USE OF GENERATION MEAN SCALING FOR ESTIMATION OF VARIANCE COMPONENTS IN MAIZE BREEDING

BY

DICKSON OTIENO LIGEYO

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DECLARATION

I declare that this thesis is my original work and has not been submitted for a degree in any other University.

Date 15/7/92 Name D. O. LIGEYO.

Signature D.O.Ligeyo

This thesis has been submitted for examination with our approval as University supervisors.

Date 17/7/92 Name DR. P.O. AYIECHO.

Signature

Date 17/7/92 Name PROF. V.K. GUPTA.

Signature V.K. Gupta

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Signature......V.K. Gupta...

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ABSTRACT

Genetic studies were carried out to estimate the variance components in maize using six crosses, A x F, A x 64, A x 8, F x 64, F x 8 and 8 x 64. The four parental inbred lines (A, F, 64 and 8), the F_1, F_2 and backcross generations of these crosses were grown in a randomized complete block design with three replicates at National Agricultural Research Centre, Kitale; Western Agricultural Research Centre, Kakamega; Soy and Sabwani, between April and October 1991. Diallel and generation mean analyses were done based on data from twelve randomly selected plants in each plot for plant height, ear height, grain yield, ear length, 200-grain weight and kernel row number. Lodging percentage was determined for the whole plot.

According to the diallel analysis, the additive gene effects were relatively more important for all the traits except grain yield, 200-grain weight and lodging percentage. Non- additive gene effects played insignificant roles in manifestation of the traits studied.

The generation mean analysis revealed that both additive and dominance genetic variances were important for grain yield, ear length, 200-grain weight, plant height, ear height and kernel row number. The variability attributable to dominance genetic variance was much greater in all cases. Lodging percentage was mainly governed by additive genes. In most crosses additive x additive and dominance x dominance genetic variances were more important than additive x dominance genetic variance at all sites. In all cases the manifestation of various genetic variance components varied according to crosses and experimental sites.

Among the parental cultivars, inbred lines F and 64 had high general combining ability estimates for yield and yield component traits at most sites, and hence were the most promising for yield improvement. The crosses 8 x 64, A x F, A x 8 and F x 64 also had high specific combining ability estimates for grain yield and could be used in further selection and hybrid development programmes. Cross 8 x 64 was the most heterotic at most sites for grain yield, plant height, ear height and ear length while crosses A x F and F x 8 were the most heterotic at most of the sites for characters, 200-grain weight and kernel row number respectively. Double cross (A x 64) x (F x 8) had the best predicted yield performance at Kitale, Kakamega and Soy.

1. INTRODUCTION

Maize (Zea mays L.) was first introduced to East Africa in the 16th century by the Portuguese traders. The introduced varieties were only suitable to the coastal areas as they had mostly come from the Carribean lowlands. The spread to the highlands took place in the 20th century when European settlers introduced varieties from South Africa (Leakey, 1970). Presently, maize is the most important food crop in Kenya, it constitutes the staple food for the majority of Kenyans. It is estimated that over one and a half million hectares of land are under the crop annually, mainly on small holdings. Approximately seventy percent of the area under maize is planted with hybrids or composites and the remaining thirty percent is planted with either local or some advanced generation of hybrids (Omollo, 1981).

Conventional maize breeding in Kenya started in early 1930's at National Plant Breeding Station, Njoro. This work was only a spare time activity of the wheat beeders and consequently made little progress. Shortly, before world War II, some single cross and double cross hybrids were produced and evaluated for yield. Because very few of the developed hybrids out-yielded open pollinated controls it was concluded that the genetic base for the populations from which the inbred lines had been derived was too narrow. This work was abandoned during the war and resumed in 1948. However, a fire in the maize crib at Njoro in 1953 which destroyed both the records and most of the breeding stocks made this work be completely abandoned.

A formal breeding program for yield was started in Kenya at Kitale in 1955. A large collection of germplasm was introduced from Central and Southern America for use in this program. At that time the local materials, the Kenya flat white complex, had acquired a high level of adaptation and disease resistance through selection (Muthoka, 1981). Crosses of Kitale synthetic II with Costa Rica 76 and with Ecuador 573 outyielded the best parent, Kitale synthetic II, by fourty percent. The varietal cross between Ecuador 573 and Kitale synthetic II was released along with classical hybrids in 1964, one of such hybrids is hybrid 611. The release of varietal cross was a breakthrough and led to the shifting of breeding strategy from the orthodox inbreeding and hybridization to population improvement. As a follow up to this, a comprehensive breeding system proposed by Eberhart, Harrison and Ogada (1967) came up as an appropriate method to exploit the situation. The outline of the comprehensive breeding system has four phases.

(1) Evaluation of local and exotic varieties to identify the best breeding material.

(2) Compositing selected breeding materials into one or more populations in such a manner that each population has a considerable genetic variation for the trait to be

improved, andthat the cross of these populations will show heterosis.

(3) Recurrent selection in each population to increase the frequency of favourable genes in order to develop populations and population crosses that are improved with each cycle of selection.

(4) Release of the commercial varieties in one of the following forms:

   (a) The cross of two populations as a varietal hybrid.

   (b) Single, three way, or double cross hybrids from inbred lines developed from the elite materials after each cycle of selection.

   (c) A synthetic variety derived from advanced generations of the population cross in areas where hybrid production is not yet feasible e.g. parts of eastern province and the coast.

Since the days of Kenya's independence, the maize breeding programme has realized tangible archievements through constant release of high yielding hybrids. Seven hybrids are currently availabe for high potential highlands, including Rift Valley, and two each for the medium, coastal and marginal rainfall areas of Kenya. The latest released varieties (1989) are hybrid H626, Makueni for dry areas and Pwani hybrid I for the coast.

The distribution of maize improvement centres in Kenya is based on agro-ecological zones. There are centres catering for late, medium and early maturing maize improvement programmes, at Kitale, Embu and Katumani respectively. Besides these there is also a high altitude maize improvement program at Ol-Joro-Orok and the coastal program which develops varieties suitable for humid coastal areas at Mtwapa.

Grain yield in maize depends on the genotype of the plant and its interaction with environment. The first work that related a theoretical concept of quantitative genetics to maize breeding was the estimation of genetic variance components by Sprague and Tatum (1942). A justification to this project is that genetic variability is a basic element necessary to any plant breeding program. If genetic variability is not present in the breeder's populations, selection will be neither effective nor possible. The methods of selection to be used and the expected selection gain will be determined by mode of gene action. The plant geneticist or breder is therefore interested in the estimation of the genetic effects in order to formulate the most advantageous breeding procedures for the improvement of the attributes in question. This study was therefore undertaken with the following objectives:-

(1) To study the genetics of yield and yield related traits in crosses involving maize

inbred lines.

(2) To estimate the combining ability and heterosis for maize hybrid combinations.

(3) To identify the best double cross hybrids that can be obtained from the crosses made.

2. LITERATURE REVIEW

2.1 Generation mean analysis:

Mather (1949) introduced tests of generation means for detection of epistasis. More general models were developed by Anderson and Kempthorne (1954), Hayman (1954) and Hayman and Mather (1955) to describe genetic variation present in two inbred lines and their descendant families. Anderson and Kempthorne (1954) showed that all the information about additive; dominance and digenic epistatic variation available in the means of generations descended from two inbred lines is contained in six parameters, namely, mean, additive, dominance, additive x additive, additive x dominance and dominance x dominance. Other models of generation mean analyses are those of Hayman (1958, 1960 a, b) and Eberhart and Gardner (1966). Anderson and Kempthorne's (1954) Model lacks simplicity in interpreting the parameters, while Eberhart and Gardner's (1966) mode can be extended only through additive x additive epistasis. Hayman's (1958, 1960 a, b) model, on the other hand, lacks the orthogonality present in the first two models. The parameters in Hayman's models were estimated by the method of least squares.

Hallauer and Miranda (1981) noted that in growing different generations of maize, one should be cognizant of two important considerations in order to have valid estimates of the generation means:

(1) Sufficient sampling of the segregating generations is necessary to have a representative sample of the genotypes. In parental and F_1 generations no sampling is involved, but F_2, F_3, F_4--- and backcross generations will be segregating and sample size has to be considered.

(2) In outbreeding crops like maize it is necessary to consider the level of inbreeding of each generation. It therefore becomes necessary to have sufficient border rows in experimental plots to minimize competition effects of the adjacent plots.

Hallauer and Miranda (1981) noted that several different possibilities exist for the type and number of generations that can be included in a generation mean experiment. Where the two parents, F_1, F_2 and F_3 generations are evaluated, there are five means for comparison. Expectations of each generation can be determined and a least squares analysis made to estimate mean (M), additive (a) and dominance (d) effects with a fair degree of precision. They concluded that generation mean analysis can be used to;

(i) Obtain some specific genetic information about a specific pair of lines.

(ii) Provide some information on the relative importance of the non-additive genetic effects for the justification of a hybrid breeding program.

(iii) Provide information on the relative importance of genetic effects.

Darrah and Hallauer (1972) indicated that one inherent property of the generation mean analysis is the cancelling of the additive effects, which would reduce the net additive effect. Based on the sample of the inbred lines, they concluded that a procedure that would detect and select favourable non-additive gene effects should result in better performing hybrids if highly heterozygous plants are to be grown.

Moreno-Gonzalez and Dudley (1981) working with maize, noted that there was no apparent association of genetic effects estimated from the generation mean analysis with crosses involving related or unrelated lines. While their study suggested that generation mean analysis was a poor method for measuring additive effects, it revealed the preponderance of dominance genetic effects for yield, plant leaf area, plant height, ear height, ear length and ear diameter. Epistatic variation was significant but smaller than additive and dominance variation. The sign of epistasis was predominantly positive for yield, suggesting that lines selected for yield may have certain combinations of genes that are expressed favourably in hybrids.

Hayman (1958, 1960 a, b) using generation mean analysis proposed a model that permits estimation of additive, dominance, additive x additive, additive x dominance and dominance x dominance effects in the cross between two inbred lines of Nicotiana rustica. Mather and Jinks (1971) described a model similar to Hayman's model using the $F\infty$ generation (population of all inbred lines derived from the cross of two inbreds) as the reference population instead of the F_2 generation. Eberhart and Gardner (1966) also published a general model for the diallel cross that separates additive, dominant, and additive x additive effects. Generation mean analysis was used to estimate epistatic effects by Gamble (1962 a) and Darrah and Hallauer (1972) for maize yield and Hughes and Hooker (1971) for resistance to Helminthosporium turcicum in maize.

Moreno-Gonzalez and Dudley (1981) noted that dominance gene effects were positive and appeared to be the most important genetic effects controlling the performance of yield, plant height, ear height, ear length, ear diamter and leaf area in maize. Dominance effects were significant in 12, 15, 15, 13, 10 and 15 out of 15 crosses for the above characters respectively. Comparing generation mean analysis with diallel analysis, these workers found that in diallel analysis the yield mean square due to dominance effects was several times larger than that due to additive effects. The large differences between the inbred and the F_1 generations were accounted for by large dominance effects. Additive effects were found to be more important than dominance effects for plant height, ear height, ear length and ear diameter. The diallel analysis was more effective in measuring additive variation than generation mean analysis of individual crosses because of differences between the two models. Variation due to epistatic effects was much smaller than variation due to additive and dominance effects. Dominance effects can be considered as a measure of heterosis if epistatic effects are negligible. The ratio of dominance to additive variation was larger for yield than for any other trait.

Stuber and Moll (1971, 1974) and Darrah and Hallauer (1972) found that the importance of epistatic effects diminished by environmental x epistatic interactions. Dominance effects were so large that their variation was not completely offset by a large location x dominance interaction. Results of the diallel analysis and the generation mean analysis agreed in showing the major importance of dominance in heterosis for grain yield in maize. The epistasis mean over all crosses was significant for yield, ear height, ear length and ear diameter. The overall epistasis mean for yield was positive. Positive differences for yield were also found by Sprague et al (1962), Stuber and Moll (1974) and Schnell and Singh (1978) when selected lines of maize were used. Results from both generation mean analysis and diallel analysis indicated that epistatic effects and their variances, though significant, were smaller than dominance effects and dominance variance.

2.2. Variance components.

The total phenotypic variance is comprised of genotypic and environmental variance components. The genotypic variance is the variance of the genotypic values and the environmental variance is the variance of environmental deviations. The genotypic component of variance is comprised of additive genetic variance, dominance genetic variance and epistatic genetic variance (Wright 1935 and Falconer, 1967). The relative magnitudes of these three genetic variance components are of importance to the plant breeder in order to plan the most effective breeding scheme. The additive variance, being the variance of the breeding values, is the most important component as it is the chief cause of resemblance between relatives. It is the main determinant of the response to selection. The dominance portion is due to allelic interactions. The epistatic genetic variance or the variance due to non-allelic interaction occurs due to teraction of additive and dominance effects involving two or more loci. Ignoring the epistatic effects will result into a bias in the estimation of the total genetic variance. The level and magnitude of the various variance components will determine the magnitude of heritability for any character.

Robinson and Comstock (1955) showed that linkage disequilibrium can bias the estimates of additive genetic variance and dominance genetic variance. The bias in the estimate of additive genetic variance in the case of an excess of coupling is always positive, and negative in the case of an excess of repulsion. The bias in the estimate of dominance genetic variance would depend upon the gene frequency, the type of gene action and the amount of linkage disequilibrium. The estimates of additive genetic variance may be biased upward due to genotype-environment interactions. Jinks and Perkins (1969) noted that additive and dominance gene action respond similarly to the different environments, with additive gene action being more responsive. The dominance and epistatic gene action was also less sensitive to the environmental differences than the additive gene action.

Robinson <u>et al</u> (1949) found little or no dominance for genes that control the expression of plant height.

They reported no dominance involvement in the expression of ear height in maize. However, Giesbretch (1961) observed that dominance gene action played a major role in the expression of ear height in maize. Moll *et al* (1963) observed that over-dominance is not of primary importance in determining genetic variation in maize. Castro *et al* (1968) found that both dominance and additive gene effects contribute significantly in the expression of grain yield in maize, although dominance gene effects contributed more (52.4% of the total genetic variation) than the additive gene effects (39.2% of the total genetic variation). Thompson *et al* (1971) noted that both dominance and additive gene effects played an important part in the inheritance of ear height in maize, although the dominant gene effects were several times greater than the additive gene effects.

Sprague and Tatum (1942) and Rojas and Sprague (1952) found more non-additive than additive variance in crosses of selected inbred lines of maize. Similar results were obtained by Matzinger *et al* (1959) while working with unselected lines from a selected population of maize. Gamble (1962a) noted that dominance effects were highly significant for crosses they made in maize. The dominance effects were positive for all crosses. This suggested that positive dominance of gene effects was important in the inheritance of yield in the generation means studied. The estimates of the six parameters, mean (m), additive(a), dominance (d), additive x additive (aa), dominance x dominance (dd) and additive x dominance (ad) for the various gene effects considered showed that dominance gene effects made the major contribution to variation in yield of grain maize in the fifteen crosses studied. Epistatic effects were also important contributors to variation for maize grain yield in most of the crosses. The estimates of additive genetic variance from F_2 generation of single crosses of inbred lines were smaller. Gamble (1962b) studied plant height, kernel row number, ear length, ear diameter and seed weight. He observed that although the majority of the crosses had significant additive gene effects, estimates of additive gene effects were less important than non-additive gene effects. Nevertheless a sufficient amount of additive variation was present for selection to be successful in any of the studied characters. Gamble (1962c) noted that the relative magnitudes of the components of variance from the different sources of variation suggested that the interaction of gene effects with years was quite important. The component of variance for the locations x crosses interactions was small and of minor importance. The relative magnitude of the variance components for the years x locations x crosses interactions suggested that this interaction was also important. Goodman (1965) observed that there was non-additive genetic variance for ear number and plant height in the West Indian composite. Williams <u>et al</u> (1965) observed that estimates of additive genetic variance were larger for ear diameter and number of kernel rows. Estimates of dominance genetic variance was preponderant for yield, ear length and weight per 100 kernels. The additive genetic variance appeared to be a relatively small fraction of the total phenotypic variance for yield. The additive genetic variance for ear length, ear diameter, weight of 100 kernels and number of kernel rows was estimated to be one fifth to a half of the total phenotypic variance.

