AN ANALYSIS OF YIELD AND OTHER TRAITS IN A DIALLEL CROSS INVOLVING ELEVEN WINTER WHEAT ALIEN-TRANSLOCATION LINES

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CHAPTER I

INTRODUCTION

Rusts have long been major disease problems in wheat (*Triticum aestivum* L. em. Thell.) and have caused substantial losses in yield and quality. Many relatives of wheat contain genes which impart resistance to those pests. To incorporate the resistance into wheat, attempts have been made to transfer specific genes from those relatives; and through the aid of irradiation and meiotic control, several translocations between wheat and a segment of alien chromatin carrying the desired gene(s) have been successfully induced in wheat.

Because the transfer of alien genes is not a precise procedure, it is rare that transfer of a single gene takes place. More often, the portion of alien chromatin is sufficiently large to contain genes conditioning other effects as well. Many of those additional effects may be eliminated by successive generations of backcrossing to wheat. In other instances, valuable portions of wheat chromatin may have been lost during the transfer process, also leading to undesirable effects. However, the alien chromatin may compensate, at least in part, for such loss.

At present, a number of alien-translocation lines conditioning resistance to several pests are available for use in wheat breeding programs. Thus the possibility exists for the combination of two or more alien translocations into the same genotype, thereby imparting multiple-pest resistance.

Due to additional genes in certain combinations, two translocations may result in an F_1 exhibiting hybrid vigor. On the other hand, if two translocations are united and either or both are missing portions of valuable wheat chromatin, a decline in the vigor of the F_1 may result. This increase or reduction in vigor may be noted by measuring agronomically and economically important characters.

The objectives of this research were to study the F_1's and parents of a diallel cross involving 11 alien-translocation lines of winter wheat to measure the response of eight performance traits and to determine the potential usefulness of these lines in a breeding program. Standard analyses of variance, analyses of general and specific combining ability, and examination of hybrid vs. parental contrasts were used to attain the above objectives.

CHAPTER II

LITERATURE REVIEW

Several relatives of wheat contain genes conditioning desirable features such as disease and insect resistance. Resistance to the rusts, powdery mildew, and several insects may be found in *Secale cereale* L. and in several of the *Aegilops* species. Species of *Agropyron* are noted for resistance to all three wheat rusts, wheat streak mosaic virus, barley yellow dwarf mosaic virus, and bunt (15). The gene pool available to wheat breeders could be greatly enlarged by exploiting the genetic variability of these wheat relatives (23). The incorporation of such desirable characters into wheat would be of great potential value in breeding programs.

Wheat is an allohexaploid composed of the A, B, and D genomes each containing seven pairs of chromosomes. Due to its hexaploid nature, unique opportunities exist for the introduction of desirable alien variation. According to Kimber (11), the relationship of the alien chromosome carrying the desired gene(s) to the chromosome(s) of wheat must be the basic consideration in any attempt to introduce such variation into cultivated wheat. If a close relationship exists between the two chromosomes, the alien character may be transferred by normal hybridization. Knott (15) further adds that a diploid species carrying one of the A, B, or D genomes can be crossed directly with common wheat or first to a tetraploid and later to a hexaploid. After a wide cross has been made, the doubled or non-doubled F_1 can be backcrossed to wheat and eventually "wheat-like" lines containing one or more characters from the alien species can be recovered. The desired character, however, is almost always accompanied by undesirable traits. These undesirable traits are present because alien chromosomes do not ordinarily pair and cross over with wheat chromosomes, so at least one entire chromosome must be added to the wheat complement or substituted for a wheat chromosome in order to retain the desired gene (22).

Besides this normal introgression of alien genes into the wheat genome through hybridization, there are two other means of introducing alien variation, i.e., by irradiation or by meiotic control (15). Sears (19) was the first to describe an irradiation technique used to transfer leaf rust resistance from Triticum umbellulatum (Aegilops umbellulata) to T. aestivum. Leaf rust resistant plants carrying an added T. umbellulatum isochromosome were X-rayed just prior to meiosis. The X-rayed pollen was then used to pollinate emasculated spikes of normal 'Chinese Spring' wheat. Resistant F_1 plants were examined for the presence of a translocation between the T. umbellulatum and a wheat chromosome. Seventeen translocations were obtained, but only one was transmitted normally through pollen. This translocation was later designated as "Transfer."

Since the pioneering work of Sears, Knott (12) and several others have used similar techniques to successfully transfer alien genes to wheat. The success of Knott's program of transferring stem rust resistance from Agropyron elongatum was attributed to two reasons: first, because wheat is an allohexaploid, it can stand the loss of up to a whole chromosome without serious deleterious effects; and second, the added Agropyron chromatin had no serious effects except on the gametes. He also found that in families segregating for one of the translocations, resistant and susceptible sibs showed no observable differences. Both X-rays and thermal neutrons were used by Sharma and Knott (29) to translocate a segment of the Agropyron chromosome contained in a wheat-like Agropyron derivative, "Agrus," to wheat. One translocation involving chromosome 7D appeared to have no detrimental effects and was normally transmitted through the gametes. This translocation is now known as "Agatha."

Not only have Aegilops and Agropyron species been used as donors of alien material, but Secale (rye) has also been used as a source of resistance. Driscoll and Jensen (7) reported the translocation of a gene for wheat leaf rust resistance from a rye chromosome to wheat. It was later shown that the translocated alien segment present in this line, "Transec," occupied a terminal position and was of considerable length. The wheat chromosome involved was identified as chromosome 4A (5) and was found to involve the loss of genetically unimportant wheat chromatin (6). More recently, Sebesta and Wood (26) have successfully transferred greenbug resistance from rye to wheat through the use of X-rays.

The major advantage of induced translocations through the use of X-rays is that the procedure will work regardless of the pairing affinity of the alien chromosome with its wheat homoeologues (15). Knott (14) considered the Agropyrons the easiest to handle and the most valuable source of potentially useful genes. Usually, lines can be produced in which the translocated segment is transmitted as though it were a dominant gene. He further added that the only real problem is that a segment of wheat chromosome will have been lost, and this could also be deleterious. According to Sears (20), a more desirable approach to this problem would be to produce a reciprocal translocation in which the desired alien chromosome segment replaces a segment of homoeologous wheat chromosome. Because the majority of transfers thus obtained are reciprocal in nature, the alien segment may then, at least partially compensate for the missing wheat segment, as well as introducing the desired alien gene. Sears (23) indicated that the attachment of a terminal segment of the alien chromosome to a nonhomoeologous chromosome would likely result in deficiencies for critical wheat genes in every case.

Because transfers of this type usually involve overall phenotypic modifications or are too arbitrary, alternative procedures have been sought. According to Knott (15), Okamoto, as well as Riley and Chapman, was among the first to report that pairing of homoeologous chromosomes in wheat is genetically controlled. Several methods utilizing homoeologous crossing over to transfer alien genes to wheat chromosomes have since been reported (15).

Riley et al. (18) were the first to report a successful technique using induced homoeologous pairing to transfer yellow rust resistance from Triticum comosum (Aegilops comosa) to wheat. An alien addition line which contained the T. comosum chromosome conditioning resistance to the disease was first produced. This was then crossed with T. speltoides (Aegilops speltoides) in order to suppress the activity of chromosome 5B which inhibits homoeologous pairing. The suppression of 5B activity permitted the T. comosum chromosome to recombine with its wheat homoeologue. A backcrossing program, combined with selection of rust-resistant plants, was undertaken to develop a 42-chromosome plant which was also resistant to yellow rust.

Through the use of a deficiency for chromosome 5B, Sears (20) was able to transfer resistance to leaf rust from two different Agropyron elongatum chromosomes to wheat chromosomes, i.e., 3D in "Tap 67" and 7D in "Agrus." For these two chromosomes, the induction of homoeologous pairing appeared to be a superior method for effecting the transfer of the desired gene when compared to those methods utilizing ionizing radiation (21).

This method of transferring desirable characters from the relatives to wheat appears to be more precise than irradiation techniques. Such transfers may have no deleterious effects, especially if the desired alien gene is near the end of one arm, permitting transfer of the gene through exchange of only a short terminal segment (20).

According to Driscoll (3), this method of induced homoeologous pairing does have limitations. The wheat chromosome that is to be involved in the translocation would presumably have to be one of the three in the pertinent homoeologous groups. For irradiation-induced transfers, any chromosome is capable of being involved in any translocation. The position of the alien gene on each of the three wheat chromosomes is also predestined, as crossing over would presumably take place between homoeologous segments of the chromosomes. If such positions were to coincide with wheat genes of significant value, the loss may not be tolerable. Some alien chromosomes with very limited possibilities for crossing over with their wheat homoeologues may never give rise to fully satisfactory transfers through induced pairing. Radiation-induced transfers from such chromosomes would have a better chance for success (18).

Sears (20) described another technique to transfer part of an alien chromosome to wheat. This transfer would be accomplished by allowing a telocentric for one arm of the alien chromosome to combine with a wheat telocentric following misdivision of two monosomes. This transfer chromosome may be useful if the alien arm is not deleterious and replaces a nonessential wheat arm.

Besides being induced through irradiation or meiotic control, alien translocations occasionally arise spontaneously. Some alien translocations have been produced in this manner, including the "Agent" (32) and "Neuzucht" (36) translocations.

Prior to the work of Sebesta (27) and of Sebesta and Smith (28), the literature did not contain information regarding the combining of translocation lines. Knott (13) , however, did test lines which had a pair of Agropyron chromosomes either added to the normal chromosome complement or substituted for wheat chromosome 6A. None of the lines equaled the check cultivar for all characters, but there was also no conclusive evidence for a detrimental effect of the Agropyron chromosome on any character studied. This work did not involve translocation lines containing segments of alien chromatin. Extensive reviews of the literature regarding translocation lines have been published by Knott (15) and Sears (20) in the last 10 years.

If alien-gene transfers are to be useful (regardless of the method used to induce them), they should be relatively free from deleterious effects associated with the exchange of alien chromatin. Driscoll (4) pointed out that an alien translocation may be acceptable in some cultivars but not in others. Thus, alien translocations should be tested in a wide variety of genetic backgrounds.

Several alien-translocation lines have been used successfully in the development of improved cultivars. 'Arthur 71,' grown commercially in the soft red winter wheat region of the U.S., contains the "Transfer" translocation (17). The "Neuzucht" translocation is present in the cultivars 'Aurora' and 'Kavkaz' grown in Eastern Europe (36). 'Sage' and 'Osage,' grown commercially in the hard red winter wheat region of the U.S., contain the "Agent" translocation (31). The "Teewon" translocation is present in the cultivar 'Payne' (30), also grown in the hard red winter wheat region of the U.S. The germplasm lines 'Amigo' and CI 15322 contain the "Amigo" and "Peethree" translocations, respectively (26, 25).

Sebesta (27) and Sebesta and Smith (28) studied the F_1's and parents of a diallel cross among six alien translocation lines of winter wheat to determine the effects on eight performance traits when two different alien gene complexes were combined two at a time. Significant GCA and SCA variances were detected for all eight characters. The GCA components were larger than those for SCA for tiller number, kernel weight, plant height, and heading date while the reverse was true for kernels/spike, grain yield, percent sterility, and percent protein. Four hybrids showed high positive heterosis for grain yield, while four other hybrids exhibited unexpectedly high levels of sterility, low values for kernels/spike, and low grain yield. The results of their study suggested that an increase in vigor may occur when certain alien translocations are combined; however, other combinations may result in detrimental effects on performance traits. Only by studying a possible combination is one likely to know whether the translocations involved are complementary or antagonistic to one another.

CHAPTER III

MATERIALS AND METHODS

Materials

Eleven winter wheat cultivars or selections were used in this study. Nine of the 11 are known to be alien-translocation lines, and two are presumed to be. The 11 lines are listed in Table I along with the designation and origin of the alien segment (known for nine lines) and the chromosome arms involved (known for six).

