DIALLEL ANALYSIS OF BARE TIP, HUSK LEAF NUMBER AND OTHER AGRONOMIC TRAITS IN MAIZE (*Zea mays* L.)

By

JENNIFER JEPKURUI CHUMO

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DECLARATION

This thesis is my original work and has not been presented for a degree in any other University.

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JENNIFER JEPKURUI CHUMO

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

Date 22nd July, 1986

DR. A.P. TYAGI
First Supervisor

Date July 31, 1986

DR. P.M. KIMANI
Second Supervisor

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Abstract

Maize (Zea mays L.) is the most important food crop in Kenya. It is consumed as roasted cobs and ground flour for making "Ugali", a staple food for over 50% of Kenya's population.

Although several hybrids and synthetic varieties are available for cultivation in Kenya, little effort has been made to study the genetics of yield and its components in local maize. The study was undertaken primarily to find out the genetics of yield and other economic traits such as bare tip in ears, which is directly associated with the quality of the maize while still in the field, and to suggest suitable breeding methods for further improvement of the yielding potential.

A diallel cross was made among six selected maize inbred lines. All 15 possible crosses (excluding reciprocals) and six parents were planted at two locations in Kitale, in a randomized block design with two replications during the 1985 rainy season. Normal agronomic practices were followed and data were recorded on twelve randomly selected plants for the following traits; bare tip ears (incomplete husk cover of ears),

ear husk leaf number, leaf number per plant, plant height, ear height (ear placement), kernel weight and grain yield. For days to pollen shed, the whole plot per entry was used to determine when 50% of the plants were shedding pollen.

Diallel analysis was carried out according to Hayman(1954ab) and Jones (1965). Both additive and dominance gene effects significantly influenced the inheritance of all the traits except grain yield. Dominance gene effects played a greater role than the additive effects in the expression of plant height, ear height, days to pollen shed, bare tip and husk leaf number, while additive effects were of major importance in the expression of leaf number and kernel weight. Dominance effects accounted for all the significant genetic variation in the inheritance of grain yield. Overdominance gene action was involved in the expression of all traits except leaf number and kernel weight whose expression was governed by partial dominance gene action. Symmetry of dominant and recessive allele distribution in the parents was indicated for kernel weight, days to pollen shed and bare tip traits, while for the other traits, asymmetry of allele distribution was suggested. Effective factors and gene or gene groups that

exhibited some degree of dominance in gene action were estimated. The effective factors ranged from one to six for the various traits and larger numbers of genes or gene groups than those of effective factors were obtained for most traits. High values of narrow and broad sense heritability were obtained for all traits (HNS = 46.6% - 84%, HBS = 67.5% - 97.3%) except for plant height, ear height and grain yield, for which low narrow sense heritability values (HNS = 1.1% - 17.9%) were obtained.

Progress under selection is possible for traits largely governed by additive gene action. However, better yielding hybrids can be obtained when parents which carry highest numbers of dominant alleles for yield and its components are used in crosses.

CHAPTER 1

INTRODUCTION

Maize (Zea mays L.) is the staple food for majority of Kenyans, (Ministry of Agriculture Development Plan 1979 - 1983; Gerhart 1975). Formal maize breeding work in Kenya begun in 1955, (Gerhart, 1975, Leakey, 1970). Maize has progressively established itself as a cash crop. It is grown by small scale farmers mainly for food and the surplus for sale, while the large scale farmers grow it primarily for sale.

Grain yield in maize depends on the genotype of the plant and its interaction with environmental factors such as soil, climate, pests, pathogens and cultural practices. Thus grain yield of a high yielding maize variety can be reduced considerably by pest and/or disease damage on leaves, stalk and ears.

Pests and pathogens can play a considerable role in reducing the yield of an otherwise high yielding variety by damaging the stalk, leaves and ears.

In maize, ear husk leaves protect the ovules, the developing and mature grains from pest, pathogen entry and water seepage into the ear. In a number of

commercial hybrids grown in Kenya, such as H 613, H 632 and H511 a considerable proportion of the ears are bare tipped. This is an undesirable trait as the short husks (shorter than the cob) fail to protect the ear from water seapage, pest and pathogen entry, leading to rotten and diseased ears and a reduction in the number of usable ears.

In breeding work, efforts are made through selection to develop a variety or varieties adoptable to a certain set of climatic conditions. Plant traits such as plant height, ear height, leaf number per plant, days to pollen shed and yield of grain also are considered.

Maximum yields are realized when the maize variety in a given environment is able to take full advantage of the growing season and complete grain filling at the end of the season. The vegetative growth contributes considerably to the final yield. Grain yield was found to be associated with plant height and ear height (Thompson, 1982). Moll et al. (1975) reported an optimum ear height for maximum grain yield. The top five leaves contributed about 40% of the plant productivity while the middle and bottom leaves contributed 35% to 40% and 5% to 25% of the total productivity, respectively, (Allison and

Watson, 1966). The upper $\frac{2}{3}$ of the maize canopy was found to contribute substantially to the productivity of the grain (Zelitch, 1971).

Maize is very sensitive to moisture stress. Moisture availability is critical during ear size determination and grain filling period. Moisture stress during this period will lead to reduction in grain yield (Aldrich et al. 1978). In a given environment therefore, the maize variety grown must reach anthesis early enough in the season so that grain filling is completed before the rains stop.

Knowledge of the gene action governing the expression of the traits that influence grain yield in Kenya's varieties is essential in planning breeding programs. The study was therefore undertaken to determine the nature of inheritance of bare tip characters, yield and yield components, and how these traits can be improved in a breeding program.

CHAPTER 2

LITERATURE REVIEW

Grain yield in maize is related to several plant traits and their interaction with the environment. Grain yield is determined by the genotype of a maize plant but is influenced in varying degrees by environmental factors such as climatic conditions, soil type and fertility level, pest and pathogens and inter and intra-species competition.

In order to realize high grain yields, each of the plant traits that influence yield must be improved through breeding procedures, to its optimum efficiency level. Positive and negative correlations between the traits should be considered in the breeding procedures so that the best compromise for each trait as determined by its contribution to grain yield is chosen.

2:1 Bare tip trait and ear husk leaf number.

Ear husk leaves play a protective role in ear development. They ensure the right environment for pollination, pollen tube growth down the style and

fertilization. The developing grain is then protected from adverse environmental effects such as pests and pathogens which upon entry into the ear would cause damage and diseases resulting in reduction of usable grain. Collins and Kempton (1917), Eden (1952) and Cameron and Anderson (1966) reported a negative correlation between husk leaf extension and earworm damage. Brewbaker and Kim (1979), in a study of highland and lowland maize types found the lowland maize types had more husk leaves and were more resistant to weevil damage than highland maize types. They reported a negative correlation ($r = -0.40$) between husk leaf number and earworm damage.

Ear husk tightness seemed to contribute more to the reduction of earworm damage than did ear husk extension, so long as the husks extended far enough to cover the tip of the ear (Starks and McMillian, 1967). Douglas (1947) concluded that a two to three inch extension beyond the tip of the ear was adequate to confer resistance to the ear against earworm damage, but suggested that ear husk extension of more than three inches beyond the tip of the ear may be necessary for resistance to other pests such as birds and weevils. Moderate extension of husk leaves

beyond the tip of the ear and tightness of the husks were suggested as desirable (Douglas, 1947). Poole (1940) however found no correlation between earworm damage and husk extension.

