Of the Fawn x Fortune crosses, treatment 15 showed the highest mean value (47.57 cm) and treatment 14 showed the lowest (34.01 cm). Of the Fortune x Fortune crosses, the highest mean performance was treatment 20 (44.98 cm), the least was treatment 23 (34.17 cm) (Table 7).

On the third measurement date, significant differences in shoot length among Fortune x Fortune crosses and among hybrids as groups were observed (Table 5). The mean performance in order from high to low was Fortune x Fortune crosses (45.35 cm), Fawn x Fortune (40.95 cm) and Fawn x Fawn (34.23 cm) (Table 8).

The GCA mean squares were significant at the one percent level of probability in July and September, but no significant SCA on either of the dates was observed. The ratio of GCA to SCA was 440:1 in July and 50:1 in September. In August, there was no significant difference among the single crosses involved in the diallel analysis (Tables 3, 4, 5).

Root Length. No significant differences in root length among the 15 single crosses were observed (Table 3).

Tiller Numbers. Significant differences in numbers of tillers per plant were observed on all three dates. The significant differences in tiller number among the Fawn x Fawn crosses were evident on all three dates measurement. This was not true for the other groups of crosses or hybrids as groups. The groups were significantly different from each other in July and September (Tables 3, 4, 5). In July, the Fawn x Fawn crosses showed the highest tiller number (4.75) compared with Fawn x Fortune (4.73) and Fortune x Fortune crosses (4.06) (Table 6). These differences were significant. In August the Fawn x Fortune crosses showed the highest tiller number (12.40) followed by the Fortune x Fortune crosses (11.84) and the Fawn x Fawn crosses (11.04). (Table 3). These differences were not significant. In September, Fawn x Fortune crosses showed the highest tiller number (19.17) followed by Fawn x Fortune crosses (13.62) and Fawn x Fawn crosses (11.97) (Table 8). These differences

were significant because of the relatively low number in the Fawn x Fawn crosses. There were significant differences among the Fawn x Fortune crosses, and the Fawn x Fawn crosses in August and September. The crosses Fortune x Fortune group did not differ from each other on any of the three dates measured (Tables 3, 4, 5).

Significant differences due to GCA effects were observed in August and September with no significant SCA effect on either date. The ratio of GCA:SCA mean square was 19:2 in August and 35:2 in September (Tables 4, 5).

Plant Spread. Differences in mean performance for plant spread among the crosses were too small to be detectable by variance analysis in August. Treatments differed, however, at the one percent level in September. Significant differences among crosses within the Fawn x Fortune, Fortune x Fortune group were observed in September (Table 5). Fortune x Fortune crosses showed the most spreading (3.63 cm) followed by Fawn x Fortune (3.43 cm) and the Fawn x Fawn crosses (3.08 cm) (Table 8).

GCA and SCA were significant in September (Table 5). The ratio of GCA to SCA was 0.5:1, indicating the importance of both additive and non additive gene action in the expression of plant spread (Table 5).

Dry Weight. The 15 single crosses were significant for dry weight in July and August but not in September. The differences

appearing in July were among the Fawn x Fortune crosses and among the hybrids as groups. There were significant differences among means at the five percent level for both Fawn x Fawn and Fawn x Fortune combinations and at the one percent level for both Fortune x Fortune combinations and crosses as groups for the August measurement (Tables 3, 4, 5).

In July the mean dry weight per pot in order from high to low was Fawn x Fawn crosses (0.278 g), Fawn x Fortune crosses (0.213 g) and Fortune x Fortune crosses (0.142 g) (Table 6). In August, the mean dry weight in order from high to low was Fawn x Fawn crosses (1.077 g), Fawn x Fortune crosses (1.048 g) and Fortune x Fortune crosses (0.801 g) (Table 7). In September the Fawn x Fortune crosses showed the highest mean dry weight (0.820 g) followed by Fawn x Fawn crosses (0.787 g) and Fortune x Fortune crosses (0.760 g) (Table 8). However, the differences among groups in September were not significant.

GCA effects were significant at the one percent level in July but not significant on the other two dates. The SCA effects were very small or negligible in all crosses (Tables 3, 4, 5).

#### Field Study

Treatment means for plant height, plant spread and anthesis date are in Table 10, panicle number, panicle length and number of

primary pedicles are in Table 13, and five panicle seed weight, seed yield, and 100 seed weight are in Table 16.

### Combining Ability

Plant Height. Significant differences in plant height were observed among groups and among crosses at the one percent probability level. The largest mean square for plant height was among the parent genotypes, the smallest was among the Fawn x Fortune crosses (Table 9). These suggest the mean differences among hybrids as groups, and among individuals within each group did not occur by chance but by the virtue of treatments themselves. The mean values for plant height of the crosses as groups in order from high to low were Fawn x Fawn crosses (71.33 cm), Fawn x Fortune crosses (69.72 cm), parent group (62.37 cm) and Fortune x Fortune crosses (61.43 cm) (Table 10).

The diallel analysis revealed a significant general combining ability contribution to these differences. Specific combining ability was negligible (Table 11). The ratio of GCA:SCA was 19:1, thus genes acting additively were the main contributors to the genetic differences observed for this trait.

Plant Spread. Treatment differences in plant spread were statistically significant among parents, Fawn x Fortune crosses, Fortune x Fortune crosses and among the groups. The highest

Table 9. Observed mean squares and levels of significance for plant height, plant spread and anthesis date in tall fescue, 1973.

Source of variation	d. f.	Plant height	Plant spread	Anthesis date
Replication	2	4,167.45**	51.47 <sup>ns</sup>	0.24 <sup>ns</sup>
Entries	21	2,024.70**	204.29**	86.78**
Among groups	3	2,998.65**	1,026.45**	368.81**
Within groups	18	1,862.37**	67.26**	39.78**
Parents	6	4,210.67**	74.51 <sup>ns</sup>	89.86**
Fawn x Fawn group	2	930.69*	1.87**	5.56**
Fawn x Fortune group	5	317.41**	95.13*	29.91**
Fortune x Fortune group	5	962.08**	56.85**	3.25**
Rep x Entries	42	345.13	36.37	2.72
Error	462	107.63	21.63	0.73

Table 10. Means, standard errors of the mean ( $\bar{S}\bar{X}$ ), coefficients of variation (CV) and least significant differences (LSD) for plant height, plant width and anthesis date in tall fescue, 1973.

Entries	Identification	Plant height (cm)	Plant spread (cm)	Anthesis date (rating)
01	Fawn	86.5	11.8	1
02	"	69.2	10.7	2
03	"	68.6	11.5	1
04	Fortune	48.5	11.3	5
05	"	51.9	14.8	5
06	"	56.5	12.8	5
07	"	55.4	15.1	5
Mean parent group		62.37	12.57	3.43
08	Fawn x Fawn	67.5	11.5	1
09	"	68.0	11.8	1
12	"	78.5	11.3	2
Mean Fawn x Fawn group		71.33	11.53	1.33
10	Fawn x Fortune	65.1	11.7	1
13	"	65.8	13.2	4
14	"	71.7	14.8	3
15	"	69.4	15.2	1
16	"	72.2	17.5	2
17	"	74.1	15.4	2
Mean Fawn x Fortune group		69.72	14.63	2.17
18	Fortune x Fortune	72.9	17.5	5
19	"	55.1	17.6	6
20	"	56.2	17.8	5
21	"	62.5	21.0	6
22	"	60.3	16.5	5
23	"	61.6	18.0	5
Mean Fortune x Fortune group		61.43	18.07	5.33
Grand mean		65.34	14.49	3.32
$\bar{S}\bar{X}$		2.12	0.95	0.17
CV		15.88	32.10	25.78
LSD .05		5.87	2.63	0.48
LSD .01		7.71	3.46	0.64



Table 11. Mean squares for replications, single crosses, general combining ability (GCA) and specific combining ability (SCA) for plant height, plant spread and anthesis date in tall fescue, 1973.