Arthur 71 and 'Purdue 6615D' (6*Arthur/Agatha) are soft red winter wheats developed at Purdue University, Lafayette, Indiana. Arthur 71 is a midtall, apically awnletted cultivar which is moderately early while Purdue 6615D is an Arthur-type wheat. Arthur 71 and Purdue 6615D contain the "Transfer" and "Agatha" translocations, respectively. Aurora is a semi-hard red winter wheat developed at Krasnodar, USSR, and contains the "Neuzucht" translocation. 'Winter Transec' contains the "Transec" translocation and is a white winter wheat developed at Cornell University, Ithaca, New York. Osage, Payne, Amigo, and CI 15322 are all hard red winter wheats developed at Oklahoma State University, Stillwater, Oklahoma. Osage is midtall in height, awned, medium late in maturity, and contains the "Agent" translocation. Payne is a medium early maturing, short-strawed, awned cultivar containing the "Teewon" translocation. Amigo and CI 15322 are both germplasm

TABLE I

ALIEN-TRANSLOCATION LINES STUDIED

Cultivar or Selection	Translocation Designation	Origin of Alien Gene Complex	Arms Involved Alien	Arms Involved Wheat	Reference
Osage	Agent	Agropyron elongatum	3Ag	3D	(32)
Arthur 71	Transfer	Triticum umbellulatum	$6C^{u}$	6Bl	(19)
Aurora	Neuzucht	Secale cereale	1R	1Bs	(36)
Winter Transec	Transec	Secale cereale	2R	4A	(7)
Purdue 6615D	Agatha	Agropyron elongatum	7el	7Dl	(29)
Payne	Teewon	Agropyron elongatum	Unknown		(24)
Salmon	Salmon	Secale cereale	1R	1B	(36)
Amigo	Amigo	Secale cereale	Unknown		(26)
CI 15322	Peethree	Agropyron elongatum	Unknown		(25)
Flex	---	?	Unknown		(35)
Plainsman V	---	?	Unknown		(1)

lines containing the "Amigo" and "Peethree" translocations, respectively. 'Salmon' is a white winter wheat obtained from the progeny of a hybrid between two strains of octaploid Triticale, as reported by Tsunewaki (34). Salmon contains the "Salmon" translocation. 'Flex' is a tall, hard red winter wheat with high grain protein developed at South Dakota State University, Brookings, South Dakota. 'Plainsman V,' also a high protein cultivar was developed by Seed Research, Inc., Scott City, Kansas. It is presumed but as yet uncertain that Flex and Plainsman V contain alien translocations. Descriptive information concerning these lines can be found elsewhere (1, 7, 8, 17, 25, 26, 29, 30, 31, 34, 35, 36).

The 55 different F_1's in this study resulted from a diallel crossing scheme involving the 11 lines listed in Table I (reciprocal crosses were not kept separate). Crosses were made in the greenhouse during the 1977-78 crossing season. Crossed and parental seed were planted in flats on October 6 and 7, 1978. The seedlings were vernalized at outside temperatures for approximately 6 weeks before transplanting.

Field Layout and Nursery Management

The seedlings were transplanted to the field on December 12, 1978. The experiment was conducted in a randomized, complete-block design with four replications. Single-row plots were spaced 30 cm apart, and the 10 plants in each plot were spaced 30 cm apart. The study was conducted during the 1978-1979 growing season at the Agronomy Research Station, Stillwater, Oklahoma, on a Bethany silt loam soil type.

A preplant application of ammonium nitrate was applied on September 5, 1978, at the rate of 30 kg/ha actual N. On March 8, 1979, a top dressing of ammonium nitrate was applied at the rate of 40 kg/ha actual N. Supplemental water was applied by sprinkler on two occasions. Insecticides were applied twice to control armyworms and greenbugs while weeds were controlled manually.

The study was harvested on June 18-25, 1979, by pulling and bagging individual plants. Eight vigorous, bordered plants from each plot were evaluated.

Characters Evaluated

The number of tillers/plant, kernels/spike, kernel weight, grain yield, percent spike fertility, plant height, heading date, and percent grain protein were evaluated in this experiment. All measurements, with the exception of percent protein and heading date, were taken on an individual plant basis. The measurements were made as follows:

Tiller Number

Tiller number/plant was recorded as the number of fertile (seed-bearing) spikes/plant at the time of threshing and was expressed on a per plant basis.

Kernels/Spike

The number of kernels/spike was determined by selecting the three best heads from each plant. These were threshed in bulk and the seed were counted and the total divided by three to determine the mean number of kernels/spike.

Kernel Weight

The weight of the seeds of the three selected heads measured to the nearest 1/10 g was divided by the number of seeds produced on the same three heads. This character was expressed as grams per 1000 kernels (per plant).

Grain Yield

Grain yield was taken as the weight of threshed grain from each individual plant including the three-spike sample and was expressed as grams per plant.

Percent Fertility

Percent fertility was determined as an average of the same three main heads used to obtain the other yield components and was expressed on a per plant basis. The number of florets/spike was counted before the three heads were threshed. This character was determined as follows: [number of seed per spike ÷ (number of spikelets per spike X 2)] X 100%. Basal and apical spikelets were excluded, as were tertiary and quaternary florets. Therefore, it is possible for fertility percentages to exceed values above 100% if any of these other florets set seed.

Plant Height

The measurement of this character was taken as the distance in centimeters from the crown (soil line) to the tip of the tallest spike, excluding awns, and was recorded on a per plant basis.

Heading Date

This character was recorded as a visual estimation of the date when 50% of the plants in a row were fully headed. This trait was determined on a per row basis and was expressed as the number of days after March 31.

Percent Protein

Percent protein of the grain was determined at the wheat quality laboratory at Oklahoma State University using an infrared analyzer. This character was determined on a per row basis.

Statistical Analyses

Standard analyses of variance were conducted on all data in order to detect the presence or absence of significant differences among the entries for the eight previously mentioned characters. The analyses for percent protein and heading date were conducted on a row basis, the other characters on a plant basis.

Heterosis was determined for all characters with respect to both the mid-parent (MP) and high-parent (HP) values. Least significant differences (LSD) were used to test each hybrid-parent contrast. The standard error (SE) of the difference between treatment means for a hybrid vs. its high-parent value was defined as $\sqrt{\frac{2\ EMS}{r}}$. Adjusted LSD values were used to test the hybrid vs. its mid-parent value because hybrid means were based on only half as many observations as mid-parent values. The SE for such comparisons was defined as $\sqrt{\frac{3\ EMS}{2r}}$ where EMS is the experimental error mean square and r represents the number of observations comprising the treatment mean.

Combining Ability Analyses

Combining ability analyses were conducted using F_1 and parental data for all eight characters according to the procedure outlined by Griffing (9) as method 2, model I. Under this model, the genotypes and blocks are regarded as fixed effects. Inferences, therefore, are restricted to the genotypes entering the diallel cross, because the experimental material was not a random sample of a definable larger population. Griffing's analysis provides for the partitioning of the sum of squares due to genotypes into general combining ability (GCA) and specific combining ability (SCA) sums of squares associated with p-1 and [p(p-1)]/2 degrees of freedom, respectively, where p represents the number of parents involved in the diallel cross. Under this model, the tests of significance for GCA and SCA are: MS_{GCA}/MS_E and MS_{SCA}/MS_E, respectively where MS_{GCA} and MS_{SCA} are the mean squares associated with GCA and SCA, respectively, and MS_E is the error mean square. The variance components for GCA and SCA were calculated according to the procedures outlined by Griffing.

All of the plants of one of the F_1's died in the seedling state. Therefore, no data could be recorded nor could means or SCA effects be calculated for this hybrid. Because of this, three separate analyses for GCA and SCA were calculated, i.e., all parents and hybrids were included except for the hybrid that died; one of the parents that resulted in the lethal combination was excluded along with all its hybrids; and the other parent and all its hybrids were excluded. Each of the last two methods excluded one parent and 10 hybrids from the

GCA and SCA analyses, respectively, while the first method excluded only one hybrid from the SCA analysis. Correlation coefficients between the first method and the other two were no lower than 0.98 for any character measured. Therefore, the data reported herein with respect to GCA and SCA are the result of the first method of analysis.

CHAPTER IV

EXPERIMENTAL RESULTS

General Considerations

No serious problems with diseases or insects were encountered during the course of this study; and in general, the yields were good. However, all plants of the Osage/Winter Transec hybrid died as seedlings prior to transplanting to the field. Therefore, no data was recorded for that entry nor could means or SCA effects be calculated for it. Several plants of the Osage/Plainsman V hybrid exhibited some degree of stunting and leaf injury at various times during the growing season. The damage to both these hybrids was apparently due to hybrid necrosis, a genetic defect as described by Hermsen (10). In the case of Osage/Winter Transec, the symptoms were severe, resulting in death of the plants. In the case of Osage/Plainsman V, the symptoms were less severe, but affecting grain yield and other traits.

After heading, an abnormal amount of spike sterility was observed in several hybrids particularly Arthur 71/Aurora, Arthur 71/Winter Transec, Aurora/Purdue 6615D, Winter Transec/Flex, Aurora/Flex, Winter Transec/Purdue 6615D, and Purdue 6615D/CI 15322. In these hybrids, however, no indication of necrosis or chlorosis was observed; the plants appeared normal throughout the season.

Analyses of Variance

Mean squares from analyses of variance for each of the eight traits are presented in Tables II and III. Because heading date and percent protein were measured on a row basis, their mean squares are presented separately (Table III) from the others. In both analyses (Tables II and III), there were only 64 degrees of freedom for entries instead of 65 because all plants of the Osage/Winter Transec hybrid died as seedlings. Highly significant entry (i.e., genotype) mean squares were obtained for all eight characters. Mean squares for replications were highly significant for six of the eight traits studied indicating that blocking of replications was effective for those traits in removing significant amounts of variation from experimental error, thus increasing the precision of the analysis. All characters measured on a plant basis (Table II) exhibited highly significant differences between replication by entry mean squares (experimental error) and residual mean squares (sampling error). This indicates that experimental error for those traits contained variation in addition to that among subsamples.

Comparisons Among Means

The means for each trait are presented in Table IV. In this and subsequent tables, the following abbreviations were used: Arthur 71 = Atr71, Aurora = Aura, Winter Transec = W.Trans, Purdue 6615D = 6615D, Salmon = Salm, CI 15322 = 15322, and Plainsman V = PmV. No abbreviations were necessary for Osage, Payne, Amigo, or Flex. All means, with the exception of those for heading date and percent protein, were based on 32 observations. The means for describing heading date and percent

TABLE II

MEAN SQUARES FOR SIX TRAITS FROM ANALYSES OF VARIANCE OF F_1 HYBRIDS AND PARENTS

Source of Variation	df	Tiller Number	Kernels/ Spike	Kernel Weight	Grain Yield	Percent Fertility	Plant Height
Replication	3	296.6**	476.1**	232.4**	826.7**	782.9	2294.8**
Entry	64	121.1**	4133.6**	672.1**	457.1**	29908.5**	2096.7**
Rep X Entry	192	21.7**	90.5**	25.3**	47.9**	593.5**	78.6**
Residual	1820	9.8	27.7	6.8	17.0	197.4	36.2

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE III

MEAN SQUARES FOR HEADING DATE AND PERCENT PROTEIN FROM THE ANALYSES OF VARIANCE OF F_1 HYBRIDS AND PARENTS

Source of Variation	df	Heading Date	Percent Protein
Replication	3	14.6	125.7**
Entry	64	599.8**	82.0**
Error	192	13.7	4.0

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE IV

MEANS FOR EIGHT CHARACTERS FROM AN 11-PARENT DIALLEL CROSS OF WINTER WHEAT ALIEN-TRANSLOCATION LINES

Entry	Tiller Number (No./Plant)	Kernels/ Spike (No.)	Kernel Weight (g/1000)	Grain Yield (g/Plant)	Percent Fertility	Plant Height (cm)	Heading Date[1]	Percent Protein
F_1 Hybrids								
Osage/Atr71	15.3	30.2	44.0	16.5	107.6	70.4	39.8	17.4
/Aura	13.4	51.3	37.5	20.0	145.9	79.2	39.5	15.2
/W.Trans	---	---	---	---	---	---	---	---
/6615D	16.8	32.6	40.8	17.2	105.2	71.4	38.0	16.0
/Payne	14.6	52.4	34.2	21.2	153.7	76.4	40.1	15.7
/Salm	12.5	41.4	41.6	17.7	130.7	85.2	45.3	18.5
/Amigo	14.4	40.4	42.8	19.6	130.8	76.0	38.5	15.3
/15322	17.2	34.2	36.7	17.8	108.3	79.5	41.0	17.9
/Flex	13.8	39.3	37.1	17.2	126.9	76.8	45.5	17.9
/PmV	10.0	32.3	30.3	8.3	121.7	64.9	38.3	16.2
Atr71/Aura	11.8	14.1	45.2	6.5	41.6	72.0	37.2	21.2
/W.Trans	14.2	13.9	36.6	6.3	41.3	76.3	41.5	20.2
/6615D	11.2	29.1	38.7	10.8	100.4	64.0	37.3	17.1
/Payne	14.3	26.7	43.1	12.9	89.0	66.9	39.0	17.6
/Salm	13.8	22.8	45.0	12.4	70.1	78.0	40.0	19.6
/Amigo	13.9	26.2	45.2	13.9	87.7	70.8	37.0	17.3
/15322	15.1	23.9	41.6	12.5	83.2	73.7	38.8	16.9
/Flex	14.9	29.6	38.3	13.8	101.6	71.7	39.8	16.8
/PmV	13.9	25.8	40.2	10.1	92.2	67.9	36.0	18.9
Aura/W.Trans	11.1	55.1	39.9	20.1	140.6	81.4	41.0	15.2
/6615D	10.4	12.4	45.2	4.9	36.9	66.0	37.8	20.9
/Payne	10.0	56.0	36.6	16.6	153.8	71.7	37.3	15.9
/Salm	10.1	45.6	43.6	17.7	134.2	80.8	40.0	18.0
/Amigo	10.3	47.5	44.0	17.1	132.6	77.3	36.5	15.8
/15322	11.6	43.6	41.7	16.7	122.9	82.8	38.0	16.5
/Flex	13.6	21.3	45.2	11.6	58.3	76.8	39.8	20.8
/PmV	10.4	49.8	39.9	14.6	147.2	70.7	36.8	16.1
W.Trans/6615D	11.8	21.6	40.4	8.5	68.8	73.6	39.5	18.6
/Payne	12.9	60.1	33.8	22.1	164.1	83.2	43.8	15.0
/Salm	12.5	34.0	38.4	13.5	88.7	94.2	49.0	19.6
/Amigo	12.5	34.5	39.0	14.9	104.4	80.3	43.0	16.2
/15322	11.6	44.4	33.8	14.6	126.2	96.6	49.3	17.7
/Flex	14.4	22.2	35.1	9.1	58.7	88.8	50.3	20.1
/PmV	14.2	49.8	29.5	16.4	152.4	75.3	38.3	16.3