Breeding for earworm resistance in maize, using recurrent selection method showed a decline after the third and fourth cycles of selection (Widstrom et al.,1970). A redefinition of the earworm damage measurement and use of a more susceptible tester or S_1 family selection per se was suggested. Zuber et al. (1971) found mass selection for resistance to earworm damage in two maize synthetics to be effective. He reported a 22.1% reduction in earworm damage after eight cycles of selection in synthetic C and 25.3% after nine cycles in synthetic S. Using different selection indexes, Widstrom et al. (1982). reported progress in resistance to earworm damage in the first cycle of selection and a decline in progress thereafter.

Robinson et al. (1949) reported heritability values of 49.5% and 35.9% for husk extension and husk score respectively. They also suggested complete dominance for husk extension and partial to complete dominance for husk score.

Husk leaves have also been reported to carry out photosynthesis. Hesketh and Musgrave (1962) found that the rate of photosynthesis of ear and normal leaves was the same. Jain (1971) found that the ear husk leaves were the most efficient photosynthetically, contributing 15% of the dry matter of the ear. Allison and Watson (1966) found that the ear husk leaves made negligible contribution to grain yield as compared to normal leaves. Husk leaves may significantly contribute to grain yield when some photosynthetic leaf area is lost in the process of detasseling during seed production, (Cantrell and Geadelman, 1981). The authors concluded that the contribution of husk leaves to grain yield was small but significant. Rasmusson and Crookston (1977), working on barley found that multiple awned lines yielded less than single awned lines. The reduction in yield was attributed to partitioning of photosynthates between the grains and the awns.

Cantrell and Geadelman (1981), reported that the mode of gene action controlling the inheritance of husk leaf area was quantitative and suggested that improvement of this trait through standard maize breeding procedures should be effective. Dominance and epistasis gene actions were suggested

to be responsible for the expression of the observed heterosis for high husk leaf area, while partially dominant genes favoured low husk leaf area.

General combining ability (gca) mean squares for husk leaf number were highly significant at Hawaii and Colombia locations (Brewbaker and Kim, 1979). Specific combining ability (sca) values were also significant but were exceeded by gca effects by a ratio of 5:1 and 20:1 in Hawaii and Colombia, respectively, (Brewbaker and Kim, 1979). These results suggest that additive gene effects are important in the inheritance of husk leaf number.

Brewbaker and Kim (1979) reported heterosis of 11% in the hybrids and a low heritability value (24%) for husk leaf number.

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2:2 Leaf number per plant

Leaves are the most important photosynthetic organs on the plant. Leaf number per plant increases with increasing plant height (Allen et al., 1973; Cross and Stuber, 1973; Rood and Major, 1981). With increasing leaf number, there was an increase in the leaf area index (LAI). Yield increases with increasing leaf area index (LAI) up to an optimum level beyond which additional LAI is counter productive. Rutger et al. (1971) reported a small but significant linear relationship between grain yield and leaf area index. Williams et al. (1965) reported a reduction in grain yield for leaf area index close to six. Removal of tassel and top leaf resulted in a 25% increase in grain yield at high plant density (89,000 plants ha^{-1}) while an increase in grain yield of 17% was realized when the tassel and top three leaves were removed, (Hunter et al., 1969). Smith and Colville (1967) reported a 77.8% and 69.2% yield of the check hybrid when all leaf tissue below and above the ear, respectively, were removed. The top five leaves contributed about 40% of the productivity of the maize plant, while the middle and bottom leaves contributed 35% to 40% and 5% to 25% of the total productivity of the plant, respectively,

(Allison and Watson, 1966).

Leaf number inheritance in field beans was found to be controlled by dominant gene effects while leaf size was found to be under the control of additive gene action, (Duarte and Adams, 1963). In maize, additive gene action, with complete dominance was found to control leaf number (Rood and Major, 1981). Russell and Stuber, (1985) suggested that general combining ability (additive gene action) was more important that specific combining ability (non additive gene action) in the expression of leaf number per plant in maize. Bonaparte, (1977) in a diallel analysis found that leaf number expression showed partial dominance. A similar finding was reported by Leng, (1951). Additive effects accounted for a bigger proportion than dominance effects in the expression of this trait. Both narrow and broad sense heritability values (95.6, 97.2) for this trait were high, (Bonaparte, 1977).

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2:3 Days from planting to pollen shed.

The period it takes a given variety of maize from planting to pollen shed determines how much stalk and leaf area develops before the onset of the reproductive phase. Climate plays a major role in determining this period. Days from planting to silking was found to be positively correlated ($r = 0.86$) with yield (Troyer and Hallauer, 1968). Mulamba et al. (1983) reported an association between days to flowering and grain yield. Troyer and Brown (1976) however reported no relationship ($r = 0.01$) between flowering date and yield, in one season and a negative correlation ($r = -0.87$) between these two traits in a second season.

Two maize inbreds which differed in the duration from planting to pollen shed took approximately the same period (about two months) to complete grain filling (Hallauer and Russell, 1962).

Heterosis for earliness in maize was reported by several workers (Yang, 1949; Leng, 1951; Bonaparte 1977). Epistasis influenced the expression of flowering in corn (Giesbrecht, 1959). Both additive and dominance gene effects also were reported to govern the expression of flowering in corn (Bonaparte, 1977; Rood and Major, 1980). This finding was however not

supported by the results of Giesbrecht (1959) who suggested that partial dominance governed earliness in corn. On the other hand, additive gene effects were attributed to largely govern days to silk in maize (Kimani and Drolsom, (in Press).

High heritability values of 56.6%, 68.7% (narrow sense) and 68.8%, and 89.0% (broad sense) for days from planting to flowering were reported by Giesbrecht (1959) and Rood and Major (1980), respectively. These values indicate that selection for earliness in corn is possible.

Asymmetry in the distribution of dominant and recessive alleles in the parents of a diallel analysis in pearl millet was suggested by Phul et al. (1970). In sorghum a similar finding was reported by Chiang and Smith (1967). Giesbrecht (1959) reported that at least five factors govern days to pollen shed in corn. A minimum of three gene pairs were reported responsible for the expression of the period between planting and pollen shed (Mohamed, 1959). One effective factor was advanced to govern flowering time in grain sorghum, by Chiang and Smith (1967).

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2:4 Plant height and ear height.

The maize stalk supports the leaves and ears apart from carrying out other functions such as transport of assimilates, nutrients and photosynthesis. A tall maize variety develops considerable vegetative growth, mainly in the form of leaves, which play a major role in determining grain yield, while a short variety would have less of this vegetative growth. Plant height is thus positively correlated ($r = 0.60$, $r = 0.71$) with leaf area and number of leaves per plant (Allen et al., 1973). Yield in maize was found to be positively correlated ($r = 0.20$) with plant height (Jenkins, 1929). Thomson (1982) and Mulamba et al. (1983) reported an association between plant height and yield in maize. Eckebil et al. (1977) reported a positive correlation ($r = .71$) between plant height and yield in sorghum.

Russell and Eberhart (1970) reported that additive gene action played a bigger role as compared to other forms of gene action, in the determination of plant height in maize. Similar results were reported by Castro et al. (1968), and Cornelius and Dudley (1976). Chiang and Smith (1967) working in sorghum found additive gene action to be

largely responsible for the expression of plant height.