Source of variation	d. f.	Plant height	Plant spread	Anthesis date
Replication	2	3776.30 <sup>**</sup>	62.75 <sup>ns</sup>	2.53 <sup>ns</sup>
Single crosses	5	993.25 <sup>**</sup>	121.88 <sup>**</sup>	53.66 <sup>**</sup>
GCA	3	1599.34 <sup>**</sup>	156.33 <sup>**</sup>	74.08 <sup>**</sup>
SCA	2	84.11 <sup>ns</sup>	70.22 <sup>*</sup>	23.03 <sup>**</sup>
R x SC	10	206.89 <sup>ns</sup>	84.01 <sup>**</sup>	4.93 <sup>**</sup>
Error	126	140.46	22.11	1.52
GCA:SCA		19:1	2.2:1	3.2:1

\*, \*\* Significant difference at .05 and .01 probability level, respectively

ns Non significant difference

significant variation was observed among the Fawn x Fortune crosses. The least significant variation was observed among the Fawn x Fawn crosses (Table 9). The mean value in order from high to low were Fortune x Fortune crosses (18.07 cm) Fawn x Fortune crosses (14.63 cm), parent group (12.57 cm) and Fawn x Fawn crosses (11.53 cm) (Table 10). This suggests that the fortune germplasm contributes to the spreading habit of growth more than the Fawn parent material.

The genetic analysis from the diallel crosses revealed significance in both GCA and SCA (Table 11). The ratio of GCA:SCA is 2.2:1. The low ratio of GCA:SCA suggests both additive and non additive gene action are involved in the expression of this characteristic.

Anthesis Date. Differences for anthesis date were significant among parents and among crosses. The higher mean square value was observed for among parents and among the Fawn x Fortune crosses. The analysis of variance indicated the largest phenotypic variation occurred among hybrids from the Fawn x Fortune crosses (Table 9). The mean value for anthesis date in order from low to high were Fawn x Fawn crosses (1.33), Fawn x Fortune crosses (2.17), parent group (3.43) and Fortune x Fortune crosses (5.33) (Table 10), so the Fortune reaches anthesis later than the Fawn germplasm.

GCA and SCA were significant at the one percent probability level (Table 11). The ratio of GCA:SCA = 3.2:1. The significant

SCA coupled with low ratio of GCA:SCA demonstrated that both types of gene action control the expression of this trait.

Panicle Numbers. Panicle number differences were apparent among the parents, Fawn x Fortune crosses, Fortune x Fortune crosses and among the groups. The relatively high mean square value among Fawn x Fortune crosses resulted from genetic variation generated by crossing two diversified sources of germ plasm (Table 12).

The mean value for panicle number in order from high to low was Fortune x Fortune crosses (27.5), Fawn x Fortune crosses (23.7), Fawn x Fawn crosses (19.3) and parent group (17.57) (Table 13). The Fawn germ plasm is one that produces few panicles than the Fortune material.

Significant GCA was observed at the five percent probability level (Table 14). The ratio of GCA:SCA = 1.4:1. This is a low ratio and because the SCA effects were not significant, it is difficult to make inferences about the relative importance of the contribution of the two types of gene action.

Panicle Length. Significant differences for panicle length were observed among parents, single crosses and among the groups (Table 12). The mean square values in order from high to low were those of Fortune x Fortune crosses, parents, Fawn x Fortune crosses and Fawn x Fawn crosses. This meant that the large differences among the Fortune x Fortune crosses indicated that one could expect

Table 12. Observed mean squares and levels of significance for panicle numbers, panicle length and number of primary pedicels in tall fescue, 1973.

Source of variation	d. f.	Panicle numbers	Panicle length	Number of primary pedicels
		**	**	**
Replication	2	2,002.62	163.61	26.76
		**	**	**
Entries	21	740.72	91.33	71.42
		**	**	**
Among groups	3	2,775.60	197.29	919.71
		**	**	**
Within groups	18	401.61	73.67	69.97
		**	**	**
Parents	6	406.88	69.06	111.72
		ns	**	ns
Fawn x Fawn group	2	248.08	40.88	4.51
		**	**	**
Fawn x Fortune group	5	611.20	51.27	57.04
		*	**	**
Fortune x Fortune group	5	247.20	114.70	58.97
		**	**	*
Rep x Entries	42	266.07	24.07	8.40
Error	462	89.64	7.50	5.34

Table 13. Means, standard errors of the mean ( $\bar{S}\bar{X}$ ), coefficients of variation (CV) and least significant differences (LSD) for panicle numbers, panicle length and number of primary pedicels in tall fescue, 1973.

Entries	Identification	Panicle numbers	Panicle length (cm)	Number of primary pedicels
01	Fawn	14	17.6	16
02	"	15	12.9	13
03	"	19	13.5	14
04	Fortune	19	13.4	15
05	"	20	15.8	19
06	"	24	14.2	14
07	"	12	13.3	16
Mean parent group		17.57	14.39	15.29
08	Fawn x Fawn	18	13.3	14
09	"	17	13.9	15
12	"	23	15.8	15
Mean Fawn x Fawn group		19.3	14.3	14.6
10	Fawn x Fortune	21	13	14
13	"	18	16.5	17
14	"	21	16.2	16
15	"	32	16.9	17
16	"	27	16.9	17
17	"	23	16.2	15
Mean Fawn x Fortune group		23.7	15.95	16.0
18	Fortune x Fortune	32	20.8	20
19	"	28	16.0	16
20	"	24	14.6	16
21	"	27	17.4	16
22	"	24	16.9	16
23	"	30	15.3	16
Mean Fortune x Fortune group		27.5	16.8	16.7
Grand mean		22.18	15.47	15.77
$\bar{S}\bar{X}$		1.93	0.56	0.47
CV		42.68	17.70	14.65
LSD <sub>.05</sub>		5.36	1.55	1.31
LSD <sub>.01</sub>		7.04	2.04	1.72

Table 14. Mean squares for replications, single crosses, general combining ability (GCA) and specific combining ability (SCA) of panicle numbers, panicle length and number of primary pedicels in tall fescue, 1973.

Source of variation	d. f.	Panicle numbers	Panicle length	Number of primary pedicels
Replication	2	320.40	131.68	27.17
Single crosses	5	217.59	4.58	23.57
GCA	3	248.00	7.23	36.03
SCA	2	171.96	0.61	4.88
R x SC	10	294.80	45.41	13.80
Error	126	76.34	10.46	5.69
GCA:SCA		1.4:1	12:1	7.4:1

\*, \*\* Significant difference at .05 and .01 probability level

ns Non significant difference

improvement by selection for this trait (Table 12). Fortune x Fortune crosses exhibited the longest average panicle length (16.8 cm), followed by the Fawn x Fortune crosses (15.95 cm) and the Fawn x Fawn crosses (14.3 cm) (Table 13). It appears that the Fortune material has genes that contribute more to panicle length than the Fawn germ plasm.

Even though large differences among entries were observed, those crosses lending themselves to the diallel analysis showed no significant differences, thus no significant genetic effects. This is peculiar to the particular crosses involved and is not consistent with inferences obtained from the overall analysis (Table 14).

Number of Primary Pedicels. Significant differences for number of primary pedicels were noted among parents, Fawn x Fawn crosses, Fortune x Fortune crosses, Fortune x Fortune crosses and among all groups. Little genetic variation was observed among the Fawn x Fawn crosses. Similar mean squares for Fawn x Fortune and Fortune x Fortune crosses (Table 12) indicated a like magnitude of genetic variation. The mean value for number of primary pedicels in order from high to low were Fortune x Fortune crosses (16.7), Fawn x Fortune crosses (16.0), parent group (15.29) and Fawn x Fawn crosses (14.6) (Table 13).