Comstock (1955) showed how the presence of epistatic gene effects will cause an upward bias in the estimates of both the additive and dominance genetic variance. Comstock et al (1957) postulated that the variance which should be attributed to epistasis in maize was not more than one tenth of the total genetic variance. Hayman (1958, 1960a, b) noted that epistasis occurs widely and it may be as important as additivity or dominance in genetic variation. Working with Nicotiana rustica he observed that there was a difficulty of specifying additive and dominance variation in the presence of epistasis. This difficulty can be overcome when epistasis is at relatively low level of intensity, but when epistatis is the major source of genetic variation no measure of additive or dominance variation is possible. Sufficiently large experiments permit accurate estimation of mean epistatic effects by simple statistical procedures. The simplest experiment supplying information on additive, dominance and the three kinds of epistatic variation should contain two inbred lines, and their F_1, F_2 and the first backcross generations. Bauman (1959), Gorsline (1961), Gamble (1962a) and Sprague et al (1962) obtained evidence that epistatic effects were significant among crosses involving specific inbred lines. Though results of Robinson and Cockerham (1961) did not suggest any evidence of epistatic gene interaction, its presence in the determination of grain yield could not be ruled out. Gamble (1962a) observed that additive x additive and additive x dominance appear to contribute more to the performance of grain yield in the crosses studied than do dominance x dominance gene effects. Such a relative importance could be expected since the F_1 population means suggested considerable heterosis. Gamble (1962b) considered additive x additive, additive x dominance and dominance x dominance estimates and realized that epistatic gene effects, although of minor importance in certain crosses for any one attribute, were important in the inheritance of plant height, kernel row number, ear length, ear diameter and seed weight in corn. Considering the individual types of digenic epistatic effects, the dominance x dominance estimates were relatively the largest in magnitude in all the crosses. Significant estimates of the additive x dominance gene effects were exhibited more frequently in all the attributes. The dominance x dominance gene effects which were significant were all negative suggesting a diminishing effect due to this type of gene effect. In contrast, the additive x additive gene effects which were significant were mostly positive, suggesting an enhancing effect in the inheritance. The additive x dominance gene effects were all positive in most crosses. Dominance x dominance gene interaction had a diminishing effect on plant height, while additive x dominance and additive x additive gene interaction had an increasing effect on plant height. This showed that epistasis played a major role in the determination of plant height in maize. Compton et al (1965) suggested that epistatic variability in maize populations are negligible, both within open-pollinated varieties and in varietal hybrids. Eberhart et al (1966) also found little evidence for siginificant amounts of epistasis in open pollinated varieties of maize. Favourable epistatic combinations of genes in the inbred lines may be important in contributing to heterosis in F_1 hybrids. If favourable epistatic genes became fixed in the inbred lines during selection, the opportunity for recombination would not be present in the production of single cross hybrids. Considering yield, ear diameter, ear length, ear height, plant height and days to tassel, the estimates of epistatic genetic variance were positive for ear number and ear diameter. The estimates of additive variance were larger than the estimates of dominance variance for all characters. Dominance variance was relatively larger for yield than for other characters. Epistasis did not contribute significantly to the total genetic variance. Estimates of epistatic variances were similar whether obtained by pooling single environment experiments, or by combining over locations and then pooling to remove the genotype x location interactions. Eberhart and Hallauer (1968) noted that the epistatic effects detected did not give any average superiority of the single crosses over the three-way or double crosses. Evidence of statistically significant variation attributable to epistatic effects has been reported for several traits in both plant and animal species (Stuber and Moll, 1971). However, evaluations of the effects of epistatic gene action in maize indicate that genotype by environmental interaction cause equal or greater errors in predictions of hybrid performances than epistatic effects. This is true when evaluations are conducted in single rather than in many environments (Otsuka _et al_., 1972 and Stuber _et al_., 1973). Dangi and Paroda (1978) observed that the magnitude as well as the type of epistasis was found to vary with the environment, suggesting that the gene effects should be studied in a wide range of environmental conditions. Moreno-Gonzalez and Dudley (1981) noted that mean epistasis over all the crosses contributed significantly to the expression of grain yield in maize.

Sprague and Tatum (1942) studied general and specific combining ability in single crosses of maize. Tests involving previously selected lines exhibited larger estimates of dominance than additive genetic variances, whereas the reverse was true for unselected lines. Thus, the presence or absence of selection resulted in a marked change in the relative importance of the two major fractions of the genetic variance. Robinson et al (1949) and Gardner et al (1953) obtained estimates of the degree of dominance for yield genes in the overdominance range in F_2 populations derived from single crosses among inbred lines. In both reports the authors recognized and discussed the possibility that such estimates of overdominance could be obtained as the result of repulsion phase linkages, even though none of the genes involved had more than partial dominance. Rojas and Sprague (1952) made comparisons among variance components in maize yield trials using selected lines. Their results showed dominance and epistatic variances to be more important than additive effects. Comstock (1955) and Comstock and Moll (1963) argued that experiments conducted in single environment may provide good estimates of the degree of dominance. Robinson et al (1955) reported that the effectiveness of intra-variety selection depends on presence of additive genetic variance. Two possibilities were advanced for reconciling presence of additive genetic variance with ineffectiveness of intra-variety selection. The first rests on negative genetic correlation between grain yield and other components of net reproductive capacity. The second envisages the additive genetic variance as rising from loci at which gene action is largely additive and gene frequency is at equilibrium between the forces of mutation and selection. Matzinger et al (1959) reported slightly smaller standard errors for genetic variance components for yield compared to theoretical standard errors. Gardner and Lonnquist (1959) obtained an estimate of the degree of dominance in the overdominance range for genes affecting yield in a study with the F_2 generation of a cross between two lines of maize. However, when the F_8 generation of the same cross was used, an estimate in the partial dominance range was obtained. These results indicated the possibility that linkage bias may have been responsible for earlier estimates in the overdominance range in studies involving the F_2 generation. Grafius (1959) found no correlation between the genes controlling the grain yield components in barley and suggested that there might be no genes for grain yield. Extrapolating his findings on maize, Grafius (1960) questined the validity of overdominance gene action for grain yield in maize. Cockerham (1961) indicated that the presence of non-additive genetic variance is the primary justification for initiating a hybrid breeding program. Lindsey et al (1962) indicated that epistasis may bias the estimates of additive and dominance genetic variance. The bias in the case of additive genetic variance is a function of the additive types of epistasis, and the bias in the estimate of dominance variance is a function of all components of epistasis. Gamble (1962a) noted that the relative magnitude of additive gene effects to the mean effects suggested that they are of minor importance in the explanation of yield variation. Comstock and Moll (1963) pointed out that when an experiment is conducted at several locations in a particular year, the estimates of genetic variances include the corresponding genotype x year interaction variance. the estimates of the genotype x location interaction variances include the corresponding genotype x year x location interaction variance. Eberhart et al (1966) showed theoretically that the magnitude of changes in genetic variances vary according to gene frequency and degree of dominance in the population. The higher the gene frequency, the greater will be the reduction of genetic variance from successful selection. Gardner and Eberhart (1966) noted that only when random selfed lines from the varieties and variety crosses are included can the additive and dominance effects be estimated separately. ElRouby and Penny (1967) considered the silking date, plant and ear heights, kernel size, lodging percentage and grain yield and they observed that the estimates of additive genetic variance differed significantly from zero for all characters. Liang and Walter (1968) noted that additive gene effects seemed to have a minor contribution to the inheritance for grain yield, head weight, kernel weight and kernel number in grain sorghum. Dominance gene effects were important in the inheritance of most of these traits. Among the three types of epistatic gene effects, additive x additive and dominance x dominance were important. Additive x dominance gene effects were of minor importance. They concluded that genetic models assuming negligible epistasis may be somewhat biased. Hallauer (1970) reported that complete dominance to overdominance govern the expression of grain yield in maize. Results obtained by Russel and Eberhart (1970) and Kimani (1979) indicate a predominant dominance gene effects in the expression of grain yield in maize. They noted that additive gene effects contributed little in the inheritance of grain yield in maize. Wright et al (1971) observed that all estimates of additive genetic variance were significant from zero. All the estimates of deviations due to dominance were non-significant for characters, silking date, plant and ear height, ear length and diameter, kernel row number, 300 kernel weight and grain yield. The largest proportion of the total genetic variance was additive for all traits. Cornelius and Dudley (1976) noted that dominance genetic variance was large for yield but negative for plant height and ear height in maize. An estimate of additive genetic variance for yield was negative and an estimate of average degree of dominance suggested extreme overdominance. Additive gene effects were reported to play a major role in the expression of ear height in maize. Ayiecho (1990) indicated that both additive and non-additive gene effects were responsible for the manifestation of variability in grain yield per plant and grains per head in barley, though the magnitude of the additive genetic variance was greater incase of grain yield. The 100-grain weight was controlled mainly by non-additive genes.

2.3 Heterosis

This is the phenomenon in which the cross of two stocks produces a hybrid that is superior in growth, size, yield or general vigour. East (1936) believed that heterosis was best described by the term hybrid vigour. He indicated that the inheritance of quantitative characters may be the key to the explanation of heterosis. Heterosis is but the reverse counterpart of inbreeding depression. East (1936), Hayes and Johnson (1939) and Johnson and Hayes (1940) observed that crosses of more distantly related parents show greater heterosis than crosses of more closely related parents. Jinks and Jones (1957) noted that there is a clear association between non-allelic interaction and heterosis. Eighty percent of all heterotic crosses showed significant non-allelic interactions. They concluded that significant heterosis in the crosses made was the result of overdominance or the dispersion of dominant increasing alleles in the parental lines. Lonnquist and Gardner (1961) showed that the average maize grain yields of parents ranged from 54.9 to 96.6 bushels per acre. The F_1 yields ranged from 81.8 to 106.9 bushels per acre. Average heterosis relative to the mid parent was 108.5 percent and relative to the better parent was 102.8 percent. Results obtained by Robinson and Cockerham (1961) showed that the relationship between performance and heterozygosity was essentially linear for both yield and ear height. Heterosis, measured from the mid parent, was manifested in the varietal cross for yield but not for ear height. They reported heterotic responses of 105 percent for grain yield in a varietial cross between two open pollinated varieties of maize. Moll _et al_ (1962), Moll _et al_ (1965) and Odongo (1986) showed that heterosis increased with increased divergence within certain limits.

Extremely divergent crosses resulted in decreased heterosis. Paterniani and Lonnquist (1963) noted that varietal crosses of maize regularly exhibit heterosis and the amount of heterosis displayed depends on the yielding ability and genetic diversity of the parental varieties. The data presented by Moll _et al_ (1965) display the same pattern. Whether expressed as the average F_1 performance, or as heterosis expressed as either the deviation from the parental mean or as the deviation from the high parent. The fact that the pattern was consistent was interpreted as supporting evidence that the levels of heterosis observed were associated with the levels of genetic divergence. Niehaus and Pickett (1966) observed that percent heterosis was greatest for grain yield and its primary components and for height in sorghum. Days to fifty percent bloom, number of leaves per plant and threshing percentages did not exhibit appreciable heterosis. The degree of inbreeding depression was somewhat related to amount of heterosis, the greatest depression occuring for grain yield. Hallauer and Eberhart (1966) showed that there was an average heterosis of eleven percent in crosses between maize synthetic varieties. Troyer and Hallauer (1968) obtained heterosis in crosses among extremely early flint varieties collected from different areas of the northern hemisphere. They reported a seventy one percent heterosis relative to the mid-parental value. Castro et al (1968) noted that only minor portions of the variation in days to flower and plant height could be attributed to heterosis. The large inbreeding depression in yield relative to the other traits explains the relatively greater portion of variation accounted for by the dominance effects in this trait. They observed that 5.1 percent of the total genetic variation was due to heterosis. Hallauer and Sears (1972) noted that the effects of inbreeding showed a reverse trend to the expression of heterosis for silk emergence and plant and ear height. The heterosis and inbreeding depression estimates indicated that the means of F_1 and F_2 populations were similar to the mid parent for leaf number.

2.4 Combining Ability and Diallel Analysis

The concept of combining ability was developed by Sprague and Tatum (1942). General combining ability (GCA) is the average performance of an inbred line in a number of hybrid combinations. Specific combining ability (SCA) is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the parental lines involved. General combining ability measures, additive effects while specific combining ability measures non-additive gene effects. Sprague and Tatum (1942) assumed that general combining ability was the result of additive gene action, while specific combining ability was dependent on dominance, epistasis and genotype-environmental interactions. They obtained estimates of the variances associated with combining ability for grain yield in maize, and they noted that in previously selected material, the variance of specific combining ability was larger than the variance of the general combining ability. In unselected material, the situation was reversed and the variance for the general combining ability was the larger.

Rojas and Sprague (1952) found that the variance components for interactions involving specific combining ability and environments were larger than the corresponding estimates involving general combining ability. Their results suggested that non-additive effects are influenced more by environment than additive effects. Griffing (1956a) proposed the statistical concept of general and specific combining ability in homozygous as well as in heterozygous base populations. Lonnquist and Gardner (1961) calculated estimates of general combining ability and specific combining ability effects for grain yield, and they observed that the additive effects were much more important than non-additive effects. This was to be expected considering the heterogenous nature of an open-pollinated variety used in the study. The components of variance attributable to the interactions of general combining ability with locations and with years were small and non-significant while those attributable to the interactions of specific combining ability with locations and years were both of a sizeable nature and in several cases statistically significant. Niehaus and Pickett (1966) showed that in the F_1 generation of sorghum, grain yield, 100 seed weight, seeds/head, heads/row, height, days to fifty percent bloom, number of leaves and threshing percentage had significant variance for both general and specific combining ability. The component for general combining ability was larger than for specific combining ability in all cases except for 100-seed weight. All F_2 components were smaller in absolute value than corresponding F_1 values. General combining ability mean squares for number of heads per row and specific combining ability mean squares for grain yield, number of seeds per head, number of heads per row and threshing percentages were not significant in the F_2 generation. The lower specific combining ability in the F_2 generation indicated that there was considerable non-additive gene action in the F_1 generation, much of which was lost in the F_2 generation.

The modern use of diallel cross started apparently with the development of the concepts of general and specific combining ability by Sprague and Tatum (1942). Jinks (1954) used diallel analysis to investigate reciprocal differences, heterosis, genotype-environmental interactions and modes of gene action for height, flowering time and leaf length for crosses involving inbreds of Nicotiana rustica. Hayman (1954), Griffing [1956a, b] and Kempthorne (1956) used diallel cross to estimate the genetic components of variation among yields of crosses. Diallel cross has also been used to estimate the actual yielding capacities of crosses. Kempthorne and Curnow (1961) used a diallel cross and considered its efficiency in estimating the genetic variance components. When a diallel crossing system is used in genetic studies, the additive and the non-additive components of the parent genotypic variance are estimated by use of general and specific combining ability components. The sort of relationship existing between these two sets of parameters was proposed and discussed by Matzinger and Kempthorne (1956), Griffing (1956a) and Kempthorne and Curnow (1961). According to them the population phenotypic variance is partitioned into various genotypic and environmental components.

$\sigma^2 p = \sigma^2 G + \sigma^2 E$, but $\sigma^2 G = \sigma^2 A + \sigma^2 NA$

$\sigma^2 p = \sigma^2 A + \sigma^2 NA + \sigma^2 E$

Where $\sigma^2 P$ = Population phenotypic variance

$\sigma^2 G$ = Population genotypic variance

$\sigma^2 A$ = Additive genetic variance

$\sigma^2 NA$ = Non-additive genetic variance

$\sigma^2 E$ = Environmental effect variance estimated from error variance.

σ^2 NA can be further partitioned into dominance and epistatic variances. For an arbitrary number of loci Griffing (1956b) gave the partitioning as follows:

$2\sigma^2$ GCA = σ^2 A + σ^2 AA + $\frac{1}{4}\sigma^2$ AAA + etc

σ^2 SCA = σ^2 D + $\frac{1}{2}\sigma^2$ AA + σ^2 AD + σ^2 DD + σ^2 AAA + σ^2 AAD + σ^2 DDD + etc.

σ^2 G = σ^2 A + σ^2 D + σ^2 AA + σ^2 AD + σ^2 DD + σ^2 AAA + σ^2 AAD + σ^2 DDD + etc

σ^2 G = σ^2 GCA + σ^2 SCA

The parameters are as follows:

σ^2 GCA = General combining ability variance

σ^2 SCA = Specific combining ability variance

σ^2 AA = Additive gene interaction variance

σ^2 AD = Additive-dominance gene interaction variance

σ^2 DD = Dominance gene interaction variance.

Ayiecho (1989), working with barley observed that the general combining ability (gca) effects were highly significant for the number of tillers per plant, the number of grains per head and 100-grain weight. The specific combining ability (SCa) effects were highly significant for 100-grain weight only.

2.5 Prediction of double-cross hybrid performance:

Double-cross hybrids have been extensively used in maize since their use was suggested by Jones (1918). Double-cross hybrids result from crosses between two single crosses that are themselves the result of crosses between two inbred lines. The best results are expected to occur when four different inbred lines are used. Double-cross hybrid breeding programs usually use two genetically divergent populations. Prediction of double cross performance in maize was first reported by Jenkins (1934) using single cross data. He suggested four alternative methods of prediction:

A. Mean performance of six possible single crosses among any set of four inbred lines.

B. Average performance of four non-parental single crosses.

C. Average performance of four inbred lines over a series of single crosses.

D. Average performance of a set of four inbred lines when tested by the top cross procedure.

The four methods of prediction differ with respect to type of gene action involved. Methods A, C and D are related only to additive gene action. While method B involves additive as well as non-additive gene effects. Otsuka _et al_ (1972) noted that accuracy of prediction depends more on number of replications and environments than on small differences in prediction methods.

CHAPTER THREE

3. MATERIALS AND METHODS

3.1. Materials

Four maize inbred lines, A, F, 8 and 64 developed at National Agricultural Research Centre, Kitale were used in this study. Inbred lines A and F were derived from Kenya Flat white complex population. Inbred line 8 was derived from a subpopulation of Kitale Synthetic II, S21 in its third cycle (S21 C_3) while inbred line 64 emanated from Kitale Synthetic II (R 11) during the second cycle (R 11 C_2).