Overdominance was however found to control the expression of plant height in maize (Bauman, 1959; Rood and Major, 1981), and sorghum (Liang and Walter, 1968). The apparent overdominance may have resulted from gene linkage (Liang and Walter, 1968). Duarte and Adams (1963) and Sinha and Khanna (1975) pointed out that apparent overdominance for a given trait could result from multiplicative effects of components that individually show partial or complete dominance. Epistasis was reported by Gamble (1962b) to play a major role in the determination of plant height in maize. Dominance x dominance gene interaction had a diminishing effect on plant height while dominance x additive and additive x additive gene interaction had an increasing effect on plant height.

Although partial dominance and dominance were reported by Yang (1949) and Gamble (1962b), respectively, to play a major role in the expression of plant height in maize, Robinson et al. (1949) found little or no dominance for genes that control the expression of plant height.

Whereas Robinson et al. (1949) reported a high heritability value (70.1%) for plant height, Rood and Major (1981) reported a low heritability value (11.5%) for plant height. A low (4.7%) and moderately high(36%) narrow sense heritability values for plant height in sorghum were reported by Chiang and Smith (1967) and Ibrahim et al. (1985), respectively.

At least two effective factors were reported to control plant height expression in sorghum, (Chiang and Smith, 1967). The authors also reported asymmetry of allele distribution in the parents for this trait.

Ear height was found to be positively associated with grain yield in maize (Thomson, 1982; Mulamba et al., 1983). Acosta and Crane (1972) found an associated response between ear height and grain yield in maize. Selection for lower ear height resulted in a 4.7% reduction in yield in cycle two and 19.7% and 30.5% yield reduction in cycles three and four, respectively, (Acosta and Crane, 1972). Moll et al. (1975) reported a non-linear relationship between ear height and grain yield, whereby the optimum ear height for maximum grain yield was found to range between 116 cm and 129cm. Seven cycles

of selection for lower plant height resulted in a reduction of ear height and grain yield from 155 cm to 143 cm and 67 q/ha to 64 q/ha respectively. In the same study, lodging percentage was reduced from 59% to 22% (Thompson, 1982). Acosta and Crane, (1972) found in one population, an increase in lodging when selection for lower ear height was effected while in second population the opposite was true. Effective selection for lower ear height has been reported by Acosta and Crane (1972). Acosta and Crane (1972) reported a 24% ear height reduction after four cycles of selection for lower ear height. Selection for lower ear height in maize using recurrent selection for seven cycles resulted in a yield increase of 18%, a 9% reduction in ear height and 35% less lodging (Horner et al., 1976). Vera and Crane (1970) found a slight reduction in yield and a considerable reduction in lodging when ear height in maize was reduced through selection. The changes observed for yield and lodging were however not significant (Vera and Crane, 1970). Troyer and Hallauer (1968) reported a 15% heterosis in ear height in crosses as compared to the varieties.

Additive gene effects were reported to play a major role in the expression of ear height in maize (Castro et al., 1968, Cornelius and Dudley, 1976). Robinson et al. (1949) reported no dominance involvement in the expression of ear height in maize. Dominance gene action was however reported to play a major role in the expression of ear height in maize (Giesbrecht, 1961; Kimani and Drolsom, in press).

Both dominance and additive gene effects were reported by Thompson et al. (1971) to be important in the inheritance of ear height in maize, although the dominant gene effects were several times greater than the additive gene effects. Epistatic gene effects also were found to significantly influence ear height expression in some of the hybrids.

The number of effective factors for ear height were reported to range from four to seven by Giesbrecht (1961).

High narrow sense heritability values (58.9%, 71.2%) for ear height were reported by Giesbrecht (1961), while Robinson et al. (1949) reported a low narrow sense heritability value 14.1% for ear height.

2:5 Kernel weight and grain yield

Large sinks are necessary for high grain yields to be realized. They influence the rate of assimilate translocation from the source (Hahn, 1977). The source of the assimilates; the effective leaf area index (LAI) should be large in order that high yields can be realized. Grain yield is thus correlated to the effective leaf area index. Leaf area index is determined by leaf size and the number of leaves on the plant, while in most cases leaf number is determined by plant height.

Grain yield in maize is determined by a number of yield components; ears per plant, rows per ear, kernels per row and kernel weight. The weight per kernel is determined by the rate and duration of grain filling (Johnson and Tanner, 1972; Frey, 1981). Poneleit and Egli (1979) reported a reduction in kernel size and grain yield when the grain filling period was reduced by 2.5 days.

Heterosis for grain yield in maize has been reported by several workers. Johnson (1973) reported heterosis for grain yield in crosses between high kernel row number and high kernel weight varieties of maize. Gerrish (1983) reported

heterosis for grain yield in varietal crosses of maize. The range of 111% to 117% and 112% to 115% heterosis were reported in crosses of dent corn varieties and crosses between dent corn and Carribean and Mexican varieties, respectively. An average heterosis of 11% was reported by Hallauer and Eberhart (1966) in crosses between maize synthetic varieties.

More heterosis was observed when crosses of unrelated maize varieties were made and evaluated (Moll et al., 1962). Heterosis for increased grain yield (128%) was realized in crosses between unrelated maize varieties and relatively low heterosis (86%) was obtained in crosses of related varieties (Moll et al., 1962). Similar results were obtained by Moreno-Gonzalez and Dudley (1981). Heterotic responses of 105% for grain yield in a varietal cross between two open pollinated varieties of maize was reported by Robinson and Cockerham (1961); while Castro et al. (1968) obtained results that indicated that 5.1% of the total genetic variation was due to heterosis. A 71% heterosis relative to mid-parental value was reported by Troyer and Hallauer (1968).

Additive gene action was reported to contribute little in the inheritance of grain yield in maize (Gamble, 1962a; and Russel and Eberhart, 1970). Results obtained by Mason and Zuber (1976) and Kimani and Drolsom (in press) indicated a predominant additive gene action for grain yield expression. Results obtained by Gamble (1962a) and Russel and Eberhart (1970) indicate a predominant dominance gene effects in the expression of grain yield. Both dominance and additive gene effects were found to contribute significantly in the expression of grain yield in maize, although dominance gene effects contributed more (52.4% of the total genetic variation) than additive gene effects (39.2% of the total genetic variation); Castro et al., 1968). Dominance effects contributed more than additive gene effects in the expression of grain yield according to the results obtained by Gamble (1962a); Darrah and Hallauer (1972); Johnson (1973); Cornelius and Dudley (1976) and Moreno-Gonzalez and Dudley (1981). Partial dominance gene action was reported by Lonnquist (1953) to be important in the expression of grain yield in maize. Complete dominance to overdominance gene action was reported by Hallauer (1970) to govern the expression of grain yield in maize

Overdominant gene action was reported to influence the expression of grain yield in maize, although this overdominance was suspected to have resulted from linked loci which otherwise show partial to complete dominance gene action (Cornelius and Dudley, 1976). Overdominance gene action was also reported by Robinson et al. (1949) to account for grain yield realization in maize, although again it was pointed out that the observed overdominance could have been due to high linkage of certain genes in the repulsion phase, which had not broken in only one generation of random mating. Gardner and Lonnquist (1959) also reported the presence of overdominance in F2 and larger additive effects in F8 than in F2. They suggested the observed overdominance in F2 could be due to linkage of loci involved in the expression of grain yield. Grafius (1959) found no correlation between the genes controlling grain yield components in barley and suggested that there might not be genes for grain yield. Extrapolating his findings on barley, Grafius (1960) questioned the validity of overdominance gene action for grain yield in maize. Mean epistasis over all crosses was found to contribute significantly to the expression of grain

yield in maize (Moreno-Gonzalez and Dudley, 1981). Although no evidence of epistatic gene interaction was suggested by the results of Robinson and Cockerham (1961) its presence in the determination of grain yield could not be ruled out either. Allard (1956) and Jana (1975) reported that inter-allelic gene effects often influence the estimation of genetic components. Epistasis of the types, additive x additive, and additive x dominance were more important than dominance x dominance gene interaction in the expression of grain yield in maize (Gamble, 1962a). Seasonal and environmental differences have been reported to influence the genetic expression of certain traits (Allard, 1956; Paroda and Hayes, 1971; and Riggs and Hayter, 1972). Specific combining ability variances were found to be more variable than general combining ability variance hence the need to have more sites for an evaluation when specific combining ability effects were involved in the expression of a given trait (Spragne, 1955).