The combining ability estimate from the diallel analysis,

indicated significant GCA and non significant SCA (Table 14) with the ratio of GCA:SCA = 7.4:1. This large ratio of GCA:SCA coupled with a non significant SCA suggested additive gene action as the main portion of the genetic system governing this trait.

Five Panicles Seed Weight. Significant differences for seed weight occurred among parents and all single cross groups and among the groups. The mean square for the Fawn x Fortune crosses was higher than that of the Fortune x Fortune group (Table 15). The mean values for five panicle seed weight were Fawn x Fawn crosses (1.612 g), parent group (1.056 g), Fortune x Fortune crosses (0.9422 g) and Fawn x Fortune crosses (0.4062 g) (Table 16).

Both GCA and SCA were significant at the one percent probability level (Table 17). The mean square ratio of GCA:SCA was 0.2:1. This suggests that non additive gene action may be of considerable importance in the expression of this characteristic.

Seed Yield. The differences in total seed weight were evident in all groups except the Fortune x Fortune crosses. The significant variation among the Fawn x Fawn crosses indicated the possibility for improvement by selection for the trait (Table 15). The Fawn x Fawn crosses produced the highest seed yield (4.807 g), followed by Fortune x Fortune crosses (2.932 g) and the Fawn x Fortune crosses (1.23 g) (Table 16). The Fawn material resulted in much higher seed yield than the Fortune germ plasm.



Table 15. Observed mean squares and levels of significance for the five panicles seed weight, seed yield per plant, and 100 seed weight in tall fescue, 1973.

Source of variation	df	Five panicles seed weight	Seed yield	100 seed weight
Replication	2	6.92	160.89	0.0076
Entries	21	7.47	66.02	0.0491
Among groups	3	25.28	212.24	0.1161
Within groups	18	4.52	41.67	0.0379
Parents	6	5.56	61.69	0.0993
Fawn x Fawn group	2	13.63	115.44	0.00059
Fawn x Fortune group	5	2.95	27.41	0.0124
Fortune x Fortune group	5	1.20	2.4	0.0047
Rep x entries	42	1.25	21.36	0.0027
Error	462	0.35	5.31	0.0011

Table 16. Means, standard errors of the mean ( $\bar{S}\bar{X}$ ), coefficients of variation (CV) and least significant differences for five panicle seed weight, seed yield per plant and 100 seed weight in tall fescue, 1973.

Entries	Identification	Five panicle seed weight (g)	Seed yield (g/plant)	100 seed weight (g)
01	Fawn	0.941	2.11	0.3289
02	"	1.182	2.94	0.2163
03	"	2.089	6.19	0.2982
04	Fortune	0.687	1.82	0.1644
05	"	0.782	1.89	0.2016
06	"	0.865	2.89	0.1966
07	"	0.849	1.51	0.1652
Mean parent group		1.056	2.76	0.2245
08	Fawn x Fawn	1.095	3.10	0.2654
09	"	1.264	4.04	0.2725
12	"	2.477	7.28	0.2746
Mean Fawn x Fawn group		1.612	4.807	0.2708
10	Fawn x Fortune	1.040	3.18	0.2589
13	"	0.080	0.14	0.1993
14	"	0.155	0.56	0.2181
15	"	0.280	0.88	0.2411
16	"	0.326	1.08	0.2545
17	"	0.556	1.56	0.2412
Mean Fawn x Fortune group		0.4062	1.23	0.2355
18	Fortune x Fortune	1.247	2.91	0.1928
19	"	0.843	2.98	0.1871
20	"	0.705	2.51	0.1803
21	"	0.880	3.34	0.2154
22	"	1.189	2.62	0.1759
23	"	0.789	3.17	0.1855
Mean Fortune x Fortune group		0.9422	2.922	0.1895
Grand mean		0.923	2.67	0.2243
$\bar{S}\bar{X}$		0.121	0.47	0.0068
CV		63.95	86.31	14.79
LSD .05		0.334	1.30	0.0188
LSD .01		0.439	1.71	0.0247

Table 17. Mean squares for replications, single crosses, general combining ability (GCA) and specific combining ability (SCA) of five panicles seed weight, seed yield per plant and 100 seed weight, in tall fescue, 1973.

Source of variation	d. f.	Five panicles seed weight	Seed yield	100 seed weight
Replication	2	6.19	119.68	0.0080
Single crosses	5	20.07	165.98	0.0320
GCA	3	7.66	96.01	0.0512
SCA	2	38.69	270.91	0.0034
R x SC	10	1.59	47.72	0.0025
Error	126	0.34	8.16	0.0012
GCA:SCA		0.2:1	0.4:1	15.1:1

\*, \*\* Significant difference at .05 and .01 probability level

ns Non significant difference

Both GCA and SCA were significant at the one percent probability level (Table 17). The ratio of GCA:SCA was 0.4:1, suggesting the relative importance of the non additive genetic scheme.

100 Seed Weight. All groups, except Fawn x Fawn crosses, showed significant difference at the the one percent probability level (Table 15). The mean value for 100 seed weight in order from high to low were Fawn x Fawn crosses (0.2708 g), Fawn x Fortune crosses (0.2355 g), parent group (0.2245 g) and Fortune x Fortune crosses (0.1895 g) (Table 16). This suggests improvement could be achieved by crossing Fawn x Fortune genotypes followed by selection among segregating progenies. This was confirmed by a significant general combining ability for this trait (Table 17). The ratio of GCA:SCA was 15.1:1; thus, genes acting additively were primarily responsible for its expression.

#### Heterosis

The error term used for heterosis study came from analysis of variance comprising of 15 single cross, 15 corresponding mid parent and 7 parent groups (Table 18).

Plant Height. The deviations from the additive scheme were statistically significant at the one percent probability level within the Fawn x Fortune and Fortune x Fortune crosses but not so among the Fawn x Fawn crosses (Table 19). The mean of Fawn x Fawn,

Table 18. Analysis of variance for 37 entries including 7 parents, 15 single crosses, and 15 mid parent values; Heterosis study, tall fescue, 1973.

Source	d. f.	Plant height	Plant spread	Anthesis date	Panicle numbers	Panicle length	Number of primary pedicels	Five panicles seed weight	Seed yield	100 seed weight
Replication	2	525.59**	13.71*	0.35 <sup>ns</sup>	279.47**	21.52**	8.25**	0.8740**	21.37**	0.00138**
Entries	36	252.77**	18.49**	9.83**	75.03**	8.79**	7.05**	0.6812**	6.02**	0.00578**
Error term	72	32.32	3.21	0.34	21.87	2.15	0.85	0.1153	1.89	0.000225

Table 19. Single cross means ( $\overline{SX}$ ), mid parent means ( $\overline{MP}$ ), single crosses as percent of their mid parents ( $\cdot/\cdot$ ), and mean squares (MS) associated with linear comparison between single crosses and their corresponding mid parents for plant height, plant spread and anthesis date in tall fescue, 1973.