TABLE IV (Continued)

Entry	Tiller Number (No./Plant)	Kernels/ Spike (No.)	Kernel Weight (g/1000)	Grain Yield (g/Plant)	Percent Fertility	Plant Height (cm)	Heading Date[1]	Percent Protein
6615D/Payne	15.2	29.2	42.8	15.7	88.8	70.7	38.0	18.2
/Salm	14.8	28.0	48.5	17.4	83.7	80.0	38.3	19.1
/Amigo	13.7	29.0	41.0	13.6	94.1	67.4	37.5	17.8
/15322	15.0	20.2	42.6	10.1	66.5	74.0	38.0	19.6
/Flex	15.7	34.4	37.9	15.0	109.8	73.8	40.3	17.1
/PmV	12.9	24.4	40.0	9.2	83.4	66.5	32.8	19.9
Payne/Salm	12.8	51.1	38.9	19.6	149.6	80.6	42.0	16.4
/Amigo	12.6	42.6	39.0	18.0	137.6	68.9	37.8	16.6
/15322	13.8	39.4	35.0	16.1	132.1	74.2	40.3	16.6
/Flex	14.9	34.3	37.7	16.3	109.0	71.4	39.5	18.5
/PmV	12.5	38.4	35.1	14.0	127.5	63.1	36.0	17.3
Salm/Amigo	13.4	40.1	43.1	19.1	126.9	80.0	38.8	16.1
/15322	11.8	35.4	35.8	12.4	107.8	90.0	46.5	19.1
/Flex	12.3	30.3	41.2	13.5	87.1	86.7	48.8	20.6
/PmV	11.8	47.6	34.3	15.3	153.6	72.6	37.8	16.6
Amigo/15322	13.2	33.2	38.3	14.3	113.2	76.0	38.5	17.8
/Flex	15.0	27.6	42.1	14.5	90.7	72.1	39.3	19.1
/PmV	13.3	33.6	40.1	14.8	116.2	65.4	34.8	17.7
15322/Flex	15.2	33.4	37.9	16.2	103.9	83.3	43.3	19.5
/PmV	13.3	36.8	33.1	13.4	130.6	69.5	37.0	17.4
Flex/PmV	15.3	27.4	30.8	12.9	95.1	67.0	37.0	20.7
Parents								
Osage	12.3	42.1	36.1	15.0	142.6	73.0	45.5	16.3
Atr71	10.8	24.1	37.6	8.2	96.9	61.1	38.0	17.7
Aura	7.9	52.3	41.2	13.8	131.4	69.7	40.3	17.5
W.Trans	8.5	60.2	27.0	11.4	154.8	93.2	53.8	16.9
6615D	11.6	32.5	34.4	9.8	111.7	62.7	37.0	16.5
Payne	11.3	51.2	32.8	16.5	160.8	69.5	43.3	16.5
Salm	9.6	47.8	35.9	13.7	135.7	81.6	49.0	18.6
Amigo	11.0	37.1	38.9	13.2	131.5	67.1	39.0	15.7
15322	11.2	32.7	28.9	9.0	116.7	73.0	40.3	17.1
Flex	12.4	39.3	30.8	13.2	124.3	77.2	49.5	18.8
PmV	10.8	34.2	28.7	8.3	132.3	56.4	32.2	18.3
F_1 Mean ($\bar{F}_1$)	13.3	34.9	39.4	14.5	108.0	75.4	39.9	17.8
Parental Mean ($\bar{P}$)	10.7	41.2	33.9	12.0	130.8	71.3	42.5	17.3
$\bar{F}_1/\bar{P}$, %	124.3	84.7	116.2	120.8	82.6	105.8	93.9	102.9
Experimental Mean	12.8	35.9	38.5	14.1	111.9	74.7	40.3	17.7
LSD (0.05)	2.3	4.7	2.5	3.4	11.9	4.4	1.8	1.0
C.V.	36.3	26.4	13.1	49.1	21.7	11.9	9.2	11.2

[1]Number of days after March 31.

protein were based on four observations (one observation/entry/replication). The performance of the hybrids expressed as a percent relative to their respective mid-parent and high-parent values are shown in Table V. Parental and hybrid means, ranked in order, along with hybrid-parent deviations may be found in the Appendix (Tables XIV-XXI) for each character separately.

As shown in Table IV, the means for tiller number ranged from 7.9 for Aurora to 17.2 for Osage/CI 15322. The parent with the highest number of tillers was Flex with 12.4. The overall means for F_1's and parents were 13.3 and 10.7, respectively, with the F_1's displaying 24.3% more tillers overall than their parents. Thirty-seven of the 54 F_1's studied exhibited significant positive mid-parent heterosis while 27 F_1's had significantly more tillers than their respective high-parents. One F_1, Osage/Plainsman V, had significantly fewer tillers than its high-parent (Table V).

The number of kernels/spike ranged from 60.2 for Winter Transec to 12.4 for Aurora/Purdue 6615D (Table IV). Winter Transec/Payne, with a value of 60.1, was the F_1 with the highest number of kernels. Arthur 71 was the lowest parent with a mean of 24.1 kernels/spike. The overall F_1 mean was 34.9 while the overall parental mean was 41.2. The mean of all F_1's expressed as a percentage of the overall parental mean was 84.7%. As shown in Table V, five hybrids were significantly higher in kernels/spike than their mid-parent while none was significantly higher than its respective high-parent. Twenty-six hybrids were significantly lower than their mid-parents while 41 were significantly lower than their high-parents.

TABLE V

MEAN PERFORMANCE OF HYBRIDS EXPRESSED AS A PERCENT OF MID-PARENT (MP) AND HIGH-PARENT (HP) VALUES

F_1 Hybrids	Tiller Number %MP	Tiller Number %HP	Kernels/Spike %MP	Kernels/Spike %HP	Kernel Weight %MP	Kernel Weight %HP	Grain Yield %MP	Grain Yield %HP	Percent Fertility %MP	Percent Fertility %HP	Plant Height %MP	Plant Height %HP	Heading Date %MP	Heading Date %HP	Percent Protein %MP	Percent Protein %HP
Osage/Atr71	132**	124**	91	72**	119**	117**	142**	110	90*	75**	105	96	95*	87**	102	98
/Aura	133**	109**	109*	98	97	91**	139**	133**	106	102	111	108	92**	87**	90**	87**
/W.Trans	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
/6615D	141**	137**	87*	77**	116**	113**	139**	115	83**	74**	105	98	92**	84**	98	97
/Payne	124**	119*	112**	102	99	95	135**	128**	89**	84**	107**	105	90**	88**	96	95
/Salm	114	102	92	87**	116**	115**	123*	118	94	92*	110	104	96**	92**	106**	99**
/Amigo	124**	117	102	96	114**	110**	139**	131**	95	92	108**	104	91**	85**	96	94
/15322	146**	140**	91	81**	113**	102	148**	119	84	76**	109	109	96*	90**	107**	105**
/Flex	112	111	97	93	111**	103	122*	115	95	89**	102	99	96*	92**	102**	95**
/PmV	87	81*	85**	77**	94*	84**	71*	55**	89**	85**	100	89**	99	84**	94	89**
Atr71/Aura	126**	109*	37**	27**	115**	110**	59**	47**	36**	32**	110**	103	95**	92**	120**	120**
/W.Trans	146**	131**	33**	23**	113**	97	64*	55**	33**	27**	99	82**	90**	77**	117**	114**
/6615D	100	97	103	90	107*	103	120	110	96	90	103	102	99	98	100	97
/Payne	129**	127**	71**	52**	122**	115**	104	78*	69**	55**	102	96	96	90**	103	99
/Salm	135**	128**	63**	48**	122**	120**	113	91	60**	52**	109**	96	92**	82**	108**	105*
/Amigo	128**	126*	86*	71**	118**	116**	130*	105	77**	67**	110**	106	96	95*	104	98
/15322	137**	135**	84**	73**	125**	111**	145**	139*	78**	71**	110**	101	99	96	97	95
/Flex	128**	120*	93	75**	112**	102	129*	105	92	82**	104	93*	91**	80**	92**	89**
/PmV	129**	129**	89	75**	121**	107*	122	122	80**	70**	116**	120**	103	95*	105*	103
Aura/W.Trans	135**	129*	98	92*	117**	97	160**	146**	98	91**	100	87**	87**	76**	88**	87**
/6615D	107	90	29**	24**	120**	110**	42**	36**	30**	28**	100	95	98	94**	123**	119**
/Payne	104	88	108	107	99	89**	110	101	105	96	103	103	89**	86**	94**	91**
/Salm	115	105	91*	87**	113**	106	129*	128*	100	99	107**	99	90**	82**	100	97
/Amigo	109	94	106	91*	110**	107*	127*	124	101	101	113**	111**	92**	91**	95*	90**
/15322	121**	104	103	83**	119**	101	146**	121	99	94	116**	113**	94*	94*	95*	94*
/Flex	134**	110	47**	41**	126**	110**	86	84	46**	44**	105	99	89**	80**	115**	111**
/PmV	111	96	115**	95	114**	97	132*	106	112**	111*	112**	101	102	91**	90**	88**

TABLE V (Continued)

F_1 Hybrids	Tiller Number %MP	Tiller Number %HP	Kernels/Spike %MP	Kernels/Spike %HP	Kernel Weight %MP	Kernel Weight %HP	Grain Yield %MP	Grain Yield %HP	Percent Fertility %MP	Percent Fertility %HP	Plant Height %MP	Plant Height %HP	Heading Date %MP	Heading Date %HP	Percent Protein %MP	Percent Protein %HP
W.Trans/6615D	117	102	47**	36**	132**	117**	80	75	52**	44**	94*	79**	87**	73**	111**	110**
/Payne	130**	114	108*	100	113**	103	158**	134**	104	102	102	89**	90**	81**	90**	89**
/Salm	137**	130*	63**	56**	122**	107*	108	99	61**	57**	108**	101	95**	91**	110**	105*
/Amigo	128**	114	71**	57**	118**	100	121	113	73**	67**	100	86**	93**	80**	99**	103**
/15322	117	104	96	74**	121**	117**	143**	128	93	82**	116**	104	105*	92**	104**	104**
/Flex	137**	116	45**	37**	121**	114**	74*	69*	42*	38**	104	95*	97	93**	113**	107**
/PmV	146**	131**	106	83**	106	103	166**	144**	106	98	101	81**	89**	71**	93**	89**
6615D/Payne	133**	131**	70**	57**	127**	124**	119	95	65**	55**	107*	102	95*	88**	110**	110**
/Salm	140**	128**	70**	59**	138**	135**	148**	127*	68**	62**	111**	98	89**	78**	109**	103
/Amigo	121*	118	83**	78**	112**	105	118	103	77**	72**	104	100	99	96	111	108**
/15322	132**	129**	62**	62**	135**	124**	107	103	58**	57**	109**	101	98	94*	117**	115**
/Flex	131**	127**	96	88*	116**	110**	130*	114	93	88*	106*	96	93**	81**	97	91**
/PmV	115	111	73**	71**	127**	116**	102	94	68**	63**	112**	106	95*	102**	114**	109**
Payne/Salm	122*	113	103	100	113**	108*	130**	119	101	93	107**	99	91**	86**	93**	88**
/Amigo	113	112	96	83**	109**	100	121*	109	94	86**	101	99	92**	97**	103	101
/15322	123**	122*	94	77**	113**	107	126*	98	95	82**	104	102	96	93**	99	97
/Flex	126**	120*	75**	67**	119**	115**	110	99	76**	68**	97	92**	85**	80**	105*	98
/PmV	113	111	90*	75**	114**	107	113	85	87**	79**	100	91**	95*	83**	99	95*
Salm/Amigo	130**	122*	94	84**	115**	111**	142**	139**	95	94	108**	98	88**	79**	94*	87**
/15322	113	105	88*	74**	110**	100	109	91	85**	79**	116**	110**	104*	95**	107**	103
/Flex	112	99	70**	63**	124**	115**	100	99	67**	64**	109**	106*	99	99	110**	110**
/PmV	116	109	116**	100	106	96	139**	112	115**	113**	105	89**	93**	77**	90**	89**
Amigo/15322	119*	118	95	89	113**	98	129*	108	91*	86**	108**	104	97	96*	109**	104
/Flex	128**	121*	72**	70**	121**	108**	110	110	71**	69**	100	93*	98**	79**	111**	102
/PmV	122*	121*	94	91	119**	103	138**	112	88**	88**	106	97	98	89**	104	97
15322/Flex	129**	123*	93	85*	127**	123**	146**	123	86**	84**	111**	108**	96	87**	109**	104
/PmV	121*	119	110	108	115**	115**	155**	149**	105	99	107*	95	102	92**	98	95
Flex/PmV	132**	123*	75**	70**	128**	124**	120	98	74**	72**	100	87**	91	75**	112**	110**

*,** Significantly different from the mid-parent (or high-parent) at the 0.05 and 0.01 levels of probability, respectively.