A low heritability value of 20.1% for grain yield in maize was reported by Robinson et al. (1949). High heritability values of 79% and 76% for grain yield in sorghum were reported by Eckebil et al. (1977) and Lothrop et al. (1985), respectively.

Additive gene effects were reported to play a major role in the determination of kernel weight in high amylose corn (Helms et al., 1971). Several other research workers (Johnson, 1973; Cornelius and Dudly, 1976; Kimani and Drolsom, in press) have reported similar findings for the expression of kernel weight in maize.

Both additive and dominance gene effects were reported by Darrah and Hallauer (1972) to contribute more or less equally in the expression of kernel weight in maize, while complete dominance and partial dominance were reported by Hallauer and Russell (1962) and Cornelius and Dudley (1976), respectively, to govern the expression of kernel weight in maize. Russell and Eberhart (1970) obtained additive gene effects values that were twice the dominant gene effects, in the expression of kernel weight in maize.

High heritability values (74%, 82%) for kernel weight in sorghum were reported by Lothrop et al. (1985).

Asymmetry of positive and negative allele distribution in the parents, in sorghum was reported by Chiang and Smith (1967).

CHAPTER 3

MATERIALS AND METHODS

3:1 Materials

Six maize inbred lines developed at Kitale Research Station were used in the present study. Three of these inbreds; A, F, and G were derived from Kenya Flat White Complex population while the other three inbreds; 100, 50 and 93 were developed from an exotic open pollinated population;- Ecuador 573. For purposes of discussing the results, the six inbred lines were designated as follows:

G - array 1
F - array 2
A - array 3
100 - array 4
50 - array 5
93 - array 6

3:2 Diallel cross

Three exotic inbred lines were planted in a crossing block at Faculty of Agriculture field station on August 15, 1984. The local inbred lines were planted two weeks later, on August 31, 1984.

The purpose of the crossing block was to raise F1 hybrid seed and to increase parental seed. Spacing between and within the rows was 75 cm and 30 cm, respectively. Rows of 20 hills were overplanted and later thinned to two plants at the end hills and one plant per hill in the inner hills. Diammonium phosphate (DAP) was applied at the rate of 173 kg DAP per hectare (80 kg P_2O_5 per hectare and 31 kg Nitrogen per hectare). Ammonium sulphate nitrate (ASN) was top dressed at the rate of 80 kg Nitrogen per hectare . One hand weeding and two spot weedings effectively controlled the weeds. Parents of intended crosses were grown adjacent to one another to ease the pollination process. Apart from supplying pollen for the female rows, the male rows were also selfed to increase parental seed. Prior to silking, ear shoots were covered and later pollinated.

3:3 Field evaluation trial

The evaluation trial was conducted at three sites; the National Agricultural Research Station, Kitale, and at two Agricultural Development Corporation (ADC) farms; Sabwani and Jabali. The approximate location of this region is 1^{o}N and 34^{o}E.

It receives between 750 mm and 1250 mm of rainfall/year, spread between March and September. The altitude is about 1890 metres above sea level. Soils are of brown friable clays to sandy clays which are well drained, deep to moderately deep. Although the trial was conducted at three sites, the results reported in this thesis are those of ADC Sabwani and Jabali farms only. In both locations, Sabwani and Jabali, the fields had been cropped with maize the previous season. Rains started on March 19, 1985 and the evaluation trials were planted on March 27 and 28, 1985 at Sabwani and Jabali, respectively.

A randomized complete block design with two replications was used. A plot had four rows with 11 hills each. Plants were spaced 30 cm within rows and 75 cm between rows. Plots were overplanted and later thinned to 44,444 plants ha^{-1}. An alley of 90 cm separated the two replications in each location and four guard rows sorrounded each trial. At planting, diammonium phosphate (DAP) was applied at the rate of 80 kg P_2O_5 and 31 kg 'N'/ha. Furadan granules were placed at each hill during planting to reduce pest damage during germination and early growth. One hand weeding and

one spot weeding adequately controlled weeds. After six weeks from planting, the trials were sidedressed with calcium ammonium nitrate (CAN) at the rate of 100 kg N /ha.

3:4 Data collection

Data were collected on twelve randomly selected plants in each plot. Data on the following traits were collected; leaf number per plant, days from planting to pollen shed, plant height, ear height, bare tipped ears, ear husk leaf number, kernel weight and grain yield. For all traits except days to pollen shed, the central two rows were used for the purpose of data collection. The whole plot (four rows) was used to collect data on days to pollen shed.

3:4:1 Leaf number per plant

The fourth leaf in a random sample of twelve plants in the central two rows was marked with wax pencil. Labels were later tied round the plants, above the eighth leaf for determination of the total leaf number per plant when the lower leaves have senesced. Total leaf score per plant was determined shortly after pollen shed.

3:4:2 Days from planting to pollen shed.

Days from planting to pollen shed were scored when 50 per cent of the plants in each plot were shedding pollen.

3:4:3 Plant height

Plant height in cm was measured from the ground to the tip of the tassel in each of 12 plants per plot.

3:4:4 Ear height

Ear height (ear placement) was measured in cm from the ground to the node bearing the ear or the uppermost ear in each of the randomly selected plants per plot.

3:4:5 Bare tip ears

Harvesting was done when the black layer formation had developed in the grain. This was checked 65 days after the latest variety shed pollen. The ears of the labelled plants were harvested carefully making sure that the ears were removed at the node with all its husk leaves intact. Any loose outer husk leaves were secured on the ear with rubber bands. The ears of the twelve harvested plants were then scored for bare tip trait.

3:4:6 Ear husk leaf number

The husk leaves of each of the harvested ears were counted and recorded.

3:4:7 Kernel weight

A sample of 500 kernels per plot was weighed and adjusted to 12.5 percent moisture content.

3:4:8 Grain yield

The harvested ears of each plot were sun dried, shelled and weighed. Grain moisture content was determined on two samples per plot. The weight per plot of harvested grain was then adjusted to 12.5 per cent moisture content.

3:5 Statistical analysis and estimation of genetic components.

3:5:1 Analysis of variance

Preliminary analysis of variance on the data was carried out to determine if there were significant differences among the treatments for the traits scored.