Groups		Plant height (cm)	Plant spread (cm)	Anthesis date (rating)
Fawn x Fawn	$\overline{SX}$	71.33	11.53	1.33
	$\overline{MP}$	74.80	11.23	1.70
	$\cdot/\cdot$	95.36 <sub>ns</sub>	102.67 <sub>ns</sub>	76.43 <sub>ns</sub>
	MS	54.18	0.41	0.62
Fawn x Fortune	$\overline{SX}$	69.72	14.63	2.17
	$\overline{MP}$	62.17	12.82	3.33
	$\cdot/\cdot$	112.14 <sub>**</sub>	114.12 <sub>**</sub>	65.17 <sub>**</sub>
	MS	513.02	29.48	12.06
Fortune x Fortune	$\overline{SX}$	61.43	18.07	5.33
	$\overline{MP}$	53.10	13.53	5.00
	$\cdot/\cdot$	115.69 <sub>**</sub>	133.56 <sub>**</sub>	106.60 <sub>ns</sub>
	MS	624.50	185.50	1.08
All crosses	$\overline{SX}$	66.73	15.39	3.27
	$\overline{MP}$	61.07	12.79	3.67
	$\cdot/\cdot$	109.27 <sub>**</sub>	120.33 <sub>**</sub>	89.10 <sub>**</sub>
	MS	720.90	152.10	3.60
Error term with 72 d. f.		32.32	3.21	0.34

Table 20. Single cross means ( $\overline{SX}$ ), mid parent means ( $\overline{MP}$ ), single crosses expressed as the percent of their corresponding mid parent ( / . ) and observed mean squares with the levels of significance for comparison between single crosses and mid parents for plant height, plant spread and anthesis date in tall fescue, 1973.

Entries	Identification	Plant height (cm)				Plant spread (cm)				Anthesis date (rating)			
		$\overline{SX}$	$\overline{MP}$	/ .	MS	$\overline{SX}$	$\overline{MP}$	/ .	MS	$\overline{SX}$	$\overline{MP}$	/ .	MS
08	Fawn x Fawn	67.5	77.9	86.65	162.24	11.5	10.9	105.50	0.54	1	2	50.00	1.50
					*				ns				*
09	"	68.0	77.6	87.63	138.24	11.8	11.7	100.85	0.02	1	1	100.00	0.00
					*				ns				ns
12	"	78.5	68.9	113.93	138.24	11.3	11.1	101.80	0.06	2	2	100.00	0.00
					*				ns				ns
10	Fawn x Fortune	65.1	69.2	94.08	25.22	11.7	13.3	87.97	3.84	1	3	33.33	6.00
					ns				ns				**
13	"	65.8	60.6	108.58	40.56	13.2	12.8	103.13	0.24	4	4	100.00	0.00
					ns				ns				ns
14	"	71.7	62.3	115.09	132.54	14.8	12.9	114.73	5.42	3	4	75.00	1.50
					*				ns				*
15	"	69.4	58.6	118.43	117.96	15.2	11.4	133.33	21.66	1	3	33.33	6.00
					*				*				**
16	"	72.2	60.3	119.73	212.42	17.5	13.2	132.58	27.74	2	3	66.67	1.50
					*				**				*
17	"	74.1	62.0	119.52	219.62	15.4	13.3	115.79	6.62	2	3	66.67	1.50
					*				ns				*
18	Fortune x Fortune	72.9	50.2	145.21	772.94	17.5	13.1	133.59	29.04	5	5	100.00	0.00
					**				**				ns
19	"	55.1	52.5	104.95	10.14	17.6	12.1	145.45	45.38	6	5	120.00	1.50
					ns				**				*
20	"	56.2	52.0	108.08	26.46	17.8	13.2	134.85	31.74	5	5	100.00	0.00
					ns				**				ns
21	"	62.5	54.2	115.31	103.34	21.0	13.8	152.17	77.76	6	5	120.00	1.50
					ns				**				*
22	"	60.3	53.7	112.29	65.34	16.5	15.0	110.00	3.38	5	5	100.00	0.00
					ns				ns				ns
23	"	61.6	56.0	110.00	47.04	18.0	14.0	128.57	24.00	5	5	100.00	0.00
					ns				**				ns
error taken with 72 d. f.					32.32				3.21				0.34

Fawn x Fortune and Fortune x Fortune crosses expressed as the percentage of the mean of their corresponding mid parent were 95.36, 112.14 and 115.69, respectively (Table 19).

The single degree of freedom analysis in the heterosis study revealed significant deviations from the additive scheme at the five percent probability level for crosses 08, 09 and 12 to 17. Cross number 18 also showed significant heterosis at the one percent level of probability. The significant positive heterosis or hybrid vigor observed in treatments 12 and 14 to 18 ranged from 13.93 to 45.21 percent above the mid parent. Negative heterosis was notably found in treatments 08, 09 with 13.35 and 12.37 percent below the performance of their corresponding mid parents (Table 20).

All single crosses of morphologically diversified groups possessed significant hybrid vigor while only two treatments from the phenotypically similar groups expressed significant hybrid vigor (Table 20).

Plant Spread. Significant hybrid vigor (.01 level) was observed within the Fawn x Fortune and Fortune x Fortune single crosses groups but not in the Fawn x Fawn group (Table 19).

The single degree of freedom analysis for heterotic responses indicated significant non additive effects for crosses 15, 16, 18 to 21 and 23. The hybrid vigor observed in those treatments was 33.33, 32.58, 33.59, 45.45, 34.85, 52.17 and 28.57 percent above the mid parent, respectively (Table 20).



The heterotic response for this trait was higher among treatments of the spreading group (Fortune x Fortune crosses) than those of the hybrid combination between spreading and non spreading groups (Fawn x Fortune crosses) or the non spreading crosses (Fawn x Fawn crosses).

Anthesis. Heterosis for anthesis was apparent only within Fawn x Fortune group (Table 19). A study of the individual crosses indicated significant heterosis for treatments 08, 10, 14 to 17, 19 and 21. Crosses 08, 10, and 14 to 17 ranged from 33.33 to 66.67 percent earlier than the mid parent, based on the anthesis date ratings. A later heterotic response was observed in crosses 19 and 21 which represent crosses of the late maturity group, Fortune x Fortune crosses (Table 20).

Five of the six crosses from among the two diversified morphological parent groups exhibited heterosis for this characteristic. Only one cross within the Fawn x Fawn and the Fortune x Fortune group expressed heterosis.

Panicle Numbers. Fawn x Fortune crosses and Fortune x Fortune crosses were significantly different at the one percent probability level for number of panicles produced. The mean square value for the Fortune x Fortune group was larger than that of Fawn x Fortune group. The analysis indicated large genetic variation for the trait and high heterosis effects were observed (Table 21). The

Table 21. Single cross means ( $\overline{SX}$ ), mid parent means ( $\overline{MP}$ ), single crosses as percent of their mid parent ( $\%.$ ) and mean squares (MS) associated with linear comparison between single crosses and their corresponding mid parents for panicle numbers, panicle length and number of primary pedicels in tall fescue, 1973.

Groups		Panicle numbers	Panicle length (cm)	Number of primary pedicels
Fawn x Fawn	$\overline{SX}$	19.3	14.3	14.6
	$\overline{MP}$	16.3	14.7	14.6
	$\%.$	118.40 <sub>ns</sub>	97.28 <sub>ns</sub>	100.00 <sub>ns</sub>
	MS	40.5	0.72	0.0
Fawn x Fortune	$\overline{SX}$	23.7	15.95	16.0
	$\overline{MP}$	17.3	14.30	16.0
	$\%.$	136.99 <sub>**</sub>	111.54 <sub>**</sub>	100.00 <sub>ns</sub>
	MS	368.64	24.5025	0.0
Fortune x Fortune	$\overline{SX}$	27.5	16.8	16.7
	$\overline{MP}$	19.0	14.2	16.3
	$\%.$	144.74 <sub>**</sub>	118.31 <sub>**</sub>	102.45 <sub>ns</sub>
	MS	650.25	60.84	1.44
All crosses	$\overline{SX}$	24.33	15.98	16.00
	$\overline{MP}$	17.80	14.34	15.87
	$\%.$	136.69 <sub>**</sub>	111.44 <sub>**</sub>	100.82 <sub>ns</sub>
	MS	959.40	60.75	0.45
Error term with 72 d. f.		21.87	2.15	0.85

Table 22. Single cross means ( $\overline{SX}$ ), mid parent means ( $\overline{MP}$ ), single crosses as the percent of their corresponding mid parent (./.) and observed mean square with the levels of significance for comparison between single crosses and mid parents for panicle numbers, panicle length and number of primary pedicels in tall fescue, 1973.