The overall F_1 mean for kernel weight was 39.4 g/1000 seeds and the overall parental mean was 33.9 g/1000 (Table IV). On the average, F_1's had 16.2% higher kernel weight than their parents. Means for kernel weight ranged from 48.5 g for Purdue 6615D/Salmon to 27.0 g for Winter Transec. Aurora was the highest parent with a kernel weight of 41.2 g. Forth-eight hybrids exceeded their mid-parent by significant margins while 30 hybrids were significantly greater than their respective high-parents (Table V). Three hybrids had significantly lower kernel weight than their high-parents, and one hybrid was significantly lower than its mid-parent.

Winter Transec/Payne was the highest yielding entry with a mean of 22.1 g/plant while Aurora/Purdue 6615D was the lowest with 4.9 g (Table IV). The overall parental mean was 12.0 g compared to the overall F_1 mean of 14.5 g, i.e., a 20.8% average yield advantage of F_1's over their parents. Thirty hybrids yielded significantly greater than their respective mid-parents while 11 hybrids yielded significantly more than their high-parents. Five and six hybrids yielded significantly less than their mid-parents and high-parents, respectively (Table V).

Percent fertility ranged from 164.1% for Winter Transec/Payne to 36.9% for Aurora/Purdue 6615D (Table IV). The parent with the highest percent fertility was Payne with 160.8% while the lowest parent was Arthur 71 with 96.9%. Eight hybrids displayed less than 80% spike fertility. Those hybrids were Arthur 71/Salmon, Winter Transec/Purdue 6615D, Purdue 6615D/CI 15322, Winter Transec/Flex, Aurora/Flex, Arthur 71/Aurora, Arthur 71/Winter Transec, and Aurora/Purdue 6615D. The possible reasons for their depressed fertility and its implications in breeding programs will be considered in the following chapter. The overall means for fertility were 108.0% and 130.8% for F_1's and parents, respectively, which is a 17.4% decline in fertility in the F_1's overall. Forty hybrids had significantly lower values for spike fertility than their respective high-parents and 31 were significantly lower than their mid-parent values for this trait. Only two hybrids, Salmon/ Plainsman V and Aurora/Plainsman V exhibited significantly greater fertility values than either their mid-parent or high-parent values (Table V).

The highest parental mean for plant height was Winter Transec with 93.2 cm (Table IV) while Winter Transec/CI 15322 was the tallest hybrid with a mean plant height of 96.6 cm. Plainsman V was the entry with the shortest stature having a mean of 56.4 cm. The shortest hybrid was Payne/Plainsman V with a mean of 63.1 cm. As shown in Table V, 14 hybrids were significantly shorter than their tallest parent while only one hybrid, Winter Transec/Purdue 6615D was significantly shorter than its mid-parent. On the other hand, 25 were significantly taller than their mid-parents; and six were significantly taller than their tallest parent.

Means for heading date ranged from the earliest value of 32.2 days for Plainsman V to the latest value of 53.8 days for Winter Transec. The earliest hybrid was Purdue 6615D/Plainsman V with a value of 32.8 days while the latest hybrid was Winter Transec/Flex with a value of 50.3 days (Table IV). The F_1's averaged 6.1% earlier than the parents with means of 39.9 and 42.5 days for the F_1's and parents, respectively, one hybrid was later than its latest parent (high-parent), and two hybrids were significantly later than their respective mid-parents

(Table V). Thirty-four of 55 hybrids were significantly earlier than their mid-parent values while 49 of 55 were significantly earlier than their respective later parent.

Percent protein means ranged from 21.3% for Arthur 71/Aurora to 15.0% for Winter Transec/Payne. The highest parent was Flex with 18.8% and the lowest was Amigo with 15.7% (Table IV). The overall means for F_1's and parents were 17.8 and 17.3%, respectively, which results in a 2.9% advantage for the F_1's. Twenty-four hybrids were significantly higher than their mid-parents while 17 hybrids were significantly higher than their high-parents. Thirteen hybrids were significantly lower than their mid-parents for percent protein while 17 were significantly lower than their high-parents (Table V).

Diallel Analyses for General and Specific Combining Ability

All available data were subjected to diallel analyses (9) for general combining ability (GCA) and specific combining ability (SCA) for each of the eight characters. As stated previously, all the plants of the Osage/Winter Transec hybrid died as seedlings; therefore, no SCA effects could be calculated for that hybrid. The mean squares from the combining ability analyses of variance are presented in Table VI. Highly significant GCA and SCA variances were observed for all characters.

The variance components for GCA (associated with additive genetic effects) and SCA (nonadditive effects) were calculated to obtain estimates of additive and nonadditive effects. Although estimates of variance components for GCA and SCA are valid in the strict sense only

TABLE VI

MEAN SQUARES FOR GENERAL COMBINING ABILITY, SPECIFIC COMBINING ABILITY, AND ERROR FOR EIGHT CHARACTERS

Trait	GCA[1]	SCA	Error
Tiller Number	41.47**	10.25**	2.70
Kernels/Spike	1795.95**	265.30**	11.31
Kernel Weight	299.90**	44.02**	3.16
Grain Yield	173.33**	35.62**	5.93
Percent Fertility	11140.11**	2367.88**	74.19
Plant Height	1421.63**	47.36**	9.78
Heading Date	350.38**	15.43**	1.71
Percent Protein	25.98**	7.34**	0.94

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

[1]The degrees of freedom for GCA, SCA, and error mean squares were 10, 54, and 192, respectively.

with random models, estimates of those components were made in this study even though the genotypes included herein were considered fixed rather than random. This was done to provide information regarding the relative magnitude of the components while recognizing at the same time that restrictions are placed on the interpretations of those estimates. The variance components, along with the GCA/SCA ratios for each trait, are presented in Table VII. The GCA components were 2.82 and 4.17 times greater than the SCA components for heading date and plant height, respectively, indicating the importance of additive genetic effects for those two traits. On the other hand, the ratios of GCA to SCA were less than unity for tiller number, kernels/spike, kernel weight, grain yield, percent fertility, and percent protein which indicates that those six traits are influenced to a greater degree by dominance, epistasis, or both.

GCA Effects

Because the GCA mean squares were significant for all traits (Table VI), GCA effects for the individual parents could be estimated for each of the eight characters studied. Those estimates and their standard errors are shown in Table VIII. The GCA effects, as expected, agreed roughly in rank with the parental means for all characters (comparisons between Tables IV and VIII). This suggests that selection of parents for use in a plant breeding program to improve these traits may be based largely on phenotypic performance of the parents themselves and also suggests the presence of considerable additive effects.

The parents Osage and Payne displayed significant positive GCA effects for grain yield, kernels/spike, and percent fertility. Those

TABLE VII

ESTIMATES OF VARIANCE COMPONENTS FOR GENERAL AND SPECIFIC COMBINING ABILITY FOR EIGHT CHARACTERS

Trait	GCA Component	SCA Component	GCA/SCA
Tiller Number	4.37	7.54	0.78
Kernels/Spike	198.29	253.99	0.78
Kernel Weight	32.97	40.86	0.81
Grain Yield	18.60	29.69	0.64
Percent Fertility	1229.50	2293.69	0.54
Plant Height	156.87	37.58	4.17
Heading Date	38.74	13.72	2.82
Percent Protein	2.83	6.85	0.41

TABLE VIII

ESTIMATES OF GENERAL COMBINING ABILITY EFFECTS AMONG ELEVEN PARENTS FOR EIGHT CHARACTERS

Parent	Tiller Number	Kernels/ Spike	Kernel Weight	Grain Yield	Percent Fertility	Plant Height	Heading Date	Percent Protein
Osage	0.89	3.85*	-0.73	2.46*	15.41*	0.94	1.45*	-1.00*
Atr71	0.46	-10.99*	2.49*	-2.89*	-25.97*	-4.98*	-1.77*	0.48
Aura	-1.98*	5.53*	3.11*	0.29	2.35	-0.06	-1.62*	-0.14
W.Trans	-0.67	5.22*	-3.56*	-0.39	3.00	9.41*	4.97*	-0.22
6615D	0.51	-8.26*	1.99*	-2.11*	-21.90*	-5.09*	-2.62*	0.39
Payne	0.16	7.64*	-1.45*	2.76*	21.59*	-2.50*	-0.37	-0.87*
Salm	-0.70	3.29*	1.65*	1.25	4.44	7.11*	2.99*	0.68
Amigo	0.01	-0.34	2.44*	1.27	3.92	-2.33	-1.98*	-0.85*
15322	0.47	-1.80	-2.03*	-0.57	-1.40	3.60*	0.44	0.10
Flex	1.22	-4.22*	-0.65	-0.24	-12.03*	1.83	2.84*	1.29*
PmV	-0.37	0.08	-3.26*	-1.83	10.59*	-7.93*	-4.33*	0.14
S.E.	0.64	1.32	0.70	0.96	3.38	1.23	0.51	0.38

two parents also exhibited the largest negative GCA effects for percent protein. Osage displayed a tendency toward later heading date in its hybrids while Payne showed tendencies toward lighter kernel weight and shorter plant height. Arthur 71 showed significant negative GCA effects for kernels/spike, grain yield, percent fertility, plant height (shorter plants) and heading date (earlier maturing) as well as a tendency toward increased kernel weight. The greatest amount of positive effects for plant height were recorded for Winter Transec, Salmon, and CI 15322 indicating that they contribute toward taller stature in their hybrids. Winter Transec and Salmon also showed trends in their offspring toward later heading dates, as did Osage and Flex. Flex showed the greatest positive effects for percent protein and tiller number (though the latter was not significant at the 0.05 probability level). The parent Aurora showed significant negative GCA effects for tiller number; however, it displayed positive effects for kernels/spike and kernel weight. Winter Transec and Plainsman V had the largest negative GCA effects for kernel weight. Arthur 71 and Purdue 6615D had significant negative effects for yield, percent fertility, and kernels/spike.

SCA Effects

The SCA effects for tiller number and kernels/spike are given in Table IX along with their respective standard errors. None of the hybrids exhibited significant positive SCA effects for tiller number. One hybrid, Osage/Plainsman V, exhibited significant negative SCA effects for this trait while Payne/Plainsman V displayed substantial, but not significant, negative effects. All hybrids with Plainsman V

TABLE IX

ESTIMATES OF SPECIFIC COMBINING ABILITY EFFECTS FOR TILLER NUMBER AND KERNELS/SPIKE

	Tiller Number (Upper Diagonal)							Kernels/Spike (Lower Diagonal)			
Parent	Osage	Atr71	Aura	W.Trans	6615D	Payne	Salm	Amigo	15322	Flex	PmV
Osage		1.13	1.66	---	2.55	0.68	-0.52	0.67	3.02	-1.10	-5.73
Atr71	1.21		0.43	1.56	-2.58	0.86	1.22	0.57	1.29	0.36	-1.93
Aura	5.77	16.52		0.90	-0.96	-1.04	-0.03	-0.62	-0.29	1.48	-1.11
W.Trans	---	-16.40	8.19		0.87	0.58	0.99	0.32	-1.05	1.01	-0.50
6615D	0.91	12.91	-21.03	-11.47		1.69	2.10	0.37	1.15	1.09	-2.28
Payne	4.83	-6.09	6.76	11.10	-6.31		0.55	-0.44	0.29	0.66	-4.22
Salm	-1.80	-5.63	4.65	-10.60	-3.10	4.09		1.23	-0.76	-1.04	-1.87
Amigo	0.74	1.44	6.17	-6.46	1.51	-0.79	1.01		-0.10	0.90	-1.08
15322	-3.93	0.58	3.72	4.82	-5.81	-2.57	-2.18	0.77		0.68	-2.22
Flex	3.55	8.70	-16.15	-14.91	10.81	-5.24	-4.91	-3.92	3.35		-1.20
PmV	-9.56	-22.50	-19.76	22.04	9.39	-5.58	-13.32	-0.60	2.60	9.66	
	S.E. (1) = 4.57		S.E. (2) = 4.37					S.E. (1) = 2.23		S.E. (2) = 2.14	

(1) Standard error between two crosses having one common parent.
(2) Standard error between two crosses having no parents in common.

as a parent showed negative SCA effects for tiller number.