3:5:2 Estimation of genetic components

When the test indicated significant differences among treatments, a diallel analysis of variance, (Hayman, 1954a) as modified by Jones, (1965) was carried out to estimate the various genetic components. Hayman's, (1954a) model estimates additive and dominant genetic components and also differences that may exist between the F1 hybrids and their reciprocals.

The Hayman 1954a model can be represented as:

$$Yrs = m + jr + js + 1 + 1r + 1s + 1rs + Kr - Ks + Krs \quad (r \neq s)$$

$$Yr = m + 2jr - (n-1)\ 1 - (n-2)\ 1r \text{ (for yrr)}$$

where:

m = mean response level

jr = additive contribution of the i^{th} line
= average dominance deviation

1r = additional dominance deviation due to the i^{th} line.

kr = differences between the effects of the i^{th} parent line used as male.

ks = differences between the effects of the i^{th} parent used as female.

yrs = entry in the r^{th} row and S^{th} column

yr = r^{th} parent (line).

Hayman (1954b) model for the estimation of genetic variances assumes:,

(i) Diploid segregation of chromosomes.

(ii) Independent action of non allelic genes in the diallel cross.

(iii) No multiple allelism

(iv) Homozygous parents

(v) Genes are distributed independently between the parents.

(vi) No reciprocal differences.

Whether a data set satisfies these assumptions is determined by the analysis of 'Wr/Vr' variance, (where Vr represents the variance of the r^{th} array and Wr represents the covariance between the parents and their offspring in the r^{th} array) and regression coefficient 'b'. Wr - Vr analysis of variance is presented in Table 1.

Table 1. Analysis of variance of Wr - Vr

Source of variation	Degrees of freedom (df)	Mean sums of squares (ms)
Total	T-1	$\sum_{ij}\sum(X_{ij}-\bar{X}..)^2/T-1$
Blocks	b-1	$b\sum_{i}(\bar{X}_{i.}-\bar{X}..)^2/b-1$
Lines	L-1	$L\sum_{j}(\bar{X}.-\bar{X}..)^2/L-1$
Error	(T-1)-(b-1)-(L-1) (=e)	$\{\sum_{i}\sum_{j}(X_{ij}-\bar{X}..)^2-b\sum(\bar{X}i.-\bar{X}..)^2 -\sum_{j}(\bar{X}._{j}-\bar{X}..)^2\}/e-1$

Estimation of components of genetic variation Table 2 was executed when the data fitted the assumptions postulated by Hayman (1954b).

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Table 2. Analysis of variance of genetic components

Source of variation	Degrees of freedom (df)	Mean sum of squares (ms)
a	n-1	$\Sigma(y_{r.}+y_{.r})^2/2n-2y^2_{..}/n^2$
b1	1	$(y_{..}-ny_{.})^2/n^2(n-1)$
b2	n-1	$\Sigma(y_{r.}+y_{.r}-ny_{r})^2/n(n-2)-(2y_{..}-n)^2/n^2(n-2)$
b3	$\frac{1}{2}n(n-3)$	$(y_{rs}+y_{rs})^2/4-\Sigma y^2_{r}-y(y_{r.}+y_{.r}-2r)^2/2(n-2)+(y_{..}-y_{.})^2/(n-1)(n-2)$
b	$\frac{1}{2}n(n-1)$	$\Sigma(y_{rs}+y_{rs})/4-\Sigma(y_{r.}+y_{.r})^2/2n+..^2/n^2$
Treatments (tr)	tr-1	
Blocks (B)	b-1	
Ba	(B-1)(n-1)	
Bb1	(B-1)(1)	
Bb2	(B-1)(n-1)	
Bb3	(B-1)($\frac{1}{2}$n(n-3)	
Btr	(B-1)(tr-1)	

Table 2. Cont.

Where;

a = measure of general combining ability.

b = measure of specific combining ability.

b1 = mean dominance deviation

b2 = further dominance deviation due to the i^{th} parent.

tr = treatments

B = Blocks (replications)

3:5:2 The variance of each array and the covariance between parents and their offspring for every array (Wr) were analysed and used to draw the Wr/Vr graph. The graph indicated the nature of dominance, whether no dominance, partial dominance, complete or overdominance prevailed for a given trait. The position of the parents along the (Wr, Vr) line revealed the relative proportions of dominant and recessive alleles in the parents. Estimation of the following genetic components was performed.

D

F

H1

H2

h2

H1/D

H2/4H1

$h^2/H2$

$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$

K

h^2

where,

D = additive genetic variance

H1 and H2 = dominance genetic variance

F = The mean of the covariance of additive and dominance effects over all arrays.

h2 = dominance effect (as the algebric sum over all loci in the heterozygous phase in all crosses).

$(H1/D)^{0.5}$ = average degree of dominance.

H2/4H1 = mean value of Ui Vi at all loci exhibiting dominance.

$h^2/H2$ = Number of groups of genes which exhibit some dominance in the control of the trait.

$(4DH1)^{0.5}$ + F/ $(4DH1)^{0.5}$ - F = Total ratio of dominant to recessive genes (alleles) in all the parents.

K = The number of effective factors in the expression of a particular trait.

h^2 = heritability; narrow sense (NS) and broad sense (BS).

1. A bare tipped ear of inbred G, taken in location II (Jabali), 1985.

CHAPTER 4

RESULTS

Mean values of parents and crosses.

Mean phenotypic values of bare tipped ears, husk leaf number, leaf number, days to pollen shed, plant height, ear height, kernel weight and grain yield are presented in Table 3 and 4, for Sabwani and Jabali sites respectively. The analysis of variance for all these traits indicated significant differences between the inbreds and the hybrids (Appendix I).

4:1 Bare tip and husk leaf number.

4:1:1 Bare tip trait

Bare tip scores were greater in the hybrids than in the parents for both Sabwani (location I) and Jabali (location II) sites, (Tables 3 and 4). The range of bare tip score in the parents was from 0.0 to 5.5 and 0.0 to 6.5 in location I and II, respectively. In both locations, inbred G was found to have the highest number of bare tip ears (5.5 and 6.5), (Table 3 and 4), among the parents. The

local inbreds (G, F and A) had highest bare tip scores relative to the exotic inbreds (100, 50 and 93). This was true for both locations (Table 3 and 4). The range of bare tip scores among the hybrids was from 0.0 to 13.5 in location I (Table 3) and from 0.0 to 13 in location II (Table 4). The hybrids which had inbred G as one of the parents had proportionately higher bare tip scores compared to the other hybrids. This was found to be true at both locations (Table 3 and 4). The crosses of exotic inbred lines had the lowest bare tip scores in both locations (Table 3 and 4). The progeny showed considerable heterosis at the two locations for this trait (Table 3 and 4).

The results of the analysis of variance of Wr-Vr for bare tip are presented in Appendix II. There was no significant difference between the lines. Regression coefficient 'b' values of 0.539 and 0.634 (Figure 1 and 2) differed significantly from zero but not from unity for both locations, respectively. Consistency of Wr-Vr differences over arrays and the nonsignificant variation of 'b' from unity indicated that the data fitted the additive - dominance model. Bartlett's test of heterogeneity of variances gave nonsignificant X^2

Table 3. Mean performance of parents and single cross hybrids (F1) for bare tip and other agronomic traits in location I (Sabwani) in 1985 season.