The four parental inbred lines were mated in half diallel series in 1990 to produce F_1's. The crosses were selfed to produce F_2 and also backcrossed to each of their respective parents. The parents were also selfed to increase parental seed. Therefore the materials for this study comprised of the four parental inbred lines, their F_1, F_2 cross generations and twelve backcrosses as given Table 1 below:

Table 1. The F_1, F_2 and backcross populations used in the study.

Crosses		Backcrosses	
F_1	F_2	B1	B2
A x F	A x F	(A x F) x A and	(A x F) x F
A x 8	A x 8	(A x 8) x A and	(A x 8) x 8
A x 64	A x 64	(A x 64) x A and	(A x 64) x 64
F x 64	F x 64	(F x 64) x F and	(F x 64) x 64
F x 8	F x 8	(F X 8) x F and	(F X 8) x 8
8 x 64	8 x 64	(8 x 64) x 8 and	(8 x 64) x 64

This gave a total of twenty eight entries for the study

3.2 Field Evaluation Trial

The twenty eight entries were planted in a three replicate randomized complete block design for evaluation at four sites, namely, National Agricultural Research Centre, Kitale, Sabwani Agricultural Development Corporation farm, Kitale, Western Agricultural Research Centre, Kakamega and East African Tannin Extract Company Chemoset farm, Soy (Uasin Gishu). The experiments were conducted between April and October, 1991. Every entry was planted in a plot of four rows each having eleven plants spaced at 75cm between rows and 30cm within rows. Spacing between replicates was 90cm. At planting diammonium phosphate (DAP) was applied at 80kg P_2O_5 and 31kg N/ha while calcium ammonium nitrate (CAN) was applied as a topdress six weeks later at the rate of 100kg N/ha.

3.3 Data Collection

Data was taken from twelve randomly chosen plants from the two middle rows in each plot for the following traits:

3.3.1 Ear Height (cm)

This was measured from the ground to the node bearing the upper most ear on each of the randomly selected plants.

3.3.2 Plant Height (cm)

This was measured from the ground to the tip of the tassel on each of the randomly selected plants.

3.3.3 Grain Yield (bags/ha)

The two middle rows were harvested, excluding the outermost hills. The harvested ears were sun-dried, shelled and weighed. Grain moisture content was determined on three samples per harvested plot. The weight of the harvested grain was then adjusted to 12.5

percent moisture content.

3.3.4 Kernel Weight (g)

A sample of 200 kernels per harvested plot was weighed and the weight adjusted to 12.5 percent moisture content.

3.3.5 Ear Length (cm)

This was determined from the twelve harvested plants per plot by measuring from the collar (base) of the ear to the tip region where grain filling ends.

3.3.6 Kernel Row Number

The average number of kernel rows was determined by counting the number of rows in each harvested ear from the twelve selected plants.

3.3.7 Lodging Percentage (%)

This was considered for both root and stalk lodging. The whole plot was used to determine the lodging percentage.

3.4 Statistical and Genetic Analysis

A fixed model was used for analysis since we are interested in genetic information about a particular set of parents.

3.4.1 Statistical Analysis

In this study a randomized complete block design with b replicates (blocks) and t- treatments (entries) was applied. The treatments included:

(i) P_1 parents, the ith parent $i = (1, 2 \ldots., P)$ is coded by (ii)

(ii) $\frac{P(P-1)}{2}$ F1 crosses, the cross between the ith female parent and the jth male ($i<j$) is coded by (ij)

The number of entries (t) = $\frac{P(P+1)}{2}$

The model for analysis of variance is:

$$Y_{ij} = M + C_{it} + B_j + E_{ij}$$

Where: Y_{ij} = Observation from the ith treatment in the jth block

i = 1, 2 ... t treatments

j = 1,2 ... r replicates/blocks

M = General mean

C_i = Effect of the ith treatment

B_j = Effect of the jth block

E_{ij} = Error effect

Based on the above model the analysis of variance is as in Table 2 below:-

Table 2. Analysis of variance table for randomized complete block design

Source	df	SS
Total	bt - 1	$\sum_{i<j} Y^2_{ij} - C$
Replicates	b - 1	$\frac{\sum_{j} Y^2_{.j}}{t} - C$
Treatments	t - 1	$\frac{\sum_{i\leq j} Y^2_{ij.}}{b} - C$
Error	(b - 1) (t - 1)	By subtraction

Where: b = replicates

t = treatments

c = correction factor

3.4.2 Genetic Analysis

A diallel analysis was performed for the crosses according to fixed model of analysis III of Gardner and Eberhart (1966) as given in Table 3.

Table 3. Diallel anova (according to analysis III and Gardner and Eberhart (1966) *

Source	*df*	*ss*
Treatment	$\frac{p(p+1)}{2}-1$	$\frac{\sum_{i\leq j} Y_{ij.}^2}{b}$
GeneralResponse	1	$\frac{2}{bp(p+1)}G^2$
Parents	$p-1$	$\frac{p-1}{b}S^2(Y_{ij.})$
ParentsVsCrosses	1	$\frac{1}{bp(p+1)(p-1)}(2G-(p+1)D)^2$
Crosses	$\frac{p(p-1)}{2}-1$	$\frac{1}{b}\sum_{i\leq j} Y_{ij.}^2-\frac{2(\sum_{i\leq j} Y_{ij})^2}{bp(p-1)}$
GCA	$p-1$	$\frac{p-1}{b(p-2)}S^2(Y_{i..}-Y_{ii.})$
SCA	$\frac{p(p-3)}{2}$	*By subtraction*

* The formulae for sums of squares are adapted from Ayiecho (1988).

SCA	$\frac{p(p-3)}{2}$	*By subtraction*

* The formulae for sums of squares are adapted from Ayiecho (1988).

The model applicable to this analysis is as follows:

$Y_{ij} = M + C + g_i + g_j + S_{ij}$ for $i < j$

$Y_{ii} = M + W + W_i$ for $i = j$

With restrictions:

$\Sigma g_i = 0, \quad \Sigma W_i = 0 \quad S_{i.} = 0$

These parameters are interpreted as below:

M = Mean (general level) for crosses and parents

C and W = Contrast parameters for parents vs crosses comparison

M + C = Mean (general level for crosses)

M + W = Mean (general leve for parents)

g_i and g_j = General combining ability for parents i and j

W_i = Parental effect of the ith parent

S_{ij} = Specific combining ability of the (ij)th cross

The notations used in the estimation of the parameters in the above model are:

b = number of replications

G = Grand total

p = number of parents

$D = \sum_{i} Y_{ii.}$ and $Y_{ii.} = \sum_{K} Y_{iik}$ = Total for parents

$$Y_{i..} = Y_{ii.} + \ldots Y_{ii.} + Y_{ii.+} \ldots Y_{ip}$$

$$Z_{i..} = Y_{i..} - Y_{ii.}$$

$$W_{i..} = Y_{i..} + Y_{ii.}$$

The parameters were estimated by

$g = \frac{D}{pb}$ = parental mean

$$h = \frac{1}{b} \frac{1}{P(p-1)} [2G - (P + 1)D]$$

$$M = g + \frac{p-1}{p=1} h$$

$$C = \frac{2}{P + 1} h$$

$$g_i = \frac{1}{2b} (Y_{ii.} - \frac{D}{P}) \frac{1}{b} \frac{1}{(P-2)} [W_{i..} - \frac{P+2}{2} Y_{ii.} - \frac{2G}{P} + \frac{(P+2)D)}{2P}]$$

$$W_i = \frac{1}{b} (Y_{ii.} - \frac{D}{p})$$

$$S_{ij} = M_{ij} - M - C - g_i - g_j$$

Where g = mean (general level) for parents

h = average heterosis

m = mean (general level) for crosses and parents c & w = contrast parameters for the parents vs crosses comparison

Estimation of generation means and variance components:

The generation mean analysis of Hayman (1958, 1960, a, b) was applied to each cross in each environment for each character. When epistasis is present the six parameters provide an exact fit to the generation means and their variance estimates are:

$$m=\overline{F_2}$$

$$d=\overline{B_1}-\overline{B_2}$$

$$h=\overline{F_1}-4\overline{F_2}-(\frac{1}{2})\overline{P_1}-(\frac{1}{2})\overline{P_2}+2\overline{B_1}+2\overline{B_2}$$

$$i=2\overline{B_1}+2\overline{B_2}-4\overline{F_2}$$

$$j=\overline{B_1}-\frac{1}{2}\overline{P_1}-\overline{B_2}+\frac{1}{2}\overline{P_2}$$

$$l=\overline{P_1}+\overline{P_2}+2\overline{F_1}+4\overline{F_2}-4\overline{B_1}-4\overline{B_2}$$

Where m,d,h,i,j and l refer to mean, additive, dominance, additive x additive, additive x dominance and dominance x dominance effects respectively.

$V_m = V(\bar{F}_2)$

$V_d = V(\bar{B}_1) + V(\bar{B}_2)$

$V_h = V(\bar{F}_1)+16V(\bar{F}_2)+1/4V(\bar{P}_1)+1/4V(\bar{P}_2)+4V(\bar{B}_1)+(\bar{B}_2)\ 4V(\bar{B}_2$

$V_i = 4V(\bar{B}_1) + 4V(\bar{B}_2) + 16V(\bar{F}_2)$

$V_j = 4V(\bar{B}_1) + 1/4V(\bar{P}_1) + 4V(\bar{B}_2) + 1/4\ V(\bar{P}_2)$

$V_l = V(\bar{P}_1) + V(\bar{P}_2) + 4V(\bar{F}_1) + 16V(\bar{F}_2) + 16V(\bar{B}_1) + 16V(B_2)$

Where the parameters V_m, V_d, V_n, V_i, V_j and V_i refer to variance of mean, additive, dominance, additive x additive, additive x dominance and dominance x dominance genetic variances respectively.

3.5 Estimation of Heterosis

Heterosis was calculated from the better parent by the following formula:

$$\text{Heterosis} = \frac{F1 - BP}{BP} \times 100$$

Where F1 = Value of the cross

BP = Better parent value

3.6 Identification of the Best Double Cross

The performance of double cross hybrids was predicted using mean yield of the four non-parental single crosses as suggested by Allard (1960).

CHAPTER FOUR

RESULTS

4.1 Plant Height (cm)

In general the data obtained from all the four sites indicate that the F_1 populations were tallest, followed by backcrosses, F_2 and the parents respectively (Table 4). The F_1 cross 8 x 64 was the tallest at all sites while inbred line A was the shortest. Plants were generally taller at Kitale, Soy and Sabwani than at Kakamega.

There was significant variation among the treatments at all the sites (Appendix 1). The analysis given in Table 5 suggests that the general combining ability effects for plant height were significant at all sites, but not specific combining ability effects. Inbred lines 8 and 64 had the highest general combining ability estimates. Inbred line 8 was the best general combiner at Kitale, Kakamega and Sabwani, while inbred line 64 was the best general combiner at Soy (Table 7). The poorest general combiner at all sites was inbred line A. Crosses A x 8 and F x 64 had the highest specific combining ability estimates at Kitale and Sabwani, while at Kakamega and Soy, the best specific combinations were A x F and 8 x 64 (Table 7).

Table 4: Mean plant height (cm) data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	237.24	189.28	213.28	209.86	212.49
F	277.11	222.77	266.58	258.20	256.17
64	319.01	268.06	310.83	291.53	297.37
8	310.44	256.81	266.56	291.39	281.30
$\underline{F_1}$					
A x F	347.47	279.72	324.72	314.03	316.49
A x 64	353.78	306.11	328.57	329.86	329.58
A x 8	374.14	297.11	332.36	338.47	335.52
F x 64	396.47	316.39	368.33	359.86	360.26
F x 8	384.72	330.70	358.61	356.39	357.60
8 x 64	405.17	358.06	381.33	380.69	381.31

<u>Backcrosses</u>					
(AxF)x4	321.64	235.83	293.33	271.81	280.65
(Ax64)xA	312.31	243.19	287.78	283.06	281.58
(Ax8)xA	328.58	285.28	314.31	310.28	309.61
(Fx64)xF	336.39	282.78	318.33	306.67	311.04
(Fx8)xF	350.00	285.56	331.25	336.67	325.87
(8x64)x8	382.75	310.00	328.33	355.42	344.13
(AxF)xF	336.20	264.17	309.31	286.39	299.01
(Ax64)x64	346.11	283.33	352.83	328.75	327.76
(Ax8)x8	362.58	324.17	344.58	354.86	346.25
(Fx64)x64	377.39	288.61	357.78	329.58	338.34
(Fx8)x8	396.89	328.47	350.08	349.50	353.74

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
(8x64)x64	377.08	303.33	327.36	351.81	339.90
$\underline{F}_2$					
(AxF) x	310.58	240.83	277.97	270.56	274.99
(Ax64) x	299.70	236.53	259.86	264.72	265.20
(Ax8) x	354.92	277.92	300.64	311.53	311.25
(Fx64) x	331.78	276.67	297.22	311.95	304.40
(Fx8) x	344.78	270.69	307.42	325.56	312.11
(8x64) x	332.44	268.06	296.11	301.25	299.47
Mean of parents	285.95	234.31	264.31	262.75	
F_1 mean	376.96	314.68	348.98	346.55	
Backcross					

mean	352.33	286.23	326.27	322.07
F_2 mean	329.03	261.78	289.87	297.60
LSD.05	24.18	21.82	21.98	21.77

Table 5: Diallel analysis mean squares for yield component traits in maize

Location	Source	df	Plant hgt.	Ear hgt.	Grain yield	Ear length	200-grain weight	Kernel row number	Lodging %
Kitale	Treatments	9	8890.38**	4405.62**	3681.30**	2466.0**	401.84**	1.25**	667.4
	Parents	3	4146.78**	910.69**	56.16	16.30**	113.87	0.35	1148.9
	Parents vs crosses	1	6625.95**	3498.42**	3595.01*	14.31*	342.76*	0.33*	206.4
	Crosses	5	1590.98**	1087.43**	749.46	8.83**	38.16	1.37**	15.75
	GCA	3	2392.60**	1714.03**	562.97	14.13**	30.82	2.20**	22.91
	SCA	2	388.47	147.42	102920	0.89	49.17	0.12	6.51
	Error	18	261.43	172.33	543.48	1.76	54.62	0.21	8.46
Kakamega	Treatments	9	7676.21**	4378.41**	1345.37**	36.41**	422.29**	2.67**	44.77
	Parents	3	3778.59**	2024.10**	317.58	12.77*	365.29*	3.03*	7.53
	Parents vs Crosses	1	5168.28**	2611.70**	1211.70**	24.57*	157.66	1.00	14.33
	Crosses	5	2246.96**	1966.29**	49.91	12.82**	256.96	1.18*	550.2
	GCA	3	3586.02**	3224.68**	60.08	21.32**	413.06*	1.80**	179.3
	SCA	2	283.38	78.72	34.66	0.07	22.81	0.25	950.0
	Error	18	133.71	57.01	129.21	3.01	101.67	0.29	274.4
Soy	Treatments	9	8260.69**	3343.59**	2233.95**	25.10**	355.39**	1.47*	136.5
	Parents	3	4779.04**	1705.51**	37.87	6.70	78.66	2.26**	46.5
	Parents vs Crosses	1	5735.71**	2138.50**	2130.23**	6.40	252.00	0.08	0.6
	Crosses	5	1677.24**	1145.85**	163.60	6.78*	138.85	1.14	21.45
	GCA	3	2700.77**	1893.94**	228.35	10.48*	224.23	1.69*	22.83
	SCA	2	141.96	23.70	66.57	1.24	10.78	0.30	20.38
	Error	18	133.71	105.88	83.69	2.22	84.65	0.43	39.10
Kabwani	Treatments	9	8054.39**	3656.16**	2734.13**	29.43**	354.03**	1.77**	36.28
	Parents	3	4466.46**	2114.72**	43.98	43.65**	135.85**	43.65**	48.33
	Parents vs Crosses	1	1123.38*	2177.90**	2587.41**	12.39*	284.23**	0.10	12.60
	Crosses	5	1704.78**	1392.08**	237.18*	5.80*	44.01	1.71**	14.58
	GCA	3	2804.83**	2214.34**	230.34*	7.07*	28.56	2.65**	10.42

SCA	2	57.71	158.68	247.67	3.91	67.19	0.31	205.82
Error	18	159.31	129.59	70.62	1.72	21.49	0.14	73.04

*,** - Significant at 5% and 1% significance level respectively.

Table 6 : Mean squares for combined anova for yield and yield related traits.