Seven hybrids, i.e., Arthur 71/Aurora, Arthur 71/Purdue 6615D, Winter Transec/Payne, Winter Transec/Plainsman V, Purdue 6615D/Flex, Purdue 6615D/Plainsman V, and Flex/Plainsman V, displayed significant positive SCA effects for kernels/spike. Winter Transec/Plainsman V exhibited the largest positive SCA effect. Ten hybrids, on the other hand, displayed significant negative SCA effects for this trait. These were Osage/Plainsman V, Arthur 71/Winter Transec, Aurora/Purdue 6615D, Aurora/Flex, Aurora/Plainsman V, Winter Transec/Purdue 6615D, Winter Transec/Salmon, Winter Transec/Flex, Salmon/Plainsman V, and Arthur 71/Plainsman V. The largest negative SCA effect was exhibited by Arthur 71/Plainsman V.

Table X contains SCA effects for kernel weight and grain yield. Purdue 6615D/Salmon had the highest positive SCA effect for kernel weight with a value of 6.43. Two other hybrids, Purdue 6615D/CI 15322 and Aurora/Flex, had considerable, though non-significant at the 0.05 level, positive effects for this trait. All the hybrids having Plainsman V as a parent displayed negative SCA effects for kernel weight with three of these hybrids, i.e., Winter Transec/Plainsman V, Salmon/Plainsman V, and CI 15322/Plainsman V, displaying negative effects of statistically significant magnitude. Three other hybrids, Osage/Aurora, Arthur 71/Purdue 6615D, and Aurora/Payne, showed considerable negative effects for kernel weight though none was significantly different from zero. These results are in good agreement with the ranked means of the F_1 hybrids for kernel weight (Table XVI).

None of the hybrids showed significant positive SCA effects for grain yield. Two hybrids, Osage/Plainsman V and Aurora/Purdue 6615D,

TABLE X

ESTIMATES OF SPECIFIC COMBINING ABILITY EFFECTS FOR
KERNEL WEIGHT AND GRAIN YIELD

	Kernel Weight (Upper Diagonal)							Grain Yield (Lower Diagonal)			
Parent	Osage	Atr71	Aura	W.Trans	6615D	Payne	Salm	Amigo	15322	Flex	PmV
Osage		3.81	-3.24	---	1.16	-2.06	2.27	2.67	1.08	0.09	-4.95
Atr71	2.75		1.22	-0.73	-4.17	3.68	2.46	1.92	2.72	-1.94	-3.21
Aura	3.06	5.02		1.92	1.69	-3.43	0.48	0.05	2.21	4.29	-1.76
W.Trans	---	-4.59	6.06		3.54	0.37	1.86	1.72	0.97	0.87	-6.28
6615D	2.70	1.69	-7.42	-3.11		3.87	6.43	-1.87	4.19	-1.84	-5.05
Payne	1.85	-1.06	-0.55	5.60	0.92		0.26	-0.35	0.12	1.44	-1.21
Salm	-0.12	-0.14	1.99	-1.51	4.13	1.42		0.64	-2.22	1.84	-8.25
Amigo	1.72	1.39	1.44	-0.15	0.28	-0.19	2.47		-0.50	1.89	-1.81
15322	1.81	1.82	2.87	1.40	-1.37	-0.21	-2.40	-0.49		2.18	-5.35
Flex	0.83	2.76	-2.62	-4.35	3.28	-0.34	-1.65	-0.69	2.83		-2.51
PmV	-10.51	0.58	1.08	2.59	-1.02	-4.26	-1.25	-2.27	-2.28	-0.40	
	S.E. (1) = 3.31		S.E. (2) = 3.17					S.E. (1) = 2.58		S.E. (2) = 2.47	

(1) Standard error between two crosses having one common parent.
(2) Standard error between two crosses having no parents in common.

displayed significant negative SCA effects for this trait. These results are in good agreement with the rank of the F_1 means.

SCA effects for percent fertility and plant height are given in Table XI. Ten hybrids, Arthur 71/Purdue 6615D, Winter Transec/Payne, Arthur 71/Flex, Purdue 6615D/Flex, Arthur 71/Plainsman V, Winter Transec/Plainsman V, Purdue 6615D/Plainsman V, Salmon/Plainsman V, Aurora/Flex, and Flex/Plainsman V exhibited significant positive SCA effects for percent fertility. The Flex/Plainsman V hybrid showed the highest positive effect. Arthur 71/Aurora, Arthur 71/Winter Transec, Aurora/Purdue 6615D, Winter Transec/Purdue 6615D, Winter Transec/Salmon, Winter Transec/Flex, and Aurora/Plainsman V displayed significant negative SCA effects for this trait with Aurora/Purdue 6615D showing the greatest negative effect.

Only Winter Transec/CI 15322 displayed significant positive SCA effects for plant height. Two hybrids, Salmon/Plainsman V and CI 15322/Plainsman V, showed significant negative SCA effects.

The SCA effects for heading date and percent protein are presented in Table XII. All the hybrids having Plainsman V as one of their parents exhibited positive SCA effects for heading date (later heading), and three of them (i.e., Aurora/Plainsman V, Payne/Plainsman V, and CI 15322/Plainsman V) showed significant positive SCA effects for this trait. Two hybrids, Winter Transec/Purdue 6615D and Payne/Flex, showed substantial but non-significant negative SCA effects.

Arthur 71/Aurora, Arthur 71/Winter Transec, Aurora/Purdue 6615D, and Aurora/Flex exhibited significant positive SCA effects for percent protein. Five hybrids, Arthur 71/Flex, Aurora/Winter Transec,

TABLE XI

ESTIMATES OF SPECIFIC COMBINING ABILITY EFFECTS FOR
PERCENT FERTILITY AND PLANT HEIGHT

	Percent Fertility (Upper Diagonal)							Plant Height (Lower Diagonal)			
Parent	Osage	Atr71	Aura	W.Trans	6615D	Payne	Salm	Amigo	15322	Flex	PmV
Osage		5.99	15.98	---	-0.58	4.51	-1.33	-0.72	-17.89	11.38	-16.95
Atr71	-0.48		-47.01	-47.94	36.17	-18.79	-20.51	-2.46	-1.56	27.38	31.18
Aura	3.44	2.11		23.07	-55.72	17.66	15.21	14.13	9.74	44.18	-51.76
W.Trans	---	-3.02	-2.88		-24.43	27.33	-30.96	-14.74	12.39	-44.46	63.14
6615D	0.63	-0.79	-3.72	-5.62		22.98	-10.95	-0.01	-22.37	31.57	25.92
Payne	3.04	-0.47	-0.68	1.41	3.41		11.41	-0.11	-0.31	-12.78	-11.42
Salm	2.23	0.94	-1.11	2.73	2.98	1.11		6.33	-7.38	-17.48	40.99
Amigo	2.53	3.26	4.80	-1.73	-0.07	-1.12	0.35		-1.54	-13.32	0.92
15322	0.03	0.20	4.37	8.68	0.59	-1.81	4.41	-0.17		5.17	16.46
Flex	-0.91	-0.06	0.08	2.60	2.14	-2.79	2.87	-2.33	2.95		67.83
PmV	-6.76	2.12	-1.32	-4.19	2.51	-1.74	-9.01	-2.39	-10.15	-3.18	
	S.E. (1) = 4.24		S.E. (2) = 4.00					S.E. (1) = 11.71		S.E. (2) = 11.19	

(1) Standard error between two crosses having one common parent.
(2) Standard error between two crosses having no parents in common.

TABLE XII

ESTIMATES OF SPECIFIC COMBINING ABILITY EFFECTS FOR HEADING DATE AND PERCENT PROTEIN

	Heading Date (Upper Diagonal)							Percent Protein (Lower Diagonal)			
Parent	Osage	Atr71	Aura	W.Trans	6615D	Payne	Salm	Amigo	15322	Flex	PmV
Osage		-0.37	-0.77	---	-1.27	-1.02	0.37	-1.40	-1.33	0.77	2.86
Atr71	0.22		0.20	-2.13	1.20	0.70	-1.67	0.32	-0.36	-1.76	2.77
Aura	-1.35	3.14		-2.79	1.55	-1.20	-1.82	-0.34	-1.26	-1.92	5.31
W.Trans	---	2.29	-2.10		-3.29	-1.29	0.59	-0.42	3.40	1.99	0.56
6615D	-1.08	-1.43	2.94	0.79		0.55	-2.57	1.66	-0.26	-0.42	1.06
Payne	-0.11	0.30	-0.85	-1.62	0.99		-1.07	-0.33	-0.26	-3.42	3.84
Salm	1.18	0.79	-0.25	1.47	0.32	-1.05		-2.70	2.62	2.46	1.22
Amigo	-0.56	-0.04	-0.92	-0.44	0.55	0.61	-1.42		-0.39	-2.05	3.12
15322	1.08	-1.37	-1.09	0.18	1.45	-0.27	0.68	0.91		-0.47	4.62
Flex	-0.05	-2.64	1.94	1.39	-2.24	0.39	0.94	1.02	0.47		1.45
PmV	0.06	-0.33	-1.52	-1.62	-1.92	1.00	-2.26	0.51	1.27	0.20	
	S.E. (1) = 0.95		S.E. (2) = 0.89					S.E. (1) = 1.78		S.E. (2) = 1.67	

(1) Standard error between two crosses having one common parent.
(2) Standard error between two crosses having no parents in common.

Purdue 6615D/Flex, Purdue 6615D/Plainsman V, and Salmon/Plainsman V, showed significant negative effects.

CHAPTER V

DISCUSSION

According to Sprague and Tatum (33) GCA provides a measure of additive gene action. Brown et al (2) and Kronstad and Foote (16) reported that most of the genetic variability of performance traits studied in wheat was due to additive effects of genes. The ratios of variance components obtained in the present study (Table VII) indicated that most of the genetic variation for plant height and heading date could be accounted for by variation due to GCA. However, SCA components were more important for the other six traits in this study.

Tiller number, kernels/spike, kernel weight, grain yield, percent fertility, and percent protein showed larger components for SCA than for GCA. The number of kernels/spike is related to percent fertility, and some of the hybrids did show unusually high levels of spike sterility. This could account, at least in part, for the larger SCA component for kernels/spike. Grain yield in wheat is a complex trait; the major components of which are tiller number, kernels/spike, and kernel weight. Interactions among these traits could also account in part for the high SCA estimate for grain yield. Yield is also associated with spike fertility; and the high SCA component for this trait could account in part for the high SCA estimate for grain yield. The occurrence of significant SCA effects for all traits in this study suggests that the genetic variation for each trait was also partly due to dominance, epistasis, or both.

The GCA effects, considering all traits, indicated Osage and Payne were the better parents of the 11 lines studied in this test, while Aurora, Salmon, Amigo, CI 15322, Flex, and Plainsman V appeared to be next in potential value. On the other hand, Arthur 71, Purdue 6615D, and Winter Transec seemed to be the least favorable in this set. Some combinations of these translocation lines resulted in heterosis for grain yield while others resulted in low fertility accompanied by a reduction in kernels/spike, low yield, and high protein content.

As shown in Appendix Tables XIV to XXI, the best hybrid exceeded the best parent for tiller number, kernel weight, grain yield, percent fertility, plant height, and percent protein. Eighteen hybrids exceeded or were equal to the highest yielding parent, Payne. Deviations of those high-yielding hybrids from their high-parents ranged from 0.1 to 6.3 g/plant while average heterosis (compared to the high-parent) of those hybrids was 123%. Three hybrids, Arthur 71/Aurora, Arthur 71/Winter Transec, and Aurora/Purdue 6615D, had lower grain yield than Arthur 71, the lowest yielding parent. Deviations of the low-yielding hybrids from their high-parents ranged from -5.1 to -8.9 while the average high-parent heterosis of the three low-yielding hybrids was only 46%. These three hybrids also exhibited the lowest values for percent fertility, ranging from 41.6 to 36.9%, and the lowest values for kernels/spike.

The relationships among the characters of grain yield, percent fertility, kernels/spike, and percent protein as observed for the 10 highest and 10 lowest yielding hybrids are illustrated in Table XIII. The highest yielding hybrids generally displayed increased levels of

TABLE XIII

HIGH-YIELDING VS. LOW-YIELDING HYBRIDS

F_1 Hybrid	Grain Yield (g/Plant)	Percent Fertility	Kernels/ Spike (No.)	Percent Protein
High-Yielding Group				
W.Trans/Payne	22.1	164.1	60.1	15.0
Osage/Payne	21.2	135.7	52.4	15.7
Aura/W.Trans	20.1	140.6	55.1	15.2
Osage/Aura	20.0	145.9	51.3	15.2
Osage/Amigo	19.6	130.8	40.4	15.3
Payne/Salm	19,6	149.6	51.1	16.4
Salm/Amigo	19.1	126.9	40.1	16.1
Payne/Amigo	18.0	137.6	42.6	16.1
Osage/15322	17.8	108.3	34.2	17.9
Osage/Salm	17.7	130.7	41.4	18.5
Low-Yielding Group				
Atr71/6615D	10.8	100.4	29.1	17.1
Atr71/PmV	10.1	92.2	25.8	18.9
6615D/15322	10.1	66.5	20.2	19.6
6615D/PmV	9.2	83.4	24.4	19.9
W.Trans/Flex	9.1	58.7	22.2	20.1
W.Trans/6615D	8.5	68.8	21.6	18.6
Osage/PmV	8.3	121.7	32.3	16.2
Atr71/Aura	6.5	41.6	14.1	21.2
Atr71/W.Trans	6.3	41.3	13.9	20.2
Aura/6615D	4.9	36.9	12.4	20.9

fertility in relation to the overall F_1 mean for that character, with the exception of the Osage/CI 15322 hybrid. This particular hybrid had the highest tiller number (which also contributes to yield) of all parents and F_1's. With the exception of Osage/CI 15322, these top 10 yielding hybrids also had increased numbers of kernels/spike and were among the lowest in percent protein.