Entries	Identification	Panicle numbers				Panicle length (cm)				Number of primary pedicels			
		$\overline{SX}$	$\overline{MP}$	./.	MS	$\overline{SX}$	$\overline{MP}$	./.	MS	$\overline{SX}$	$\overline{MP}$	./.	MS
08	Fawn x Fawn	18	15	120.00	13.5 <sup>ns</sup>	13.3	15.3	86.93	6.0 <sup>ns</sup>	14	15	93.33	1.5 <sup>ns</sup>
09	"	17	17	100.00	0.0 <sup>ns</sup>	13.9	15.6	89.10	4.34 <sup>ns</sup>	15	15	100.00	0.0 <sup>ns</sup>
12	"	23	17	135.29	54.0 <sup>ns</sup>	15.8	13.2	119.70	10.14 <sup>*</sup>	15	14	107.14	1.5 <sup>ns</sup>
10	Fawn x Fortune	21	17	123.53	24.0 <sup>ns</sup>	13.0	16.7	77.84	20.54 <sup>**</sup>	14	18	77.78	24.0 <sup>**</sup>
13	"	18	18	100.00	0.0 <sup>ns</sup>	16.5	14.4	114.58	6.62 <sup>ns</sup>	17	16	106.25	1.5 <sup>ns</sup>
14	"	21	14	150.00	73.5 <sup>ns</sup>	16.2	13.1	123.74	14.42 <sup>*</sup>	16	15	106.67	1.5 <sup>ns</sup>
15	"	32	19	168.42	253.5 <sup>**</sup>	16.9	13.5	125.19	17.34 <sup>**</sup>	17	15	113.33	6.0 <sup>*</sup>
16	"	27	20	135.00	73.5 <sup>ns</sup>	16.9	14.7	114.97	7.26 <sup>ns</sup>	17	17	100.00	0.0 <sup>ns</sup>
17	"	23	16	143.75	73.5 <sup>ns</sup>	16.2	13.4	120.90	11.76 <sup>*</sup>	15	15	100.00	0.0 <sup>ns</sup>
18	Fortune x Fortune	32	20	160.00	216.0 <sup>**</sup>	20.8	14.6	142.47	57.66 <sup>**</sup>	20	17	117.65	13.5 <sup>**</sup>
19	"	28	22	127.27	54.0 <sup>ns</sup>	16.0	13.8	115.94	7.26 <sup>ns</sup>	16	15	106.67	1.5 <sup>ns</sup>
20	"	24	16	150.00	96.0 <sup>*</sup>	14.6	13.4	108.96	2.16 <sup>ns</sup>	16	16	100.00	0.0 <sup>ns</sup>
21	"	27	22	122.73	37.5 <sup>ns</sup>	17.4	15.0	116.00	8.64 <sup>*</sup>	16	17	94.12	1.5 <sup>ns</sup>
22	"	24	16	150.00	96.0 <sup>*</sup>	16.9	14.6	115.75	7.94 <sup>ns</sup>	16	18	88.89	6.0 <sup>*</sup>
23	"	30	18	166.67	216.0 <sup>**</sup>	15.3	13.8	110.87	3.38 <sup>ns</sup>	16	15	106.67	1.5 <sup>ns</sup>
error with 72 d. f.					21.87				2.15				0.85

difference among the Fawn x Fortune crosses was larger than that among the Fawn x Fawn crosses, but less than the differences among the Fortune x Fortune crosses.

Only cross 15 of the Fawn x Fortune crosses exhibited significant positive heterosis; 68 percent above the mid parent. Three crosses of the Fortune x Fortune group showed hybrid vigor ranging from 50 to 66.67 percent above the mid parent (Table 22). None of the crosses showed a significant negative heterosis effect for panicle number.

Panicle Length. Significant heterosis was observed in the Fawn x Fortune and Fortune x Fortune groups. The mean squares of both groups were 24.50 and 60.84 respectively (Table 21).

The analysis of variance for the individual treatments revealed significant positive heterosis response for crosses 12, 14, 15, 17, 18 and 21. The heterosis ranged from 19.70 to 42.47 percent above the mid parent. A negative heterosis of 22.16 percent below the mid parent was observed in treatment 10, a Fawn x Fortune cross (Table 22). This is an example of negative heterosis in a group of crosses obtained from crossing diverse sources of germ plasm.

Number of Primary Pedicels. A deviation from the additive scheme was not apparent when single crosses were considered as groups, for primary pedicel number (Table 21). However treatments 15 and 18 showed 13.33 and 17.65 percent positive heterosis whereas

treatment 22 expressed 11.11 percent negative heterosis (Table 22).

Five Panicles Seed Weight and Seed Yield. Significant heterosis for five panicle seed weight and seed yield were apparent in the Fawn x Fortune crosses but not in other single crosses (Table 23). In each case it was negative in its response.

The low fertility in crosses of diversified germ plasm (Fawn x Fortune crosses) suggested the irregularities in the meiotic process. The inter and intraallelic interaction pertaining to paternal and maternal chromosomes of the hybrids from diversified germ plasm, evidently conditioned a genetic imbalance and gametes which failed to fertilize was the result. This was subsequently expressed as negative heterosis for members of the group of crosses (Table 24).

100 Seed Weight. There was no apparent heterosis expressed in any of the single crosses group for 100 seed weight (Table 23).

### Heritability

The 15 single crosses were regressed on their corresponding mid parents for the nine characteristics studied (Table 25). The simple regression coefficients (b) for plant height, plant spread, anthesis date, panicle numbers, panicle length, primary pedicel numbers, best five panicle seed weight, seed yield and 100 seed weight were 0.2636, 0.9668, 1.2143, 1.1781, 0.4436, 0.2789, 0.2419, 0.3096 and 0.7417, respectively. The regression

Table 23. Single cross means ( $\overline{SX}$ ), mid parent means ( $\overline{MP}$ ), single crosses as percent mid parent ( $\cdot/\cdot$ ) and mean squares (MS) associated with linear comparisons between single crosses and their corresponding mid parents for five panicles seed weight, seed yield per plant, and 100 seed weight in tall fescue, 1973.

Groups		Five panicles seed weight (g)	Seed yield (g/plant)	100 seed weight (g)
Fawn x Fawn	$\overline{SX}$	1.612	4.807	0.2708
	$\overline{MP}$	1.404	3.750	0.2812
	$\cdot/\cdot$	114.81 <sup>ns</sup>	128.19 <sup>ns</sup>	96.30 <sup>ns</sup>
	MS	0.1947	5.0276	0.000486
Fawn x Fortune	$\overline{SX}$	0.4062	1.23	0.2355
	$\overline{MP}$	1.1922	3.092	3.2283
	$\cdot/\cdot$	34.07 <sup>**</sup>	39.78 <sup>**</sup>	103.15 <sup>ns</sup>
	MS	5.5601	31.2034	0.000468
Fortune x Fortune	$\overline{SX}$	0.9422	2.922	0.1895
	$\overline{MP}$	0.7938 <sup>ns</sup>	2.03	0.1820
	$\cdot/\cdot$	118.69 <sup>ns</sup>	143.94 <sup>ns</sup>	104.12 <sup>ns</sup>
	MS	0.1982	7.1609	0.000504
All crosses	$\overline{SX}$	0.8617	2.62	0.2242
	$\overline{MP}$	1.0753	2.80	0.2209
	$\cdot/\cdot$	80.14 <sup>**</sup>	93.57 <sup>ns</sup>	101.49 <sup>ns</sup>
	MS	1.026	0.45	0.00027
Error term with 72 d. f.		0.1153	1.89	0.000225

Table 24. Single cross means ( $\overline{SX}$ ), mid parent means ( $\overline{MP}$ ), single crosses as the percent of their corresponding mid parent ( $\prime / .$ ) and observed mean square with the levels of significance for comparison between single crosses and mid parents for five panicles seed weight seed yield per plant and 100 seed weight in tall fescue, 1973.