Source	df	Plant height	Ear height	Grain yield	Ear length	200 - Grain weight	Kernel row number	Lodging %
Total	119							
Locations	3	16923.42**	9404.16**	2223.38**	19.36**	2615.79**	0.86*	5496.69**
Replications in Locations	8	828.33**	399.55**	229.71	12.24**	141.76*	0.78*	730.43**
Genotypes	9	32354.30**	15404.33**	9281.26**	110.69**	1292.26**	6.04**	428.35**
Genotypes x locations	27	175.96	126.48	237.83	1.63	80.43	0.37	394.20*
Parents	3	16433.93	6361.67**	89.92	42.51**	405.33**	6.30**	883.07**
Parents x locations	-9	1362.30	712.64	326.15	73.10	562.64	8.42	670.02*
Parents vs crosses	1	207904.43	92860.24**	80212.74**	714.97**	9161.90**	10.66**	445.89
Crosses	5	6796.50**	5338.75**	609.76*	30.75**	250.49*	4.95**	152.01
Crosses x locations	15	5302.86	853.92	123.04	90.73	154.52	6.84	215.85
GCA	3	11200.34**	8783.46**	725.75*	49.77**	396.11**	8.0**	151.52
GCA x locations	9	83.97	87.85	118.61	1.08	100.18	0.10	192.26
SCA	2	190.74	171.68	435.79	2.22	32.06	0.32	152.75
SCA x locations	6	318.62	193.07	102.95	94.02	158.11	2.04	256.13
Error	72	192.54	116.24	206.75	2.18	65.61	0.27	206.83

*, ** - Significant at 5% and 1% Significance level respectively.

Table 7: GCA effects (diagonal) and SCA effects (off diagonal) for plant height

Parents	Sites	A	F	8	64
A	Kitale	-27.74a*	-0.64a*	8.35c	-7.71b*
	Kakamega	-30.55b*	4.21a	-7.93b*	3.72a
	Soy	-30.66a*	4.04a	1.36c	-5.40b*
	Sabwani	-28.64a*	0.81a	2.62b	-3.43c*
F	Kitale		-1.10b*	-7.71b*	8.35c
	Kakamega		-8.62c*	3.72a	-7.93b*
	Soy		2.35b	-5.40b*	1.36c
	Sabwani		-4.69b*	-3.43c*	2.62b
8	Kitale			16.58d	-0.64a*
	Kakamega			20.91a	4.21a
	Soy			12.67c	4.04a
	Sabwani			17.95c	0.81a
64	Kitale				12.27c
	Kakamega				18.25a
	Soy				15.63c
	Sabwani				15.38c

Values followed by the same lettering for each trait (a,b,c) are not significantly different,(Duncan's multiple range test, $p \leq 0.05$).

* - Significant, $p \leq 0.05$

The poorest specific combinations at Kitale, Soy and Sabwani were A x 64 and F x 8, while at Kakamega the lowest specific combining ability estimates were obtained for crosses A x 8 and F x 64.

According to the generation mean analysis (Table 8) four crosses (A x F, A x 64, A x 8 and F x 8) exhibited significant additive genetic variance at Kakamega. The crosses did not have consistent additive genetic variance manifestation at the other sites. Most of the crosses exhibited significant dominance genetic variance at each of the sites, except crosses A xF at Kitale and Sabwani and A x 8 at Kitale. Epistatic genetic variances were not consistently exhibited by the six crosses at the four sites. Significant additive x dominance genetic variance was shown by crosses A x F at Kitale, A x 64 at Soy and F x 8 at Kitale and Kakamega. Significant x dominance variances were manifested at all the sites for cross F x 8.

Table 9 shows mean heterosis for plant height at the four sites. Cross 8 x 64 was the most heterotic at Kitale, Kakamega and Sabwani, while cross F x 8 had the highest heterosis estimate at Soy. The least heterotic cross at all the sites was A x 64.

Table 8: Mean estimates of genetic effects and variance components for plant height for the crosses over the four environments

		Genetic effects and variance components											
Crosses	Sites	m	v_m	d	v_d	h	v_h	i	v_i	j	v_j	l	v_l
A x F	Kitale	310.58**	2.95**	-14.56	241.70	53.21	1072.36	73.14**	1013.96	242.62	264.47**	179.71**	4350.25**
	Kakam.	240.83**	5.27**	-28.33**	50.69**	110.21**	347.35**	36.67**	287.04	-11.74	54.15	-64.87	1136.60
	Soy	277.97**	66.15**	-15.97	53.55	178.18**	1458.97**	93.39**	1272.63**	10.68**	148.66	-169.36	2660.06**
	Sabwani	270.56**	81.50**	-14.58	170.06	114.17	2117.08	34.17**	1984.27	9.58	178.44	-54.44	4556.27
A x 64	Kitale	299.70**	122.08**	-33.81	232.75	193.68**	3043.41**	118.05	2884.34	7.10	289.71	-171.03	6313.60
	Kakam.	236.53**	18.21**	-40.14**	226.93**	184.23**	1257.02**	106.94**	1230.59**	-0.90	260.19	-90.14	4149.44
	Soy	259.86**	23.40**	-65.06**	491.27**	308.29**	2725.47**	241.78**	2339.46**	-16.28**	578.73**	-341.76**	9778.73**
	Sabwani	264.72**	49.91**	-45.69**	243.25**	243.89**	1903.10**	164.72**	1771.46**	-4.86	297.90	-227.23**	5216.97**
A x 8	Kitale	354.92**	4.11**	-34.00	192.29	62.96	893.10	-37.34	834.94	2.60	212.53	-49.04	3375.06
	Kakam.	277.92**	155.79**	-38.89**	93.94**	181.14**	2906.06**	107.22	2868.37	-5.28	106.89	-285.50**	3146.47**
	Soy	300.64**	385.93**	-30.28	294.82	207.67**	3094.10**	115.22	2723.00	-3.64	415.84	-288.44**	7745.19**
	Sabwani	311.53**	69.24**	-144.58**	99.95**	172.01**	1531.89**	84.16	1507.59	-3.82	106.30	-236.24**	2804.25**

F x 64	Kitale	331.78**	59.34**	-41.00**	134.53**	198.83**
	Kakam.	276.67**	106.65**	-5.83	145.17	130.98**
	Soy	297.22**	245.74**	-39.45**	134.22**	242.96**
	Sabwani	311.95**	52.16**	-22.92	119.04	119.72**
F x 8	Kitale	344.78	39.09**	-46.89**	86.34**	205.61**
	Kakam.	270.69**	53.32**	-42.92**	187.20**	236.19**
	Soy	307.42**	207.92**	-18.83	79.82	225.04**
	Sabwani	325.56**	17.84**	-10.83	212.97	147.71**
8 x 64	Kitale	332.44**	16.90**	5.67	35.91	280.31**
	Kakam.	268.06**	48.69**	6.67	236.51	250.07**
	Soy	296.11**	154.88**	0.97	407.08	219.58**
	Sabwani	301.25**	1.45**	3.61	185.84	298.68**

** Significant at 1% significant level

V_m = Variance of mean

V_d = Additive variance

m = Mean effects

d = Additive effects

1554.60**	100.44**	1487.60**	-20.03	196.44	-138.89	3370.03
2376.07**	36.11	2287.16	16.81	180.48	-235.29**	4303.61**
4575.26**	163.33	4468.73	-17.32	169.68	-201.47	6505.51
1467.87**	24.72	1310.74	-6.25	171.87	-121.70	3367.78
1011.73**	114.67**	970.75**	-30.22**	111.53**	-251.45**	2170.74**
1691.95**	145.28**	1601.88**	-25.90**	202.19**	-232.37**	4208.51**
3765.38**	133.00	3646.06	-18.85	148.84	-245.30**	5081.20**
1160.47**	56.11	1137.35	5.76	217.49	-172.08**	3785.45**
790.15**	186.90**	414.10**	9.97	95.30	-269.72**	2349.26**
1787.85**	154.45	1725.09	12.29	281.32	-140.14	4814.31
4263.41**	126.94	4106.38	23.11	468.45	-98.28	9619.46
833.79**	209.44**	766.52**	3.68	236.65	-279.58**	3264.88**

V_h = Dominance variance	h = Dominance effects
V_i = Additive x additive variance	i = Additive x Additive effects
V_j = Additive x dominance variance	j = Additive x Dominance effects
V_l = Dominance x dominance variance	l = Dominance x Dominance effects

Table 9: Heterosis for yield and yield related characters at four experimental sites

Site	Cross	Characters						
		Plant height	Ear height	Lodging percent	Ear length	Kernel row No.	200-grain weight	Grain yield
N.A.R.C. KITALE	A x F	25.39f	39.98a	-60.75f	15.52abc	-1.08d	37.18ab	276.56g
	A x 64	10.88d	21.73ab	-82.54d	3.22c	0.87e	10.36c	204.63ef
	A x 8	20.52e	29.19c	-85.87d	8.80b	-2.10d	27.03a	185.05e
	F x 64	24.26f	42.97a	-65.03de	25.43a	6.49g	16.66b	244.78f
	F x 8	23.93f	37.12a	-88.77e	23.65a	8.17f	30.03a	226.69f
	8 x 64	26.99f	51.14abc	-92.51e	24.96a	5.87g	17.39b	265.75g
WARC-KAKAMEGA	A x F	25.57ab	50.72d	-40.84a	20.42e	0.55abc	21.16a	84.87g
	A x 64	14.20c	21.30f	60.56ab	19.70e	5.53b	25.16b	133.83e
	A x 8	15.70c	14.30ef	76.92b	15.85ef	-0.71c	11.33ab	150.26ef
	F x 64	18.03d	35.65e	100.79c	44.88g	8.10a	16.57c	92.71f
	F x 8	28.77ab	33.83e	16.55bc	43.44g	7.26a	1.61ac	76.76g
	8 x 64	38.58abc	50.72d	5.44abc	37.72d	1.81ab	-4.03abc	280.12fg

SOY	A x F	21.81g	32.93ab	-17.64g	38.15f	-3.20e	38.53ab	215.01ab
	A x 64	5.71f	4.07a	19.02e	6.79ef	-0.33f	19.59c	116.14ac
	A x 8	24.69g	22.24b	-31.91f	22.10e	-5.70fg	14.69a	163.95a
	F x 64	18.50ef	17.47c	0.25c	29.75g	5.37ef	28.61ab	175.70a
	F x 8	34.52efg	37.72abc	9.52d	40.68f	-3.35e	33.87ac	196.71c
	8 x 64	22.68g	32.36ab	-7.94ef	24.94e	-1.75efg	14.89a	146.57b
SABWANI	A x F	21.62g	35.44g	-41.56a	20.25c	-3.37a	30.27g	161.38b
	A x 64	6.85e	10.57f	-77.36b	24.33a	1.75b	22.48e	225.59a
	A x 8	14.57f	12.40f	-58.49c	12.83b	-8.69c	30.72g	134.18c
	F x 64	23.44g	24.69e	-49.11ab	25.53a	0.07ab	16.55f	177.28ab
	F x 8	22.31g	19.88ef	-88.13ac	30.86ab	-0.06ac	27.66ef	187.03ac
	8 x 64	30.59fg	35.94g	-38.67a	38.29ac	-1.24abc	16.95f	220.26a

Values followed by the same lettering for each trait (a,b,c,d,e,f,g) are not significantly different, $P \leq 0.05$.

4.2 Ear Height (cm)

At all the four sites, the F_1, populations had the highest ear heights followed by backcrosses, F_2 and the parents respectively (Table 10). The F_1 for cross 8 x 64 displayed highest ear height at Kakamega, Soy and Sabwani.

At Kitale a backcross [(F x 8) x 8] had the highest ear heights. Lower ear heights were displayed by inbred line A at all sites. The ear heights observed at Kakamega were generally low. There was significant variation among the genotypes at all the sites (Appendix 1). Diallel analysis also suggests that general combining ability effects were significant at all the sites (Table 5). Inbred line 8 had the highest general combining ability estimates at all the sites while inbred line A had the lowest estimates (Table 11). Crosses A x F and 8 x 64 were the best specific combinations at Kakamega, Soy and Sabwani. At Kitale the best specific combinations were A x 8 and F x 64. Crosses A x 64 and F x 8 were the poorest specific combinations at Kitale and Sabwani. At Kakamega and Soy the poorest specific combinations were A x 8 and F x 64.

The estimates of genetic variance components (Table 12) suggest that cross F x 8 exhibited significant additive genetic variance at all the sites.

Table 10: Mean ear height (cm) data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	124.24	82.36	109.31	111.11	106.74
F	133.00	86.71	125.28	123.06	117.01
64	153.66	121.94	162.22	156.39	148.56
8	161.50	135.00	149.86	166.94	153.33
F_1					
A x F	186.17	130.70	166.53	166.67	162.51
A x 64	187.06	147.92	168.83	172.92	169.18
A x 8	208.64	154.31	183.19	187.64	183.45
F x 64	219.70	165.42	190.56	195.00	192.67
F x 8	221.45	180.00	206.39	200.14	201.99

8 x 64	232.25	203.47	214.72	226.94	219.35
<u>Backcrosses</u>					
(AxF)xA	165.53	113.89	154.72	145.42	144.89
(Ax64)xA	163.75	109.17	149.17	150.69	143.20
(Ax8)xA	172.22	144.31	170.14	170.42	164.27
(Fx64)xF	170.78	133.89	168.33	163.75	159.19
(Fx8)xF	187.44	134.03	176.67	172.78	167.43
(8x64)x8	215.94	169.44	185.69	197.36	192.11
(AxF)xF	176.39	124.03	165.56	150.83	154.20
(Ax64)x64	186.25	131.94	195.56	170.56	171.49
(Ax8)x8	202.36	175.00	191.67	201.67	192.67
(Fx64)x64	205.58	142.22	196.53	174.72	179.74
(Fx8)x8	235.86	179.58	208.89	208.67	206.50

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
(8x64)x64	206.44	158.33	179.72	188.06	183.14
F_2					
(AxF) x	168.11	113.19	144.58	147.36	142.06
(Ax64) x	162.03	103.19	139.31	145.28	137.45
(Ax8) x	199.64	140.94	166.39	172.22	169.80
(Fx64) x	168.06	132.78	161.67	155.56	154.51
(Fx8) x	185.17	141.53	173.89	178.61	169.80
(8x64) x	186.86	141.67	169.31	170.70	167.13
Mean of parents	143.08	106.50	136.67	139.38	
F_1 mean	209.21	163.64	188.37	191.55	
Backcross mean	190.71	142.99	178.55	174.58	
F_2 mean	178.31	128.88	159.19	161.62	
LSD .05	19.01	15.19	16.82	15.30	

Table 11: GCA effects (diagonal) and SCA effects (off diagonal) for ear height

Parents	Sites	A	F	8	64
A	Kitale	-22.88a*	-0.01a*	4.95c*	- 4.95b
	Kakamega	-28.99a*	3.45a	-3.77c*	0.32b
	Soy	-23.28a*	2.26b	-1.49a*	-0.76a*
	Sabwani	-23.72a*	5.25a	-0.23b*	-5.02c*
F	Kitale		-0.16b*	-4.96b*	4.96c
	Kakamega		-7.40a*	0.32b	-3.77c*
	Soy		-0.82b*	-0.76a*	-1.49a*
	Sabwani		-6.42b*	-5.02c*	-0.23b*
8	Kitale			17.35d	-0.01a*

	Kakamega	23.44d	3.45a
	Soy	19.60d	2.26b
	Sabwani	20.03d	5.25a
64	Kitale		5.69c
	Kakamega		12.95c
	Soy		4.50c
	Sabwani		10.10c

Values followed by the same lettering for each trait (a,b,c,d,) are not significattly different, (Duncan's multiple range test, $p \leq 0.05$)

* Significant, $p \leq 0.05$

Table 12: Mean estimates of genetic effects and variance components for ear height for the crosses over the four environments

		Genetic effects and Variance Components											
Crosses	Sites	m	v_m	d	v_d	h	v_h	i	v_i	j	v_j	l	v_l
A x F	Kitale	168.07**	15.61**	-10.87	79.31	68.96**	638.18**	8.76	333.27	-47.82**	95.34**	-189.84	1803.45**
	Kakam.	113.19*	5.34**	-10.14	13.41**	69.21**	150.25**	23.06	139.13	-7.96	14.73	-68.42**	344.51**
	Soy	144.58**	19.15**	-10.83	135.34	111.46**	953.17**	62.22	847.81	-2.85	155.37	-133.14	2893.30
	Sabwani	147.36**	31.39**	-5.42	12.27	52.64**	594.30	3.06	551.26	0.56	21.80	-28.06	870.64
A x 64	Kitale	162.03**	47.41**	-22.50	117.97	100.03**	1065.61**	51.90	1230.40	-7.75	132.31	-99.94	294.15
	Kakam.	103.19**	14.02**	-22.78	85.27	115.21**	605.76**	69.45**	565.46**	-2.99	97.27	-51.53	1749.44
	Soy	139.31**	24.67**	-46.39**	157.02**	165.28**	1241.21**	132.22**	1022.84**	-19.93	178.32	-212.49**	3780.53**
	Sabwani	145.28**	15.18**	-19.86**	52.06**	100.56**	563.94**	61.39**	451.14**	2.78	84.60	-90.55	1527.09
A x 8	Kitale	199.64**	14.18**	-30.14**	87.59**	84.45**	684.76**	103.16**	577.18**	-11.47	157.43	-149.39	1960.67**
	Kakam.	140.94**	127.94**	-30.69**	39.89**	120.46	2221.79	74.84	2206.59	-4.37	51.78	-187.48**	2746.11**
	Soy	166.39**	128.32**	-21.53	146.37	111.67	2747.09	58.05	2638.61	-1.25	187.64	-156.12	4829.01
	Sabwani	172.22**	1.23**	-31.25**	107.00**	103.89**	462.85**	55.28**	447.76**	-3.33	116.46	-146.12**	1792.14**