The 10 lowest yielding hybrids generally had depressed levels of spike fertility, fewer kernels/spike, and increased levels of protein with two exceptions, Arthur 71/Purdue 6615D and Osage/Plainsman V. These two hybrids were also among the lowest hybrids for tiller number and kernel weight, respectively. Both of those traits are components of yield. The reduction in kernel weight exhibited by Osage/Plainsman V was probably due to the hybrid necrosis of this hybrid. Four of the parents associated with the high-yielding hybrids were also present in combinations which resulted in low yield and low fertility, i.e., Aurora, Winter Transec, Osage, and CI 15322. Either Payne, Osage, or both were parents in eight of the 10 high-yielding F_1's while Osage was present in only one of the lowest yielding hybrids.

If the chromosomes involved in the translocations are considered (Table I), it should be noted that those F_1's which exhibited positive heterosis for yield contained either the 2R-4A of Winter Transec, the 3Ag-3D of Osage, the 1R-1Bs of Aurora, the 1R-1B of Salmon, or the unknown translocations of Payne, Amigo, or CI 15322. The F_1's having reduced yield contained either the $6C^u$-6Bl translocation of Arthur 71 or the 7el-7Dl translocation of Purdue 6615D. There are two exceptions, the Winter Transec/Flex and the Osage/Plainsman V F_1's. These contain the 2R-4A and 3Ag-3D translocations of Winter Transec and

Osage, respectively, along with the unknown translocations of Flex and Plainsman V.

The extra vigor for yield apparently imparted by Osage and Payne may or may not have been due to the particular alien translocation involved in these two lines. It should be noted that these two were developed specifically for the Southern Great Plains region within which this study was conducted. Their potency for yield may be due to their background genotypes rather than the particular alien-gene complex involved. To make a completely definitive study of the effects of combining alien translocation lines, each translocation should be in a common genetic background which, in this case, could be approached by backcrossing each line onto a single adapted cultivar.

In a previous study (27, 28), F_1's and parents of a diallel cross among six alien translocation lines were examined. The results of that study were that GCA components were larger than those for SCA for tiller number, kernel weight, plant height, and heading date, while SCA components were larger for kernels/spike, grain yield, percent sterility, and percent protein. Four hybrids were found to have high positive heterosis for grain yield while four others exhibited high levels of sterility, low values for kernels/spike, and low grain yields. It was also found that two parents, Aurora and Purdue 6615D, were involved as parents in the four highest, as well as the four lowest yielding hybrids.

In the present study GCA components were larger than those for SCA for plant height and heading date while SCA components were larger for kernels/spike, tiller number, kernel weight, grain yield, percent fertility, and percent protein. Several hybrids were found to have high positive heterosis for grain yield. Several others displayed low levels of spike fertility accompanied by low grain yield, decreased kernels/spike, and increased levels of protein. It is noteworthy that four of the five lowest yielding hybrids in this present study were also the four lowest yielding hybrids in the previous study. It is of further interest to note that one of the four parents present in combinations common to both high-yielding and low-yielding groups in the present study, was also common to both groups in the previous study. The results of this study are in good general agreement with those of the previous study.

The number of kernels/spike in the hybrids in this, as well as in the previous study (27), were lower than the parental mean. In the previous study, only one hybrid had a significantly greater number of kernels/spike than its high-parent while two hybrids had significantly more kernels/spike than their respective mid-parents. In the present study, no hybrid had significantly more kernels/spike than its high-parent while six hybrids had a significantly greater number of kernels/spike than their mid-parents. On the other hand, in both studies there was a preponderance of hybrids with significantly fewer kernels/spike than both their high- and mid-parents.

The low values for kernels/spike, as well as the low levels of spike fertility exhibited by some of these hybrids, may have been due to the loss of portions of wheat chromatin when two of the alien translocation lines were brought together. The loss of wheat chromatin may result in reduction of chromosome pairing which could result in chromosome imbalance. This would cause a decrease in spike fertility, which in turn would result in a decrease in kernels/spike.

Wheat breeding programs in the Hard Red Winter Wheat Area have progressed to the point that more attention is now being given to the development of cultivars having multiple-pest resistance. Because many of the pest-resistant sources now available are alien translocation lines, it is important to know something about possible beneficial vs. detrimental effects when those translocations are combined into a single genotype.

The results of this study indicate that while certain combinations of these alien translocation lines give an increase in fertility accompanied by increased yield, other combinations should probably be avoided in breeding programs on the Southern Great Plains, e.g. Arthur 71/Aurora, Arthur 71/Winter Transec, Aurora/Purdue 6615D, Osage/Plainsman V, and Winter Transec/Purdue 6615D.

CHAPTER VI

SUMMARY AND CONCLUSIONS

The F_1's and parents of a diallel cross among 11 alien-translocation lines of winter wheat were studied to determine the response of eight performance traits when alien gene complexes were combined in all possible two-way combinations. The 11 parents and 54 F_1's (one F_1 died in the seedling stage) were grown in a space-planted nursery on the Agronomy Research Station, Stillwater, Oklahoma, during the 1978-79 season. The experiment was conducted in a randomized, complete-block design with four replications. Eight vigorous, bordered plants from each single-row plot were evaluated. Measurements were taken on tiller number, kernels/spike, kernel weight, grain yield, percent fertility, plant height, heading date, and percent protein. All data were subjected to standard analyses of variance, as well as Griffing's analyses for GCA and SCA. Hybrid-parent contrasts were also examined for each trait.

The GCA components were larger than those for SCA for plant height and heading date, indicating that additive gene effects were more important for those two traits than were nonadditive effects. On the other hand, SCA components were larger for tiller number, kernels/spike, kernel weight, grain yield, percent fertility, and percent protein, indicating that in this particular set of genotypes nonadditive gene effects for those traits were more important than additive effects.

The combining ability data for yield and yield components indicated that Osage and Payne were probably the better parents in this set while Arthur 71, Winter Transec, and Purdue 6615D were the least so. Eleven hybrids, i.e., Winter Transec/Payne, Osage/Payne, Aurora/Winter Transec, Osage/Aurora, Osage/Amigo, Salmon/Amigo, Aurora/Salmon, Purdue 6615D/Salmon, Winter Transec/Plainsman V, CI 15322/Plainsman V, and Arthur 71/CI 15322 showed significant positive high-parent heterosis for yield. On the other hand, several exhibited low levels of fertility, low numbers of kernels/spike, and low grain yields.

Aurora, Winter Transec, Osage, and CI 15322 were involved as parents in some of the highest yielding hybrids as well as some of the lowest yielding. This indicates that specific combinations of alien-translocation lines could do very well; whereas, others would do very poorly. Certain combinations of alien-translocation lines might present some problems in a wheat breeding program on the Southern Great Plains, e.g., Aurora/Purdue 6615D, Arthur 71/Winter Transec, Arthur 71/Aurora, Osage/Plainsman V, and Winter Transec/Purdue 6615D. This situation would have important implications in wheat breeding programs for multiple-pest resistance because many of the present sources of pest resistance exist in alien-translocation lines.

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APPENDIX

TABLE XIV

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR TILLER NUMBER

Parent or F_1 Hybrid	Rank	Tiller Number (No./Plant)	Hybrid-Parent Deviation Mid-Parent	Hybrid-Parent Deviation High-Parent
Osage/15322	1	17.2	5.4**	4.9**
Osage/6615D	2	16.8	4.9**	4.5**
6615D/Flex	3	15.7	3.6**	3.4**
Osage/Atr71	4	15.3	3.8**	3.0**
Flex/PmV	4	15.3	3.7**	2.9*
15322/Flex	6	15.2	3.4**	2.8*
6615D/Payne	6	15.2	3.8**	3.6**
Atr71/15322	8	15.1	4.1**	3.9**
Amigo/Flex	9	15.0	3.3**	2.6*
6615D/15322	9	15.0	3.6**	3.4**
Atr71/Flex	11	14.9	3.3**	2.5*
Payne/Flex	11	14.9	3.1**	2.5*
6615D/Salm	13	14.8	4.2**	3.2**
Osage/Payne	14	14.6	2.8**	2.3*
W.Trans/Flex	15	14.4	3.9**	2.0
Osage/Amigo	15	14.4	2.8**	2.1
Atr71/Payne	17	14.3	3.3**	3.0**
Atr71/W.Trans	18	14.2	4.5**	3.4**
W.Trans/PmV	18	14.2	4.5**	3.4**
Atr71/PmV	20	13.9	3.1**	3.1**
Atr71/Amigo	20	13.9	3.0**	2.9*
Atr71/Salm	22	13.8	3.6**	3.0**
Osage/Flex	22	13.8	1.5	1.4
Payne/15322	22	13.8	2.6**	2.5*
6615D/Amigo	25	13.7	2.4*	2.1
Aura/Flex	26	13.6	3.5**	1.2
Osage/Aura	27	13.4	5.6**	5.0**
Salm/Amigo	27	13.4	3.1**	2.4*
Amigo/PmV	29	13.3	2.4*	2.3*
15322/PmV	29	13.3	2.3*	2.1
Amigo/15322	31	13.2	2.1*	2.0
W.Trans/Payne	32	12.9	3.0**	1.6
6615D/PmV	32	12.9	1.7	1.3
Payne/Salm	34	12.8	2.4*	1.5
Payne/Amigo	35	12.6	1.5	1.3
W.Trans/Amigo	36	12.5	2.7**	1.5
W.Trans/Salm	36	12.5	3.4**	2.9*
Payne/PmV	36	12.5	1.5	1.2
Osage/Salm	36	12.5	1.6	0.2
Flex	40	12.4	---	---
Salm/Flex	41	12.3	1.3	-0.1
Osage	41	12.3	---	---
Atr71/Aura	43	11.8	6.6**	2.3*
Salm/15322	43	11.8	1.4	0.6
Salm/PmV	43	11.8	1.6	1.0
W.Trans/6615D	43	11.8	1.7	0.2
W.Trans/15322	47	11.6	1.7	0.4
Aura/15322	47	11.6	2.1**	0.4
6615D	47	11.6	---	---
Payne	50	11.3	---	---
Atr71/6615D	51	11.2	0.0	-0.4
15322	51	11.2	---	---
Aura/W.Trans	53	11.1	2.9**	2.5*
Amigo	54	11.0	---	---
Atr71	55	10.8	---	---
PmV	55	10.8	---	---
Aura/PmV	57	10.4	1.1	-0.4
Aura/6615D	57	10.4	0.6	-1.2
Aura/Amigo	59	10.3	0.9	-0.7
Aura/Salm	60	10.1	1.4	0.5
Aura/Payne	61	10.0	0.4	-1.3
Osage/PmV	61	10.0	-1.5	-2.3*
Salm	63	9.6	---	---
W.Trans	64	8.6	---	---
Aura	65	7.9	---	---
Osage/W.Trans	66	---	Seedling Lethal	