Entry	Trait							
	Bare tip	Husk leaf number	Leaf number	Day to pollen shed	Plant height (cm)	Ear height (cm)	500 Kernel weight (g)	Grain yield $Kgha^{-1}$
G	5.5	9.2	21.7	112.0	225.8	115.2	110.0	1481.5
F	3.5	10.9	22.3	104.5	267.0	132.3	154.5	2222.2
A	1.5	7.3	21.4	103.5	250.2	133.3	150.0	2222.2
100	0.5	9.2	23.7	117.5	293.2	162.1	114.8	4074.0
50	0	9.2	22.6	117.5	288.6	172.7	108.5	2592.6
93	0	9.7	23.7	118.0	275.4	150.0	99.9	2592.6
GXF	10.5	10.6	22.0	104.0	327.5	176.8	122.1	4814.8
GXA	8.5	9.2	21.9	101.0	321.3	168.8	138.8	5555.5
GX100	9.0	11.4	23.0	104.0	355.3	204.9	110.4	6296.2
GX 50	8.5	10.6	23.2	103.0	345.3	195.9	123.9	6666.6
GX 93	13.5	10.8	23.5	102.5	368.0	214.9	132.8	6296.2

Table 3. Cont.

Entry	Bare tip	Husk leaf number	Leaf number	Day to pollen shed	Plant height (cm)	Ear height (cm)	500 Kernel weight (g)	Grain yield $Kgha^{-1}$
F X A	1.5	10.4	22.1	100.0	340.0	181.1	143.5	6296.2
F X100	3.0	9.9	23.3	104.5	359.6	205.9	137.3	6296.2
F X50	1.5	10.0	23.4	101.5	385.3	231.1	142.8	6666.6
F X93	8.0	10.5	23.4	102.5	378.4	223.6	149.9	7407.3
A X 100	0.5	9.6	22.9	101.0	354.9	192.9	144.2	5925.9
A X 50	0	8.8	23.1	100.5	362.0	218.0	139.0	7037.0
A X 93	3.0	9.2	23.3	100.0	357.9	206.5	142.1	6666.6
100X50	2.5	10.5	24.2	112.0	348.9	207.3	127.8	6296.2
100X93	0	10.3	24.1	110.5	346.3	197.7	113.5	4814.8
50X93	1.0	9.6	24.1	113.0	327.1	192.3	102.4	4074.0

Table 3. Cont.

Entry	Bare tip	Husk leaf number	Leaf number	Day to pollen shed	Plant height (cm)	Ear height (cm)	500 Kernel weight (g)	Grain yield $Kgha^{-1}$
Mean	3.90	9.85	23.0	106.33	327.52	184.92	128.96	5061.68
SE($\bar{X}$)	1.311	0.285	0.254	1.918	13.617	9.839	5.258	0.154
C.V. %	31.7	6.4	1.4	1.6	4.6	5.3	6.4	2.3
$\bar{F}1$	4.73	10.09	23.17	104.00	351.85	201.18	131.37	7286.35
$\bar{P}1$	1.25	9.25	22.57	112.17	266.70	144.27	122.95	2530.85

Where; $\bar{F}1$ = Mean of the single cross hybrids

$\bar{P}1$ = Mean of the inbred lines (parents)

Table 4. Mean performance of parents and single cross hybrids (F1) for bare tip and other agronomic traits in location II (Jabali) in 1985 season

Entry	Trait							
	Bare tip	Husk leaf number	Leaf number	Days to pollen shed	Plant height (cm)	Ear height (cm)	Kernel weight (g)	Grain yield Kg ha^{-1}
G	6.5	10.1	21.9	110.0	245.3	126.9	116.6	1481.5
F	3.5	12.8	22.4	103.5	290.9	147.3	181.0	4814.8
A	1.0	8.2	21.2	102.0	247.4	130.4	175.8	4444.4
100	0.5	9.9	24.2	111.0	302.4	192.4	153.0	4814.8
50	0	9.7	24.0	115.5	286.8	178.7	119.3	3333.3
93	0	10.2	23.9	114.5	287.2	165.3	126.0	3333.3
GXF	12.5	11.2	22.1	100.0	358.9	192.3	151.6	6296.2
GXA	9.0	9.1	22.2	99.5	343.1	177.7	173.5	8888.8
GX100	13.0	10.3	23.2	101.0	379.3	224.3	135.5	6666.6
GX50	11.0	11.1	23.3	102.5	373.0	217.0	152.5	8518.4
GX93	8.5	11.4	23.7	102.0	380.7	218.4	137.0	12,222.1

Table 4. Cont.

Entry	Bare tip	Husk leaf number	Leaf number	Days to pollen shed	Plant height (cm)	Ear height (cm)	500 Kernel weight (g)	Grain yield kg ha^{-1}
FxA	2.0	11.7	21.8	98.0	354.8	186.9	207.3	7407.3
FX100	1.5	11.2	23.4	100.0	390.3	221.0	186.6	9259.2
FX50	2.0	9.9	23.1	99.5	372.2	201.2	140.6	7777.7
FX93	7.5	10.5	23.3	100.5	382.3	220.8	180.6	8888.8
AX100	0.5	10.2	22.9	99.0	379.3	213.3	173.8	8518.4
AX50	0	9.1	23.3	100.0	375.9	215.4	160.0	8148.1
AX93	4.5	9.4	23.2	98.0	384.3	221.5	173.2	8888.8
100X50	2.5	10.3	24.6	115.5	357.2	217.2	142.4	6296.2
100X93	0	11.3	24.1	109.5	347.9	204.1	147.0	5555.5
50X93	1.5	10.2	24.1	111.0	342.1	208.4	142.9	4814.8

Table 4. Cont.

Entry	Bare tip	Husk leaf number	Leaf number	Days to pollen shed	Plant height (cm)	Ear height (cm)	Kernel weight (g)	Grain yield Kg ha^{-1}
Mean	4.17	10.37	23.14	104.40	341.97	194.74	156.01	6684.24
SE($\bar{X}$)	1.356	0.320	0.282	1.843	14.191	9.421	7.375	0.214
C.V.%	20.3	4.7	1.2	0.9	2.4	0.5	3.6-	5.7
$\bar{F}1$	5.07	10.46	23.22	102.13	368.09	209.90	160.30	7876.46
$\bar{P}1$	1.92	10.15	22.93	109.42	276.67	156.83	145.28	3703.68

Where; $\bar{F}1$ = Mean of single cross hybrids

$\bar{P}1$ = Mean of inbred lines (parents).