F x 64	Kitale	168.06**	50.76**	-34.72**	39.47**	156.69**	984.57**
	Kakam.	132.80**	48.40**	-8.33	100.44	82.20	1190.15
	Soy	161.67**	45.89**	-28.20**	53.90**	129.86**	1058.83**
	Sabwani	155.56**	4.42**	-10.97	39.84	110.11**	272.94**
F x 8	Kitale	185.17**	32.10**	-48.42**	45.37**	91.70**	800.58**
	Kakam.	141.53**	21.84**	-45.60**	14.02**	130.25**	460.86**
	Soy	173.89**	55.23**	-32.22**	26.23**	144.38**	1026.15**
	Sabwani	178.61**	6.27**	-28.89**	76.69**	109.59**	412.88**
8 x 64	Kitale	186.86**	63.71**	9.50	69.44	172.00**	1541.67**
	Kakam.	141.67**	82.35**	11.11	54.70	163.89**	1568.42**
	Soy	169.31**	56.56**	5.97	225.33	112.29**	1845.41**
	Sabwani	170.70**	23.86**	9.31	103.97	153.33**	930.33**

** Significant at 1% significant level

V_m = Variance of mean

V_d = Additive variance

V_h = Dominance variance

V_i = Additive x additive variance

V_j = Additive x dominance variance

V_l = Dominance x dominance variance

m = Mean effects

d = Additive effects

h = Dominance effects

i = Additive x Additive effects

j = Additive x Dominance effects

l = Dominance x Dominance effects

80.33**	970.07**	-24.39**	50.99**	-106.83**	1501.69**
21.11	1176.11	9.28	113.04	-33.84	2437.60
83.05**	947.83**	-9.72**	60.50**	-144.16**	2032.58**
54.72**	230.01**	5.70	66.96	-62.22	879.72
105.94**	695.05**	-34.17**	112.38**	-215.16**	1661.62**
61.11**	405.51**	-21.41**	26.40**	-106.62**	795.21**
75.56	988.57	-19.93**	52.81**	-158.75**	1453.73**
34.45	407.08	-6.95	80.74	-93.06	1350.62
97.33**	1296.98**	5.58	134.73	-162.46**	3108.60**
88.87	1536.45	4.58	77.86	-80.55	2320.77
53.61	1806.24	12.15	253.18	-42.91	4663.90
88.05**	797.70**	4.03	131.03	-81.67	2575.91

F x 64	Kitale	168.06**	50.76**	-34.72**	39.47**	156.69**	984.57**	80.33**	970.07**	-24.39**	50.99**	-106.83**	1501.69**
	Kakam.	132.80**	48.40**	-8.33	100.44	82.20	1190.15	21.11	1176.11	9.28	113.04	-33.84	2437.60
	Soy	161.67**	45.89**	-28.20**	53.90**	129.86**	1058.83**	83.05**	947.83**	-9.72**	60.50**	-144.16**	2032.58**
	Sabwani	155.56**	4.42**	-10.97	39.84	110.11**	272.94**	54.72**	230.01**	5.70	66.96	-62.22	879.72
F x 8	Kitale	185.17**	32.10**	-48.42**	45.37**	91.70**	800.58**	105.94**	695.05**	-34.17**	112.38**	-215.16**	1661.62**
	Kakam.	141.53**	21.84**	-45.60**	14.02**	130.25**	460.86**	61.11**	405.51**	-21.41**	26.40**	-106.62**	795.21**
	Soy	173.89**	55.23**	-32.22**	26.23**	144.38**	1026.15**	75.56	988.57	-19.93**	52.81**	-158.75**	1453.73**
	Sabwani	178.61**	6.27**	-28.89**	76.69**	109.59**	412.88**	34.45	407.08	-6.95	80.74	-93.06	1350.62
8 x 64	Kitale	186.86**	63.71**	9.50	69.44	172.00**	1541.67**	97.33**	1296.98**	5.58	134.73	-162.46**	3108.60**
	Kakam.	141.67**	82.35**	11.11	54.70	163.89**	1568.42**	88.87	1536.45	4.58	77.86	-80.55	2320.77
	Soy	169.31**	56.56**	5.97	225.33	112.29**	1845.41**	53.61	1806.24	12.15	253.18	-42.91	4663.90
	Sabwani	170.70**	23.86**	9.31	103.97	153.33**	930.33**	88.05**	797.70**	4.03	131.03	-81.67	2575.91

** Significant at 1% significant level

V_m = Variance of mean

V_d = Additive variance

V_h = Dominance variance

V_i = Additive x additive variance

V_j = Additive x dominance variance

V_l = Dominance x dominance variance

m = Mean effects

d = Additive effects

h = Dominance effects

i = Additive x Additive effects

j = Additive x Dominance effects

l = Dominance x Dominance effects

Significant dominance genetic variances were detected for the crosses at most of the sites. Manifestation of epistatic variance components was not consistent across the sites. Cross A x F exhibited no significant additive x additive genetic variance in all sites. Significant additive x dominance genetic variance estimates were exhibited by three crosses (A x F, F x 64, F x 8) at Kitale, Soy and Kakamega. No significant additive x dominance genetic variance was observed for crosses A x 64, A x 8 and 8 x 64. A number of crosses exhibited significant dominance x dominance genetic variance at some of the sites.

4.3 Grain Yield (Kgs/ha)

In general the data obtained from all the four sites show that the F_1 populations had the highest means for the grain yields followed by backcrosses, F_2 and parents respectively (Table 13). The F_1 for cross 8 x 64 had the highest yields at Kitale, Soy and Sabwani, while at Kakamega F x 64 had the highest grain yields. Relatively lower yields for all populations was observed at Kakamega.

Table 13: Mean grain yield (Kgs/ha) data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	1692.90	2132.10	2228.40	2477.70	2133.00
F	2355.30	3060.90	2348.10	2754.90	2629.80
64	2219.40	1307.70	2952.90	1976.40	2114.10
8	2618.10	992.70	2425.50	2648.70	2171.70
F_1					
A x F	8868.60	5658.30	7396.20	7200.90	7281.00
A x 64	6947.10	4984.208	6381.90	8065.80	6595.20
A x 8	7462.80	5334.30	6401.70	6201.90	6350.40
F x 64	8120.70	5898.604	8140.50	7639.20	7449.30

F x 8	8554.70	5410.80	7196.40	7907.40	7266.60
8 x 64	9576.00	4969.80	7281.00	8481.60	7577.10
<u>Backcrosses</u>					
(AxF)xA	5542.20	3730.50	4909.50	5953.50	5033.70
(Ax64)xA	5157.00	2676.60	5909.40	5985.90	4954.50
(Ax8)xA	6113.70	3353.40	5038.20	5756.40	5065.20
(Fx64)xF	6044.40	3828.60	6376.50	5699.70	5119.20
(Fx8)xF	6239.70	4900.50	4890.60	6698.70	5718.60
(8x64)x8	7616.70	4109.40	4941.00	7830.00	6124.50
(AxF)xF	6772.50	4556.70	4781.70	6070.50	5634.90
(Ax64)x64	7671.60	4082.40	6845.40	7486.20	6521.40
(Ax8)x8	6125.40	4650.30	5246.10	5862.60	5471.10
(Fx64)x64	8359.20	3416.40	5988.60	6468.30	3105.00
(Fx8)x8	5736.60	3662.10	6021.00	8195.40	5907.60

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
(8x64)x64	6890.40	3942.90	6678.90	6354.00	5967.00
$\underline{F}_2$					
(AxF) x	5400.90	4249.80	4646.70	4875.30	4793.40
(Ax64) x	4617.90	2494.80	3710.70	4591.80	3853.80
(Ax8) x	5455.80	3081.60	4646.70	4658.40	4459.50
(Fx64) x	4096.80	3843.90	3564.90	5460.30	4241.70
(Fx8) x	5265.00	2488.50	4640.40	5265.00	4414.50
(8x64) x	4833.00	3366.90	4561.20	5140.80	4550.40
Mean of parents	2221.20	1873.80	2488.50	2464.20	
F_1 mean	8254.80	5375.70	7133.40	7582.50	

Backcross mean	6522.30	3909.60	5635.80	6530.40
F_2 mean	4944.60	3254.40	4294.80	4998.60
LSD .05	1387.80	1923.30	206.00	1584.90

While the analysis in Appendix 1 suggest that there were significant variation among the treatments, the diallel analysis in table 5 indicates that the general combining ability effects were only significant at Sabwani. No significant specific combining ability effects were observed at any of the sites. Considering the general combining ability, inbred line F was the best general combiner at Kitale, Kakamega and Soy while inbred line 64 was the best general combiner at Sabwani (Table 14). The poorest general combiner at Kitale, Soy and Sabwani was inbred line A, while inbred line 8 was poorest general combiner at Kakamega. The best specific combinations at Kitale were A x F and 8 x 64, while the best specific combinations at Sabwani were A x 64 and F x 8. The poorest specific combinations at Kitale and Sabwani were A x 8 and F x 64, while the poorest specific combinations at Kakamega and Soy were A x 64 and F x 8.

The estimates of variance components (Table 15) indicated that four crosses (A x 64, A x 8 F x 64 and 8 x 64) exhibited significant additive genetic variation at Kakamega, Kitale and Soy respectively. Crosses A x F and F x 8 did not show any significant additive genetic variance at any of the sites. With a few exceptions, all crosses exhibited significant dominance genetic variance at all sites. Significant additive x additive genetic variance was exhibited by A x 64 at all the sites. Four crosses exhibited significant additive x dominance genetic variance at a few sites. On the other hand crosses A x F and F x 8 did not show significant additive x additive genetic variance at any of the sites. The manifestation of additive x dominance and dominance x dominance epistatic variance was also inconsistent for six crosses at the four sites.

Table 14: GCA effects (diagonal) and SCA effects (off diagonal) for grain yield

Parents		A	F	8	64
	Sites				
A	Kitale	-13.25a*	14.09a	-11.81c*	-2.28b*
	Kakamega	-0.84a*	-0.69a*	2.67b	-1.98a*
	Soy	-6.77a*	2.28a	1.53a	-3.82c*
	Sabwani	-7.11a*	2.87a	-7.36b*	4.49c
F	Kitale		9.32b	-2.28b*	-11.81c*
	Kakamega		4.66b	-1.98a*	2.67b
	Soy		7.41b	-3.82c*	1.53a
	Sabwani		-0.01b*	4.49c	-7.36b*

8	Kitale	-0.40d*	14.09a
	Kakamega	-2.30a*	-0.69a*
	Soy	-2.89a*	2.28a
	Sabwani	-0.88d*	2.87a
64	Kitale		4.33c
	Kakamega		1.53a*
	Soy		2.24c
	Sabwani		7.99c

Values followed by the same lettering for each trait (a,b,c,d,) are not significantly different (Duncan's multiple range test, $p \le 0.05$

* Significant, $p \le 0.05$

Table 15: Mean estimates of genetic effects and variance components for grain yield for the crosses over the four environments

		Genetic effects and Variance components											
Crosses	Sites	m	v_m	d	v_d	h	v_h	i	v_i	j	v_j	l	v_l
A x F	Kitale	60.01**	9.77**	-13.66	114.46	109.67**	1400.97**	33.61**	614.12	-9.98	123.11	-65.27	5135.10
	Kakam.	47.22**	3.75**	-9.19	187.35	29.31**	943.48	-4.72	809.39	-4.02	210.44	3.99	3593.92
	Soy	51.63**	33.18**	1.42	28.50	65.62	683.64	8.86	644.81	2.08	49.51	-9.00	1142.15
	Sabwani	54.17**	26.07**	-1.30	60.24	101.96**	761.35**	51.02**	658.08	0.25	68.14	-100.05	1794.02
A x 64	Kitale	51.31**	19.34**	-27.94**	50.30**	135.28**	564.12**	79.83**	510.66**	-25.01**	65.42**	-167.05	1328.07**
	Kakam.	27.72**	3.50**	-15.61	245.46	75.58**	1066.92**	39.30**	1037.82**	-20.19	247.90	-40.52	4099.69
	Soy	41.23**	22.96**	-10.40	51.64	160.68**	625.89**	118.55**	573.91**	-6.38	72.90	-202.61**	1401.51**
	Sabwani	51.02**	13.07**	-16.68	137.85	160.15	776.52**	95.28**	760.59**	-19.46	150.83	-165.91**	2478.50**
A x 8	Kitale	60.62**	1.99**	-0.13	134.06	84.50**	612.59**	29.53	568.09	5.02	139.28	-87.78	2354.80
	Kakam.	34.21**	40.76**	-14.41**	18.59**	82.82**	729.87**	40.91	726.42	-20.73**	21.95**	-65.49	963.26
	Soy	51.63**	45.44**	-2.32	74.87	67.29	1083.55	22.01	1026.46	-1.22	103.50	-56.56	2153.21
	Sabwani	51.76**	2.95**	-1.18	69.79	91.59**	348.54**	51.15**	326.35**	-0.23	75.21	-114.58**	1252.62**

F x 64	Kitale	45.52**	31.21**	-25.72**	58.52**
	Kakam.	42.71**	10.47**	4.58	68.17
	Soy	39.61**	90.37**	4.31	76.80
	Sabwani	60.67**	0.13**	-8.54	13.57
F x 8	Kitale	58.50**	27.99**	5.59	103.32
	Kakam.	27.65	14.81**	13.76	463.15
	Soy	51.56	43.79**	-12.56	94.14
	Sabwani	58.50**	41.02**	-16.64	239.55
8 x 64	Kitale	53.70**	4.64**	8.07	88.94
	Kakam.	37.41**	21.27**	1.86	59.94
	Soy	50.68**	23.09**	-19.32**	20.85**
	Sabwani	57.12**	27.52**	16.40	148.97

** Significant at 1% significant level

V_m = Variance of mean m =

V_d = Additive variance d =

V_h = Dominance variance h =

V_i = Additive x additive variance i =

V_j = Additive x dominance variance j =

V_l = Dominance x dominance variance l =

202.78**	773.39**	137.98**	733.37**	-26.47**	73.65**	-227.25**	1595.69**
31.42	535.54	-9.84	489.53	-5.16	90.88	28.45	1808.57
177.32**	1777.66**	116.32**	1753.04**	7.67	77.90	-151.29**	2773.08**
86.30**	82.48**	27.71**	56.33**	-12.87**	24.22**	-75.76**	323.79**
99.56**	878.66**	32.16	61.12	7.05	108.56	-52.98	2171.16
117.30	2147.30	79.70	2089.48	2.28	486.78	-104.72	7878.56
89.71	1328.57	36.26	1185.64	-12.13	102.61	-65.78	2994.28
154.84**	1731.06**	96.99	1614.08	-17.23	242.63	-192.21**	4955.38**
187.11**	460.47**	117.59**	430.03**	5.86	100.65	-163.42**	1619.01**
71.72**	697.71**	29.28	580.07	3.60	62.92	-72.22	1769.87
106.52**	501.11**	55.50**	452.85**	-16.39**	29.58**	-92.17**	896.02**
155.28**	1068.54**	86.73**	1032.84**	12.67	156.29	-162.07**	2953.10**

Mean effects

Additive effects

Dominance effects

Additive x Additive effects

Additive x Dominance effects

Dominance x Dominance effects

Crosses A x F and F x 8 did not exhibit significant additive x dominance genetic variance at any of the sites. Similarly cross A x F showed no significant dominance x dominance genetic variance at any of the sites. However, significant dominance x dominance genetic variance was exhibited by crosses A x 64, F x 64 and 8 x 64 at Kitale, Soy and Sabwani.

Values of heterosis estimates given in Table 9 show that cross A x F was the most heterotic for grain yield at Kitale and Soy while cross 8 x 64 was the most heterotic at Kakamega and Sabwani.

Predictions for double cross yield performances (Table 16) indicated that double cross (A x 64) x (F x 8) would have the best yields at Kitale, Kakamega and Soy. Double cross (A x 8) x (F x 64) would also perform well at Sabwani. The range in yield performance of the double crosses was very small at all the sites.

Table 16: Double cross yield performance (Kgs/ha) data at the four environments

Double Crosses	Means of non-parental crosses at the four sites			
	Kitale	Kakamega	Soy	Sabwani
(A x F) x (8 x 64)	7770.60	5407.20	7030.80	7453.80
(A x 64) x (F x 8)	8506.80	5465.70	7305.30	7380.90
(A x 8) x (F x 64)	8486.10	5256.00	7064.10	7914.60

4.4 Ear Length (cm)

The F_1 population had the longest ears followed by backcrosses, F_2 and parents respectively at all the sites. Longest ears were observed at Kitale while shortest ears were observed at Kakamega (Table 17).