Entries	Identification	Five panicles seed weight (g)				Seed yield (g/plant)				100 seed weight (g)			
		$\overline{SX}$	$\overline{MP}$	$\prime / .$	$MS_{ns}$	$\overline{SX}$	$\overline{MP}$	$\prime / .$	$MS_{ns}$	$\overline{SX}$	$\overline{MP}$	$\prime / .$	$MS_{ns}$
08	Fawn x Fawn	1.095	1.062	103.11	0.0016 <sup>ns</sup>	3.10	2.53	122.53	0.489 <sup>ns</sup>	0.2654	0.2726	97.36	0.078 x 10 <sup>-3</sup>
09	"	1.264	1.515	83.43	0.0945 <sup>ns</sup>	4.04	4.15	97.35	0.018 <sup>ns</sup>	0.2725	0.3136	86.89	2.532 x 10 <sup>-3</sup> **
12	"	2.477	1.636	151.41	1.0609 <sup>**</sup>	7.28	4.57	159.30	11.016 <sup>*</sup>	0.2746	0.2573	106.72	0.045 x 10 <sup>-3</sup> <sup>ns</sup>
10	Fawn x Fortune	1.040	0.862	120.65	0.0475 <sup>ns</sup>	3.18	2.00	159.00	2.088 <sup>ns</sup>	0.2589	0.2653	97.59	.006 x 10 <sup>-3</sup> <sup>ns</sup>
13	"	0.080	0.982	8.15	1.2204 <sup>**</sup>	0.14	2.42	5.79	7.797 <sup>*</sup>	0.1993	0.2090	95.36	0.014 x 10 <sup>-3</sup> <sup>ns</sup>
14	"	0.155	1.016	15.26	1.1120 <sup>**</sup>	0.56	2.23	25.11	4.185 <sup>ns</sup>	0.2181	0.1908	114.31	0.112 x 10 <sup>-3</sup> <sup>ns</sup>
15	"	0.280	1.388	20.17	1.8415 <sup>**</sup>	0.88	4.01	21.95	14.670 <sup>**</sup>	0.2411	0.2313	104.24	0.144 x 10 <sup>-3</sup> <sup>ns</sup>
16	"	0.326	1.436	22.70	1.8482 <sup>**</sup>	1.08	4.04	26.73	13.143 <sup>**</sup>	0.2545	0.2499	101.84	0.003 x 10 <sup>-3</sup> <sup>ns</sup>
17	"	0.556	1.469	37.85	1.2504 <sup>**</sup>	1.56	3.85	40.52	7.866 <sup>*</sup>	0.2412	0.2317	104.10	0.135 x 10 <sup>-3</sup> <sup>ns</sup>
18	Fortune x Fortune	1.247	0.735	109.66	0.3930 <sup>ns</sup>	2.91	1.86	156.45	1.656 <sup>ns</sup>	0.1928	0.1830	105.36	0.144 x 10 <sup>-3</sup> <sup>ns</sup>
19	"	0.843	0.772	109.20	0.0076 <sup>ns</sup>	2.98	2.36	126.27	0.576 <sup>ns</sup>	0.1871	0.1805	103.66	0.063 x 10 <sup>-3</sup> <sup>ns</sup>
20	"	0.705	0.768	91.80	0.0059 <sup>ns</sup>	2.51	1.67	150.30	1.059 <sup>ns</sup>	0.1803	0.1648	109.41	0.036 x 10 <sup>-3</sup> <sup>ns</sup>
21	"	0.880	0.819	107.45	0.0056 <sup>ns</sup>	3.34	2.39	139.75	1.356 <sup>ns</sup>	0.2154	0.1991	108.19	0.399 x 10 <sup>-3</sup> <sup>ns</sup>
22	"	1.189	0.816	145.71	0.2087 <sup>ns</sup>	2.62	1.70	154.12	1.270 <sup>ns</sup>	0.1759	0.1834	95.91	0.087 x 10 <sup>-3</sup> <sup>ns</sup>
23	"	0.789	0.853	92.50	0.0061 <sup>ns</sup>	3.17	2.20	144.09	1.413 <sup>ns</sup>	0.1855	0.1809	102.54	0.030 x 10 <sup>-3</sup> <sup>ns</sup>
error with 72 d. f.					0.1153				1.89				0.225 x 10 <sup>-3</sup>

Table 25. Three estimates of heritability, and coefficients of determination between single crosses and their corresponding mid parents for nine characteristics in tall fescue, 1973.

Identification	Plant height	Plant spread	Anthesis date
$H =  b $	0.2636	0.9668	1.2143
$H =  b'  =  b  \left(\frac{SX}{SY}\right)$	0.2495	0.4319	0.8446
$H = \frac{ b  (\overline{MP})}{\overline{SX}}$	0.2412	0.8036	1.4373
$r^2$	0.0623	0.1865	0.7133
-----			
Identification	Panicle numbers	Panicle length	Number of primary pedicels
$H =  b $	1.1781	0.4436	0.2789
$H =  b'  =  b  \left(\frac{SX}{SY}\right)$	0.5079	0.2236	0.2327
$H = \frac{ b  (\overline{MP})}{\overline{SX}}$	0.8642	0.3978	0.2762
$r^2$	0.2580	0.0500	0.0541
-----			
Identification	Five panicles seed weight	Seed yield	100 seed weight
$H =  b $	0.2419	0.3096	0.7417
$H =  b'  =  b  \left(\frac{SX}{SY}\right)$	0.1287	0.1615	0.8130
$H = \frac{ b  (\overline{MP})}{\overline{SX}}$	0.3017	0.3300	0.7311
$r^2$	0.0166	0.0261	0.6610



coefficients were also determined from the data coded in terms of standard deviation (Frey, 1957) which is the standardized regression coefficient ( $b'$ ). This value ( $b'$ ) is equivalent to the simple correlation coefficient when only two variables are involved. These coefficients range from 0.13 for five panicle seed weight to 0.84 for anthesis date (Table 25).

Three heritability estimates were computed. The first two were estimated as the  $b$  and  $b'$  value. The third one was an estimate where the regression was adjusted a function of a ratio of the mid parent to progeny. It was calculated from the formulas  $H = \frac{b \times \overline{MP}}{\overline{sx}}$  where  $\overline{MP}$  and  $\overline{sx}$  designated mid parent and single cross mean (Mahmud and Kramer, 1951). The heritability (estimates with the Mahmud and Kramer method were 0.2412, 0.8036, 1.4373, 0.8642, 0.3978, 0.2762, 0.3017, 0.3300 and 0.7311 for plant height, plant spread, anthesis date, panicle numbers, panicle length, number of primary pedicel, best five panicle seed weight, seed yield and 100 seed weight, respectively. The first and third methods resulted in heritable values for some characteristics over 100 percent. The standardized regression coefficient ( $b'$ ) placed a ceiling of 100 percent on the heritability estimate (Table 25).

Association between Anthesis Date and Various Agronomic Traits. Anthesis date was rated from one to six which represented the range from early to late floral readiness. A high anthesis rating

Table 26. All possible simple correlation coefficients (n= 66) among nine characteristics in tall fescue, 1973.