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE XV

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR KERNELS/SPIKE

Parent or F_1 Hybrid	Rank	Kernels/ Spike (No.)	Hybrid-Parent Deviation Mid-Parent	High-Parent
W.Trans	1	60.2	---	---
W.Trans/Payne	2	60.1	4.4*	-0.1
Aura/Payne	3	56.0	2.8	3.7
Aura/W.Trans	4	55.1	-1.1	-5.1*
Osage/Payne	5	52.4	5.8**	1.2
Aura	6	52.3	---	---
Osage/Aura	7	51.3	4.0*	-1.0
Payne	8	51.2	---	---
Payne/Salm	9	51.1	1.6	-0.1
Aura/PmV	10	49.8	6.6**	-2.5
W.Trans/PmV	10	49.8	2.6	-10.4**
Salm	12	47.8	---	---
Salm/PmV	13	47.6	6.6**	-0.2
Aura/Amigo	14	47.5	2.8	-4.8*
Aura/Salm	15	45.6	-4.4*	-6.7**
W.Trans/15322	16	44.4	-2.1	-15.8**
Aura/15322	17	43.6	1.1	-8.7**
Payne/Amigo	18	42.6	-1.5	-8.6**
Osage	19	42.1	---	---
Osage/Salm	20	41.4	-3.6	-6.4**
Osage/Amigo	21	40.4	0.8	-1.7
Salm/Amigo	22	40.1	-2.3	-7.7**
Payne/15322	23	39.4	-2.6	-11.8**
Osage/Flex	24	39.3	-1.4	-2.8
Flex	24	39.3	---	---
Payne/PmV	26	38.4	-4.3*	-12.8**
Amigo	27	37.1	---	---
15322/PmV	28	36.8	3.4	2.6
Salm/15322	29	35.4	-4.9*	-12.4**
W.Trans/Amigo	30	34.5	-14.1**	-25.7**
6615D/Flex	31	34.4	-1.5	-4.9*
Payne/Flex	32	34.3	-10.9**	-16.9**
Osage/15322	33	34.2	-3.2	-7.9**
PmV	33	34.2	---	---
W.Trans/Salm	35	34.0	-20.0**	-26.2**
Amigo/PmV	36	33.6	-2.0	-3.5
15322/Flex	37	33.4	-2.6	-5.9*
Amigo/15322	38	33.2	-1.7	-3.9
15322	39	32.7	---	---
Osage/6615D	40	32.6	-4.7*	-9.5**
6615D	41	32.5	---	---
Osage/PmV	42	32.3	-5.8**	-9.8**
Salm/Flex	43	30.3	-13.3**	-17.5**
Osage/Atr71	44	30.2	-2.9	-11.9**
Atr71/Flex	45	29.6	-2.1	-9.7**
6615D/Payne	46	29.2	-12.6**	-22.0**
Atr71/6615D	47	29.1	0.8	-3.4
6615D/Amigo	48	29.0	-5.8**	-8.1**
6615D/Salm	49	28.0	-12.1**	-19.8**
Amigo/Flex	50	27.6	-10.6**	-11.7**
Flex/PmV	51	27.4	-9.4**	-11.9**
Atr71/Payne	52	26.7	-10.9**	-24.5**
Atr71/Amigo	53	26.2	-4.4*	-10.9**
Atr71/PmV	54	25.8	-3.3	-8.4**
6615D/PmV	55	24.4	-8.9**	-9.8**
Atr71	56	24.1	---	---
Atr71/15322	57	23.9	-4.5**	-8.8**
Atr71/Salm	58	22.8	-13.1**	-25.0**
W.Trans/Flex	59	22.2	-27.6**	-38.0**
W.Trans/6615D	60	21.6	-24.7**	-38.6**
Aura/Flex	61	21.3	-24.5**	-31.0**
6615D/15322	62	20.2	-12.4**	-12.5**
Atr71/Aura	63	14.1	-24.1**	-38.2**
Atr71/W.Trans	64	13.9	-28.2**	-46.3**
Aura/6615D	65	12.4	-30.0**	-39.9**
Osage/W.Trans	66	---	Seedling Lethal	

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE XVI

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR KERNEL WEIGHT

Parent or F_1 Hybrid	Rank	Kernel Weight (g/1000)	Hybrid-Parent Deviation Mid-Parent	Hybrid-Parent Deviation High-Parent
6615D/Salm	1	48.5	13.4**	12.6**
Aura/6615D	2	45.2	7.4**	4.0**
Aura/Flex	2	45.2	9.2**	4.0**
Atr71/Aura	2	45.2	5.8**	4.0**
Atr71/Amigo	2	45.2	6.9**	6.3**
Atr71/Salm	6	45.0	8.3**	7.4**
Osage/Atr71	7	44.0	7.1**	6.4**
Aura/Amigo	7	44.0	4.0**	2.8*
Aura/Salm	9	43.6	5.1**	2.4
Salm/Amigo	10	43.1	5.7**	4.2**
Atr71/Payne	10	43.1	7.9**	5.5**
Osage/Amigo	12	42.8	5.3**	3.9**
6615D/Payne	12	42.8	9.2**	8.4**
6615D/15322	14	42.6	11.0**	8.2**
Amigo/Flex	15	42.1	7.3**	3.2**
Aura/15322	16	41.7	6.7**	0.5
Atr71/15322	17	41.6	8.4**	4.0**
Osage/Salm	17	41.6	6.1**	5.5**
Aura	19	41.2	---	---
Salm/Flex	19	41.2	7.9**	5.3**
6615D/Amigo	21	41.0	4.4**	2.1
Osage/6615D	22	40.8	5.6**	4.7**
W.Trans/6615D	23	40.4	9.7**	6.0**
Atr71/PmV	24	40.2	7.1**	2.6*
Amigo/PmV	25	40.1	6.3**	1.2
6615D/PmV	26	40.0	8.5**	5.6**
Aura/W.Trans	27	39.9	5.8**	-1.3
Aura/PmV	27	39.9	4.9**	-1.3
W.Trans/Amigo	29	39.0	6.1**	0.1
Payne/Amigo	29	39.0	3.2**	0.1
Payne/Salm	31	38.9	4.6**	3.0*
Amigo	31	38.9	---	---
Atr71/6615D	33	38.7	2.7*	1.1
W.Trans/Salm	34	38.4	6.9**	2.5*
Atr71/Flex	35	38.3	4.1**	0.7
Amigo/15322	35	38.3	4.4**	-0.6
Flex/PmV	37	38.2	8.4**	7.4**
15322/Flex	38	37.9	8.1**	7.1**
6615D/Flex	38	37.9	5.3**	3.5**
Payne/Flex	40	37.7	5.9**	4.9**
Atr71	41	37.6	---	---
Osage/Aura	42	37.5	-1.1	-3.7**
Osage/Flex	43	37.1	3.7**	1.0
Osage/15322	44	36.7	4.2**	0.6
Aura/Payne	45	36.6	-0.4	-4.6**
Atr71/W.Trans	45	36.6	4.3**	-1.0
Osage	47	36.1	---	---
Salm	48	35.9	---	---
Salm/15322	49	35.8	3.4**	-0.1
W.Trans/Flex	50	35.1	6.2**	4.3**
Payne/PmV	50	35.1	4.4**	2.3
Payne/15322	52	35.0	4.2**	2.2
6615D	53	34.4	---	---
Salm/PmV	54	34.3	2.0	-1.6
Osage/Payne	55	34.2	-0.3	-1.9
W.Trans/Payne	56	33.8	3.9**	1.0
W.Trans/15322	56	33.8	5.9**	4.9**
15322/PmV	58	33.1	4.3**	4.2**
Payne	59	32.8	---	---
Flex	60	30.8	---	---
Osage/PmV	61	30.3	-2.1*	-5.8**
W.Trans/PmV	62	29.5	1.7	0.8
15322	63	28.9	---	---
PmV	64	28.7	---	---
W.Trans	65	27.0	---	---
Osage/W.Trans	66	---	Seedling Lethal	

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE XVII

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR GRAIN YIELD

Parent or F_1 Hybrid	Rank	Grain Yield (g/Plant)	Hybrid-Parent Deviation Mid-Parent	Hybrid-Parent Deviation High-Parent
W.Trans/Payne	1	22.1	8.2**	5.6**
Osage/Payne	2	21.2	5.4**	4.7**
Aura/W.Trans	3	20.1	7.5**	6.3**
Osage/Aura	4	20.0	5.6**	5.0**
Osage/Amigo	5	19.6	5.5**	4.6**
Payne/Salm	5	19.6	4.5**	3.1
Salm/Amigo	7	19.1	5.7**	5.4**
Payne/Amigo	8	18.0	3.2*	1.5
Osage/15322	9	17.8	5.8**	2.8
Osage/Salm	10	17.7	3.3*	2.7
Aura/Salm	10	17.7	3.9**	3.9*
6615D/Salm	12	17.4	5.6**	3.7*
Osage/6615D	13	17.2	4.8**	2.2
Osage/Flex	13	17.2	3.1*	2.2
Aura/Amigo	15	17.1	3.6*	3.3
Aura/15322	16	16.7	5.3**	2.9
Aura/Payne	17	16.6	1.5	0.1
Osage/Atr71	18	16.5	4.9**	1.5
Payne	18	16.5	---	---
W.Trans/PmV	20	16.4	6.5**	5.0**
Payne/Flex	21	16.3	1.5	-0.2
15322/Flex	22	16.2	5.1**	3.0
Payne/15322	23	16.1	3.4*	-0.4
6615D/Payne	24	15.7	2.6	-0.8
Salm/PmV	25	15.3	4.3**	1.6
Osage	26	15.0	---	---
6615D/Flex	26	15.0	3.5*	1.8
W.Trans/Amigo	28	14.9	2.6	1.7
Amigo/PmV	29	14.8	4.1**	1.6
W.Trans/15322	30	14.6	4.4**	3.2
Aura/PmV	30	14.6	3.6*	0.8
Amigo/Flex	32	14.5	1.3	1.3
Amigo/15322	33	14.3	3.2*	1.1
Payne/PmV	34	14.0	1.6	-2.5
Atr71/Amigo	35	13.9	3.2*	0.7
Atr71/Flex	36	13.8	3.1*	0.6
Aura	36	13.8	---	---
Salm	38	13.7	---	---
6615D/Amigo	39	13.6	2.1	0.4
W.Trans/Salm	40	13.5	1.0	-0.2
Salm/Flex	40	13.5	0.1	-0.2
15322/PmV	42	13.4	4.8**	4.4*
Flex	43	13.2	---	---
Amigo	43	13.2	---	---
Flex/PmV	45	12.9	2.1	-0.3
Atr71/Payne	45	12.9	0.6	-3.6*
Atr71/15322	47	12.5	3.9**	3.5*
Atr71/Salm	48	12.4	1.5	-1.3
Salm/15322	48	12.4	1.1	-1.3
Aura/Flex	50	11.6	-1.9	-2.2
W.Trans	51	11.4	---	---
Atr71/6615D	52	10.8	1.8	1.0
Atr71/PmV	53	10.1	1.9	1.8
6615D/15322	53	10.1	0.7	0.3
6615D	55	9.8	---	---
6615D/PmV	56	9.2	0.2	-0.6
W.Trans/Flex	57	9.1	-3.2*	-4.1*
15322	58	9.0	---	---
W.Trans/6615D	59	8.5	-2.1	-2.9
Osage/PmV	60	8.3	-3.3*	-6.7**
PmV	60	8.3	---	---
Atr71	62	8.2	---	---
Atr71/Aura	63	6.5	-4.5**	-7.3**
Atr71/W.Trans	64	6.3	-3.5*	-5.1**
Aura/6615D	65	4.9	-6.9**	-8.9**
Osage/W.Trans	66	---	Seedling Lethal	

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE XVIII

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR PERCENT FERTILITY

Parent or F_1 Hybrid	Rank	Percent Fertility	Hybrid-Parent Deviation Mid-Parent	Hybrid-Parent Deviation High-Parent
W.Trans/Payne	1	164.1	6.3	3.3
Payne	2	160.8	---	---
W.Trans	3	154.8	---	---
Aura/Payne	4	153.8	7.7	-7.0
Salm/PmV	5	153.6	19.6**	17.9**
W.Trans/PmV	6	152.4	8.9	-2.4
Payne/Salm	7	149.6	1.4	-11.2
Aura/PmV	8	147.2	15.4**	14.9*
Osage/Aura	9	145.9	-8.9	3.3
Osage	10	142.6	---	---
Aura/W.Trans	11	140.6	-2.5	-14.2**
Payne/Amigo	12	137.6	-8.5	-23.2**
Osage/Payne	13	135.7	-16.0**	-25.1**
Salm	13	135.7	---	---
Aura/Salm	15	134.2	0.7	-1.5
Aura/Amigo	16	132.6	1.2	1.1
PmV	17	132.3	---	---
Payne/15322	18	132.1	-6.6	-28.7**
Amigo	19	131.5	---	---
Aura	20	131.4	---	---
Osage/Amigo	21	130.8	-6.2	-11.8
Osage/Salm	22	130.7	-8.4	-11.9*
15322/PmV	23	130.6	6.1	-1.7
Payne/PmV	24	127.5	-19.0**	-33.3**
Osage/Flex	25	126.9	-6.5	-15.7**
Salm/Amigo	25	126.9	-6.7	-8.8
W.Trans/15322	27	126.2	-9.6	-28.6**
Flex	28	124.3	---	---
Aura/15322	29	122.9	-1.1	-8.5
Osage/PmV	30	121.7	-15.7**	-20.9**
15322	31	116.7	---	---
Amigo/PmV	32	116.2	-15.7**	-16.1**
Amigo/15322	33	113.2	-10.9*	-18.3**
6615D	34	111.7	---	---
6615D/Flex	35	109.8	-8.2	-14.5**
Payne/Flex	36	109.0	-33.5**	-51.8**
Osage/15322	37	108.3	-8.4	-34.3**
Salm/15322	38	107.8	-18.4**	-27.9**
Osage/Atr71	39	107.6	-12.1*	-35.0**
Osage/6615D	40	105.2	-21.9**	-37.4**
W.Trans/Amigo	41	104.4	-38.7**	-50.4**
15322/Flex	42	103.9	-16.6**	-20.4**
Atr71/Flex	43	101.6	-9.0	-22.7**
Atr71/6615D	44	100.4	-3.9	-11.3
Atr71	45	96.9	---	---
Flex/PmV	46	95.1	-33.2**	-37.2**
6615D/Amigo	47	94.1	-27.5**	-37.4**
Atr71/PmV	48	92.2	-22.4**	-40.1**
Amigo/Flex	49	90.7	-37.2**	-40.8**
Atr71/Payne	50	89.0	-39.8**	-71.8**
6615D/Payne	51	88.8	-47.4**	-72.0**
W.Trans/Salm	52	88.7	-56.6**	-66.1**
Atr71/Amigo	53	87.7	-26.5**	-43.8**
Salm/Flex	54	87.1	-42.9**	-48.6**
6615D/Salm	55	83.7	-40.0**	-52.0**
6615D/PmV	56	83.4	-38.6**	-48.9**
Atr71/15322	57	83.2	-23.6**	-33.5**
Atr71/Salm	58	70.1	-46.2**	-65.6**
W.Trans/6615D	59	68.8	-64.4**	-86.0**
6615D/15322	60	66.5	-47.7**	-50.2**
W.Trans/Flex	61	58.7	-80.8**	-96.1**
Aura/Flex	62	58.3	-69.5**	-73.1**
Atr71/Aura	63	41.6	-72.5**	-89.8**
Atr71/W.Trans	64	41.3	-84.5**	-113.5**
Aura/6615D	65	36.9	-84.6**	-94.5**
Osage/W.Trans	66	---	Seedling Lethal	