The analyses in Table 5 and Appendix 1, revealed significant variation among the treatments at all sites. General combining ability effects were also significant at all the sites. Considering the general combining ability estimates, inbred line F was the best general combiner at Kitale, Kakamega and Soy, while inbred line 64 was the best general combiner at Sambwani (Table 18). Inbred line A was the poorest general combiner at all sites. Crosses A x F and 8 x 64 were the best specific combinations at Kitale, Soy and Sabwani, while at Kakamega A x 64 and Fx8 were the best specific combinations. The poorest specific combinations at Kitale and Soy were A x 64 and F x 8, while in Kakamega and Sabwani the poorest specific combinations were A x 8 and F x 64.

In the generation mean analysis, the estimates of the variance components (Table 19) indicated that cross A x F exhibited significant additive genetic variance estimates at Kitale, Kakamega and Sabwani.

Table 17: Mean ear length (cm) data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	12.56	10.28	12.63	11.08	11.64
F	16.74	14.21	13.58	15.71	15.06
64	17.44	14.34	16.16	15.15	15.77
8	17.36	14.63	14.13	15.30	15.23
$\underline{F_1}$					
A x F	19.33	17.12	18.76	18.89	18.53
A x 64	18.00	17.17	17.26	18.83	17.82
A x 8	18.89	16.95	17.25	17.26	17.59
F x 64	21.87	20.78	20.79	19.72	20.77
F x 8	21.65	20.98	19.88	20.56	20.76

8 x 64	21.79	20.44	20.20	21.16	20.98
Backcrosses					
(AxF)xA	17.50	15.31	15.54	16.60	16.24
(Ax64)xA	17.33	15.36	17.62	16.89	16.80
(Ax8)xA	16.83	14.48	14.78	16.16	15.56
(Fx64)xF	20.15	15.61	18.79	18.68	18.31
(Fx8)xF	20.46	17.92	18.67	20.00	19.26
(8x64)x8	19.22	18.66	17.97	19.03	18.72
(AxF)xF	20.07	17.53	16.42	18.91	18.23
(Ax64)x64	19.73	18.45	18.75	19.45	10.09
(Ax8)x8	17.81	17.90	17.33	17.67	17.68
(Fx64)x64	22.14	17.04	17.97	19.66	19.29
(Fx8)x8	19.25	18.08	18.97	18.46	18.69

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
(8x64)x64	21.21	17.44	18.13	21.14	19.48
F_2					
(AxF) x	17.67	14.77	14.81	15.53	15.59
(Ax64) x	16.01	13.97	14.62	14.89	14.87
(Ax8) x	16.57	12.52	15.33	16.11	15.13
(Fx64) x	17.73	17.92	15.37	17.55	17.14
(Fx8) x	18.60	16.17	16.20	17.14	16.93
(8x64) x	18.04	15.57	15.69	16.29	16.40
Mean of parents	16.03	13.37	14.13	14.31	
F_1 mean	20.26	18.91	19.02	19.40	

Backcross mean	19.31	16.98	17.58	18.55
F_2 mean	17.44	15.15	15.34	16.25
LSD .05	1.95	2.42	2.34	1.72

Table 18: GCA effects (diagonal) and SCA effects (off diagonal) for ear length

Parents	Sites	A	F	8	64
A	Kitale	-2.27b*	0.31a	0.13a	-0.43b*
	Kakamega	-2.83a*	-0.01a*	-0.10a*	0.11a
	Soy	-1.88a*	0.47a	-0.02c*	-0.44b*
	Sabwani	-1.61a*	0.62a	-0.91b*	0.29c
F	Kitale		1.04a	-0.43b*	0.13a
	Kakamega		0.99b	0.11a	-0.10a*
	Soy		1.16c	-0.44b*	-0.02c*
	Sabwani		0.48bc	0.29c	-0.91b*
8	Kitale			0.78ac	0.31a
	Kakamega			0.91b	-0.01a*
	Soy			0.14b	0.47a
	Sabwani			0.38c	0.62a
64	Kitale				0.45c
	Kakamega				0.92b
	Soy				0.57b
	Sabwani				0.75b

Values followed by the same lettering for each trait (a,b,c,) are not significantly different (Duncan's multiple range test, $p \leq 0.05$)

* Significant, $p \leq 0.05$

Table 19: Mean estimates of genetic effects and variance components for ear length for the crosses over the four environments

		Genetic effects and variance components											
Crosses	Sites	m	v_m	d	v_d	h	v_h	i	v_i	j	v_j	l	v_l
A x F	Kitale	17.67**	0.40**	-2.56**	0.52**	9.16**	10.37**	4.47**	8.41	-0.48	0.88	-11.65	22.50
	Kakam.	14.77**	0.26**	-2.23**	0.72**	11.49	8.62**	6.62	6.99	0.26	0.85	-13.58**	22.22**
	Soy	14.81**	0.82**	-0.88	0.73	10.32**	17.30	4.66	16.06	-0.41	1.64	-4.85	29.70
	Sabwani	15.53**	0.11**	-2.31**	0.52**	14.36**	5.13**	8.87**	3.77**	-0.01	0.91	-15.31**	15.48**
A x 64	Kitale	16.01**	0.17**	-2.40	2.88	13.07**	14.99**	10.07**	14.08**	0.04	3.10	-18.19	51.74
	Kakam.	13.97**	0.04**	-3.09	1.81	16.59**	8.40**	11.73**	7.82**	-1.06	2.31	-20.38**	31.89**
	Soy	14.62**	0.28**	-1.13	0.86	17.11**	9.85**	14.24**	7.94**	0.64	2.31	-23.65**	25.87**
	Sabwani	14.89**	0.33**	-2.56**	0.36**	18.86**	8.49**	13.14**	6.78**	-0.52	0.74	-21.94**	17.93**
A x 8	Kitale	16.57**	0.45**	-0.97	0.26	6.93	9.11	3.00	8.37	1.43	0.54	-4.58	14.49
	Kakam.	12.52**	0.96**	-3.42**	0.57**	19.18**	18.53**	14.69**	17.58**	-1.25	1.30	-20.66**	26.87**
	Soy	15.33**	1.23**	-2.55	3.00	6.78	33.88	2.91	31.72	-1.80	4.28	-5.87	76.37
	Sabwani	16.11**	0.28**	-1.52	1.13	7.29	10.09	3.21	8.92	0.59	1.64	-9.96	27.14

F x 64	Kitale	17.13**	2.03**	-1.99	1.74	18.46**	42.58**	13.67	39.55	-1.64	1.98	-20.33	72.53
	Kakam.	17.92**	0.21**	-1.43	2.71	0.14	16.50	-6.36	14.17	-1.37	3.24	11.17	56.07
	Soy	15.37**	0.63**	0.83	2.06	17.95**	20.24**	12.03**	18.28**	2.12	2.61	-14.22	50.90
	Sabwani	17.55**	0.60**	-0.98	0.76	10.76**	14.16**	6.47	12.57	-1.26	1.11	-12.86	28.08
F x 8	Kitale	18.60**	1.45**	1.21	0.69	9.60	27.35	5.00	25.94	1.52	1.00	-7.03	39.92
	Kakam.	16.17**	0.04**	-0.15	3.59	13.88**	17.08**	7.32	14.95	0.05	4.01	-8.51	66.54
	Soy	16.20**	1.29**	-0.29	1.38	15.95**	27.73**	10.46	26.09	-0.02	1.76	-18.29**	49.20**
	Sabwani	17.14**	0.29**	1.54**	0.34**	13.41**	6.97**	8.36**	5.94**	1.34	0.81	-13.16**	14.09**
8 x 64	Kitale	18.04**	0.20**	-1.99	1.78	13.20**	10.99**	8.70**	10.22**	-1.95	1.94	-10.98	34.62
	Kakam.	15.57**	0.46**	1.21	3.62	15.88**	23.94**	9.92	21.92	1.07	4.41	-12.28	73.48
	Soy	15.69**	1.09**	-0.34	0.75	14.46**	23.27**	9.41	20.49	0.86	1.66	-10.92	38.60
	Sabwani	16.29**	1.54**	-2.10**	0.35**	21.10**	26.60**	15.17**	26.10**	-2.18	0.82	-2.74**	32.32**

** Significant at 1% significant level

V_m = Variance of mean
V_d = Additive variance
V_h = Dominance variance
V_i = Additive x additive variance
V_j = Additive x dominance variance
V_l = Dominance x dominance variance

m = Mean effects
d = Additive effects
h = Dominance effects
i = Additive x Additive effects
j = Additive x Dominance effects
l = Dominance x Dominance effects

Most crosses exhibited significant dominance genetic variance in at least three sites, except A x 8. Significant additive x additive genetic variance was exhibited by cross A x 64 at all the sites. No significant additive x dominance genetic variance was shown by any cross. Manifestation of dominance x dominance genetic variance was also not consistent for the crosses at the four sites.

Values of heterosis estimates given in Table 9 show that cross F x 64 was the most heterotic for ear length at Kitale and Kakamega, while crosses F x 8 and 8 x 64 were most heterotic in Soy and Sabwani respectively.

4.5 200-Grain Weight (g)

Data obtained from all the four sites indicate that the F_1 population had the highest means for 200-grain weight followed by backcrosses, F_2 and parental populations respectively (Table 20). Higher means for 200-grain weight for all populations were observed at Kitale, while lower weights were observed at Kakamega. The analyses in appendix 1 and Table S indicated significant differences for the treatments at all sites. However, there were no significant variations among the crosses and for the general combining ability (gca) and specific combining ability (sca) effects. The general combining ability effects were only significant at Kakamega. Considering the general combining ability estimates, inbred line F was the best general combiner at Kitale, Kakamega and Sabwani, while inbred line 64 was the best general combiner at Soy (Table 21). Inbred line 8 was the poorest general combinerat Kakamega, Soy and Sabwani, while inbred line 64 was the poorest general combiner at Kitale.

The best specific combinations at Soy and sabwani were A x 64 and F x 8. A x F and 8 x 64 were the best specific combinations at Kitale while at Kakamega A x 8 and F x 64 were the best specific combinations. At Kitale and Kakamega the poorest specific combinations were A x 64 and F x 8, while at Soy and Sabwani A x 8 and F x 64 were the poorest specific combinations.

Table 20: Mean 200-grain weight (g) data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	63.33	37.82	56.03	50.29	51.88
F	70.67	64.41	56.09	60.73	62.98
64	78.35	50.71	66.09	64.64	64.95
8	69.72	55.16	55.47	52.69	58.26
$\underline{F_1}$					
A x F	96.95	78.04	77.70	79.11	82.87
A x 64	86.46	63.47	79.04	79.17	77.03
A x 8	88.56	61.40	64.26	68.88	70.78
F x 64	91.40	75.08	84.99	75.33	81.71
F x 8	91.89	65.45	75.09	77.53	77.48
8 x 64	92.04	52.94	75.93	75.60	74.12
<u>Backcrosses</u>					
(AxF)xA	76.63	54.77	68.17	74.23	68.45
(Ax64)xA	81.01	53.76	72.53	70.58	69.47

(Ax8)xA	78.69	47.30	65.25	67.76	64.75
(Fx64)xF	94.17	68.46	75.03	79.60	79.27
(Fx8)xF	86.21	65.63	68.60	72.81	74.06
(8x64)x8	94.67	65.85	77.81	77.60	78.98
(AxF)xF	79.79	62.31	65.22	67.24	68.64
(Ax64)x64	92.39	69.87	78.04	82.21	80.63
(Ax8)x8	72.27	52.13	62.30	58.16	61.21
(Fx64)x64	90.80	63.14	76.54	72.14	76.15
(Fx8)x8	80.61	58.53	67.59	72.85	69.90
(8x64)x64	88.46	66.90	82.11	76.89	78.59
$\underline{F}_2$					
(AxF) x	72.15	61.45	65.81	64.81	64.39
(Ax64) x	89.09	69.27	73.83	73.84	77.01
(Ax8) x	77.56	51.68	63.44	60.91	63.40
(Fx64) x	78.43	63.26	71.90	68.26	70.46
(Fx8) x	75.14	53.19	63.48	65.55	64.34
(8x64) x	72.98	59.16	62.66	65.21	64.25

Mean of parents	70.51	52.03	58.42	57.09
F_1 mean	91.22	66.06	76.17	75.94
Backcross mean	84.64	60.72	71.60	72.67
F_2 mean	77.56	59.65	66.85	66.43
LSD .05	11.56	15.02	15.45	11.03

Table 21: GCA effects (diagonal) and SCA effects (off diagonal) 200-grain weight

Parents	Sites	A	F	8	64
A	Kitale	-0.84a*	3.27a	-1.23b*	-2.04b*
	Kakamega	2.39a	-0.54a*	2.16b	-1.62a*
	Soy	-3.75a*	0.65a	-1.54b*	0.89a
	Sabwani	-0.33a*	1.41a	-3.82b*	2.41c
F	Kitale		3.29b	-2.04b*	-1.23b*
	Kakamega		10.21b	-1.62a*	2.16b
	Soy		4.64b	0.89a	-1.54b*
	Sabwani		2.09b	2.41c	-3.82b*
8	Kitale			-0.58a*	3.27a
	Kakamega			-9.23d*	-0.54a*
	Soy			-6.61a*	0.65a

Sabwani	-2.91a*	1.41a
Kitale		-1.88a*
Kakamega		-3.37c*
Soy		5.73b
Sabwani		1.15b

Values followed with the same lettering for each trait (a,b,c,d,) are not significantly different (Duncan's multiple range test, $p \leq 0.05$)

* Significant, $p \leq 0.05$

	Sabwani	-2.91a*	1.41a
64	Kitale		-1.88a*
	Kakamega		-3.37c*
	Soy		5.73b
	Sabwani		1.15b

Values followed with the same lettering for each trait (a,b,c,d,) are not significantly different (Duncan's multiple range test, $p \leq 0.05$)

* Significant, $p \leq 0.05$

In the generation mean analysis, the estimates of the variance components (Table 22) indicated that only A x 64 and A x 8 exhibited significant additive genetic variance at Kakamega. Similarly significant dominance genetic variance was exhibited only by A x F at Sabwani, F x 64 at Kitale and Sabwani and 8 x 64 at Kitale, Soy and Sabwani. Significant additive x additive and dominance x dominance genetic variances was manifested by F x 64 at Kitale and 8 x 64 at Soy and Sabwani. The cross 8 x 64 also had significant dominance x dominance genetic variance at Kitale.

The heterosis values in Table 9 suggest that cross A x F was the most heterotic for 200-grain weight at Kitale and Soy while crosses A x 64 and A x 8 were the most heterotic at Kakamega and Sabwani respectively.

Table 22: Mean estimates of genetic effects and variance components for 200-grain weight for the crosses over the four environments

		Genetic effects and variance components											
Crosses	Site	m	v_m	d	v_d	h	v_h	i	v_i	j	v_j	l	v_l
A x F	Kitale	72.15**	13.30**	-3.16	47.34	54.20**	485.95	24.26	402.14	0.51	72.68	-9.21	1305.48
	Kakam.	61.45**	42.30**	-7.55	9.47	15.28	743.69	-11.64	714.60	5.75	10.82	35.80	944.55
	Soy	65.81**	4.58**	2.95	43.55	25.20**	264.08	3.56	247.51	2.98	44.93	-2.84	836.43
	Sabwani	64.81**	1.87**	6.99	63.74	47.29**	291.71**	23.69	284.75	12.21	64.92	-37.38	1077.30
A x 64	Kitale	89.09**	1.78**	-11.38	24.59	6.07	164.46	-9.55	126.81	-3.88	45.14	-22.63	572.53
	Kakam.	69.27**	64.26**	-16.11**	28.56**	-10.61	1149.50	-29.82	1142.36	-9.67	29.76	-1.98	1513.64
	Soy	73.83**	24.85**	-5.51	22.15	23.81	512.18	5.83	486.24	-0.48	36.87	-26.78	855.75
	Sabwani	73.84**	24.21**	-11.63	50.82	31.91	609.49	10.21	590.66	-4.46	53.45	-42.53	1276.74
A x 8	Kitale	77.56**	1.59**	6.43	44.58	13.71	226.34	-8.33	203.68	9.62	65.53	16.59	829.29
	Kakam.	51.68**	4.87**	-4.84**	31.05**	7.06	207.34	-7.85	202.02	3.83	34.91	24.77	595.84
	Soy	63.44**	12.21**	2.95	48.04	9.87	500.21	1.36	387.48	2.67	49.87	-16.45	1414.86
	Sabwani	60.91**	1.35**	9.60	25.12	25.57	127.16	8.18	122.06	10.80	29.54	-19.28	443.98
F x 64	Kitale	78.43**	14.98**	3.37	19.81	73.10**	329.92**	56.21**	318.97**	7.21	28.51	-94.32**	600.43**
	Kakam.	63.26**	2.35**	5.32	14.24	27.69	101.47	10.16	94.62	-1.53	15.20	-8.07	292.91
	Soy	71.90**	270.94**	-1.51	12.41	39.45	4464.05	15.55	4384.65	3.49	26.58	-26.53	4851.16
	Sabwani	68.26**	4.56**	7.47	40.43	43.09**	246.49**	30.44	234.70	9.42	43.86	-57.88	766.98
F x 8	Kitale	75.14**	26.34**	5.59	8.30	54.76	466.25	33.06	454.58	5.11	17.41	-42.52	600.84
	Kakam.	53.19**	12.14**	7.10	44.19	41.25	387.98	35.59	370.94	2.47	47.82	-33.46	969.41
	Soy	63.48**	9.63**	1.02	92.31	37.79	549.24	18.48	523.32	0.71	93.59	-29.13	936.47
	Sabwani	65.55**	36.68**	-0.04	34.21	49.92	766.13	29.10	723.70	-4.06	39.42	-51.93	1303.95
8 x 64	Kitale	72.98**	52.96**	6.20	17.87	92.35**	938.36**	74.35	918.82	10.52	22.18	-108.74**	1211.43**

Kakam.	59.16**	1.79**	-1.05	46.75	28.87	474.48	28.87	215.67	-3.28	50.23	-82.63	1811.92
Soy	62.66**	20.73**	-4.30	64.79	84.35**	621.46**	59.19**	590.84**	1.01	79.41	-115.62**	1490.76**
Sabwani	62.21**	18.90**	0.71	19.70	77.09**	412.07**	60.16**	381.12**	6.69	26.34	-100.63**	741.26**

** Significant at 1% significant level

V_m = Variance of mean

V_d = Additive variance

V_h = Dominance variance

V_i = Additive x additive variance

V_j = Additive x dominance variance

V_l = Dominance x dominance variance

m = Mean effects

d = Additive effects

h = Dominance effects

i = Additive x Additive effects

j = Additive x Dominance effects

l = Dominance x Dominance effects

4.6 Kernel Row Number

Data obtained from Kitale, Kakamega and Soy reveal that the F_1 populations had the highest kernel row number, followed by backcrosses, F_2 and then parents (Table 23). At Sabwani, the backcrosses had more kernel row numbers followed by F_2, F_1 and then the parents.

