

LINE X TESTER ANALYSIS FOR COMBINING ABILITY IN SORGHUM  
(*SORGHUM BICOLOR* (L.) MOENCH)

BY

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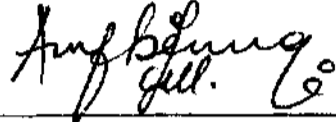
A Thesis Submitted to *the* Postgraduate School,  
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Department of Plant Science  
Faculty of Agriculture  
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Zaria, Nigeria

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DECLARATION

I hereby declare that this work presented in this thesis is original. No part of this thesis has previously been submitted for a degree or any other qualification. References made to published and unpublished literature have been duly acknowledged.

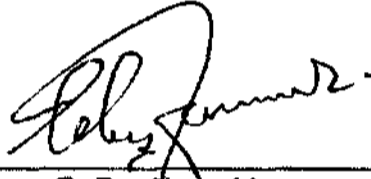


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CERTIFICATION

This thesis titled "LINE X TESTER ANALYSIS FOR COMBINING ABILITY IN SORGHUM (*SORGHUM ~~bicolor~~* (L.) MOENCH)" BY KIMBENG, COLLINS ANYE meets the regulations governing the award of the degree of Master of Science of Ahmadu Bello University, Zaria and is approved for its scientific contribution to knowledge and literary presentation.



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DEDICATION

To Mum and Dad  
for caring so much about my education

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ABSTRACT

A line X tester analysis in sorghum involving fifteen F<sub>1</sub> hybrids obtained by crossing five restorer lines onto each of three male sterile lines showed significant general combining ability among males for plant height and 1000-seed weight and among females for days to 50% flowering, plant height, head weight, number of kernels/panicle and 1000-seed weight. Specific combining ability variances were significant for percentage protein, panicle length and grain yield. The  $\sigma^2_a/\sigma^2_b$  ratio revealed the preponderance of non-additive gene action for all characters except plant height, days to 50% flowering and 1000-seed weight.

Narrow sense heritability estimates were high for plant height, days to 50% flowering and 1000-seed weight; moderate for head weight, seedling vigour and number of kernels/panicle; low for panicle length, percentage protein and grain yield.

The presence of heterosis for low x low, low x high, high x low hybrids for grain yield, supports that an appreciable amount of non-allelic genic interaction exist for this trait.

The restorer NR 71178 and male sterile 2219A are good general combiners for grain yield, while hybrid combinations M60042A x NR71156, 2219A x NR 71167 and MA9 x NR71178 excelled in their specific combining ability for this trait.

High genetic correlation between number of kernels/panicle and grain yield, indicates that selection of plant types from this population which produce large number of kernels/panicle would enhance the attainment of lines or hybrids with high yield potentials.

TABLE OF CONTENTS

<u>Contents</u>	Page
Title	i
Certification	ii
Declaration	iii
Dedication	iv
Acknowledgements	v
Abstract	vi
Table of Contents	vii
List of Tables	viii
List of Appendices	ix
CHAPTER ONE <u>INTRODUCTION</u>	1
CHAPTER TWO <u>LITERATURE REVIEW</u>	
Combining ability	4
Maturity	8
Plant height	11
Yield and yield components	13
Protein and lysine	17
Intercharacter correlation	20
CHAPTER THREE <u>MATERIALS AND METHODS</u>	24
Statistical methods	27
CHAPTER FOUR <u>RESULTS</u>	34
CHAPTER FIVE <u>DISCUSSIONS</u>	55
Summary and conclusions	66
REFERENCES	69
APPENDIX	82

LIST OF TABLES

<u>Tables</u>	<u>Page</u>
1 Description of parents	24
2 Form of analysis of variance for parents and hybrids	27
3 Form of analysis of variance for hybrids	28
4 Form of analysis of variance and covariance for all pairs of characters	33
5 Analysis of variance showing sources of variations, degrees of freedom (d.f.) and mean squares (m.s.) of nine traits in sorghum	35
6 Analysis of variance showing sources of variations, degrees of freedom (d.f.) and mean squares (m.s.) for combining ability estimates using of nine traits in sorghum	37
7 Estimates of components of variance and heritability for nine traits	38
8 Estimates of general and specific combining ability effects for seedling vigour	40
9 Estimates of general and specific combining ability effects for days to 50% flowering	41
10 Estimates of general and specific combining ability effects for plant height	42
11 Estimates of general and specific combining ability effects for number of kernels/panicle	43
12 Estimates of general and specific combining ability effects for head weight	45
13 Estimates of general and specific combining ability effects for 1000-grain weight	46
14 Estimates of general and specific combining ability effects for panicle length	47
15 Estimates of general and specific combining ability effects for protein	48
16 Estimates of general and specific combining ability effects for grain yield	49
17 Heterosis of hybrids over superior (sp) and mid-parent (mp) for all characters measured in this study	51
18 Genotypic ( $r_g$ ), phenotypic ( $r_{pn}$ ) (in brackets) and error ( $r_e$ ) correlation coefficients for all pairs of traits	54



## LIST OF APPENDICES

<u>Appendix</u>	Page
I Mean values for eight parental lines for characters measured	82
II Mean values of the hybrids for all characters measured	83
III Means, standard errors, ranges and coefficient of variation (%) of entries (E), Parents (P) and hybrids (H) for all traits measured	84

## CHAPTER ONE

### INTRODUCTION

Sorghum (*Sorghum bicolor* (L.) Moench) is the fourth most important cereal crop in the world, behind wheat, rice and maize (Purseglove, 1972). The crop is an important source of food, livestock feed and industrial raw material.

In Nigeria, it is the most important cereal food crop but its cultivation is restricted to the Savanna zones. It forms the staple food for millions of people in these areas because the grains are used to produce various local foods and drinks. The leaves and grains are also used as livestock feed, while the stalks are used for fencing, fuel, making baskets, mats, huts and a variety of other purposes (Curtis, 1965; Doggett, 1970).

As well as its importance as a food crop, sorghum is also used in the industries for various purposes. It is used in making bread, cakes, wax, syrup, starch, beverage food and drinks, and for brewing (Nwasike, 1982; 1987). The Nigerian Federal Government's ban on the importation of other cereal products like wheat and barley will likely increase the industrial demand of sorghum. Thus, the present level of production of sorghum, of which 80-85% is consumed mainly as food, must be doubled so as to accommodate the impending industrial demand of the crop (Nwasike, 1987). The present land area devoted to sorghum production is approximately 6 million

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hectares (Nwasike, 1982; 1987; Obilana, 1983), with a total annual production of between 4.8 to 6 million tonnes and an average yield of 800 to 1087 kg/ha (Obilana 1983; Nwasike, 1982; F.A.O, 1987).

In a crop improvement programme, the ultimate goal is to evolve cultivars that perform better than the existing ones. One way of achieving this goal is through hybridization of inbred lines. The choice of suitable parents in the development of superior hybrids is a matter of constant concern to breeders. This is because the performance of an inbred line *per se* is not always a good indicator of their superior combining ability. It is a common experience of the breeder that certain combinations nick well to produce superior hybrids whereas others involving equally promising parents produce disappointing progeny. It is therefore necessary to assess the genetic potential of the parents by estimating their combining ability before they are used in hybridization programmes.

Sorghum being essentially a self-pollinated crop does not lend itself naturally to rapid genetic manipulations, like hybridization, as do other open pollinated crop species like maize and millet. However, with the discovery of cytoplasmic genetic male sterility and the sterility-restorer system in sorghum, breeders have been able to develop superior sorghum hybrids with much rapidity. Thus, besides eliminating the burden of emasculations in sorghum,

the line  $\times$  tester technique gives a useful opportunity for rapid development of hybrids and is more comprehensive than other breeding techniques like diallel, which are generally based on fewer parents (Chandra *et al.*, 1969).

The objectives of this study are therefore:

- a) To assess the combining ability of some sorghum lines (to be used) in hybrid combinations;
- b) To determine the gene action governing the inheritance of some desired agronomic traits and per cent protein; and
- c) To estimate phenotypic and genotypic correlations among the traits, so as to determine the degree of association among them.

## CHAPTER TWO

## LITERATURE REVIEW

## COMBINING ABILITY

The term combining ability is commonly used by breeders to express the relative performance of a line in hybrid combinations and is usually divided into two, general and specific combining ability, which will herein be denoted as g.c.a and s.c.a respectively. Sprague and Tatum (1942) defined g.c.a as the average performance of a line in hybrid combination. They used the term s.c.a to designate instances in which certain hybrid combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved. A low variance for s.c.a effect was said to indicate that hybrids involving a particular line have performed as expected on the basis of their g.c.a.

General combining ability in particular, is directly related to the breeding value of the parent (Falconer, 1981), and is associated with additive gene action. Specific combining ability on the other hand, is commonly associated with all effects which cannot be accounted for by the additive scheme, such as dominance, epistasis and genotype - environment interaction (Rosenow, 1970).

Estimates of g.c.a and s.c.a variances from a set of crosses relate to estimates of genetic

variance for the base population from which the parent varieties are samples (Matzinger and Kempthorne, 1956). General combining ability is relatively more important than s.c.a in previously unselected materials, while s.c.a assumes greater importance in materials which have been previously selected for g.c.a (Sprague and Tatum, 1942; Kambal and Webster, 1965; Beil, 1965). Their interactions with the environment also vary. Kambal and Webster (1965) and later Niehaus and Pickett (1966) found g.c.a to be more stable than s.c.a over locations and years, while a contrary result where s.c.a was more stable was reported by Beil and Atkin (1967). Matzinger *et al.* (1959) had earlier found the following interactions to be significant in a diallel analysis of yield data obtained from several crosses in maize; g.c.a  $\times$  years, g.c.a  $\times$  years  $\times$  locations and s.c.a  $\times$  locations. They concluded that estimates of combining ability obtained from a single environment are subject to large bias from interactions of general effects with years and locations.

Several studies on combining ability indicate that general combining ability is more important than specific combining ability, although specific effects are of sufficient importance to merit attention in breeding programmes (Rosenow, 1970). Beil and Atkins (1967) found significant differences among g.c.a of all the lines for all characters measured, while significant differences among s.c.a

were expressed only for 1000-seed weight. Mukuru (1970) reported significant g.c.a mean squares for all characters studied, although s.c.a mean squares were also significant for 1000-seed weight, days to 50% bloom and per cent oil. Out of eleven characters studied, Karale *et al.* (1984) found both g.c.a and s.c.a variances to be highly significant but g.c.a components were consistently of higher magnitude than those for s.c.a for most of the characters studied.

Niehaus and Pickett (1966) computed g.c.a and s.c.a components from a diallel cross involving 8 inbred lines in the  $F_1$  and  $F_2$  generations. General combining ability was important in both the  $F_1$  and  $F_2$  generations, whereas s.c.a was influential only in the  $F_1$  generation but still to a lesser degree. Though variances for g.c.a and s.c.a effects were both significant, general effects were consistently larger in magnitude than specific effects (Rosenow, 1970; Singhana, 1980). A similar trend was reported for forage yield in sorghum where general effects were 20.5 times larger than those for specific effects (Blum, 1968). Thus, Doggett (1972) concluded that additive genetic variance is the most important part of total genetic variance in sorghum.

Reports on some other cereals have shown the same trend. Badwal (1970) studied g.c.a and s.c.a for yield and yield components in millet using a 5 x 5 diallel analysis. For yield components, the

magnitude of variances was higher for g.c.a than for s.c.a, although for grain yield s.c.a was more important. Singh *et al.* (1980) obtained significant g.c.a and s.c.a mean squares for all characters studied in a diallel cross in millet; but the general effects were predominant. Hallauer (1981), working with rye hybrids made from diallel crosses with selected and unselected inbred lines, found that g.c.a accounted for most of the genetic variability among crosses. Studies on wheat (Gyawali *et al.*, 1968; Brown, 1966) as well as barley (Hayes and Paroda, 1974) showed that s.c.a and g.c.a were both significant but g.c.a was more important.

Contrary results where s.c.a was more important have been reported. Cox and Frey (1984) for example, estimated combining ability variances using  $F_2$  populations of oats. Maximum specific effects exceeded general effects for all traits in both males and females. Khaugura *et al.* (1980) computed g.c.a and s.c.a variances using a 13 x 13 diallel in pearl millet and obtained a dominant effect of s.c.a variance over that of g.c.a.