	Plant height	Plant spread	Anthesis date	Panicle number	Panicle length	Number of primary pedicels	Five panicles seed weight	Seed yield	100 seed weight
Plant height		-0.0293	** -0.5980	0.2254	** 0.5465	0.1293	** 0.3628	** 0.3732	** 0.6939
Plant spread			** 0.4762	** 0.5575	** 0.5478	** 0.5130	* -0.2615	-0.0378	** -0.3146
Anthesis date				0.1468	0.1374	** 0.3266	-0.2297	-0.1133	** -0.8100
Panicle number					** 0.5662	** 0.3292	0.0577	** 0.3869	-0.1197
Panicle length						** 0.7067	0.0408	0.2182	0.0593
Number of primary pedicels							-0.0804	0.0762	-0.1823
Five panicles seed weight								** 0.8563	** 0.4022
Seed yield									* 0.2731

\*, \*\* significant at 5 and 1% level, respectively.

of 6 corresponded to the late flowering types while a low rating, 1, represents early flowering types. Anthesis date was significantly associated with plant height ( $r = -0.5980$ ), 100 seed weight ( $r = -0.8100$ ), plant spread ( $r = 0.4762$ ), and number of primary pedicels ( $r = 0.3266$ ) (Table 26). This indicated that the genotypes showing an early anthesis date tend to be taller, narrower in plant spread, have fewer primary pedicels and possess higher 100 seed weight.

Association among Seed Yield and Other Agronomic Traits. Seed yield was not associated with plant spread, anthesis date, panicle length and number of primary pedicels. Nevertheless significant associations were observed between seed yield and plant height, panicle number, best five panicle seed weight and 100 seed weight. The simple correlation coefficient for seed yield and their characteristics were .3732, .3869, .8563 and .2731, respectively (Table 26). Thus, five panicles seed weight showed the highest relationship to seed yield (Table 26). This we would expect because in some cases this observation represented nearly the total seed yield of the plant.

Regression and Path Coefficient Analysis. Six characteristics were entered into a multiple regression analysis with seed yield per plant as the dependent variable,  $y$ . The independent variables were 100 seed weight, best five panicle seed weight, numbers of primary pedicels, panicle length and panicle number, designated  $x_1$  to  $x_5$ , respectively. All variables were entered into the regression model

Table 27. Stepwise multiple regression models for five independent variables on seed yield, tall fescue, 1973.

n = 66

Dependent variable	Independent variables	Regression models	Coefficient of determination ( $R^2$ )
Seed yield (y)	Five panicles seed weight ( $X_2$ )	$Y = -0.3465 + 3.4291 X_2$	0.7332
Seed yield (y)	Five panicles seed weight ( $X_2$ )	$Y = -2.8372 + 0.1157 X_5 + 3.3509 X_2$	0.8475
Seed yield (y)	Panicle numbers ( $X_5$ )		
	Five panicles seed weight ( $X_2$ )	$Y = -3.5428 + 0.1154 X_5 + 0.497 X_3$	0.8487
	Panicle numbers ( $X_5$ )	$+ 3.3654 X_2$	
Seed yield (y)	Number of primary pedicels ( $X_3$ )		
	Five panicles seed weight ( $X_2$ )	$Y = -3.5113 + 0.1205 X_5 - 0.0751 X_4$	0.8506
	Panicle numbers ( $X_5$ )	$+ 0.1075 X_3 + 3.3846 X_2$	
	Number of primary pedicels ( $X_3$ )		
Seed yield (y)	Panicle length ( $X_4$ )		
	Five panicles seed weight ( $X_2$ )	$Y = -3.3928 + 0.1197 X_5$	0.8506
	Panicle numbers ( $X_5$ )	$-0.0707 X_4 + 0.1028 X_3$	
	Number of primary pedicels ( $X_3$ )	$+ 3.3970 X_2 - 0.4682 X_1$	
	Panicle length ( $X_4$ )		
	100 seed weight ( $X_1$ )		

Table 28. Path-coefficient analysis for five variables on seed yield in tall fescue, 1973.

Panicle numbers		Panicle length	
Direct	.3503	Direct	-.0674
via panicle length	-.0381	via panicle numbers	.1984
via number of primary pedicels	.0247	via number of primary pedicels	.0531
via five panicles seed weight	.0490	via five panicles seed weight	.0346
via 100 seed weight	<u>.0010</u>	via 100 seed weight	<u>-.0005</u>
	r=.3869		r=.2182
-----			
Numbers of primary pedicels		Five panicles seed weight	
Direct	.0752	Direct	.8482
via panicle numbers	.1153	via panicle numbers	.0202
via panicle length	-.0476	via panicle length	-.0027
via five panicles seed weight	-.0682	via number of primary pedicels	-.0060
via 100 seed weight	<u>.0015</u>	via 100 seed weight	<u>-.0034</u>
	r=.0762		r=.8563
-----			
100 seed weight			
Direct	-.0084		
via panicle numbers	-.0419		
via panicle length	-.0040		
via number of primary pedicels	-.0137		
via five panicles seed weight	<u>.3411</u>		
	r=.2731		

in a sequence determined by a stepwise selection procedure. In each step the entering independent variable was the one which expressed the highest partial correlation with the dependent variable. All stepwise regression equations are shown in Table 27. The effects of the independent variables on seed yield were partitioned by the path-coefficient analysis and are shown in Table 28. This regression analysis demonstrated the primary character influencing seed yield was five panicle seed weight. The second major effect on yield was from panicle numbers while the remaining characteristics showed little additional influence (Table 27). The coefficients of determination,  $R^2$  of five independent variable on seed yield was 0.8506 (Table 27), thus indicating 85.06 percent of the variation in seed yield was accounted for by variation in the five independent variables. Nevertheless, from the stepwise regression models shown in Table 27, 73.32 percent and an additional 11.43 percent of variation in seed yield were accounted for by variation in the best five panicle seed weight and panicle numbers, respectively. Then, only 0.31 percent of the variation in seed yield could be explained by variation among the remaining three independent variables. This is shown, also, by the path-coefficient analysis (Table 28). In this analysis the standardized partial regression coefficients represented the direct effect of an independent variable on seed yield. It was shown that best five panicle seed weight and panicle numbers had the greatest direct

effect on yield, with  $b'$  values equal to .8482 and .3503, respectively (Table 28).

## DISCUSSION AND CONCLUSION

### Greenhouse Study

An experiment was conducted in the greenhouse in 1972 to examine the genetic potential of growth and regrowth for several plant characteristics in 15 single crosses of tall fescue.

The experiment indicated that under sufficient nutrient supply there was greater genetic expression of some characteristics measured as the plant grew older. There were greater differences among the single crosses at the second harvest date, two months from the establishment date (Tables 3, 4, 6, 7). Under limited nutrient supply the differences among crosses were smaller and non significant for dry matter. The limited nutrient supply may have marked the full genetic expression for the trait (Tables 5, 8). Nutrient stress was found to reduce dry matter yield. The overall mean dry weight on the second date of measurement was 0.96 g /pot compared with 0.789 g /pot on the third date of measurement (Tables 7, 8).

The general and specific combining ability estimate of plant height and tiller numbers at different development period were relatively persistent. They differed only in the magnitude of GCA:SCA ratio (Tables 3, 4, 5). This suggested that the types of gene action governed the traits were relatively persistent throughout the developmental period of plants themselves.



Age of the plant and nutrient supply influenced genetic expression of traits. Selection for any plant characteristics should be made at the specific period of plant development and under adequate nutrient supply where maximum genetic expression could be observed.