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE XIX

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR PLANT HEIGHT

Parent or F_1 Hybrid	Rank	Plant Height (cm)	Hybrid-Parent Deviation Mid-Parent	Hybrid-Parent Deviation High-Parent
W.Trans/15322	1	96.6	13.5**	3.4
W.Trans/Salm	2	94.2	6.8**	1.0
W.Trans	3	93.2	---	---
Salm/15322	4	90.0	12.7**	8.4**
W.Trans/Flex	5	88.8	3.6	-4.4*
Salm/Flex	6	86.7	7.3**	5.1*
Osage/Salm	7	85.2	1.1	-0.1
15322/Flex	8	83.3	8.2**	6.1**
W.Trans/Payne	9	83.2	1.9	-10.0**
Aura/15322	10	82.8	11.5**	9.8**
Salm	11	81.6	---	---
Aura/W.Trans	12	81.4	-0.1	-11.8**
Aura/Salm	13	80.8	5.2**	-0.8
Payne/Salm	14	80.6	5.1**	-1.0
W.Trans/Amigo	15	80.3	0.2	-12.9**
6615D/Salm	16	80.0	7.9**	-1.6
Salm/Amigo	16	80.0	5.6**	-1.6
Osage/15322	18	79.5	1.2	0.8
Osage/Aura	19	79.2	-1.7	-2.3
Atr71/Salm	20	78.0	6.6**	-3.6
Aura/Amigo	21	77.3	8.9**	7.6**
Flex	22	77.2	---	---
Aura/Flex	23	76.8	3.4	-0.4
Osage/Flex	23	76.8	1.7	-0.4
Osage/Payne	25	76.4	5.1**	3.4
Atr71/W.Trans	26	76.3	-0.8	-16.9**
Osage/Amigo	27	76.0	5.9**	3.0
Amigo/15322	27	76.0	5.9**	3.0
W.Trans/PmV	29	75.3	0.5	-17.9**
Payne/15322	30	74.2	2.9	1.2
6615D/15322	31	74.0	6.2**	1.0
6615D/Flex	32	73.8	3.9*	-3.4
Atr71/15322	33	73.7	6.6**	0.7
W.Trans/6615D	34	73.6	-4.3*	-19.6**
Osage	35	73.0	---	---
15322	35	73.0	---	---
Salm/PmV	37	72.6	3.6	-9.0**
Amigo/Flex	38	72.1	-0.1	-5.1*
Atr71/Aura	39	72.0	6.6**	2.3
Atr71/Flex	40	71.7	2.6	-5.5*
Aura/Payne	40	71.7	2.1	2.0
Payne/Flex	42	71.4	-1.9	-5.8**
Osage/6615D	42	71.4	3.6	-1.6
Atr71/Amigo	44	70.8	6.7**	3.7
Aura/PmV	45	70.7	7.7**	1.0
6615D/Payne	45	70.7	4.6*	1.2
Osage/Atr71	47	70.4	3.3	-2.6
Aura	48	69.7	---	---
15322/PmV	49	69.5	4.8*	-3.5
Payne	49	69.5	---	---
Payne/Amigo	51	68.9	0.6	-0.6
Atr71/PmV	52	67.9	9.1**	6.8**
6615D/Amigo	53	67.4	2.5	0.3
Amigo	54	67.1	---	---
Flex/PmV	55	67.0	0.1	-10.2**
Atr71/Payne	56	66.9	1.6	-2.6
6615D/PmV	57	66.5	7.0**	3.8
Aura/6615D	58	66.0	-0.2	-3.7
Amigo/PmV	59	65.4	3.6	-1.7
Osage/PmV	60	64.9	0.2	-8.1**
Atr71/6615D	61	64.0	2.1	1.3
Payne/PmV	62	63.1	0.2	-6.4**
6615D	63	62.7	---	---
Atr71	64	61.1	---	---
PmV	65	56.4	---	---
Osage/W.Trans	66	---	Seedling Lethal	

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE XX

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR HEADING DATE

Parent or F_1 Hybrid	Rank	Heading Date[1]	Hybrid-Parent Deviation Mid-Parent	High-Parent
W.Trans	1	53.8	---	---
W.Trans/Flex	2	50.3	-1.3	-3.5**
Flex	3	49.5	---	---
W.Trans/15322	4	49.3	2.3*	-4.5**
Salm	5	49.0	---	---
W.Trans/Salm	5	49.0	-2.4**	-4.8**
Salm/Flex	7	48.8	-0.4	-0.7
Salm/15322	8	46.5	1.9*	-2.5**
Osage	9	45.5	---	---
Osage/Flex	9	45.5	-2.0*	-4.0**
Osage/Salm	11	45.3	-1.9**	-3.7**
W.Trans/Payne	12	43.8	-4.8**	-10.0**
15322/Flex	13	43.3	-1.6	-6.2**
Payne	13	43.3	---	---
W.Trans/Amigo	15	43.0	-3.4**	-10.8**
Payne/Salm	16	42.0	-4.1**	-7.0**
Atr71/W.Trans	17	41.5	-4.4**	-12.3**
Osage/15322	18	41.0	-1.9*	-4.5**
Aura/W.Trans	18	41.0	-6.1**	-12.8**
6615D/Flex	20	40.3	-2.9**	-9.2**
Payne/15322	20	40.3	-1.5	-3.0**
Aura	20	40.3	---	---
15322	20	40.3	---	---
Osage/Payne	24	40.1	-4.3**	-5.4**
Aura/Salm	25	40.0	-4.6**	-9.0**
Atr71/Salm	25	40.0	-3.5**	-9.0**
Osage/Atr71	27	39.8	-1.9*	-5.7**
Atr71/Flex	27	39.8	-3.9**	-9.7**
Aura/Flex	27	39.8	-5.1**	-9.7**
W.Trans/6615D	30	39.5	-5.9**	-14.3**
Payne/Flex	30	39.5	-6.9**	-10.0**
Osage/Aura	30	39.5	-3.4**	-6.0**
Amigo/Flex	33	39.3	-4.9**	-10.2**
Amigo	34	39.0	---	---
Atr71/Payne	34	39.0	-1.6	-4.3**
Salm/Amigo	36	38.8	-5.2**	-10.2**
Atr71/15322	36	38.8	-0.3	-1.5
Osage/Amigo	38	38.5	-3.8**	-7.0**
Amigo/15322	38	38.5	-1.1	-1.8*
W.Trans/PmV	40	38.3	-4.7**	-15.5**
6615D/Salm	40	38.3	-4.7**	-10.7**
Osage/PmV	40	38.3	-0.5	-7.2**
Atr71	43	38.0	---	---
Osage/6615D	43	38.0	-3.3**	-7.5**
6615D/Payne	43	38.0	-2.1*	-5.3**
6615D/15322	43	38.0	-0.6	-2.3*
Aura/15322	43	38.0	-2.3*	-2.3*
Aura/6615D	48	37.8	-0.8	-2.5**
Salm/PmV	48	37.8	-2.8**	-11.2**
Payne/Amigo	48	37.8	-3.3**	-5.5**
6615D/Amigo	51	37.5	-0.5	-1.5
Aura/Payne	52	37.3	-4.5**	-3.0**
Atr71/6615D	52	37.3	-0.2	-0.7
Atr71/Aura	54	37.2	-1.9**	-3.1**
Flex/PmV	55	37.0	-3.8	-12.5**
15322/PmV	55	37.0	0.8	-3.3**
Atr71/Amigo	55	37.0	-1.5	-2.0*
6615D	55	37.0	---	---
Aura/PmV	59	36.8	0.6	-3.5**
Aura/Amigo	60	36.5	-3.1**	-3.8**
Atr71/PmV	61	36.0	0.9	-2.0*
Payne/PmV	61	36.0	-1.8*	-7.3**
Amigo/PmV	63	34.8	-0.8	-4.2**
6615D/PmV	64	32.8	-1.8*	-4.2**
PmV	65	32.2	---	---
Osage/W.Trans	66	---	Seedling Lethal	

[1]Number of days after March 31.

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

TABLE XXI

PARENTAL AND F_1 RANKED MEANS AND HYBRID-PARENT DEVIATIONS FOR PERCENT PROTEIN

Parent or		Percent	Hybrid-Parent Deviation	
F_1 Hybrid	Rank	Protein	Mid-Parent	High-Parent
Atr71/Aura	1	21.2	3.6**	3.5**
Aura/6615D	2	20.9	3.9**	3.4**
Aura/Flex	3	20.8	2.7**	2.0**
Flex/PmV	4	20.7	2.1**	1.9**
Salm/Flex	5	20.6	1.9**	1.8**
Atr71/W.Trans	6	20.2	2.9**	2.5**
W.Trans/Flex	7	20.1	2.5**	1.3**
6615D/PmV	8	19.9	2.5**	1.6**
Atr71/Salm	9	19.6	1.5**	1.0*
W.Trans/Salm	9	19.6	1.9**	1.0*
6615D/15322	11	19.6	2.8**	2.5**
15322/Flex	12	19.5	1.6**	0.7
Amigo/Flex	13	19.1	1.9**	0.3
6615D/Salm	13	19.1	1.6**	0.5
Salm/15322	13	19.1	1.3**	0.5
Atr71/PmV	16	18.9	0.9*	0.6
Flex	17	18.8	---	---
Salm	18	18.6	---	---
W.Trans/6615D	18	18.6	1.9**	1.7**
Payne/Flex	20	18.5	0.9*	-0.3
Osage/Salm	20	18.5	1.1**	-0.1
PmV	22	18.3	---	---
6615D/Payne	23	18.2	1.7**	1.7**
Aura/Salm	24	18.0	-0.1	-0.6
Osage/15322	25	17.9	1.2**	0.8
Osage/Flex	25	17.9	0.3	-0.9
6615D/Amigo	27	17.8	1.7	1.3**
Amigo/15322	27	17.8	1.4**	0.7
Amigo/PmV	29	17.7	0.7	-0.6
W.Trans/15322	29	17.7	0.7	0.6
Atr71	29	17.7	---	---
Atr71/Payne	32	17.6	0.5	-0.1
Aura	33	17.5	---	---
15322/PmV	34	17.4	-0.3	-0.9
Osage/Atr71	34	17.4	0.4	-0.3
Atr71/Amigo	36	17.3	0.6	-0.4
Payne/PmV	36	17.3	-0.1	-1.0*
6615D/Flex	38	17.1	-0.5	-1.7**
Atr71/6615D	38	17.1	0.0	-0.6
15322	38	17.1	---	---
W.Trans	41	16.9	---	---
Atr71/15322	41	16.9	-0.5	-0.8
Atr71/Flex	43	16.8	-1.4**	-2.0**
Salm/PmV	44	16.6	-1.8**	-2.0**
Payne/15322	44	16.6	-0.2	-0.5
Payne/Amigo	44	16.6	0.5	0.1
6615D	47	16.5	---	---
Payne	47	16.5	---	---
Aura/15322	47	16.5	-0.8*	-1.0*
Payne/Salm	50	16.4	-1.2**	-2.2**
W.Trans/PmV	51	16.3	-1.3**	-2.0**
Osage	51	16.3	---	---
Osage/PmV	53	16.2	-1.1**	-2.1**
W.Trans/Amigo	53	16.2	-0.1	-0.7
Salm/Amigo	55	16.1	-1.0*	-2.5**
Aura/PmV	55	16.1	-1.8**	-2.2**
Osage/6615D	57	16.0	-0.4	-0.5
Aura/Payne	58	15.9	-1.1**	-1.6**
Aura/Amigo	59	15.8	-0.8*	-1.7**
Amigo	60	15.7	---	---
Osage/Payne	60	15.7	-0.7	-0.8
Osage/Amigo	62	15.3	-0.7	-1.0*
Osage/Aura	63	15.2	-1.7**	-2.3**
Aura/W.Trans	63	15.2	-2.0**	-2.3**
W.Trans/Payne	65	15.0	-1.7**	-1.9**
Osage/W.Trans	66	---	Seedling Lethal	

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

VITA 2

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Doctor of Philosophy

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