In a study of harvest index in sorghum using 6A-lines; 10 R- lines and their 60  $F_1$  hybrids (Palanisamy and Subramanian, 1984) all the 16 parents exhibited the preponderance of non-additive gene action in governing the trait. The females contributed more to total general effects than the males, 0.05 to 0.036 as opposed to 0.006 to 0.025, respectively. Crook and Casady (1974) studied



combining ability in sorghum for 10 characters and found significant s.c.a for all the characters.

Other studies have shown the importance of both g.c.a and s.c.a variances in expressing characters in grain sorghum. Dabholkar *et al.* (1986) studied gene action for yield, 1000-grain weight and three other plant characters in a 6 x 6 diallel without reciprocals and found relatively equal and significant g.c.a and s.c.a variances for all the characters. Analysis of data on several agronomic characters from 40 F<sub>1</sub> hybrids and their parents grown at two locations revealed that general and specific effects and additive and non-additive components of variances were of equal importance for all characters (Chaudhary *et al.*, 1983).

#### MATURITY

Nigerian sorghums are planted at the beginning of the rainy season, flower as the rains stop and ripen on residual soil moisture. They are tall, late maturing and low yielding since they have a low proportion of grain to stem and leaf, and they mature under moisture stressed condition (Andrews, 1977). Exotic varieties and hybrids on the other hand have short growing season with higher yields (Norman *et al.*, 1976; Andrews, 1976). However, they mature during the rains and are affected by mould, giving poor grain quality and yield losses. Time of maturity and moisture availability are two important factors that must be considered when

improving sorghum grain yield and quality in Nigeria.

Quinby (1967) suggested that floral initiation is controlled by four gene loci, based on a small number of major genes with continuous variation due solely to multiple allelic variants of these genes. Lateness was said to be dominant over earliness but this relationship could be reversed by dominant alleles at other loci.

The nature of gene action controlling flowering has been variously reported. Evidence of greater influence of additive gene action over non-additive gene action has been reported by several authors. Kukadia *et al.* (1983a, 1983b), working with a 5 x 5 diallel cross reported significant additive components for days to 50% bloom and days to maturity. Similarly, Nandanwankar and Katepallewa (1984) found considerable additive gene effect for days to 50% flowering in rabi sorghum. Bittinger and Cantrell (1979) crossed 50 random pollen parents and three random seed parents of diverse origin. Their analysis revealed the preponderance of additive gene action in controlling this character. The results of Rao (1972) which were based on sorghum of equally diverse origin (exotic x indian) also showed that additive gene effect had a major influence on days to 50% flowering.

Similar results indicating the importance of additive gene action for this trait have been reported by Rao *et al.* (1978), Rao and Goud (1977a), Indi and Goud (1980), Singhania (1980) and ChandrasheKharappa (1987). Based on  $F_2$  means, Basal (1971) obtained high heritability values and greatest genetic advance for days to 50% flowering which are all indices of high additive type of gene action.

However, the findings of Govil and Murty (1980) showed that both additive and non-additive gene actions were important in influencing days to 50% flowering. They evaluated 10 diverse varieties and their 45  $F_1$  hybrids, and found g.c.a and s.c.a to be both significant for this character, although the g.c.a variance was of greater magnitude. Similarly, Karade *et al.* (1984) analysed a 9 x 9 diallel cross and found that g.c.a variance was of greater value however g.c.a and s.c.a variances were both significant for this character. In a line x tester analysis involving 5 lines and 7 testers, Huga *et al.* (1987) noticed that maturity was under non-additive gene control while days to 50% flowering was controlled by both additive and non-additive gene effects. Days to 50% flowering has been shown to be polygenic in inheritance and under the influence of both additive and dominance gene effects (Bello and Ohilana, 1985). Rao (1973) reported significant reciprocal effects for days to 50% flowering only, among all characters measured, while

Nimbalkar and Bapat (1987) obtained moderate heritability for this trait.

On the contrary, Khotyleva *et al.* (1983) in the Soviet Union reported the preponderance of dominance and epistasis effects in controlling emergence to flowering period. Their analysis was based on 120 hybrids, 30 R-lines and 4 A-lines. Using five generation mean analysis to estimate gene effect in grain sorghum, Desai *et al.* (1984) also reported dominance effect for days to 50% flowering. Heterosis has been reported for this character (Sodani and Chaturvedi, 1978).

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#### PLANT HEIGHT

Plant height is an important trait in sorghum and has been associated with grain yield. The *DW<sub>2</sub>* locus for height and *ma* locus governing maturity are closely linked (Quinby and Karper, 1954). Plant height was also shown to be governed by four independently inherited genes, plus a modifying complex, and tallness was found to be dominant to dwarfness. Rao and Goud (1977b) showed that internode length was highly correlated with plant height ( $r = 0.96$ ). Genes that reduced the length of internodes in sorghum were considered as dwarfing genes while genes that reduced the size of plant parts other than the internodes were excluded from the category of dwarfing genes (Quinby, 1963a). Chavda and Drolsom (1970a) reported heterosis for plant height along with other characters like larger and longer

leaves, higher dry matter yield and more nodes as well.

Chandak and Nandanwankar (1984) studied gene action for plant height at different growth stages (60, 75 and 90 days) using five crosses, their parents,  $F_2$ ,  $B_1$ , and  $B_2$  generations. Additive gene action was obtained for all crosses after 60 days, while dominance gene action became prominent in some crosses after 75 and 90 days. Dominance x Dominance gene action was not found significant in most cases, leading the authors to conclude that gene action in most of the cases depended on the parents used. The analysis of parents,  $F_1$ ,  $F_2$  and  $F_3$  populations from 2 tall late x 2 short early materials revealed that plant height was under polygenic inheritance and was under additive and non-additive gene influence (Bello and Obilana, 1985). In another study involving 3 tall x 5 dwarf varieties, analysis from 28 hybrids and  $F_2$  populations excluding reciprocals revealed that additive as well as non-additive gene action were operative in the inheritance of the trait (Nimbalkar and Papat, 1987). They also obtained moderate heritability value for this character.

The results of Shahane and Papat (1981) on the other hand showed the importance of non-additive gene action alone in the control of plant height. Ross *et al.* (1983) working with forage sorghum obtained high values for g.c.a components for all characters except plant height where the s.c.a

component was significantly higher. These results are in agreement with those of Foster and Weng (1979), Khoiyleva *et al.* (1980), while further evidence was given by Desai and Kukadia (1985) who recorded the highest positive heterosis for plant height.

Contrasting results were reported by Nandanwankar and Katepallewar (1984) who found considerable additive gene action for plant height in "rabi" sorghum. In a study of American x African sorghum Rao *et al.* (1978) reported plant height to be under additive gene control. Other studies based on 7 x 7 and 9 x 9 diallel analysis by Kanaka (1982) and Karale *et al.* (1984) respectively, revealed the influence of additive gene action on plant height. Similar findings have been reported for forage sorghum (Lodhi *et al.*, 1978; Sharma, 1980), and in grain sorghum Finker *et al.* (1976) who obtained high narrow sense heritability value for this character.

#### YIELD AND YIELD COMPONENTS

A knowledge of the genetic control of grain yield as well as its attributes is essential for the development of relevant breeding procedures. Some of the yield attributes include head weight, head length, 1000-seed weight and seed number.

a) Head weight

The analysis of  $F_1$ ,  $F_2$  and backcrosses by Indi and Goud (1981) revealed the presence of overdominance for head weight in an analysis of African x American crosses in sorghum. Gao (1984) reported additive gene action for all characters measured except ear weight while Birada and Borikar (1984) also found epistatic effect for this character. High positive heterosis (147%) was reported for this trait. These findings denote the importance of non-additive gene action in the inheritance of this character.

Syihari and Nagari (1980) on the other hand found significant g.c.a and s.c.a variances for head weight, meaning that both additive and non-additive gene effects were important in controlling the character. Variances due to g.c.a and s.c.a were both significant for head weight, although s.c.a variance was of greater magnitude (Deshmukh, 1983).

Contrasting results on the prevalence of additive gene action for head weight were recorded by Bittinger and Cantrell (1979). Goud *et al.* (1980) later obtained a high heritability value for this character.

b) Ear length

Ear length was reported to be under additive gene control (Birada and Borikar, 1984). Their analysis was based on data from  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ , and  $R_2$  generations. Their results agree

with that of Singhana (1980) and is complemented with high heritability value obtained for this character by Rao and Goud (1977a) and Goud *et al.* (1980). Indi and Goud (1981) obtained heterosis for all other characters measured except ear length.

Conflicting results showing high heterosis for this character were however reported by Perez Cabrera and Miller (1985) and Desai *et al.* (1980) in a line x tester analysis over locations. Raju *et al.* (1980) presented evidence for dominance and epistatic effect for ear length. Partial dominance has also been reported for this character in forage sorghum (Kukadia and Singhania, 1980).

c) Grain weight

Govil and Murty (1980) using data based on 10 diverse sorghum lines and their 45 F<sub>1</sub> hybrids revealed the presence of additive gene action for 1000 - grain weight. Similar results were obtained by Bawazir (1983). However, the findings of Dabholkarr *et al.* (1986) stressed the importance of both additive and non-additive gene control for this character. Significant g.c.a and s.c.a variances were obtained for this trait, although s.c.a estimates were of higher magnitude (Rao and Goud, 1977a). Dabholkar and Baghel (1980) on the other hand reported a range of complete dominance to overdominance for this character while Perez Cabrera and Miller (1985) later obtained high negative



heterosis for 300-grain weight. But according to Rao (1973) this trait is predominantly under dominance gene action.

d) Grain yield

Grain yield has been reported to be under non-additive gene influence. Indi and Goud (1981) for example analysed  $F_1S$ ,  $F_2S$  and their backcrosses and found overdominance effect for grain yield. This result is in agreement with those of Rao (1973), Dabholkar and Baghel (1980), Khotyleva *et al.* (1980) and Lazanyi *et al.* (1983), and was complimented by Harer and Bapat (1982) who obtained high positive heterosis of 197% for grain yield. Kachave and Nandanwankar (1980) studied gene effect for grain yield in six crosses for six generations. Dominance gene effect was found to be higher than additive, additive  $\times$  additive, additive  $\times$  dominance gene effects in five out of the six crosses. In an inheritance study involving two "rabi" sorghum crosses, dominance and epistasis gene effects were found to be more important than additive gene effect for grain yield per plant. Using a line  $\times$  tester analysis, Desai *et al.* (1980) Desai and Kukadia (1985) and Kulkarai and Shinde (1985) obtained highest positive heterosis (16.67-91.3%), (21-44%) and 65.5%, respectively, for this trait. The

findings of Jan-Orn *et al.* (1976), Bhale and Borikar (1982) and Nandanwanker and Chandak (1984) also revealed the importance of non-additive gene action in governing this character.

However, evidences of additive gene effect for grain yield exist. Spivakov (1988) studied five forms of "Kafircorn", three of grain sorghum and two "banty corn" all (*S. bicolor*) in a diallel scheme. Only the g.c.a variance was found significant for grain yield. In another study, based on 6 A - lines x 10 R-lines (line x tester), Palanisamy and Subramanian (1986) obtained significant g.c.a variance for this trait. Similar results were reported by Nandan-wankar and Kalepallewar (1984).

#### PROTEIN AND LYSINE

The nutritional quality of sorghum is rather low compared with other cereals since lysine, an essential amino acid, is present in low concentrations, and leucine, which has been shown to be pellagrigenic in nature is present in high amounts. However, the discovery of the opaque - 2 and floury - 2 mutant genes in maize (Meriz *et al.*, 1964) which increased the proportion of lysine in the seed has given a lot of impetus to sorghum breeders. In an effort to improve the nutritional quality of sorghum grains, two genetic mutants, one natural and one induced, that increased the lysine concentration in the endosperm and improved protein quality of the grain were identified; the natural mutant gene (*hl*)

was found in two floury endosperm sorghum "IS 11167" and "IS 11738" from Ethiopia (Singh and Axtell, 1973); while the second "P-721q" was induced by chemical mutagenesis of a normal sorghum line (Mohan, 1975). The nutritional quality of these mutants is comparable to that of opaque - 2 maize when fed to rats (Singh and Axtell, 1973; Axtell, 1981). It is evident therefore that genetic improvement in sorghum grain protein content and quality is possible through selection, since variations exist for this trait. Earlier reports by Lowe (1958) gave the average protein content of sorghum as 8.8 per cent. Reports from several other workers (Pickett, 1969; Singh and Axtell, 1973; Rana and Murty, 1975 and Axtell, 1981) indicated a range of 5.9 to 20 per cent.