The analysis of variance for kernel row number (Appendx 1 indicated significant differences among the treatments at all sites. The diallel analysis (Table 5) suggests that the general combining ability effects were significant at all the sites. Inbred line 8 had the highest general combining ability (gca) estimates at all the sites, while inbred line A had the lowest general combining ability estimates at the four sites (Table 24). The best specific combinations at Kitale, Kakamega and Sabwani were A x 64 and F x 8, while at Soy A x 8 and F x 64 were the best specific combinations. The poorest specific combinations at Kakamega and Sabwani were A x F and 8 x 64. At Kitale the poorest specific combinations were A x 8 and F x 64, while at Soy they were A x 64 and Fx8.

The estimates of the genetic variance components (Table 25) show that crosses A x F and F x 64 exhibited significant additive genetic variance at Kitale, and cross A x 8 had significant additive genetic variation at Kitale, Kakamega and Sabwani.

Table 23: Mean kernel row number data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	12.75	11.95	12.49	12.59	12.44
F	12.86	12.49	12.97	12.29	12.65
64	12.30	10.87	12.16	12.67	12.00
8	13.25	13.26	14.14	14.18	13.71
<u>F_1</u>					
A x F	12.72	12.56	12.56	12.17	12.50
A x 64	12.86	12.61	12.44	12.89	12.70
A x 8	12.97	13.17	13.33	12.94	13.10
F x 64	13.70	13.50	13.67	13.50	13.59
F x 8	14.33	14.22	13.67	14.17	14.10

Table 23: Mean kernel row number data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	12.75	11.95	12.49	12.59	12.44
F	12.86	12.49	12.97	12.29	12.65
64	12.30	10.87	12.16	12.67	12.00
8	13.25	13.26	14.14	14.18	13.71
<u>F_1</u>					
A x F	12.72	12.56	12.56	12.17	12.50
A x 64	12.86	12.61	12.44	12.89	12.70
A x 8	12.97	13.17	13.33	12.94	13.10
F x 64	13.70	13.50	13.67	13.50	13.59
F x 8	14.33	14.22	13.67	14.17	14.10

8 x 64	14.03	13.50	13.89	14.00	13.86
<u>Backcrosses</u>					
(AxF)xA	12.78	12.61	12.86	12.73	12.76
(Ax64)xA	12.69	14.89	12.56	12.75	13.22
(Ax8)xA	13.098	12.53	13.34	13.42	13.09
(Fx64)xF	13.14	13.71	13.45	13.39	13.42
(Fx8)xF	13.28	12.87	13.32	13.44	13.23
(8x64)x8	13.56	13.48	12.94	13.95	13.48
(AxF)xF	13.50	12.68	12.75	13.20	13.03
(Ax64)x64	12.50	11.85	12.60	12.32	12.32
(Ax8)x8	14.28	13.61	13.58	14.45	13.97
(Fx64)x64	14.06	12.76	13.19	12.94	13.24
(Fx8)x8	14.00	14.22	14.16	14.50	14.22

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
(8x64)x64	13.45	12.94	13.78	13.69	13.44
F_2					
(AxF) x	13.17	12.83	12.64	12.67	12.83
(Ax64) x	12.08	10.41	12.47	12.17	11.78
(Ax8) x	13.31	13.18	13.49	13.42	14.35
(Fx64) x	13.25	13.97	13.35	13.93	13.62
(Fx8) x	14.04	13.40	13.56	14.72	13.93
(8x64) x	13.67	12.50	13.33	13.36	13.22
Mean of parents	12.79	12.14	12.94	12.93	
F_1 mean	13.44	13.26	13.26	13.28	
Backcross mean	13.36	13.18	13.21	13.40	
F_2 mean	13.25	12.72	13.14	13.39	
LSD .05	0.76	0.96	0.92	0.80	

Table 24: GCA effects (diagonal) and SCA effects (off diagonal) for kernel row number

Parents	Sites	A	F	8	64
A	Kitale	-0.88a*	-0.06a*	-0.10a*	0.16b
	Kakamega	-0.72b*	-0.23b*	0.07a	0.16a
	Soy	-0.72a*	-0.04a*	0.24b	-0.20a*
	Sabwani	-0.9a*	-0.19b*	-0.06b*	0.25a
F	Kitale		0.22cd	0.16b	-0.10a*
	Kakamega		0.25a	0.16a	0.07a
	Soy		0.06a	-0.20a*	0.24b
	Sabwani		0.00b	0.25a	-0.06b*
8	Kitale			0.51c	-0.06a*
	Kakamega			0.56a	-0.23b*
	Soy			0.56b	-0.04a*
	Sabwani			0.64d	-0.19b*
64	Kitale				0.14bd
	Kakamega				-0.08c*
	Soy				0.11a
	Sabwani				0.28c

Values followed by the same lettering (a,b,c,d) are not significantly different (Duncans multiple range test p ≤ 0.05)

* Significant, p ≤ 0.05

Table 25: Mean estimates of genetic effects and variance components for Kernel row number for the crosses over the four environments

		Genetic effects and variance components											
Crosses	Sites	m	v_m	d	v_d	h	v_h	i	v_i	j	v_j	l	v_l
A x F	Kitale	13.17**	0.07**	-0.72	0.07**	-0.20	1.37	-0.12	1.31	-0.67**	0.08	-1.38	2.38
	Kakam.	12.83**	0.10**	-0.07	0.03	-0.40	1.84	-0.74	1.70	0.20	0.11	-0.30	2.60
	Soy	12.64**	0.03**	0.11	0.32	0.49	12.05	0.67	11.82	0.35	0.46	-1.32	6.60
	Sabwani	12.67**	0.07**	-0.47**	0.20	0.92	1.87	1.19	1.83	-0.62	0.23	-3.84	4.39
A x 64	Kitale	12.08	0.23**	0.19	0.19	2.39	4.48	2.05	4.35	-0.03	0.31	-26.71	7.12**
	Kakam.	10.41**	0.17**	3.04	5.62	13.06**	25.34**	11.85	25.12	2.50	5.68	-17.30	93.39
	Soy	12.47**	0.02**	-2.05	0.11	0.57	1.21	0.44	0.73	-0.21	0.19	-1.23	3.90
	Sabwani	12.17**	0.04**	0.43	0.03	1.73	0.85	1.47	0.71	0.47	0.08	-0.58	1.63
A x 8	Kitale	13.31	0.17**	-1.20	0.10**	1.47	3.09	1.50	3.07	-0.95	0.12**	-4.28	4.35
	Kakam.	13.18**	0.02**	-1.08**	0.13**	0.12	0.84	-0.44	0.78	-0.43	0.16	-0.29	2.57
	Soy	13.49**	0.45**	-0.24	0.01	-0.08	2.52	-0.10	2.43	0.59	0.10	-0.48	2.95
	Sabwani	13.42**	0.17**	-1.03**	0.05	1.62	3.16	2.06	2.98	-0.24	0.07	-5.13	4.13

F x 64	Kitale	13.25	0.06**	-0.92
	Kakam.	13.97**	0.07**	0.95
	Soy	13.35	0.03**	0.35
	Sabwani	13.93**	0.09**	0.45
F x 8	Kitale	14.04	0.04**	-0.72
	Kakam.	13.40**	0.35	-1.35
	Soy	13.56**	0.16**	-0.84
	Sabwani	14.72**	0.04**	-1.07
8 x 64	Kitale	13.67	0.12**	0.11
	Kakam.	12.50**	0.23**	0.54
	Soy	13.33**	0.26**	-0.84
	Sabwani	13.36**	0.34**	0.25

** Significant at 1% significant level

V_m = Variance of mean m

V_d = Additive variance d

V_h = Dominance variance h

V_i = Additive x additive variance i

V_j = Additive x dominance variance j

V_l = Dominance x dominance variance l

0.07**	2.51	1.47	1.39	1.27	-1.20	0.18**	-3.23	2.88
2.63	-1.11	11.92	-2.93	11.71	0.14	2.75	0.34	44.10
0.03	0.94	0.67	-0.11	0.56	-0.16	0.11	-0.71	1.41
0.04	-2.02	1.91	-3.04	1.59	0.64	0.10	2.33	3.38
0.24	-0.33	1.68	-1.61	1.63	-0.53	0.24	1.83	46.63
0.45	1.93	7.48	0.58	7.34	-0.96	0.54	-0.58	13.26
0.20	0.84	3.66	0.73	3.38	-0.25	0.29	-1.24	6.94
0.29	-2.06	1.84	-3.00	1.80	-0.11	0.32	1.91	5.44
0.04	0.59	2.25	-0.67	2.10	-0.37	0.16	0.27	3.10
0.05	4.27	4.06	2.83	3.90	-0.66	0.13	-4.54	5.16
0.21	0.85	5.05	0.11	5.00	-1.83**	0.25**	0.53	7.76
0.03	2.41	5.85	1.83	5.55	-0.50	0.08	-2.67	7.14

= Mean effects

= Additive effects

= Dominance effects

= Additive x Additive effects

= Additive x Dominance effects

= Dominance x Dominance effects

Significant dominance genetic variance was only exhibited by cross A x 64 at Kakamega. No cross exhibited significant additive x additive genetic variance. No cross except A x 8 and F x 64 at Kitale and 8 x 64 at Soy showed significant additive x dominance genetic variance. Similarly significant dominance x dominance genetic variance was only exhibited by cross A x 64 at Kitale.

Generaly heterosis values were low (Table 9) and i some cases negative heterosis was shown by some crosses.

4.7 Lodging Percent (%)

The data from Kitale and Sabwani indicate that the F_1 populations had the lowest lodging percentage, while the parents had the highest lodging percentages (Table 26). This is contrary to the results obtained at Kakamega and Soy where the backcrosses exhibited higher lodging percentages.

Table 26: Mean lodging percent (%) data on parents, their F_1, F_2 and backcrosses grown in four environments in Kenya

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
A	51.67	33.44	44.46	40.15	42.16
F	8.62	23.66	37.95	31.90	25.53
64	12.17	23.53	46.39	13.64	23.93
8	21.20	30.86	39.80	16.23	27.02
F_1					
A x F	20.28	19.78	36.62	23.47	25.04
A x 64	9.02	53.69	55.22	9.09	29.26
A x 8	7.30	59.17	30.27	16.67	28.35
F x 64	4.26	47.51	46.51	16.23	28.60
F x 8	2.38	35.97	43.18	3.79	22.00
8 x 64	1.59	32.54	42.71	9.96	21.70
Backcrosses					
(AxF)xA	33.45	57.73	23.13	35.20	37.38

(Ax64)xA	31.86	48.86	50.13	14.87	41.43
(Ax8)xA	27.89	63.75	68.17	19.46	44.99
(Fx64)xF	18.60	77.27	43.72	10.46	37.51
(Fx8)xF	20.24	43.49	59.24	12.56	33.88
(8x64)x8	7.08	46.11	46.95	9.09	26.89
(AxF)xF	13.81	49.02	57.58	13.94	33.59
(Ax64)x64	12.98	49.92	22.95	10.75	24.15
(Ax8)x8	12.76	43.90	40.00	18.43	28.70
(Fx64)x64	9.09	63.89	40.15	17.42	32.64
(Fx8)x8	5.30	42.30	46.93	18.94	28.42

Entries	Sites				Mean
Parents	Kitale	Kakamega	Soy	Sabwani	
(8x64)x64	11.59	63.06	68.59	8.33	37.89
F_2					
(AxF) x	23.81	68.05	54.44	18.95	41.31
(Ax64) x	10.97	38.44	29.55	24.24	25.80
(Ax8) x	27.80	68.04	42.05	21.97	39.96
(Fx64) x	13.49	41.16	60.35	10.61	31.40
(Fx8) x	13.79	54.04	34.49	13.94	29.07
(8x64) x	4.55	46.55	21.06	14.39	21.64
Mean of parents	23.42	27.87	42.15	25.48	
F_1 mean	7.47	41.44	42.42	13.20	
Backcross mean	17.05	54.13	47.30	15.79	
F_2 mean	15.74	52.71	40.32	17.35	
LSD .05	13.37	18.24	24.47	17.69	

The analysis of variance for lodging percent (Appendix 1) revealed significant differences for the treatments at Kitale, Kakamega and Sabwani. Diallel analysis (Table 5) indicated that neither general combining ability effects nor specific combining ability effects were significant at any of the sites. This suggests that the variation in lodging percentage was mainly environmental. Considering general combining ability inbred line F was the best general combiner at Kakamega and Soy respectively. The poorest general combiner at Kitale and Sabwani was inbred line A, while at Kakamega and Soy they were inbred lines 8 and 64 respectively (Table 27). The best specific combinations at Kitale and Soy were crosses A x 8, F x 64. At Kakamega the best specific combinations were A x F and 8 x 64 while at Sabwani they were A x 64 and F x 8. The poorest specific combinations at Kitale and Sabwani were A x F and 8 x 64. At Kakamega the poorest specific combinations were A x 8 and F x 64 while at Soy they were A x F and 8 x 64.

Table 27: GCA effects (diagonal) and SCA effects (off diagonal) for lodging percent (%)

Parents	Sites	A	F	8	64
A	Kitale	7.37a	3.82b	-1.90a*	-1.92a*
	Kakamega	1.66a	-13.61a*	13.56c	0.05b
	Soy	-2.57ac*	-2.76a*	-4.03a*	6.78b
	Sabwani	4.81a	3.51a	3.25a	-6.76b*
F	Kitale		2.47b	-1.92a*	-1.90a*
	Kakamega		-8.03b*	0.05b	13.56c
	Soy		-0.47a*	6.78b	-4.03a*
	Sabwani		1.97b	-6.76b*	3.25a
8	Kitale			-5.79c*	3.82b
	Kakamega			4.17c	-13.61a*
	Soy			-5.55c*	-2.76a*
	Sabwani			-4.60c*	3.51a
64	Kitale				-4.05c*
	Kakamega				2.21a
	Soy				8.59b
	Sabwani				-2.16c*

Values followed by the same lettering for each trait (a,b,c) are not significantly different, $P \leq 0.05$

* Significant, $p \leq 0.05$

In the generation mean analysis, the estimates of the genetic variance components (Table 28) show that significant additive genetic variance was exhibited by A x F and A x 64 at Kitale and A x 8 at Kitale,Kakamega and Sabwani. Significant dominance genetic variance was only expressed in one cross (A x 64) at Kakamega. The same cross exhibited significant additive x additive genetic variance at Kitale. None of the crosses exhibited significant additive x dominance genetic variance at any of the sites. However, one cross (F x 64) exhibited significant dominance x dominance genetic variance at Kakamega.

Values of heterosis estimates given in Table 9 indicate that most crosses showed favourable negative heterosis for this trait at Kitale, Soy and Sabwani.