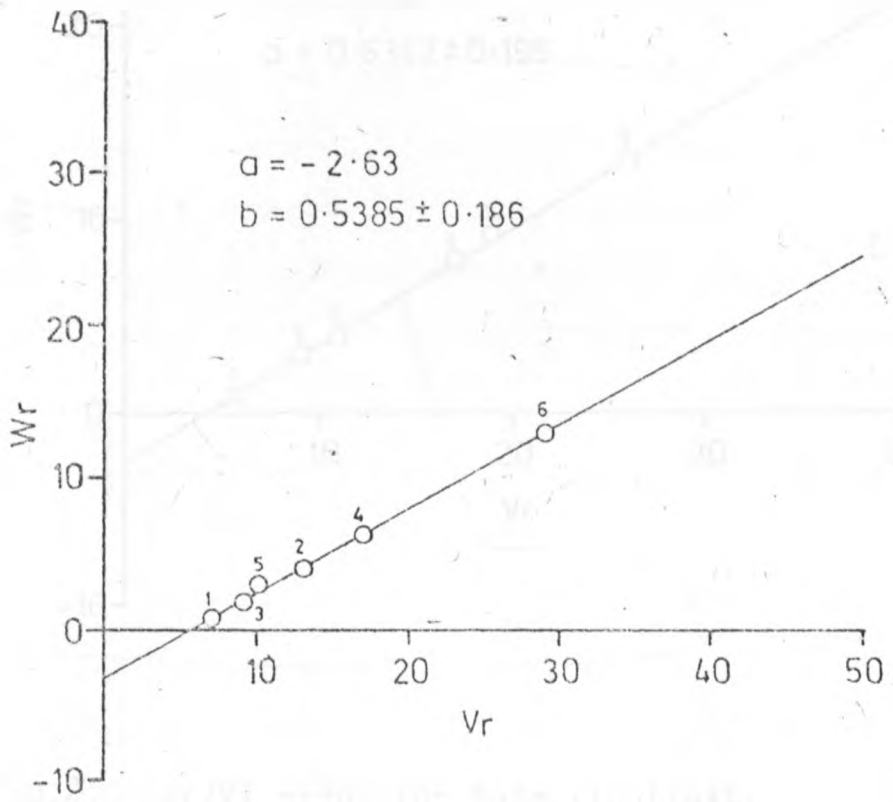

Fig. 1. Wr/Vr graph for Bare tip trait.
Location I (Sabwani), 1985

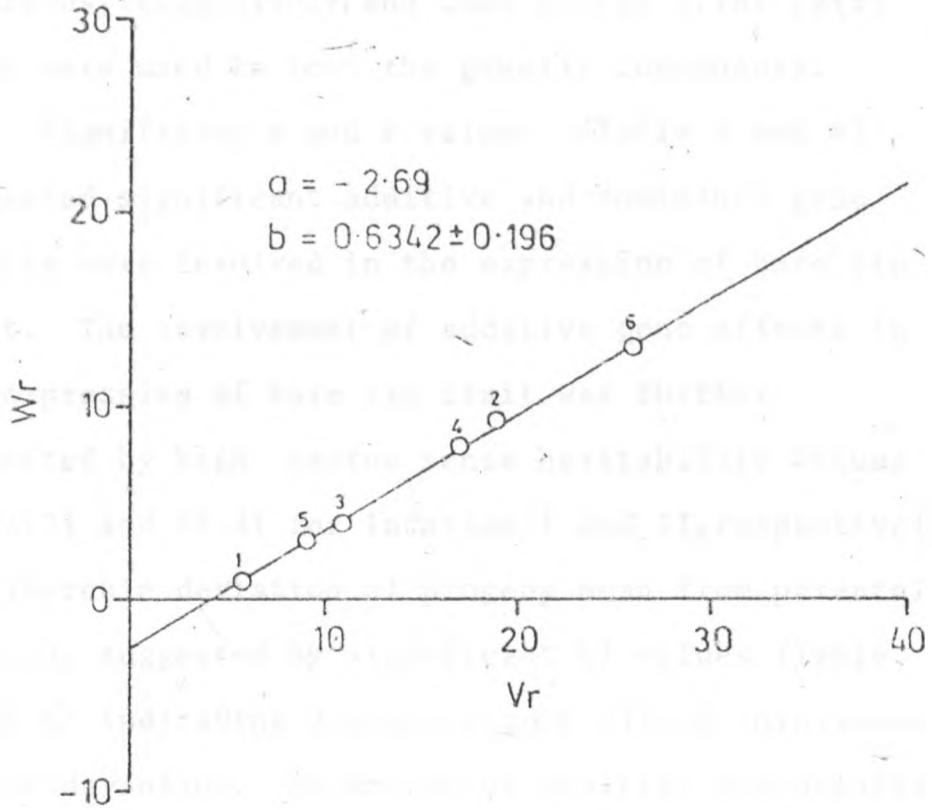

Fig.2. Wr/Vr graph for Bare tip trait.
Location II (Jabali), 1985.

values of 1.8628 and 2.0898 for Sabwani and Jabali locations, respectively, and thus pooled error (Btr) terms were used to test the genetic components.

Significant a and b values (Table 5 and 6) suggested significant additive and dominance gene effects were involved in the expression of bare tip trait. The involvement of additive gene effects in the expression of bare tip trait was further suggested by high narrow sense heritability values of 62.7% and 69.3% for location I and II, respectively. Considerable deviation of progeny mean from parental mean was suggested by significant b1 values (Table 5 and 6) indicating dominance gene effect involvement in the deviation. Asymmetry of positive and negative allele distribution in the parents was implied by significant b_2 values for the two locations, (Table 5 and 6). The values of H1 and H2 and H2/4H1 ratio (Table 7 and 8) confirm the suggested asymmetry of allele distribution. The values of $(4DH1)^{0.5} + F$ $(4DH1)^{0.5} - F$; 0.35 for location I and 0.37 for location II (Tables 7 and 8) were not close to unity implying unequal proportions of dominant and recessive alleles in the parents. Negative F values (Tables 7 and 8) for the two locations suggested that there were more recessive than dominant alleles in the

Table 5. Analysis of genetic variances for bare tip trait in location I (Sabwani) furing 1985 season.

Source of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	80.87	25.1215**	53.0526**
b1		1	78.87	13145.0000**	51.8882**
b2		5	29,92	62.7254**	12.0792**
b3		9	10.04	46.2673**	6.6053**
b		15	21.25	22.2048**	13.9803**
(treatments)	tr	20	220.47		
(Blocks)	B	1	9.52		
	Ba	5	3.210		
	Bb1	1	0.006		
Error terms	Bb2	5	2.477		
	Bb3	9	0.217		
	Bb	15	0.957		
	Btr	20	1.520		

\+ Each item tested against its own block interaction

++ All items tested against pooled block interaction (Btr)

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

Table 6. Analysis of genetic variances for bare tip trait in location II (Jabali) during 1985 season.

Sourse of variation		Degree of freedom (df)	Mean squre	VR+	VR++.
a		5	97.49	82.1314**	135.4028**
b1		1	85.05	733.1897*	118.1250**
b2		5	28.43	59.2292**	39.4861**
b3		9	6.41	3.8475*	8.9028**
b		15	18.99	18.2772**	26.3750**
(Treatments)	tr	20			
(Blocks)	B	1			
	Ba	5			
Error	Bb1	1			
Terms	Bb2	5			
	Bb3	9			
	Bb	15			
	Btr	20			

+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

parents. The estimates of H1 (42.85, 39.94) were several times larger than D. (3.78, 6.30) for both locations (Table 7 and 8) and the ratio $(H1/D)^{0.5}$ indicate apparent overdominance to be involved in the expression of bare tip trait. In Fig 1 and 2, overdominance was suggested by the negative 'a' intercept values (-2.63, -2.69), to influence the expression of this trait at the two locations. The number of genes that had dominant effects in influencing this trait were estimated to be at least five in location I and at most one in location II (Table 7 and 8). At least one effective factor was suggested to control bare tip expression at both locations. There was a large difference between the number of genes or gene groups for the two locations (5.39, and 0.06 for locations I and II, respectively).

The large difference between narrow and broad sense heritability values (Table 7 and 8) suggested existence of a high proportion of nonfixable genetic variation resulting from interaction of genes. Array 1 (inbred G) was indicated to carry the highest proportion of dominant alleles in the parents (Fig. 1 and 2), while (inbred 93) array 6 was suggested to carry the highest proportion of

Table 7. Estimates of components of genetic viariation for bare tip trait in location I (Sabwani) during 1985 seaston.