Genetic variations for sorghum grain protein has been attributed to both additive (Collins and Pickett, 1972a; 1972b Nanda and Rao, 1980; Monyo *et al.*, 1988) and non-additive (Rana and Murty, 1975) gene effects although additive effect has been more widely reported.

Collins and Pickett (1972a, 1972b) using line x tester and diallel analysis respectively, found considerable additive gene effect for per cent protein in grain sorghum. Monyo *et al.* (1988) tested 10 high lysine lines derived from "P-721 q" using three male sterile lines also derived from "P 721 q" by backcrossing to male - sterile lines. Their analysis of variance showed significant differences

in general combining ability effects for grain protein. Predominantly additive gene action (Nanda and Rao, 1980) and high heritability values (Crook and Casady, 1974; Eckeibel *et al.*, 1977) have also been reported for this trait.

Rana and Murty (1975) however using both line x tester and diallel design obtained evidence of both additive and non-additive gene action for grain protein in both designs. Analysis of crosses between grain and fodder sorghum, Rao and Ahluwalia (1980) also obtained significant g.c.a and s.c.a for per cent protein in grains. Rao (1972) had attributed the increased rate of nitrogen uptake to non-additive gene effect and the total uptake of nitrogen to be additive in inheritance.

The findings of Rana and Murty (1975) showed that protein was under the control of three sets of genes, while one set controlled lysine in grain sorghum. Axtell (1981) also revealed that the high lysine character in "P-721" is conditioned by a single gene that is partially dominant. Evidence from the experiments of Rana and Murty (1975) and Collins and Pickett (1972b) showed the importance of non-additive gene action in governing the inheritance of lysine in protein. Nayeem and Bapat (1984) obtained significant s.c.a variance for lysine in protein in their analysis involving 8 A-lines, 10 R-lines and their 80 F<sub>1</sub> hybrids. Contradictory results of predominantly additive gene action for lysine in protein was however reported by Govil and Murty (1973) and Monyo *et al.* (1988).

## INTERCHARACTER CORRELATION

Since the most important characters like yield and protein are complex in inheritance and may involve several related characters, the degree of genotypic and phenotypic correlations between yield, protein and other characters are important. Breeders are looking for characters that are correlated to yield and quality. These attributes are easier to select since they are most easily seen, and moreover, it is expensive to analyse for traits like protein and lysine. Correlated characters are important to a plant breeder because he can predict the change brought in by one of them when selection is practised for the other (Falconer, 1981).

The earlier work of Quinby and Karper (1945) showed linkage between height gene and the maturity gene Ma. Later Quinby (1972) gave evidence that maturity genes control time of floral initiation and in addition influence rate of growth as measured by leaf size and panicle weight. The state of DW<sub>2</sub> gene at 1 and 2 dwarf height levels influenced main head yield, tiller yield, total yield, kernels per head, heads per plant, 1000-seed weight, kernel weight and panicle length (Campbell and Casady, 1969). Node number was not affected, which indicated that maturity was not influenced by this gene. Palanisamy and Prasad (1984) studied the association between plant height, number of days to flowering and grain yield in a set of 32 grain sorghum varieties of diverse geographical origin.

Their results revealed that days to 50% flowering was significantly associated with plant height ( $r = 0.428$ ) and grain yield ( $r = 0.390$ ). The association between plant height and grain yield was also highly significant ( $r = 0.69$ ). The relationship between yield, maturity, and plant height was studied for up to five generations (Reddy and Rao, 1971). A positive relationship was found between days to 50% flowering and yield, days to 50% flowering and plant height, plant height and yield. On the contrary, early flowering and seed weight were also reported to be the most important factors influencing grain yield (Mishra and Rao, 1980). Eckerbeil *et al.* (1977) obtained a negative and significant association between grain yield and days to 50% flowering.

Agunbiade (1984) referred to three yield components (seed number, seed weight, and panicles per plant) of sorghum as the yield triangle. Any factor that causes reduction in size of any of the three attributes will ultimately reduce crop yield. Positive correlations have been reported between yield and seed number (Singhania, 1980; Axtell, 1981; Jimenez and Casas 1983; Monyo *et al.*, 1988); yield and seed weight (Mishra and Rao, 1980; Mauder, 1972; Ramasam *et al.*, 1986; Spivakov, 1988); yield and panicle per plant (Jain and Aulakh, 1971; Agunbiade, 1984), but number of seeds per head had the greatest and most consistent effect on total grain yield (Fischer and Kertisz, 1976; Quinby, 1943b; Nieuhaus and Pickett, 1966; Singhania, 1980;

Jimenez and Casas, 1983). The results of Monyo *et al.* (1988) showed that the increase in yield of lines in hybrid combinations derived from "P-721" "opaque stock" occurred without affecting kernel weight but number of kernels per panicle was the most important component for yield. Axtell (1981) had earlier reported that the number of kernels per panicle and/or number of panicles per unit area of land were the most important components for grain yield in lines containing the "O" genes (opaque - 2 genes).

The relationship between seedling vigour and grain yield was reported to be positive (Chlina and Phul, 1987). The same workers obtained a negative correlation between seedling vigour and grain protein, while with lysine and tryptophane it was positively correlated.

The relationships between yield and protein, yield and lysine and lysine and protein have also been studied (Abifarin, 1969; Abifarin and Pickett, 1969; Rana and Murty, 1975; Axtell, 1981; Monyo *et al.*, 1988). Monyo *et al.* (1988) studied inter-character correlation using "P-721" opaque endosperm stock. The correlations between grain yield and protein in 30 F<sub>1</sub> hybrids were negative ( $r = -0.63$ ) and significant, while that with lysine concentration in protein was also negative but non-significant. An almost similar correlation value ( $r = -0.64$ ) for grain yield and protein had earlier been reported (Collins and Pickett, 1972a). Rana

and Murty (1975) obtained negative but low correlations between grain yield and lysine. Negative correlations between grain yield and protein have also been reported (Abifarin, 1969; Abifarin and Pickett, 1969; Crook and Casady, 1972; Axiell, 1981) on the contrary positive correlations were reported by Ajakaiye (1981). Studies between protein and lysine have shown negative relationships (Rana and Murty, 1975; Collins and Pickett, 1972a).



## CHAPTER THREE

## MATERIALS AND METHODS

In the growing season of 1988 five male parents (restorers) NR71156, NR71176, NR71177, NR71178, NR71167, three female parents (male steriles) 2219A, MA9 and M60042A were sown in a breeding nursery. Fifteen hybrids were made between the five R-lines and the three A-lines using factorial mating design or Design II of Comstock and Robinson (1952). The description of the parental materials are presented in Table 1.

Table 1 Description of parents

Parent	Agronomic characters	Origin
NR71156	White grains, loose head	Are restorer lines developed from breeding programmes in Institute for Agricultural Research Samaru
NR71176	White grains, loose head	
NR71177	loose head	
NR71178	White grain, compact head	
NR71167	White grain, loose head	
2219A	Yellow grain, loose head	Are exotic male sterile lines obtained from International Crop Research Institute in the Semi-Arid Tropics, ICRISAT, India
M60042A	Semi compact head	
MA9	Yellow grains, compact oval head	

During the rainy season of 1989 the 15 hybrids, and their parents were sown in replicated trials at two locations, Samaru (Northern guinea savanna) and Kano (Sudan Savanna). The design was a randomised complete block with four (4) replications. Plot size was 2 rows each 6 m in length. Inter and intra row spacings of 75 x 30 cm was used.

About five seeds/hill were sown and later thinned down to two seedlings per stand two weeks after sowing during which missing hills were compensated for by transplanting to give a population of 40 plants per 6 m row, about 88,888 plants/ha.

Thirty-two kilograms per hectare of single superphosphate fertilizer ( $P_2O_5$ ) was applied as basal dressing prior to ridging and sowing, while 62 kg/ha of nitrogen (urea) fertilizer was applied in split doses, as basal and top dressing. The first 32 kg/ha of Nitrogen (urea) was applied as basal while 30 kg/ha three weeks after sowing, just after thinning. A mixture of gramoxone and sorghoprim A was sprayed as pre-emergence herbicide. Thereafter, weeds were controlled by hoe-weeding twice, as follows, three weeks and six weeks after sowing. The plants were sprayed with Vertox 85 to control stem borer. The following data were collected from each trial before and after harvest:

1. Seedling vigour: Vigour of the plant 20 days after sowing, based on a 5-1 scale.  
5 - most vigorous plot  
1 - least vigorous plot
2. Plant height: The distance between ground level to the base of the flag leaf at maturity.
3. Days to 50% flowering: The number of days from sowing to when one half of the plants in a plot are at anthesis.
4. 1000-seed weight: The weight of 1000 randomly selected seeds.
5. Head weight: The weight of the dry head, ear or panicle.
6. Number of kernels/panicle: This was calculated based on the following formula (Jan-Orn, 1973):

$$\frac{\text{Weight of grains/panicle} \times 1000}{1000\text{-grain weight}}$$

that is,

if 1000 grains weigh X grams

1 grain will weigh  $\frac{X}{1000}$

1000 grain weight

therefore if  $\frac{X}{1000}$  is weight of 1 gram,  
1000 grain weight

Y grams is weight of  $Y \times \frac{1000}{X}$  grains

where X = 1000 grain weight

Y = grain weight per panicle

7. Head (panicle) length: The distance between the base and the tip of the panicle.
8. Grain yield: The weight of threshed grains.

9. Proteins: Nitrogen value of seeds were analysed using micro-Kjeldahl's method and per cent protein was estimated by multiplying nitrogen per cent by 6.25.

The data collected from the Kano field was unreliable and was thus not included in the statistical analysis.

#### STATISTICAL METHODS

A randomised complete block design with four replications was used.

In the analysis of variance (ANOVA), sources of variations are partitioned into variation among parents and hybrids (Table 2).

Table 2 Form of analysis of variance for parents and hybrids

Sources of variations	Degrees of freedom (d.f.)	Sums of squares (S.S.)	Mean squares (M.S.)
Replications (r-1)	3	R	R/3
Entries (e-1)	22	E	E/22
Parents (p-1)	7	P	P/7
Hybrids (h-1)	14	H	H/14
Parents vs Hybrids (n-1)	1	N	N/1
Error (r-1)(e-1)	66	E	E/66

Hybrids are further subdivided into males, females and males x females, which provide test for g.c.a and s.c.a (Table 3).

Table 3 Form of analysis of variance for hybrids

Sources of variations	Degrees of freedom (d.f.)	Expected mean squares (E.M.S.)
Replications (r-1)	3	
Males (m-1)	4	$\sigma^2_e + r\sigma^2_{mxf} + fr\sigma^2_m$
Females (f-1)	2	$\sigma^2_e + r\sigma^2_{mxf} + mr\sigma^2_f$
Males x Females (m-1)(f-1)	8	$\sigma^2_e + r\sigma^2_{mxf}$
Error (mf-1)(r-1)	42	$\sigma^2_e$
Total mfr-1	59	

The hybrids (males effects, females effects, males x females effects) was analysed based on the following linear model.

$$Y_{ijk} = \mu + g_i + q_j + S_{ij} + E_{ijk}$$

where  $i = 1, 2, \dots, 5;$

$j = 1, 2, \dots, 3,$

$Y_{ijk}$  = the observation on the hybrid between the  
ith male and jth female in the kth  
replication

$\mu$  = population mean

$g_i$  = effect common to all progeny of the ith  
R-line

$g_j$  = effect common to all progeny of the  $j^{\text{th}}$  A-line

$S_{i,j}$  = effect specific to the progeny of mating the  $i^{\text{th}}$  R-line and  $j^{\text{th}}$  A-line

$e_{i,j,k}$  = random experimental error

The form of analysis of variation among  $F_1$  hybrids is presented in Table 3.