Table 28: Mean estimates of genetic effects and variance components for lodging percent for the crosses over the four environments

Crosses	Sites	Genetic effects and variance components											
		m	v_m	d	v_d	h	v_h	i	v_i	j	v_j	l	v_l
A x F	Kitale	23.81**	1.43**	19.64**	20.93**	-10.56	213.47	-0.70	106.52	-1.89**	43.08	7.02	785.44
	Kakam.	68.05**	38.30**	8.71	238.68	-67.47	1756.89	-58.70	1567.48	3.82	371.07	-58.11	5189.24
	Soy	54.44**	156.67**	-34.45	252.47	-60.95	3856.06	-56.36	3516.52	-37.70	440.43	50.60	7404.27
	Sabwani	18.95**	10.90**	21.26	129.54	9.94	777.79	22.50**	692.57	17.14	147.48	-1.80	8587.94
A x 64	Kitale	10.97**	2.77**	18.88**	35.00**	22.98	229.38	45.81**	140.00**	-0.87	57.90	-53.62	784.18
	Kakam.	38.44**	21.77**	-1.07	47.56	69.00**	668.45**	43.79	538.59	-6.02	173.81	-76.99	1628.73
	Soy	29.55	136.02	27.19	154.51	37.77	2744.64	27.97	2526.33	28.16	339.28	27.16	4449.42
	Sabwani	24.24	127.99	4.12	5.53	-63.53	2093.75	-45.73	2069.93	-9.14	17.29	66.46	2231.55
A x 8	Kitale	27.80**	30.41**	15.13**	13.67**	-59.04	557.87	-29.90	541.27	-0.10	28.90	36.06	771.68
	Kakam.	68.04**	132.76**	19.84**	35.87**	-29.84	2413.39	-56.86	2267.59	18.55	170.72	24.20	3281.25
	Soy	42.05**	166.58**	28.17	214.60	36.29	3880.29	48.15	3523.69	25.84	445.93	-119.69	7525.33
	Sabwani	21.97**	4.02**	1.03**	18.99**	-23.61	168.03	-12.09	140.23	-10.93	30.72	26.01	479.30
F x 64	Kitale	13.49**	14.23**	9.51	137.50	-4.70	801.04	1.43	777.66	11.28	156.16	-27.52	2521.20
	Kakam.	41.16	259.48	13.38	137.91	141.59	4733.01	117.68	3703.26	13.32	146.00	-257.79**	6477.19**
	Soy	60.35**	354.72**	3.57	336.86	-69.33	7321.47	-73.66	7102.99	7.79	391.65	83.28	12019.25
	Sabwani	10.61**	7.46**	-6.97	97.82	6.80	534.77	13.33	510.66	-16.10	115.18	8.92	1780.94
F x 8	Kitale	13.79**	21.03**	14.94	67.34	-16.60	622.48	-4.07	605.82	21.23	78.33	-12.44	1480.52
	Kakam.	54.04**	41.58**	0.99	119.32	-35.50	1198.35	-44.20	1142.51	4.59	136.01	-1.30	2797.68
	Soy	34.49**	81.04**	12.30	369.03	78.69	3208.90	74.38	2772.73	13.23	470.37	-122.60	8945.92
	Sabwani	13.94	34.20	-6.38	79.30	-13.05	882.23	7.23	864.33	-14.21	96.63	-14.42	1887.56

8 x 64	Kitale	4.55	5.17	-4.51
	Kakam.	46.55**	38.80**	-16.95
	Soy	21.06**	4.16**	-121.64
	Sabwani	14.39	76.33	0.76

** Significant at 1% significant level

V_m = Variance of mean m =

V_d = Additive variance d =

V_h = Dominance variance h =

V_i = Additive x additive variance i =

V_j = Additive x dominance variance j =

V_l = Dominance x dominance variance l =

10.87	4.07	140.39	19.17	126.13	-9.03	22.62	-19.97	313.65
165.45	37.49	1356.90	32.14	1282.62	-20.61	176.00	-131.02	3565.18
975.99	146.44	4147.82	146.83	3969.63	-18.34	1074.15	-206.30	16391.84
14.85	-27.71	1298.73	-22.73	1278.71	-0.54	25.51	37.67	1530.98

= Mean effects

= Additive effects

= Dominance effects

= Additive x Additive effects

= Additive x Dominance effects

= Dominance x Dominance effects

CHAPTER FIVE

5. DISCUSSION

5.1 Plant Height

The results indicate that the F_1 population had greater means for plant height than the backcross, F_2 and parent populations. Plants were taller at Kitale, Soy and Sabwani (all > 1800m a.s.l) than at Kakamega (1585m a.s.l). This indicates that altitude has an influence on the expression of plant height. The F_1 population mean was greater than the top parental mean in all crosses. This fact was even more evident where inbred line 8 was used as one of the parents, since it was the best general combiner for this trait at most sites. Inbred line A which was the poorest general combiner and crosses A x 64 and F x 8 which were the poorest specific combinations at most of the sites could be used in hybrid production to ensure shorter plant heights hence reduced lodging. With regard to this trait the general combining ability estimates differed less from site to site compared to specific combining ability estimates. The general combining ability effects were significant at all sites indicating that additive genetic effects contributed towards the variability in plant height.

An important observation arises from the specific combining ability estimates in Table 7 where it can be noted that, the six crosses can be grouped into three pairs. In each pair the specific combining ability estimates are equal in magnitude. These observations probably resulted from the limited number of parents used in the analysis.

The generation mean analysis showed the presence of both additive and dominance genetic variance. The dominance genetic variation was preponderant compared to additive genetic variation for all crosses at most sites. Similar results were reported by Gamble (1962a), Darrah and Hallauer (1972) and Chumo (1986). The additive genetic variation displayed in the inheritance of this character is mainly due to the additive gene effects which is fixable and hence can be easily exploited by single plant selection. Additive x additive genetic variance was significant for most crosses at all sites. This is in agreement with results of Hayman (1958). In most sites additive x additive and dominance x dominance epistatic variances appear to contribute more to the performance of plant height than do additive x dominance epistatic genetic variance. The magnitude and the type of epistatis varied with the environment (Table 8). Such a relationship had been pointed out by Dangi and Paroda (1978).

The diallel analysis was more effective in measuring additive genetic variation than generation mean analysis. However, generation mean analysis approach was more effective in revealing non-additive variance components.

Hybrid 8 x 64 was the most heterotic at Kitale, Kakamega and Sabwani, while cross A x 64 exhibited the least heterosis at all sites. Generally heterosis was low where the difference in performance of the two parents was remarkable. Heterosis was linked to specific combining ability in that the most heterotic crosses were more often the the best specific combinations and vice versa.

5.2 Ear Height

The F_1 population exhibited higher ear heights than the backcrosses, F_2 and the parental populations at all sites. There was a relationship between ear height and plant height in that the generations and or genotypes with greater plant heights had ears placed relatively high on the plant and vice versa (Tables 4 and 10).

The general combining ability effects were significant at all sites revealing that additive gene effects contributed to the manifestation of ear height in maize. Presence of additive variance for most crosses was confirmed by generation mean analysis. The specific combining ability effects were not significant indicating the absence of exploitable non-additive gene effects in the inheritance of ear height in maize. This could be due to the fact that the parental material originated from the same population. However, generation mean analysis approach revealed substancial dominance and epistatic variances. Inbred line 8 was consistently the best general combiner at all sites while inbred A was the poorest. This implies that a breeding programme aimed at reducing the ear heights hence lodging, could utilize inbred line A as one of the parents. Results show that at Kitale the best specific combinations were A x 8 and F x 64, paradoxically these crosses were the poorest specific combinations at Kakamega. This showed that there is an environmental influence on the performance of genotypes.

Cross 8 x 64 was the most heterotic at Kitale, Kakamega and Sabwani. Least heterosis was exhibited by cross A x 64 in most of the sites. Most crosses showed high heterosis for ear height. High heterosis for higher ear placement was also reported by Giesbretch (1961).

5.3 Grain Yield

Data from all the four sites indicate that the F_1 population had higher means for grain yield than the other populations. The yields were higher at Kitale, Soy and Sabwani (>1800m a.s.l), but relatively lower at Kakamega (1585m a.s.l). This can be explained by the fact that the materials used were late maturing germplasm and they made use of the long growing season at high altitude to accumulate more photosynthates.

The general combining ability effects were not found to be significant except at Sabwani. This surgested that additive gene effects played little role in the determination of grain yield. Similar results were noted for specific combining ability variances surgesting insignificant role played by dominant epistatic effects involving dominance. However, generation mean analysis revealed substantial additive and non-additive variance components. For example dominance genetic variance contributed largely in the inheritance of grain yield for most crosses and at most of the sites than additive genetic variance. Similar results were reported by Castro et al (1968), Darrah and Hallauer (1972) and Moreno-Gonzalez and Dudley (1981). Some crosses exhibited significant additive x additive genetic variance at Kitale,Soy and Sabwani denoting that it is important in the manifestation of grain yield in maize. Similar results were reported for maize by Gamble (1962a). Significant additive x dominance and dominance x dominance genetic variance was noted in some of the crosses. This observations suggest potential for improvement by selection and hybrid development involving the inbred lines used in the present study.

Inbred lines F and 64 which were the best general combiners for grain yield at most of the sites, appear to be the most promising parental lines for future breeding work. The superior crosses A x F, 8 x 64, A x 8 and F x 64 could be used in further selection programmes.

The F_1, F_2 and backcross performance was very superior to the top parent performance which is indicative of a high heterotic effect and potential for hybrid development. Cross A x F was the most heterotic at Kitale and Soy while cross 8 x 64 was the most heterotic at Kakamega and Sabwani. High heterosis for grain yield was also reported by Castro et al (1968). A promising double cross that could be considered for further development is (A x 64) x (F x 8) since it had the best predicted yield performance at Kitale, Kakamega and Soy.

5.4 Ear Length

In general genotypes with longer ears had high yields. This was also noted by Giesbretch (1961). For example the F_1 had longer ears and hence greater yields (Table 13 and 17). This implies that selection for longer ears would lead to higher yields. The general combining ability variances were significant at all sites indicating the importance of additive genes in the manifestation of ear length in maize.

The generation mean analysis also revealed the presence of some additive and dominance genetic variances, but there was preponderance of dominance genetic variance compared to additive genetic variance. The preponderance of dominance genetic variation for ear length in maize was also reported by Williams et al. (1965). The epistatic variance components were not equally important.

Cross F x 64 was the most heterotic for ear length at Kitale and Kakamega, while crosses F x 8 and 8 x 64 were the most heterotic at Soy and Sabwani respectively. This showed that environment had influence on the heterotic performance. Generally crosses involving inbred lines 8 and 64 had high manifestations of heterosis for this character.

5.5 200-Grain Weight

The F_1 populations had the highest means for 200-grain weight at all the sites. Higher means for 200-grain weight for all populations were observed at Kitale, while lower weights were observed at Kakamega. This could be due to the fact that Kakamega being at a lower altitude (1585m a.s.l), the materials were forced to mature earlier compared to Kitale (1890m a.s.l), hence the difference in the accumulation of photosynthates in the grains.

The general combining ability variances were not significant (except at Kakamega) indicating little role played by additive genes in the manifestation of this trait. Similarly non-additive variance played no role in the manifestation of this trait as reflected by diallel analysis. However, the generation mean anlysis revealed the presence of additive and non-additive components for some crosses. Williams et al. (1965) also noted non-additive variance components in maize. Environmental effects also influenced the combining ability performances of the crosses and the parents. Crosses A x 64 and F x 8 which were the best specific combinations at Soy and Sabwani were the poorest specific combinations at Kitale and Kakamega. This revealed that environment had influence in the performance of genotypes.

5.6 Kernel Row Number

In general the F_1 population had more kernel row number at most of the sites. the mean performance for kernel row number at the four sites (Table 23) do not show any considerable differences in kernel row number across the environments. Data from all the sites indicate that most of the ears had between 12 and 14 kernel rows. The general observation was that whenever grains were smaller the kernel row number tended to be greater.

The general combining ability effects were significant at all sites indicating the involvement of additive gene effects in the expression of this trait. Generation mean analysis also revealed additive variance for some of the crosses. With regard to individual epistatic genetic variances additive x dominance genetic variance made a contribution to the inheritance of kernel row number in the generation means studied, as shown by three crosses at Kitale and Soy.

Comstock (1955) had also noted the importance of epistasis for kernel row number in maize.

The mean kernel row number performance (Table 21) showed that the performance of F_1, F_2 and backcross populations were not considerably higher than the best parent. This could be the major reason behind the low and negative heterosis values. Low heterosis for this character could be due to the predominant genetic variation as indicated in this same study.

5.7 Lodging Percent

The results reveal that there was no consistency as to which populations were prone to lodging or resistant to lodging. The high lodging percentages at Kakamega and Soy could be due to the fact that the data was taken when most plots had been brought down by wind. Data on this trait should be taken more than once during the growing season to avoid over-estimation especially where wind has been involved.

Crosses with low specific combining ability estimates could be used to develop lodging resistant varieties. According to generation mean analysis three crosses exhibited significant additive genetic variance at Kitale and Kakamega. This is indicative of the involvement of additive genetic variance in the inheritance of this trait. Similar results were reported by ElRouby and Penny (1967). Results show that non-additive genes played a negligible role in the inheritance of this trait.

Heterosis was in most cases negative and this could be due to the fact that the inbred parents have been selected against lodging and any cross resulting from them should exhibit resistance to lodging.

5.8 Summary and Conclusions

1. The data in the present study indicated that both additive and dominance genetic variances were responsible for the manifestation of variability in the traits studied here. In most crosses and for all characters additive x additive and dominance x dominance genetic variances were also important contributors to inheritance.

2. The magnitude of genetic variance components varied with the environment, suggesting that such studies should be carried out in a wide range of environmental conditions.

3. The general combining ability effects were significant for most of the traits except grain yield, 200-grain weight and lodging percentage.

4. Among the parental cultivars inbred line F and inbred

line 64 appear to be the most promising for use in breeding for grain yield since they had high general combining abilities at most sites. These inbred lines also had high general combining ability values for ear length. Generally inbred line A was the poorest general combiner for most of the traits at all sites.

5. The crosses A x F and 8 x 64 which had high specific combining ability estimates for grain yield at Kitale and Sabwani and A x 8 and F x 64 which had high specific combining ability estimates at Kakamega and Soy could be used for further selection programmes.

6. The generation mean analysis was more effective in genetic variance components analysis than diallel analysis. However, the failure of diallel analysis to reveal the significance of variance components, especially non-additive components could be attributed to the lilmited number of parents used in the study.

7. Failure of diallel analysis to reveal significant genetic variation, particularly non-additive variation may also be attributable to the relationship among the lines, hence narrow diversity among them. Inbred lines A and F were originally developed from the same population. Similarly lines 8 and 64 could be related through their parental population, Kitale synthetic II. It is notable that even by generation mean analysis a number of crosses

did not show significant genetic variance components at some sites.

8. Results obtained in this study show that cross 8 x 64 was the most heterotic for plant height, ear height, grain yield and ear length at most of the sites. However, crosses A x F and F x 8 were the most heterotic for 200-grain weight and kernel row number respectively at most of the sites. These crosses could be used in further selection to improve the character in question. Heterosis was not consistent across the sites indicating environmental influence on the expression of heterosis. Heterosis should therefore be studied under a wide of environmental conditions.

5.9 RECOMMENDATIONS:

(a). Further studies should be carried out with a sufficient number of parents to give a good comparison of the diallel analysis and the generation mean analysis. The use of more parents will avoid pairing of crosses due to equal specific combining ability estimates.

(b). In order to have more valid estimates of the generation means, sufficient sampling of the generations is necessary in order to have a representative sample of genotypes. The experiments should be replicated over sites and years.

(c). It is necessary to have sufficient border rows in experimental plots to minimise competition effects of the adjacent plots.

(d). Double cross (A x 64) x (F x 8) could be improved as a potential hybrid variety. It could be improved by improving the parental lines.

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Appendix 1. Analysis of variance mean squares for yield and yield related traits in maize

Location	Source	df	Plant height	Ear height	Grain yield	Ear length	200-Grain weight	Kernel row number	Lodging %
Kitale	Total	83							
	Replicates	2	259.90	368.56	56.02	29.66**	110.66	0.13	2.54
	Treatments	27	4334.27**	2309.16**	1856.26**	13.58**	245.94**	1.08**	382.62**
	Error	54	219.15	135.55	90.21	1.22	50.13	0.22	67.07
Kakamega	Total	83							
	Replicates	2	478.10	64.43	52.06	9.64	42.06	1.58	1639.63**
	Treatments	27	12066.91**	2366.46**	571.67**	16.52**	201.36**	36.70**	761.90**
	Error	54	531.38	86.51	170.40	3.29	84.30	1.15	126.57
Soy	Total	83							
	Replicates	2	7205.40**	2974.65**	596.43**	34.23**	568.49**	0.98*	4189.17**
	Treatments	27	4144.08**	1797.93**	927.99**	12.32**	189.76**	0.89**	553.53
	Error	54	180.67	82.92	77.61	2.07	82.62	0.30	401.99
Sabwani	Total	83							
	Replicates	2	2183.60**	217.63	171.25	19.70**	290.76**	0.91*	77.35
	Treatments	27	4362.88**	1875.51**	1179.00**	18.51**	207.65**	1.63**	201.17**
	Error	54	130.23	87.81	117.60	1.11	38.90	0.24	91.92

*, ** - Significant 5% and 1% significance level respectively.

Appendix 2 — Mean monthly rainfall in millimetres recorded at the four experimental sites from January
September 1991

Site	Months								
	January	February	March	April	May	June	July	August	September
NARC-Kitale	68.6	13.5	130.0	128.5	152.0	129.1	187.1	195.1	46.6
WARC-Kakamega	129.3	86.8	203.0	196.6	469.3	95.2	92.7	210.2	118.6
Soy	97.7	13.9	170.5	109.5	17.94	208.0	237.2	207.9	65.9
Sabwani	59.4	22.4	92.10	66.5	181.8	127.9	177.3	145.2	33.2