### Field Study

#### Combining Ability, Heterosis and Heritability Estimate

Combining ability was calculated from the analysis of variance for a four clones diallel using method 4, fixed model, as outlined by Griffing (1956). Mean squares for linear comparison between 15 single crosses and their corresponding mid parents were used to test for significant heterosis. The error term for testing the heterosis effects was derived from the analysis of variance, where the entries consisted of seven parents, 15 single crosses and 15 corresponding mid parent values (Table 18). The performance of offspring in relation to the mid parent was expressed in percent, and heterosis was examined in terms of how far this value deviated from 100. Three parent-offspring relationship estimates of heritability were determined. The absolute value for heritability varied among methods. However if we assigned our heritability estimates to three classes where those in the range of 0.0 to .35 are considered low, .36 to .70 are medium and .71 or above are high, then the estimates were

quite consistent (Table 29). The coefficient of determination between single crosses and their corresponding mid parents for nine plant characteristics were also calculated to determine the percentage of variation in the offspring that can be explained by the variation in mid parents (Table 25). The  $r^2$  of all plant characteristics except anthesis date and 100 seed weight were quite low, ranged from 5 to 26 percent (Table 25). The  $r^2$  for anthesis date and 100 seed weight were 71 and 66 percent, respectively (Table 25). This is in agreement with the relatively high heritability estimates. These two characteristics are sufficiently influenced by the additive type of gene action to render heritability value for predictive purpose.

Generally we expect close association among the combining ability, heterosis and heritability estimate. Whenever the characteristic of interests possessed significant general combining ability we would expect lower heterosis and higher heritability estimate than those disclosing significant specific combining ability. In this study, the relationship was true for five of the nine characteristics examined. Plant spread and anthesis date which showed significant differences in both general and specific combining ability revealed, as expected, significant heterosis and also medium to high heritability estimates (Tables 11, 19, 29). The 100 seed weight which exhibited significant general combining ability with negligible specific combining ability showed no heterosis and a high heritability estimate (Tables 17, 23, 29).

Table 29. Comparison of methods used to estimate heritability, with estimates assigned to three classes, low, medium and high heritability values.

Identification	Plant height	Plant spread	Anthesis date	Panicle numbers	Panicle length	Number of primary pedicels	Five panicles seed weight	Seed yield	100 seed weight
$H =  b $	Low	High	High	High	Medium	Low	Low	Low	High
$H =  b'  =  b  \left( \frac{sx}{sy} \right)$	Low	Medium	High	Medium	Low	Low	Low	Low	High
$H = \frac{ b (\overline{MP})}{\overline{sx}}$	Low	High	High	High	Medium	Low	Low	Low	High

Low = Heritability estimate range from 0-35 percentage

Medium = Heritability estimate range from 36-70 percentage

High = Heritability estimate from 71 percentage and up

Significant specific combining ability were found on both five panicles seed weight and seed yields and as expected, both showed high heterosis and also low heritability estimates (Tables 15, 23, 29). However, a discrepancy from this generalized situation was observed in plant height, panicle numbers and numbers of primary pedicels. Plant height and number of primary pedicels showed significant general combining ability, non significant specific combining ability but a significant positive heterosis and low heritability estimate (Tables 11, 14, 19, 21, 29). Significant GCA and medium to high heritability estimates were observed for panicle number (Table 14), but it also expressed a significant positive heterosis (Table 21). Though no significant combining ability was observed for panicle length (Table 19) the data did exhibit significant heterosis and low to medium heritability (Tables 21, 29).

This observed discrepancy for certain characteristics may very well be due to the small diallel (six single crosses) involved in the combining ability analysis, whereas the heterosis and heritability estimates were based on all 15 single crosses. Also, the characteristics displaying significant general combining ability may indeed not possess only additive gene action but also the balance of plus and minus effects of gene interactions which result in the expression of an additive scheme. A characteristic with significant general combining ability in one population may not be the same in another

population; thus, unpredictable estimates of heterosis and heritability may be observed. This variation in estimates for the various genetic constants strengthens the premise that their true value is for the population from which they are derived.

#### Association among Plant Characteristics

All possible single correlation coefficients were calculated for nine characteristics measured (Table 26). Six of the nine characteristics of interests were used in a multiple regression model where seed yield was chosen as the dependent variable, while panicle number, panicle length, number of primary pedicels, five panicles seed weight and 100 seed weight were the independent variables (Table 27). The path-coefficient analysis was used to study direct and indirect effects of the independent variables on seed yield (Table 28).

The experiment indicated that anthesis date was negatively associated with plant height and 100 seed weight and positively associated with plant spread and number of primary pedicels. Even though there were significant differences among entries in anthesis date rating, there was no apparent association between anthesis date and seed yield in this study (Table 26).

Seed yield was significantly related to plant height, panicle numbers, five panicle seed weight, and 100 seed weight (Table 26).

The significant coefficients of determination for seed yield and other characteristics were low except for five panicle seed weight which was 77.33 percent (Table 27). This relationship, as expected, agrees with the stepwise multiple regression study and the pathway analysis (Tables 27, 28). In the stepwise multiple regression model we observed 73 and an additional 11 percent of the variation in seed yield to be accounted for by the variation in five panicle seed weight and panicle numbers, respectively. The direct influences of seed weight and panicle numbers were 84 and 35 percent of the simple correlation coefficient between the characteristics and seed yield (Tables 27, 28).

Significant differences were observed for panicle length and number of primary pedicels (Table 12). The two variables were also significantly associated as measured by the correlation coefficient (Table 26). However, neither variable was associated with seed yield even when those single crosses low in fertility (Fawn x Fortune crosses) were eliminated from the analysis. These characteristics were measured on the five panicles used for five panicle seed yield and even here, they were not related to seed yield. This suggests that branching of the panicles (not measured) may be an important panicle characteristic related to seed yield and should be investigated in future studies.

Five panicle seed weight, although in some cases it resembled

the total seed yield, contained the most productive tillers of a given plant. This represented the maximum genetic expression for yield of a given plant. The high correlation coefficients between this trait and seed yield indicated this might be a selection tool for seed yield. Phenotypic selection for the best five panicle seed weight were somewhat similar to single head selection in cereal crops, a practice used for many years. However, some differences between the two may exist. Selection for the best five panicle seed weight was used to identify superior clones whereas seeds from a selected single head in  $F_2$  generation of cereal crop are used to generate  $F_3$  families for further selection. Using the five best panicle seed weight as the selection criterion for seed yield is a time consuming method but this may be overcome by a rating procedure for seed yield and panicle characteristics.

## SUMMARY

### Greenhouse Study

1. Genetic expression for some plant characteristics measured, was greater as the plant grew older.
2. Limited nutrient supply marked some genetic effects. This phenomenon was evident by reducing dry matter yield.

### Field Study

1. Significant general combining ability was observed for plant height, panicle numbers, number of primary pedicels and 100 seed weight. Both significant GCA and SCA were observed for plant spread, anthesis date, five panicle seed weight and seed yield. Non significant combining ability was observed for panicle length.

GCA was found to be more important than SCA in all traits except five panicle seed weight and seed yield which was in reverse.

2. Fawn x Fawn single crosses exhibited no heterosis in all characteristics measured Fawn x Fortune crosses exhibited hybrid vigor for plant height, plant spread, anthesis date, panicle numbers and panicle length. Negative heterosis was observed for five panicle seed weight and seed yield. Fortune x



Fortune crosses also exhibited hybrid vigor for plant height, plant spread, panicle numbers and panicle length.

3. Three methods of heritability estimate led to similar results when used as approximations. Hundred seed weight was high in heritability while plant spread, anthesis date, panicle numbers was shown medium to high. Medium to low heritability values were observed for panicle length and low heritability values were evident for plant height, number of primary pedicels, five panicle seed weight and seed yield.
4. Five panicle seed weight and panicle numbers were significantly associated with seed yield while panicle length, number of primary pedicels and 100 seed weight revealed little relationship.

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