In this analysis, males and females express the g.c.a while males x females interaction represent the s.c.a. Genetic components of variance was estimated from the expectations of mean squares according to Singh and Chaudhary (1985):

$$\sigma^2_m = \frac{MS_m - MS_{m \times f}}{rf} = g_a = \text{Cov H.S.} = 1/4\sigma^2_A = \sigma^2_{gca m}$$

$$\sigma^2_f = \frac{MS_f - MS_{m \times f}}{rm} = g_a = \text{Cov H.S.} = 1/4\sigma^2_A = \sigma^2_{gca f}$$

$$\sigma^2_{m \times f} = \frac{MS_{m \times f} - MS_e}{r} = \text{Cov (F.S.)} - 2\text{Cov (H.S.)} = 1/4\sigma^2_D = \sigma^2_{sca}$$

where

$MS_m$  = mean square males

$MS_f$  = mean square females

$MS_{m \times f}$  = males x females interaction mean square

$MS_e$  = error mean square

$r$  = number of replications;  $r = 4$

$f$  = number of females;  $f = 3$

$m$  = number of males;  $m = 5$

$A$  = additive gene effect

$D$  = dominance gene effect

and the average additive genetic variance ( $\sigma^2A'$ )

$$\begin{aligned} \sigma^2A' &= \text{Cov (H.S) average} \\ &= \frac{1}{r(2mf - m - f)} \left[ \frac{(f-1)MS_e + (m-1)MS_m - MS_{mf}}{m + f - 2} \right] \end{aligned}$$

The g.c.a and s.c.a effects for each character will be estimated as per Beil and Atkins (1967)

$$\text{g.c.a. (male)} = \bar{V}_1 - \bar{V}$$

$$\text{g.c.a. (female)} = \bar{V}_2 - \bar{V}; \text{ and}$$

$$\text{s.c.a (hybrids)} = \bar{V}_{12} - \bar{V}_1 - \bar{V}_2 + \bar{V}$$

where

$\bar{V}_1$  = mean performance of hybrids with a given male parent averaged over all replications and females

$\bar{V}_2$  = mean performance of hybrids with a given female parent averaged over all replications and males

$\bar{V}_{12}$  = mean of a given hybrid averaged over replications.

$\bar{V}$  = experimental mean (mean performance of all hybrids).

The significance of general and specific combining ability effects for each character was tested using formulae analogous to those proposed by Bailey Jr as used by Cox and Frey (1984) and Monyo et al. (1988).

$$t = \frac{g.c.a}{S.E.gca}$$

$$S.E_{g_m} = \sqrt{\frac{MS_m(m-1)}{mfr}}$$

$$S.E_{g_f} = \sqrt{\frac{MS_f(f-1)}{mfr}}$$

where

$MS_m$  = mean square males

$MS_f$  = mean square females

$S.E_{g_m}$  = standard error of g.c.a for males

$S.E_{g_f}$  = standard error of g.c.a for females

$r$  = number of replications

$f$  = number of females

$m$  = number of males

Similarly, significance for s.c.a effects:

$$t = \frac{g.c.a}{S.F.sca}$$

$$S.E.s.c.a = \sqrt{\frac{MS_{mf}(m-1)(f-1)}{mfr}}$$

where

$MS_{mf}$  = mean square males x females

$S.E.sca$  = standard error for s.c.a

Narrow sense heritability was estimated using Grafius et al. (1952) formula as used by Abifarin (1969).



$$h^2 = \frac{\sigma^2_f + \sigma^2_m}{\sigma^2_f + \sigma^2_m + \sigma^2_{fm} + \sigma^2_{e/r}}$$

Heterotic effect was determined, as increase or decrease of  $F_1$  mean over that of the superior parent as follows:

$$H = \frac{\bar{F}_1 - \bar{M}_{sp}}{\bar{M}_{sp}} \times 100$$

and as increase or decrease over the mid-parent value as follows:

$$H = \frac{\bar{F}_1 - (\bar{P}_1 + \bar{P}_2)/2}{(\bar{P}_1 + \bar{P}_2)/2} \times 100$$

Where

$\bar{F}_1$  = mean performance of hybrid formed between the i'th male and j'th female parent.

$\bar{M}_{sp}$  = mean performance of superior parent of a common hybrid

$\bar{P}_1$  = mean of parent one

$\bar{P}_2$  = mean of parent two

Duncan's New Multiple Range Test (DNMRT) was used to test significant differences between means.

Genotypic and phenotypic correlations were estimated for pairs of all traits studied from mean squares and mean cross products as follows:

$$r_{oxy} = \frac{M_{gx.gy} - M_{ex.ey}}{(M_{gx}-M_{ex})(M_{gy}-M_{ey})^{1/2}}$$

$$r_{ph(xy)} = \frac{\bar{m}_{gx.gy}}{(\bar{m}_{gx} \cdot \bar{m}_{gy})^{1/2}}$$

$$r_e = \frac{\bar{m}_{ex.ey}}{(\bar{m}_{ex} \cdot \bar{m}_{ey})^{1/2}}$$

where

$\bar{m}_{gx.gy}$  = mean product of traits X and Y and,

$\bar{m}_{gx}$  and  $\bar{m}_{gy}$  = mean squares of traits X and Y, respectively

$\bar{m}_{ex.ey}$  = error mean product of traits X and Y and,

$\bar{m}_{ex}$  and  $\bar{m}_{ey}$  = error mean squares of traits X and Y respectively

Table 4 Form of analysis of variance and covariance  
for all pairs of characters

Sources of variations	d.f.	Trait X	Trait Y	Mean product
Reps (r-1)	3	-	-	-
Entry (e-1)	22	$\bar{m}_{gx}$	$\bar{m}_{gy}$	$\bar{m}_{gx.gy}$
Error (r-1)(e-1)	66	$\bar{m}_{ex}$	$\bar{m}_{ey}$	$\bar{m}_{ex.ey}$
Total	91			

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## CHAPTER 4

## RESULTS

The analysis of variance of parents and hybrids for nine characters is presented in Table 5. Highly significant differences ( $P = 0.01$ ) were shown among all entries for all the characters, except per cent protein which showed significant difference ( $P = 0.05$ ). The parents revealed highly significant differences ( $P = 0.01$ ) for seedling vigour, days to 50% flowering, plant height, panicle length and grain yield, but significant differences ( $P = 0.05$ ), for head weight. No significant differences were observed among the parents for number of kernels/panicle, 1000-seed weight and protein. The females among the parents showed highly significant differences ( $P = 0.01$ ) for plant height, while the males showed highly significant differences ( $P = 0.01$ ) for seedling vigour, days to 50% flowering, plant height and panicle length. Females vs males differed at ( $P = 0.01$ ) for seedling vigour, plant height, head weight and grain yield but at ( $P = 0.05$ ) for panicle length.

Hybrids were highly significantly different ( $P = 0.01$ ) for all the characters studied except for seedling vigour and per cent protein where the differences were significant ( $P = 0.05$ ). Parents Vs hybrids contrast was highly significant ( $P = 0.0.1$ ) for all characters except seedling vigour and per cent protein.

Table 5 Analysis of variance showing sources of variations, degrees of freedom (d.f.), and mean squares (m.s.) of nine traits in sorghum

Sources of variations	d.f.	Seedling vigour	Days to 50% flowering	Plant height	No. of kernels/panicle	Mean Squares
Replications	3	0.812	7.84	254.88**	379766	
Entries	22	2.488**	59.07**	1384.90**	1482257**	
Parents (P)	7	2.482**	56.90**	1582.90**	671452	
Females (F)	2	0.333	17.60	798.10**	168513	
Males (M)	4	1.625**	88.50**	1065.80**	642797	
Female Vs Male	1	10.208**	8.80	5221.00**	758669	
Hybrids (H)	14	2.650*	28.20**	899.50**	1476558**	
P Vs H	1	0.264	506.60**	679.50**	7237683**	
Error	66	0.433	6.49	27.40	426083	

\*, \*\* Significant at  $P = 0.05$  and  $P = 0.01$ , respectively

Table 5 (Cont'd)

Sources of variations	Head weight	1000-grain weight	Panicle length	Protein %	Grain yield
Replications	0.001305**	5.94	4.29	3.81	2429434
Entries	0.001388**	23.80**	21.52**	6.72*	4184747**
Parents (P)	0.000722*	8.61	36.35**	4.34	4370295**
Females (F)	0.000577	16.74	1.79	6.76	3760366
Males (M)	0.000425	3.39	59.61**	3.38	2882996
F Vs M	0.002197**	13.24	12.42*	3.30	11539348**
Hybrids (H)	0.000955**	24.53**	7.13**	8.38*	26245544**
P Vs H	0.012107**	115.77**	117.29**	0.19	24728060**
Error	0.000305	6.24	1.88	3.64	1345284

\*, \*\* Significant at  $P = 0.05$  and  $P = 0.01$ , respectively

Table 6 shows the analysis of variance for combining ability for nine characters. Highly significant differences among males were observed in their g.c.a for plant height ( $P = 0.01$ ) and significant differences observed for 1000-seed weight ( $P = 0.05$ ). The g.c.a estimated from the female effects were highly significant ( $P = 0.01$ ) for days to 50% flowering, plant height, head weight and 1000-grain weight and significant ( $P = 0.05$ ) for seedling vigour and number of kernels/panicle. Significant variations for s.c.a (males x females) were obtained for seedling vigour, per cent protein, grain yield at ( $P = 0.05$ ) and for panicle length at ( $P = 0.01$ ).

Estimates of male, female, males x females components of variance are presented in Table 7. Female components of variance were larger in magnitude than those for males for all the characters except for per cent protein and panicle length. This further indicates the predominance of female variances over those for males as already shown by their mean squares (Table 6).

The  $\sigma^2_A$  provides estimate for average g.c.a (average additive gene effect) while  $\sigma^2_D$  gives the estimate of average s.c.a (average dominance gene effect). In general, there was a preponderance of non-additive component ( $\sigma^2_D$ ) over the additive component ( $\sigma^2_A$ ) of variance for six out of the nine characters studied, as indicated by the  $\sigma^2_A/\sigma^2_D$  ratio. However,

Table 6 Analysis of variance showing sources of variations, degrees of freedom (d.f.), and mean squares (m.s.) for combining ability for nine traits in sorghum

Sources of variations	d.f.	Seedling vigour	Days to 50% flowering	Plant height	No. of kernels/panicle	Mean Squares
Replications	3	0.378	7.39	165.71**	59260	
Males	4	3.692	12.42	1389.70**	678330	
Females	2	6.350*	147.82**	3291.60**	5909900*	
Males x Females	8	1.204*	6.19	56.442	767340	
Error	42	0.437	4.23	27.568	427820	

\*, \*\* Significant at P = 0.05 and P = 0.01, respectively.

Table 6 (Cont'd)

Sources of variations	Head weight	1000-grain weight	Panicle length	Protein %	Grain yield
Mean Squares					
Replications	0.00167**	4.6777	7.978	1.1508	16003
Males	0.0003371	31.098*	9.683	11.863	881600
Females	0.004305**	83.966**	7.453	6.1613	3265300
Males x Females	0.000426	6.9038	5.765**	7.1850*	3335923*
Error	0.0002955	5.1572	1.3503	2.9925	1414391

\*, \*\* Significant at P = 0.05 and P = 0.01, respectively.



Table 7 Estimates of components of variance and heritability (%) for nine traits

	Seedling vigour	Days to 50% flowering	Plant height	No. of kernels/panicle
$\sigma^2_{\mu}$	0.20729	0.5188	111.11**	-7400
$\sigma^2_{\mu}$	0.25729*	7.08**	161.76**	257000*
$\sigma^2_{\mu}$	0.19173*	0.4910	7.22	84900
$\sigma^2_{\mu}$	0.038	0.58	22.35	18805
$\sigma^2_{\mu}$	0.19173	0.4910	7.22**	84900
$\sigma^2_{\mu}/\sigma^2_{\epsilon}$	0.198	1.189	3.095	0.22
$h^2$ (ns)	42.48	83.08	93.08	56.55

\*, \*\* Significant at  $P = 0.05$  and  $P = 0.01$ , respectively  
 ns = narrow sense

Table 7 (Cont'd)

	Head weight	1000-grain weight	Panicle length	Protein %	Grain yield
$\hat{\beta}_a$	0.00000742	2.016*	0.327	0.3898	-204500
$\hat{\beta}_b$	0.000194**	3.85**	0.084	-0.0512	-3530
$\hat{\beta}_{a_1}$	0.0000327	0.437	1.104**	1.0481*	480400*
$\hat{\beta}_c$	0.000014	0.475	0.0361	0.0316	-18930.18
$\hat{\beta}_d$	0.0000327	0.437	1.104	1.0481	480400
$\hat{\beta}_a/\hat{\beta}_d$	0.429	1.087	0.033	0.030	-0.039
$h^2$ (ns)	63.66	77.28	22.19	15.86	-33

\*, \*\* Significant at  $P = 0.05$  and  $P = 0.01$ , respectively  
 ns = narrow sense

variance components due to average additive effect of genes were predominant for plant height, days to 50% flowering and 1000-grain weight.

Narrow sense heritability estimates (Table 7) were as low as -33% for grain yield and as high as 95.08% for plant height. Similarly, heritability estimates were low for per cent protein (15.86%) and panicle length (22.19%), moderate for seedling vigour (45.48%), number of kernels/panicle (56.55%), head weight (63.66%), high for days to 50% flowering (83.08%) and 1000-grain weight (77.28%).

The estimates of g.c.a and s.c.a effects are presented in Tables 8 to 16. Concluding from the g.c.a effects for seedling vigour (Table 8), NR 71177 was the most influential male parent while 2219A was the most influential female parent for this character. For days to 50% flowering, the restorer NR 71178 and male sterile 2219A were very important in reducing flowering date (Table 9). Estimates of g.c.a for plant height (Table 10) showed that NR 71156 and MA9 were important in reducing plant height. Incidentally, hybrid MA9 x NR 71156 had the lowest mean grain yield (Rank 15, Appendix II), and the lowest heterosis value (Table 17) for plant height.

The estimates of g.c.a effects for number of kernels/panicle (Table 11) indicated that MA9 was the most influential among the female parents. NR 71156 and NR 71176 had high non-significant g.c.a effects among the males, while the highest value for

Table 8 Estimates of general and specific combining ability effects for seedling vigour

Parent	Specific effect (S <sub>ij</sub> ) <sup>+</sup>			General effect (g <sub>i</sub> ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	0.35	0.35	-0.70	-0.70
NR 71176	-0.23	0.27	-0.03	0.13
NR 71177	-0.65	0.10	0.55	0.55
NR 71178	-0.07	-0.07	0.13	0.47
NR 71167	0.60	-0.65	0.05	-0.55
General effect (g <sub>i</sub> ) <sup>*</sup>	0.65	-0.35	-0.30	

++ S.E (g<sub>i</sub>) = t<sub>0.05</sub>, t<sub>0.01</sub> (0.46) = 1.30, 2.2

\* S.E (g<sub>i</sub>) = t<sub>0.05</sub>, t<sub>0.01</sub> (0.46) = 1.50, 2.7

+ S.E (S<sub>ij</sub>) = t<sub>0.05</sub>, t<sub>0.01</sub> (0.40) = 0.86, 1.2

Table 9 Estimates of general and specific combining ability effects for days to 50 per cent flowering

Parent	Specific effect ( $S_{ij}$ ) <sup>+</sup>			General effect ( $g_i$ ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	0.347	-0.551	0.20	-0.75
NR 71176	1.767	-1.130	-0.633	1.58
NR 71177	1.067	0.537	0.537	-0.09
NR 71178	0.600	-0.303	-0.303	-1.00
NR 71167	-1.650	3.450**	0.197	0.25
General effect * ( $g_j$ )	-2.52	-0.37	2.88	

\*\* Significantly different from zero at the 0.01 probability level.

++ S.E ( $g_i$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.91) = 2.53, 4.19

\* S.E ( $g_j$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (2.22) = 7.06, 12.97

+ S.E ( $S_{ij}$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.91) = 1.95, 2.71

Table 10 Estimates of general and specific combining ability effects for plant height

Parent	Specific effect ( $S_{ij}$ ) <sup>+</sup>			General effect ( $g_i$ ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	0.85	3.45	-4.30	-18.70
NR 71176	-5.48	0.62	4.87	3.38
NR 71177	3.18	-2.97	-0.22	8.97
NR 71178	-0.65	0.70	-0.05	2.30
NR 71167	2.10	-1.80	-0.30	4.05
General effect <sup>*</sup> ( $g_j$ )	4.40	10.05	-14.45	

<sup>++</sup> S.E ( $g_i$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (9.63) = 26.77, 44.30  
<sup>\*</sup> S.E ( $g_j$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (10.47) = 33.29, 61.14  
<sup>+</sup> S.E ( $S_{ij}$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (2.70) = 5.78, 8.05

Table 11 Estimates of general and specific combining ability effects for number of kernels/head

Parent	Specific effect (S <sub>ij</sub> ) <sup>+</sup>			General effect (g <sub>i</sub> ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	-222.30	390.60	-168.30	138.07
NR 71176	414.85	-286.45	-128.40	132.65
NR 71177	115.80	301.47	-417.23	-255.27
NR 71178	-35.80	-527.87	563.70	-236.18
NR 71167	272.50	122.22	150.27	220.73
General effect * (g <sub>j</sub> )	-396.60	-204.55	601.15	

<sup>++</sup> S.E (g<sub>i</sub>) = t<sub>0.05</sub>, t<sub>0.01</sub> (211) = 587, 971.00  
<sup>\*</sup> S.E (g<sub>j</sub>) = t<sub>0.05</sub>, t<sub>0.01</sub> (443.5) = 1412, 2592.96  
<sup>+</sup> S.E (S<sub>ij</sub>) = t<sub>0.05</sub>, t<sub>0.01</sub> (318) = 680.5, 948.00

s.c.a was with the cross MA9 x NR 71178 followed by 2219A x NR71176. Although NR71167 and MA9 were good general combiners, significant values for s.c.a were recorded for head weight (Table 12) in the hybrids M60042A x NR71177, and MA9 x NR 71177. Another yield component, 1000-seed weight, exhibited negative significant s.c.a value for hybrid M60042A x NR 71178 and high positive non-significant s.c.a value for hybrid 2219A x NR 71178 (Table 13). Lines NR 71178 and 2219A were the most influential male and female parents, respectively, for this trait. With regards to panicle length (Table 14), male parents NR 71167 and NR 71177 were important while MA9 was important among the females in influencing this character.

The g.c.a effects for per cent protein (Table 15) indicated that NR 71167 was the most important male parent for this character and NR 71177 the least. Similarly, 2219A was the most important female parent and MA9 the least. However, judging from the s.c.a value, hybrid M60042A x NR 71178 was the most important for this trait. It also accounted for the highest mean per cent protein among the hybrids (Appendix II).

From estimates of g.c.a for grain yield (Table 16), MA9 and NR 71156 were the least influential parents for this character. Their hybrid, MA9 x NR 71156, was the least in terms of grain yield (Appendix II), and had a significant negative s.c.a value (Table 16). Lines NR 71178 and 2219A were the most



Table 12 Estimates of general and specific combining ability effects for head weight

Parent	Specific effect ( $S_{ij}$ ) <sup>+</sup>			General effect ( $g_i$ ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	0.0089	0.0008	-0.0098	0.00097
NR 71176	0.0041	-0.008	0.0044	0.0025
NR 71177	0.0001	0.017*	-0.0161*	-0.01
NR 71178	-0.0034	-0.0035	0.0069	-0.0017
NR 71167	-0.0089	-0.0055	0.0154	0.0086
General effect * ( $g_j$ )	-0.0151	-0.003	0.0181	

\* Significantly different from zero at 0.05 probability level.

++ S.E ( $g_i$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.0047) = 0.13, 0.02

\* S.E ( $g_j$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.012) = 0.038, 0.07

+ S.E ( $S_{ij}$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.0075) = 0.016, 0.022

Table 13 Estimates of general and specific combining ability effects for 1000-grain weight

Parent	Specific effect ( $S_{ij}$ )+			General effect ( $g_i$ )++
	2219A	M60042A	MA9	
NR 71156	0.41	-0.504	0.025	-0.39
NR 71176	-1.136	1.11	0.06	-0.84
NR 71177	-1.185	1.127	1.26	-5.23
NR 71178	1.37	-2.63*	-0.84	2.54
NR 71167	0.541	0.302	0.094	0.92
General effect * ( $g_i$ )	1.71	0.17	-1.88	

\* Significantly different from zero at 0.05 probability level.

++ S.E ( $g_i$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (1.4) = 3.9, 6.4

\* S.E ( $g_i$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (1.7) = 5.04, 9.8

+ S.E ( $S_{ij}$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.96) = 2.05, 2.9

Table 14 Estimates of general and specific combining ability effects for panicle length

Parent	Specific effect ( $S_{ij}$ ) <sup>+</sup>			General effect ( $g_i$ ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	0.655	0.584	-1.215	-0.24
NR 71176	-0.203	-0.578	0.778	-0.56
NR 71177	1.063	0.664	-1.731	0.85
NR 71178	-0.812	-0.266	1.069	-1.07
NR 71167	-0.703	0.403	1.102	0.995
General effect ( $g_j$ ) <sup>*</sup>	-0.63	0.025	0.595	

<sup>++</sup> S.E ( $g_i$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.8) = 2.2, 3.68  
<sup>\*</sup> S.E ( $g_j$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (1.5) = 1.59, 2.92  
<sup>+</sup> S.E ( $S_{ij}$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (0.87) = 1.86, 2.60

Table 15 Estimates of general and specific combining ability effects for protein

Parent	Specific effect ( $S_{ij}$ ) <sup>+</sup>			General effect ( $g_i$ ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	0.24	-1.052	0.812	-0.252
NR 71176	-0.57	-0.742	1.322	-0.859
NR 71177	1.53	-0.242	-1.270	-0.959
NR 71178	-0.806	1.948	-1.098	0.825
NR 71167	-0.34	0.088	0.242	1.245
General effect * ( $g_j$ )	0.47	0.142	-0.612	

<sup>++</sup> S.E ( $g_i$ ) =  $t_{0.05}, t_{0.01}$  (0.89) = 2.47, 4.1  
<sup>\*</sup> S.E ( $g_j$ ) =  $t_{0.05}, t_{0.01}$  (0.45) = 1.40, 2.6  
<sup>+</sup> S.E ( $S_{ij}$ ) =  $t_{0.05}, t_{0.01}$  (0.98) = 2.10, 2.9

Table 16 Estimates of general and specific combining ability effects for grain yield

Parent	Specific effect ( $S_{ij}$ ) <sup>+</sup>			General effect ( $g_i$ ) <sup>++</sup>
	2219A	M60042A	MA9	
NR 71156	202.27	1409.26	-1611.52*	-474.03
NR 71176	-50.53	-330.74	381.27	114.86
NR 71177	-170.50	-96.31	266.81	99.29
NR 71178	-442.75	-439.06	881.81	192.06
NR 71167	461.52	-543.15	81.63	37.82
General effect <sup>*</sup> ( $g_j$ )	398.29	11.30	-409.60	

\* Significantly different from zero at 0.05 probability level

++ S.E ( $g_i$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (242) = 672, 1113.2

<sup>\*</sup> S.E ( $g_j$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (329.6) = 1048, 1925.0

+ S.E ( $S_{ij}$ ) =  $t_{0.05}$ ,  $t_{0.01}$  (667) = 1427, 1988.0

influential male and female parents, respectively. However, the highest positive s.c.a value was obtained for hybrid M60042A x NR 71156 which gave the highest mean grain yield among the hybrids (Appendix II).

The highest mean heterosis was obtained for grain yield (24.84%) and lowest (-7.7%) for Days to 50% flowering (Table 17). Heterosis for individual crosses expressed as percentage increase or decrease of hybrid mean over the mean of the superior parent (%SP) or, the mid-parent (%MP) is presented in Table 17. Both positive and negative heterosis were obtained for all the characters. Estimates expressed as %SP were generally, smaller than corresponding estimates expressed as %MP. It is more meaningful to compare the  $F_1$  vigour with the superior parent rather than the mid-parent, since this gives an estimate of improvement made.

In Table 17, heterosis on this basis is expressed for yield in twelve out of the fifteen  $F_1$  lines. It is interesting to note that the highest heterosis for grain yield (74.21% SP, 120.57% MP) was exhibited by hybrid 2219A x NR 71178 (yield Rank 6, Appendix II) and both parents are relatively low in grain yield (Appendix Table 1) but are good general combiners (Table 16).

For protein content, most of the hybrids were lower than their superior parents as indicated by the many unfavourable (negative) heterosis. The highest favourable heterosis was exhibited by hybrid M60042AxNR 71178 with yield ranking 12 (Appendix II)

Table 17 Heterosis of hybrids over superior (sp) and mid-parent (mp) for all characters measured in this study

Cross	Rank†	Seedling vigour		Days to 50% flowering		Plant height		Number of kernels/head		Head weight		1000-grain weight	
		(%MP)	(%SP)	(%MP)	(%SP)	(%MP)	(%SP)	(%MP)	(%SP)	(%MP)	(%SP)	(%MP)	(%SP)
2219A x NR7115A	7	-20.00	-3.61	-6.87	-7.08	41.53	27.30	6.38	41.58	44.29	46.38	11.63	20.35
W60042A x NR7115A	1	-40.00	-23.08	-4.88	-7.57	23.56	18.30	40.95	46.01	50.00	62.79	0.83	8.35
NA9 x NR7115A	15	-60.00	-51.8	11.27	-1.78	-3.02	-5.26	36.27	43.48	43.75	53.33	-6.80	-6.17
2219A x NR7117A	4	0.00	-0.76	24.36	10.42	60.00	19.04	21.18	66.42	10.23	6.17	7.68	13.63
W60042A x NR7117A	11	20.83	0.00	-1.73	-4.55	1.23	-4.55	30.51	15.13	1.32	9.86	5.93	11.41
NA9 x NR7117A	8	-27.08	-13.58	4.63	0.97	28.40	5.02	37.55	38.22	48.86	55.95	-4.33	-1.49
2219A x NR71177	5	13.16	21.13	-8.36	-11.52	76.82	35.10	-11.53	23.95	-18.37	-3.61	16.89	21.17
W60042A x NR71177	9	5.26	21.21	-7.65	-8.44	32.27	19.48	2.27	14.17	11.22	38.85	3.53	6.95
NA9 x NR71177	10	18.42	-13.58	-3.16	-3.86	28.90	8.11	5.45	8.36	-1.02	8.99	-10.26	-5.93
2219A x NR71178	6	37.14	41.18	-7.29	-14.26	64.47	40.29	20.15	48.86	1.18	12.42	35.93	42.85
W60042A x NR71178	12	8.57	20.63	-10.10	-14.54	29.67	29.03	-8.20	-2.30	15.29	36.11	28.28	34.35
NA9 x NR71178	3	14.29	17.65	-5.75	-10.27	22.36	13.76	50.03	72.90	52.94	57.58	-5.93	-2.73
2219A x NR71167	2	65.00	18.42	-8.81	-10.98	69.76	35.17	-14.83	21.92	-3.23	11.80	15.77	25.88
W60042A x NR71167	14	-46.51	-35.21	-5.44	-5.64	28.92	20.78	5.09	21.11	13.98	39.47	3.19	11.84
NA9 x NR71167	13	-30.23	-21.05	-2.46	-2.81	23.87	7.99	33.39	41.96	59.14	71.10	-0.78	-0.52
Average heterosis (%)		-2.7	-7.7**		13.48**		19.18**		24.53**		9.64**		

\*\* Significant at 1% level of probability

† Means of grain yield are ranked from highest (1) to lowest (15)

Table 17 (Cont'd)

Cross	Rank†	Panicle length		Protein		Grain yield	
		(% SP)	(TMP)	(% SP)	(TMP)	(% SP)	(TMP)
Z219A x NR71156	7	3.82	5.49	-10.20	-2.13	21.44	72.76
M60042A x NR71156	1	5.90	9.71	-7.01	-6.55	43.52	68.56
MA9 x NR71156	15	1.74	6.35	2.87	2.92	49.16	-47.22
Z219A x NR71176	4	1.77	2.86	-20.80	-12.05	31.50	86.98
M60042A x NR71176	11	2.47	5.26	-8.80	-7.17	13.50	33.22
MA9 x NR71176	8	9.54	13.55	1.97	4.22	21.35	25.90
Z219A x NR71177	5	-1.88	5.19	-5.85	2.12	24.68	78.24
M60042A x NR71177	9	-0.94	7.82	-7.11	-6.15	16.40	37.67
MA9 x NR71177	10	-6.56	2.57	-23.02	-22.64	14.87	20.24
Z219A x NR71178	6	-0.36	11.52	-10.28	1.79	74.21	120.57
M60042A x NR71178	12	7.46	26.34	36.94	36.20	58.88	59.17
MA9 x NR71178	3	16.73	27.65	-4.58	-0.24	46.72	67.11
Z219A x NR71167	2	-1.33	2.94	-3.30	-0.69	5.60	62.34
M60042A x NR71167	14	1.99	8.07	2.85	9.85	-22.20	2.23
MA9 x NR71167	13	8.61	16.11	-1.90	4.25	-18.12	-2.99
Average heterosis (%)		7.99**		0.26		24.84**	

\*\* Significant at 1% level of probability

† Means of grain yield are ranked from highest (1) to lowest (15)



Shorter plants and early maturing plant types were considered superior to taller plants and late maturing plants respectively. Except for hybrid MA9 x NR 71156 yield ranking 15 (Appendix II) all the hybrids were taller than their respective parents. Twelve out of fifteen hybrids flowered earlier than their superior parents, as is indicated by the negative heterosis values. For seedling vigour, seven hybrids indicated positive heterosis.

Negative heterosis was expressed in two hybrids for number of kernels/panicle and in three hybrids for head weight. Five out of fifteen heterotic values were negative for the 1000-grain weight and panicle length. The highest heterotic effect for 1000-grain weight, (35.93% SP, 42.85% MP) was expressed in hybrid 2219A x NR 71178 with yield ranking 6 (Appendix II). This hybrid also gave the highest heterotic effect for grain yield. Hybrid 2219A x NR 71178 had the third highest heterotic value (20.15% SP, 48.86% MP) for number of kernels/panicle while hybrid M60042A x NR 71156 with yield ranking 1 (Appendix II), gave the fourth highest heterotic values. For panicle length, the highest heterotic values were for hybrid MA9 x NR 71178 with yield ranking 3 (Appendix II) and hybrid M60042AA x 71156 with yield ranking 1 (Appendix II) had the fifth. A similar trend was recorded for plant height and days to 50% flowering where highest heterotic effects for these characters were exhibited for the same hybrid (2219A x NR 7178) as well as for grain yield.

Phenotypic ( $r_{ph}$ ), genotypic ( $r_g$ ) and error ( $r_e$ ) correlations are presented in Table 18. All the correlation coefficients determined were positive, while the rest were indeterminable, because the values were greater than 1. For phenotypic correlation coefficients ( $r_{ph}$ ), only number of kernels/panicle was significantly correlated ( $P = 0.01$ ) with grain yield. Percentage protein was highly correlated ( $P = 0.01$ ) with 1000-grain weight ( $r_{ph} = 0.909$ ), and seedling vigour ( $r_{ph}=0.455$ ). Highly significant phenotypic correlations ( $P = 0.01$ ) were also obtained between seedling vigour, 1000-grain weight, with panicle length, while 1000-grain weight, panicle length with days to 50% flowering followed a similar trend.

The genotypic correlation coefficient ( $r_g$ ) for yield was highly significant ( $P = 0.01$ ) with number of kernels/panicle, and non-significant for all other traits. Percentage protein was significantly correlated ( $P = 0.01$ ) with 1000-grain weight, seedling vigour, and non-significant with grain yield and plant height. Correlation between panicle length with seedling vigour, 1000-grain weight and days to 50% flowering was significant at  $P = 0.01$  level. The strongest association was obtained for protein and 1000-grain weight ( $r_g = 0.956$ ), followed by yield and number of kernels/panicle ( $r_g=0.523$ ). The error correlation coefficient for yield with number of kernels/panicle ( $r_e=0.563$ ) was highly significant, ( $P=0.01$ ) meaning that these two characters are influenced by the same differences of environmental conditions.

Table 18 Genotypic ( $r_g$ ) and phenotypic ( $r_{ph}$ ) in brackets correlation coefficients are in upper triangle, error correlation coefficients ( $r_e$ ) are in lower triangle

	Seedling vigour	Days to 50 % flowering	Plant height	No. of kernels/panicle
Seedling vigour	1.00	(0.207) 0.177	(0.047) 0.033	(0.001) 0.001
Days to 50 % flowering	0.258**	1.00	( - ) -	( - ) -
Plant height	0.126	2.05**	1.00	( - ) -
No. of kernels/panicle	0.001	-	-	(1.00)
Head weight	-	-	0.003	0.00003
1000-grain weight	0.283*	0.98**	0.477**	0.004
Panicle length	0.480**	0.539**	0.260**	0.002
Protein (%)	0.345**	0.002	0.365**	-
Grain yield	0.0001	0.005	0.563**	

\*, \*\* denote significant at 0.05 and 0.01 probability levels, respectively;  
-, (-) denote genotypic and phenotypic correlation coefficients greater than 1, respectively.

Table 18 (Cont'd)

	Head weight	1000-grain weight	Panicle length	Protein %	Grain yield
Seedling vigour	( - ) -	(0.18) 0.15	(0.36)** 0.33**	(0.46)** 0.79**	(0.006) 0.007
Days to 50% flowering	( - ) -	(0.364)** 0.139	(0.509)** 0.497**	( - ) -	(0.003) 0.004
Plant height	(0.001) -	(0.093) 0.038	(0.120) 0.101	(0.109) 0.048	(0.01) 0.016
No. of kernels/panicle	(0.001) 0.008	(0.002) 0.002	(0.002) 0.003	( - ) -	(0.548)** 0.523**
Head weight	1.00 -	( - ) -	( - ) -	( - ) 0.001	(0.001)
1000-grain weight	- -	1.00 0.469**	(0.489)** 0.956**	(0.909)** 0.002	(0.001)
Panicle length	- -	0.550** 0.002	1.00	( - )	(0.001)
Protein %	- 0.001	-	0.720**	1.00	( - )
Grain yield	-	0.002	-	0.002	1.00

\*, \*\* denote significant at 0.05 and 0.01 probability levels, respectively;  
-, (-) denote genotypic and phenotypic correlation coefficients greater than 1, respectively.

## CHAPTER FIVE

## DISCUSSION

The significant differences observed among the genotypes (entries) for all traits (Table 5) indicate that an appreciable amount of genetic variation exists among the entries for the traits measured. This is expected since wide ranges in means were recorded for most of the characters. Falconer (1981) has pointed out that the amount of improvement that can be made by selection among a number of crosses depends on the amount of variation between the crosses and on the intensity of selection since selection is ultimately applied to the crosses. In this study the hybrids differed significantly for all the characters measured therefore these characters could be easily selected for a breeding programme.

Analysis of variance for combining ability gives the relative importance of g.c.a or s.c.a effects to the total genetic variability present in a population. This serves as a useful tool to plant breeders since breeding methodologies may depend upon the nature of gene action that controls a particular character within a population.

In this study, the present significant differences for g.c.a variances for seedling vigour, days to 50% flowering, plant height, head weight, number of kernels/panicles and 1000-seed weight reveals the importance of additive gene action in controlling these characters.



Percentage protein, grain yield, panicle length and seedling vigour were shown to be under non-additive gene influence since the male x female interaction mean squares were significant for these characters.

However, the relative contributions of the  $g_m$  (male effects),  $g_f$  (female effects) and  $s_{mf}$  (male x female effects) to the total genetic variability present in a population remains obscured until these various variance components are partitioned. Components of variance (Table 7) revealed that the female effects were more influential than the male effects in the expression of most characters in the hybrids. Ahifarin (1969) reported higher variance components for male effects for all characters while Kambai and Webster (1965) reported same for grain yield. Beil (1965) on the other hand obtained larger variance component for female effects for grain yield. All authors attributed larger variance components to high level of genetic diversity of either the R-line (male parents) or A-line (female parents). An examination of the mean squares for comparisons among male and female parents (Table 5) showed that the male parents were generally more diverse than the females. However, a study of variance components showed that the  $g_f$  (female) effects were more important than the  $g_m$  (male) effects for most characters. Falconer (1981) had earlier noted that the performance of an inbred line is correlated with its performance in crosses to some extent depending on how much of the

variance is due to additive genes. It is thus likely that only a small portion of the variation found among the male parents was additive.

Dhaliwal (1977) reported that seed protein content of  $F_1$  hybrid seeds in bread wheat, corn and soybean is regulated by genotypes of the maternal parent rather than the hybrid endosperm or hybrid seed. In this study, the male component effect although not significant, was more influential than the female effect for this character. However, this character is under non-additive gene control as indicated by the significant males  $\times$  females interaction (Table 6), and low  $\sigma^2_a/\sigma^2_d$  ratio (Table 7) and high significant s.c.a effects (Table 15). This result contradicts those of Mongo *et al.*, (1988) and Nanda and Rao (1980) who reported predominantly additive gene action for this character, but tends to support the findings of Rana and Murty (1975) that non-additive gene action was important for per cent protein.

Specific combining ability has been shown to assume greater importance than g.c.a on materials that have been previously tested and selected for g.c.a (Sprague and Tatum, 1942; Kambal and Webster 1965; Beil, 1965). The lines in this study constitute elite lines among the Samaru breeding stock and have therefore been highly selected for grain yield over the years. Thus the s.c.a portion of total genetic variance was high and significant for grain yield. This result agrees with those of Nandanwanker and

Chandak (1984, Lazanyi *et al.* (1983) and Bhale and Borikar (1982). On the contrary, Spivakov (1988) reported predominantly additive gene action for this trait.

The major emphasis in this study was for grain yield. A closer look at the yield attributes was therefore worthwhile. Variance components (Table 7) revealed that although the mean squares for female effects were significant for head weight and number of kernels/panicle (Table 6) indicating presence of additive gene effect, their estimates of  $\sigma^2_D$  were twice and seven times, larger than for  $\sigma^2_A$ . This suggests that the degree of dominance was higher for total performance than for its individual component, indicating that these characters were more under non-additive gene influence. The  $\sigma^2_A/\sigma^2_D$  ratio (Table 7) further confirms that panicle length and grain yield were predominantly under non-additive gene control, while additive gene action predominated for 1000-grain weight. Thus the inheritance of yield and its components did not follow the same trend as 1000-grain weight was predominantly under additive gene control. Grain yield is a quantitative character, and its expression is complex, based on the interaction of a few to many genes, although the inheritance of yield components may be either additive, non-additive or both.

The high values of  $\sigma^2_A/\sigma^2_D$  ratio ( $> 1$ ) obtained for plant height and days to 50% flowering



stress the importance of additive portion of genetic variance in controlling the inheritance of these characters. Similar results have been reported for plant height (Sharma, 1980; Karale *et al.*, 1984) and days to 50% flowering (Kukadai *et al.*, 1983a; Ghandrashe Kharappa, 1987).

Although this experiment was designed to study combining ability, information on heritability is useful in predicting the relative importance of g.c.a and s.c.a. Narrow-sense heritability measures the relative importance of the additive portion of the genetic variance that can be transmitted to the next generation of offspring (Fehr, 1987). A high value for narrow-sense heritability therefore indicates that additive gene action is important for controlling the character while a low value signifies non-additive gene influence. Moderate narrow-sense heritability value would mean that both additive and non-additive gene action are important in influencing the expression of the character, and that an appreciable amount of additive effect exist for improvement.

The high estimates of narrow-sense heritability obtained for plant height, days to 50% flowering and 1000-grain weight in this study supports the high  $\sigma^2_a/\sigma^2_p$  ratio earlier reported for these characters and indicates that these characters are largely controlled by additive gene action. These characters could be easily selected in a breeding programme since they are fixable. High estimates of heritability have also been reported by Basal (1971)

for days to 50% flowering and Finkner *et al.* (1976) for plant height.

Moderate narrow-sense heritability estimates for head weight, seedling vigour, and number of kernels/panicle indicate that an appreciable amount of improvement is expected through selection since a significant amount additive genetic variance is present within the total genetic variance for these characters. For the economically important characters, grain yield and protein quality, narrow-sense heritability was low, emphasizing the importance of non-additive gene action and the environment in controlling their expression. These characters incidentally had high coefficients of variation (Appendix III) thus lending credence to the fact that most of the variation was not heritable and was therefore due to genic interaction and the environment.

The negative value of heritability estimated for grain yield in this study was simply considered as low. Negative components of variance have been reported in grain sorghum (Jan-Orn, 1973; Marquez-Sanchez and Hallauer, 1970). They attributed this to

- a) Sample size
- b) Assortative mating
- c) Deficiency in the genetic model
- d) linkage and estimates of actual zero values.

Estimates of components of variance also depend on the relative magnitude of the mean squares in the analysis, which in turn depend on the degree of freedom

(Marquez-Sanchez and Hallauer, 1970). In this study, the male  $\times$  female interaction mean square was of larger magnitude than those for males and females for grain yield, and heritability was estimated using variance components.

In an experiment such as this, heterosis is the main attraction. As far as breeders for agriculturally important self-pollinating crops are concerned, the major considerations are, first, whether or not it is possible to obtain sufficient heterosis for characters of economic importance under conditions which also give high yield per unit area of land, and, secondly, whether or not it is possible to fix such heterosis in pure breeding lines (Kraljevic-Balalic *et al.*, 1976).

In this study, significant heterosis was exhibited for all the characters except percentage protein and seedling vigour, as indicated by the parent versus hybrids contrast. Heterosis is expected since some amount of genetic variability exists between and among the parental lines (Table 5).

The highest mean heterosis was obtained for grain yield (24.84%), followed by head weight (24.53%) and then number of grains/panicle (19.18%). Grain yield has been observed to be the most heterotic character in sorghum, closely followed by number of grains per panicle (Kambal and Webster, 1965; Singhana, 1980).

Heterosis for grain yield in sorghum is well documented. Desai and Kukadia (1985), Harer and Baput (1982), Kulkaric (1985) all obtained the highest

positive heterosis of (16.67-91.33%), (21-44%), (197%) and (65%) respectively for grain yield. This compares favourably with the range (5.6-120%) of positive heterosis obtained for this trait in this study.

Previous studies with grain sorghum have also shown heterosis for other characters as reported in this study. Solani and Chaturvedi (1978) reported high heterosis for days to 50% flowering, while Desai and Kukadia (1985) reported heterosis for plant height. For head weight, Birada and Borikar (1984) recorded high positive heterosis (147%), while Perez Cabrera and Miller (1985) reported heterosis for panicle length and grain weight.

Based on investigations on heterosis, it appears that the factors that contribute to grain yield include 1000-seed weight, number of kernels per panicle, panicle length, greater plant height, and earlier flowering since hybrids that showed high heterosis for yield exhibited high heterosis for these traits. Studies on the expression of hybrid vigour in grain sorghum in the United States of America have shown that the main increase comes from more grains per plant (Quinby, 1963b). It was also suggested that greater yield of hybrids may be attributed to more rapid cell division of the apical meristem, as with corn.

In heterosis studies, the breeder is also interested in the amount of heterosis that can be useful for improvement. He is particularly interested in that hybrid combination that differs significantly

from the mean performance, of the parents, the best parent, or from the highest yielding commercial variety. Parents of such hybrids are selected for their g or s.c.a, since the ultimate goal in a hybrid programme is to indentify genotypes which could excel in their combining ability.

In the present study, the F<sub>1</sub> vigour compared with the superior parent (%SP) was considered in more details than with the mid-parent (%UP) since this gives an estimate of the improvement made. A similar approach was used by Fonseca and Patterson (1968), but is herein referred to as heterosis rather than heterobeltosis.

It is therefore noteworthy that the highest heterosis for grain yield was exhibited by hybrid 2219A (high) x NR71178 (high), yield ranking 4 (Appendix II) whose parents have high g.c.a effects for this trait. This means a portion of the s.c.a effect may be fixable, therefore these parents could be selected for their g.c.a in a hybrid programme, since their high g.c.a effect is reflected in their s.c.a. Hybrids formed with female parents 2219A gave consistently high grain yield, ranking second, fourth, fifth, sixth and seventh (Appendix II). However, the high s.c.a effects for M60042A (low) x NR71156 (low) > 2219A (high) x NR71167 (low) > MA9 (low) x NR 71178 (high) hybrids which were the top three hybrids in terms of grain yield, reveal the importance of genic interaction for this character. Such cross combinations are not likely to give good segregants

but the parents could be selected for their s.c.a effects. Therefore crossing such "good lines" with subsequent testing and selection in hybrid combinations, may be an effective breeding method.

Grain protein has been shown to be under non-additive gene influence. Among the hybrids, hybrids MA9 (low) x NR 71167 (high), M60042A (low) x NR71178 (high) were significantly higher in per cent protein than the others. This indicates that hybrids with high percentage protein involved at least one high general combiner. Since these hybrids are low yielding (Ranks 12 and 15 respectively, Appendix II), selection intensity for this character among the hybrids must be low, unless the main objective of the breeding programme is for protein quality.

The predominance of non-additive components of variance and the high level of dominance for grain yield and protein, impose some limits on the progress of improvement through direct selection for these characters. In such a situation, a selection procedure that gives proper weight to related characters becomes necessary since this may cause a simultaneous improvement in yield and quality. The success of this strategy depends to a large extent on the nature and magnitude of intercharacter associations, and the heritability ratios of the characters concerned.

Positive significant correlation ( $P = 0.01$ ) between protein with seedling vigour and 1000-seed weight at both genotypic and phenotypic levels,

implies that selecting for more vigorous plants and heavier seeds might increase the chances of improving grain protein. Positive correlation between 1000-grain weight and protein, have been reported by Abifarín (1969).

The rather weak positive association between grain yield with days to 50% flowering and plant height, suggest that shorter plant types or early flowering plants could be bred successfully to some extent without offsetting grain yield. Percentage protein, head weight, 1000-grain weight, and panicle length all showed weak association with grain yield, indicating that these characters behave independent of yield.

That number of kernels/panicle is the most influential character in grain yield is clearly brought out by this study, as it was the only character so correlated with yield. Several authors including Quinby (1963b), Niehaus and Pickett (1966), Fisher and Kertisz (1976), Singhana (1980), Axtell (1981), Jimenez and Casas (1983) and Nandanwankar and Chandak (1984) agree that number of kernels/panicle has the greatest and most consistent effect on total grain yield in sorghum. In this study, the heritability estimated for number of kernels/panicle was moderate so although the  $\sigma^2_a/\sigma^2_p$  ratio was low, an appreciable amount of additive genetic variance exists for this trait. Therefore, significant progress in selecting for grain yield is expected when screening segregations on the basis of number of kernels/panicle.

## SUMMARY AND CONCLUSION

Each of five pollen fertility restoring (R) lines was crossed onto three male sterile (A) lines to obtain fifteen  $F_1$  hybrids. The hybrids and their parents were grown at two locations with two rows each randomised four times. The loss of an experiment at one location limited the analysis to one location thus biasing the result to an unknown extent.

Line  $\times$  tester procedure was used to estimate the g.c.a and s.c.a variances among the  $F_1$  hybrids. The linear model assumed for this analysis included; an effect due to the g.c.a of an A-line, an effect due to the g.c.a of an R-line, an effect due to the s.c.a of the male  $\times$  female interaction plus an effect due to random error.

Significant differences among males were observed in their g.c.a for plant height and 1000-seed weight. The females differed significantly in their g.c.a for days to 50% flowering, plant height, head weight, number of kernels/-panicle, seedling vigour and 1000-seed weight. Significant variation for s.c.a were obtained for percentage protein, panicle length, seedling vigour and grain yield.

Evaluation of variance components  $\sigma^2_a/\sigma^2_b$  revealed that most characters were more under the influence of non-additive effect of genes except for plant height, days to 50% flowering and 1000-seed weight.

The following values were obtained for estimates of narrow sense heritability; seedling vigour



(42.48%), days to 50% flowering (83.08), plant height (95.08%), number of kernels/panicle (56.55%), head weight (63.66%), 1000-seed weight (77.28%), and panicle length (22.19%), percentage protein (15.86%), grain yield (-33%),.

Wide ranges in means were recorded for most of the characters. Grain yield ranged from 1887.78-5329.45 kg/ha while percentage protein ranged from 8.66-14.43%. Hybrid means were generally higher than the means of the parents except for the characters seedling vigour and days to 50% flowering. The greatest average heterosis was obtained for grain yield (24.84%) followed by head weight (24.53%), number of kernels/panicle (19.18%), plant height (13.48), 1000-grain weight (9.64%), panicle length (7.99%), days to 50% flowering (-7.7%), seedling vigour (-2.7%), and least for percentage protein (0.265).

For individual hybrids, hybrid 2219A x NR71178, which were both good general combiners for grain yield, gave the highest positive heterosis value (74.21% SP and 120.57% MP). Hybrid M60042A x NR71178 gave the highest positive heterosis for percentage protein (30.94% SP, 36.20% MP).

Values for the general response of parental lines as expressed in hybrid combinations indicate that for grain yield, lines (NR71178) and (2219A) are parents with good g.c.a and are expected to perform well when included in most hybrid programmes. Based on the specific combining ability effect, and the per se ,

performance of the hybrids, hybrids M60042A x NR71156 2219A x NR71167 and MA9 x NR71178 which were the top three hybrids, and yielded better than the highest yielding parent could be selected as superior hybrids for grain yield. Superior specific combiners for percentage protein were M60042A x NA71178) and MA9 x NR71167.

Per cent protein was significantly correlated with seedling vigour and 1000-grain weight, while grain yield was significantly correlated only with number of kernels/panicle.

The results in this study indicate that most of the characters measured in this population including grain yield, were more under non-additive effect of genes. Selection of inbred lines to be used in hybrid programmes should be on the basis of specific combining ability of the lines. Once some high yielding hybrids are identified, they could then be capitalised on, in further testing and selection, for the development of hybrid grain sorghum. Owing to the significant genotypic correlation between grain yield and number of kernels/panicle ( $r_g = 0.523$ ), it is concluded that selecting plant types from this population that produce large number of seeds/head would increase the possibility of obtaining lines or hybrids with high yield potentials.

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Appendix I Mean values of the eight parental lines for characters measured

Parent	Seedling vigour	Days to 50% flowering	Plant height	No. of kernels/panicle	Head weight
NR7115A	5.0a ± 0.0	65.5b ± 0.65	105.6d ± 3.87	2328.5ab ± 202.7	0.070abc ± 0.0080
NR71176	4.75ab ± 0.25	64.8b ± 1.03	143.5a ± 3.77	2565.6ab ± 382.3	0.088abc ± 0.010
NR71177	3.75bcd ± 0.48	70.5b ± 1.5	137.0a ± 3.84	2737.25ab ± 539.3	0.098a ± 0.010
NR71178	3.5cd ± 0.5	76.5a ± 1.19	114.0c ± 2.46	1905.25ab ± 252.6	0.085abc ± 0.0080
NR71167	4.25abc ± 0.48	69.0b ± 1.58	128.0b ± 4.11	2946.25a ± 223.6	0.093ab ± 0.0090
Z219A	3.25cd ± 0.25	65.8b ± 1.30	85.0e ± 1.58	1770.5b ± 302.0	0.068br ± 0.0090
NA0042A	2.75d ± 0.25	69.3b ± 3.04	113.25c ± 1.49	2167.0ab ± 337.3	0.059c ± 0.0031
NA9	3.25cd ± 0.25	69.5b ± 1.60	77.25d ± 1.89	2598.0ab ± 359.7	0.083abc ± 0.0048

\* = Means within columns followed by the same letter are not significantly different at the 0.05 level of probability

DNRRT = Duncan's New Multiple Range Test



## Appendix I (Cont'd)

Parent	1000-grain weight	Panicle	Protein	Grain yield
NR71154	22.78a ± 2.17	28.83bc ± 1.0	11.17a ± 0.51	3713.3ab* ± 425
NR71174	21.75a ± 1.85	28.33bc ± 0.94	10.66a ± 0.89	3707.78ab ± 877.6
NR71177	20.96a ± 0.78	32.00a ± 1.1	11.25a ± 1.89	3777.78ab ± 928.38
NR71178	21.57a ± 1.0	21.8d ± 0.51	10.17a ± 0.97	2400.55bc ± 411.9
NR71167	23.21a ± 1.4	30.15ab ± 0.59	12.63a ± 2.04	4998.33a ± 525.4
2219A	19.48a ± 1.3	27.63bc ± 0.76	13.33a ± 0.45	1507.28c ± 168
W600428	19.62a ± 1.3	26.83c ± 0.33	11.02a ± 0.52	2610.15bc ± 179.4
W69	23.09a ± 1.1	26.33c ± 0.53	11.14a ± 0.37	3440.03ab ± 651.12

\* = Means within columns followed by the same letter are not significantly different at the 0.05 level of probability

DWRT = Duncan's New Multiple Range Test.

Appendix II Mean values of the hybrids for all characters measured

Hybrid	Rank	Seedling vigour	Days to 50% flowering	Plant height	No. of kernels/panicle	Head weight
M60042A x NR 71156	1	3.0c ± 0.0	62.3bcd ± 0.63	128.5de ± 3.60	3282abcd ± 235.6	0.1045bc ± 0.0032
2219A x NR 71167	2	4.5ah ± 0.29	60.0d ± 0.58	144.3abc ± 2.20	2509.5cde ± 264.4	0.09bc ± 0.01
NA9 x NR 71178	3	4.00abc ± 0.0	65.5a ± 0.87	121.5e ± 2.80	3886.5ab ± 315.3	0.149a ± 0.02
2219A x NR 71176	4	4.3ab ± 0.48	64.8ah ± 1.03	136.4cd ± 4.00	3108.8abcd ± 290.0	0.097bc ± 0.007
2219A x NR 71177	5	4.30ab ± 0.48	60.3d ± 0.25	150.3a ± 2.3	2421.8de ± 340.0	0.08c ± 0.02
2219A x NR 71178	6	4.80a ± 0.25	61.0cd ± 0.41	139.8bc ± 3.2	2289.3de ± 210.0	0.09bc ± 0.013
2219A x NR 71156	7	4.00abc ± 0.41	61.0cd ± 0.71	170.30e ± 5.3	2532.0cde ± 201.8	0.10bc ± 0.007
NA9 x NR 71176	8	3.5bc ± 0.29	67.8a ± 1.90	127.50de ± 3.50	3563.3abc ± 361.0	0.013a ± 0.007
M60042A x NR 71177	9	4.0abc ± 0.0	64.0abc ± 1.00	149.8a ± 1.40	2780bcde ± 268.0	0.11bc ± 0.009
NA9 x NR 71177	10	4.5ah ± 0.29	67.3a ± 2.1	128.0de ± 3.40	2887.0abcd ± 349.0	0.10bc ± 0.008
M60042A x NR 71176	11	3.8abc ± 0.63	64.0abc ± 1.20	147.8ab ± 2.00	2600.00cde ± 241.0	0.10bc ± 0.006
M60042A x NR 71178	12	3.8abc ± 0.63	62.3bcd ± 0.75	146.8ab ± 3.60	1999.00e ± 224.0	0.10bc ± 0.009
NA9 x NR 71167	13	4.0abc ± 0.0	67.3a ± 0.63	123.0e ± 2.5	3930.0a ± 110.0	0.13a ± 0.005
M60042A x NR 71167	14	4.3ah ± 0.49	65.3ab ± 0.85	146.00ab ± 1.5	3296.0abcd ± 622.0	0.11bc ± 0.02
NA9 x NR 71175	15	2.0d ± 0.0	66.3a ± 1.10	96.30f ± 1.40	3229.0abcd ± 153.0	0.12ab ± 0.006

\* Means for grain yield are ranked from highest to lowest

\*\* Means within columns followed by the same letter are not significantly different at the 0.05 level of probability as determined by DMRT

Appendix II (Cont'd)

Hybrid	Rank	1000-grain weight	Panicle length	Protein	Grain yield
M60042A x NR 71156	1	22.97cde ± 0.45	30.5abcde ± 0.16	10.35bc ± 0.53	5329.17+ ± 659a**
2219A x NR 71167	2	24.87abc ± 0.67	29.80bcde ± 0.88	12.89ab ± 0.60	5280.6 ± 877.6a
NA9 x NR 71178	3	21.72de ± 0.84	30.73abcd ± 0.64	10.63bc ± 0.53	5047.2 ± 569.5a
2219A x NR 71176	4	23.43cde ± 1.36	28.75fg ± 0.78	10.58bc ± 0.78	4875.6 ± 372.5a
2219A x NR 71177	5	24.50bcde ± 0.97bcde	31.43ab ± 0.92	12.55ab ± 0.75	4710.0 ± 638.92a
2219A x NR 71178	6	29.32a ± 1.85	27.63g ± 0.68	11.96ab ± 1.45	4530.5 ± 387.1a
2219A x NR 71156	7	25.43abcd ± 1.87	29.93bcde ± 0.44	11.97ab ± 0.51	4509.5 ± 659a
NA9 x NR 71176	8	22.09de ± 0.92	30.95abc ± 0.57	11.36bc ± 0.63	4499.5 ± 443a
M60042A x NR 71177	9	21.79de ± 1.06	31.68ab ± 0.86	10.45bc ± 0.83	4397.2 ± 530.6a
NA9 x NR 71177	10	20.72e ± 1.4	29.85bcde ± 0.58	8.66c ± 0.75	4339.4 ± 542.9a
M60042A x NR 71176	11	23.05cde ± 1.2	29.03cdefg ± 0.66	10.05bc ± 0.13	4208.4 ± 526.5a
M60042A x NR 71178	12	27.67ab ± 0.88	28.83defg ± 1.12	14.43a ± 1.35	4147.0 ± 653a
NA9 x NR 71167	13	23.03cde ± 0.90	32.83a ± 0.19	12.39a ± 0.51	4092.8 ± 391a
M60042A x NR 71167	14	23.95bcde ± 0.80	30.75abc ± 0.33	12.99ab ± 1.54	3888.9 ± 1091.5a
NA9 x NR 71175	15	21.38e ± 0.75	29.28bcde ± 0.40	11.46abc ± 0.44	1887.8 ± 175.3b

\* Means for grain yield are ranked from highest to lowest

\*\* Means within columns followed by the same letter are not significantly different at the 0.05 level of probability as determined by DMRRT

Appendix III Means, standard errors, ranges and coefficient of variations (%) of entries (E), Parents (P) and hybrids (H) for all traits studied

Character		Mean	S.E	Range	Coefficient of variation (%)
Seedling vigour	E	3.74	± 0.47	2.00 - 5.00	17.59
	P	3.80	± 0.47	2.75 - 5.00	17.57
	H	3.70	± 0.47	2.00 - 4.75	17.87
Days to 50% flowering	E	65.63	± 1.90	60.00 - 76.50	3.88
	P	68.84	± 2.27	64.75 - 76.50	3.70
	H	63.92	± 1.46	60.00 - 67.75	3.99
Plant height	E	127.39	± 3.70	85.00 - 150.30	4.11
	P	115.70	± 3.86	85.00 - 143.50	4.72
	H	133.73	± 3.70	96.00 - 150.00	3.93
Number of kernels/panicle	E	2745.26	± 461.56	1770.50 - 3930.00	23.78
	P	2377.28	± 459.50	1770.50 - 2946.25	27.33
	H	2941.52	± 462.50	1989.25 - 3930.00	22.24
Head weight	E	0.097	± 0.012	0.059 - 0.149	18.60
	P	0.080	± 0.013	0.059 - 0.098	22.10
	H	0.106	± 0.012	0.080 - 0.149	16.25
1000-grain weight	E	23.06	± 1.77	19.48 - 25.43	10.83
	P	21.56	± 2.09	19.48 - 23.21	13.69
	H	23.86	± 1.61	20.72 - 29.32	9.52
Panicle length	E	29.31	± 0.97	21.80 - 32.83	4.68
	P	27.74	± 1.14	21.80 - 28.83	5.80
	H	30.15	± 0.87	27.63 - 32.83	3.85
Protein	E	11.48	± 1.35	8.66 - 14.43	16.82
	P	11.42	± 1.63	10.17 - 13.33	20.20
	H	11.51	± 1.22	8.66 - 14.43	15.02
Grain yield	E	4004.31	± 820.15	1507.28 - 5329.45	28.97
	P	3294.40	± 805.19	1507.28 - 4998.33	34.57
	H	4382.93	± 840.71	1887.78 - 5329.45	27.13

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