Genetic component	Mean value
D	3.78 ± 2.209
H1	42.85 ± 12.019
H2	29.16 ± 10.737
h2	152.56 ± 7.227
F	-12.28 ± 11.567
E	1.52 ± 1.790
Derivatives	
$(H1/D)^{0.5}$	3.37
H2/4H1	0.17
h2/H2	5.23
K	1.32
$(4DH1)^{0.5} + F/(4DH1)^{0.5}-F$	0.35
Heritabilities	
+HNS	62.7
#HBS	93.2

+ HNS - Narrow sense heritability

HBS - Broad sense heritability

Table 8. Estimates of components of genetic variation for bare tip in location II (Jabali) during 1985 season.

Genetic component	Mean value
D	6.30 ± 4.247
H1	39.94 ± 10.779
H2	27.08 ± 9.629
h2	1.63 ± 26.546
F	-14.61 ± 10.374
E	0.72 ± 1.606
Derivatives	
$(H1/D)^{0.5}$	2.52
H2/4H1	0.17
h2/H2	0.06
K	1.49
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	0.37
Heritabilities	
+HNS	69.3
#HBS	97.0

+HNS - Narrow sense heritability

#HBS - Broad sense heritability

recessive alleles for this trait. The rest of the inbreds were intermediate in position, indicating that they carried about equal proportions of dominant and recessive alleles, although arrays 3, 5 and 2 carried proportionately more dominant than recessive alleles (Fig. 1 and 2). Dominance for greater numbers of bare tip ears and recessiveness for fewer bare tip ear (complete husk cover) was suggested by the data presented in Tables 3 and 4 and Figures 1 and 2.

4:1:2 Husk leaf number

There was a small difference of 0.84 and 0.31 between the progeny and parental mean husk leaf number for Sabwani and Jabali locations, respectively, (Table 3 and 4). A range of 3.6 and 4.6 husk leaves between the highest and the lowest husk leaf scores for location I and II, respectively, (Table 3 and 4) was observed among the parental values. The range between the lowest and highest husk leaf scores among the hybrids was 2.6 and 2.3 for Sabwani and Jabali locations, respectively, (Table 3 and 4). Among the parents, inbred F was found to have the largest number of husk leaves while inbred A had the least

(Table 3 and 4). The other inbreds had husks leaf number scores between these two extremes.

Consistency of Wr-Vr differences over arrays (Appendix II) indicated conformity of the data to the additive - dominance model with independent gene distribution. The non significance of the regression coefficient 'b' (0.844 and 1.104) from unity furhter indicated conformity of data to the additive - dominance model.

Apart from using individual block interaction error terms to test the genetic components, pooled block interaction error term (Btr) as well was used since Bartlett's test of heterogeneity of variances (x^2 = 7.1912, 2.4299) was not significant in the two locations.

In both locations (Table 9 and 10) additive genetic effects were found to contribute significantly to the inheritance of husk leaf number. Deviation of progeny mean from parental mean as a result of dominance gene effects was not significant when bl was tested against its own block interaction error term (Table 9) for location I, but was significant when tested against the pooled error (Btr) term. In location II however, this genetic component was not significant (Table 10).

Table 9. Analysis of genetic variances for husk leaf number in location I (Sabwani) during 1985 season.

Sourse of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	3.83	16.3675**	9.3415**
b1		1	6.29	17.5209	15.3415**
b2		5	0.72	1.2743	1.7561
b3		9	0.55	1.2761	1.3415
b		15	0.99	2.1019	2.4146*
(Treatments)	tr	20	1.70		
(Blocks)	B	1	0.09		
	Ba	5	0.234		
Error	Bb1	1	0.359		
Terms	Bb2	5	0.565		
	Bb3	9	0.431		
	Bb	15	0.471		
	Btr	20	0.410		

+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

,** Significant at £% and 1% level respectively.

Table 10. Analysis of genetic variances for husk leaf number in location II (Jabali) during 1985 season.

Source of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	5.45	32.6547**	20.4887**
b1		1	0.82	1.8345	3.0827
b2		5	0.73	1.8296	2.7444*
b3		9	1.24	3.5821	4.6617**
b		15	1.04	2.5366*	3.9098**
(Treatments)	tr	20	2.15		
(Blocks)	B	1	0.004		
	Ba	5	0.167		
	Bb1	1	0.447		
Error	Bb2	5	0.399		
Terms	Bb3	9	0.413		
	Bb	15	0.410		
	Btr	20	0.266		

\+ Each item tested against its block interaction.

++ All items tested against pooled block interaction (Btr)

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

Asymmetry of positive and negative alleles in the parents was indicated in location II (Table 10) by the significant b2 component and H2/4H1 estimate of 0.22 (Table 12). All the dominance gene effects were however not explained by b1 and b2 components in location II (Table 10) as was indicated by the significant b3 component.

The estimate of D (1.04) for location I (Table 11) was slightly lower than H1 value (1.54), and the opposite was true for location II (Table 12), so that the estimated average degree of dominance $(H1/D)^{0.5}$ tended to overdominance (1.22) for location I and complete dominance (0.94) in location II.

The estimate of the number of genes or gene groups (h2/H2) was found to vary so much between the two locations that its reliability is questionable (Table 11 and 12). At least one and four effective factors for this trait were estimated for location II and I, respectively, (Table 12 and 11). The ratio $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ indicated an excess of dominant over recessive alleles for both locations (Table 11 and 12). The results of F were positive (0.33, 1.15)

Table 11. Estimates of components of genetic variation for husk leaf number trait in location I (Sabwani) during 1985 season.

Genetic component	mean value
D	1.04 ± 0.301
H1	1.54 ± 0.763
H2	0.80 ± 0.680
h2	12.77 ± 0.459
F	0.33 ± 0.734
E	0.41 ± 0.113
Derivatives	
$(H1/D)^{0.5}$	1.22
H2/4H1	0.13
h2/H2	15.96
K	3.85
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.30
Heritabilities	
+HNS	51.7
*HBS	67.5

\+ HNS - Narrow sense heritability

* HBS - Broad sense heritability

Table 12. Estimates of components of genetic variation for husk leaf number trait in location II (Jabali) during 1985 season.

Genetic component	Mean value
D	2.04 ± 0.265
H1	1.69 ± 0.673
H2	1.47 ± 0.601
h2	793.42 ± 0.405
F	1.15 ± 0.648
E	0.27 ± 0.100
Derivatives	
$(H1/D)^{0.5}$	0.94
H2/4H1	0.22
h2/H2	568.35
K	0.61
$(4DH1)^{0.5} + F/DH1)^{0.5} - F$	1.99
Heritabilities	
+HNS	46.6
*HBS	77.3

+ HNS - Narrow sense heritability

* HBS - Broad sense heritability

and supported the presence of more dominant than receisive alleles in the parents.

In Figure 3 and 4, the relative positions of inbreds (arrays) are presented. In both locations, inbred A was found to have the highest number of recessive alleles among the parents. This inbred also had the lowest husk leaf number score. Inbred F (array 2) was found to carry the highest proportion of dominant alleles in location I (Fig. 3), while inbred 100 (array 4) was indicated to carry the highest propotion of dominant alleles in location II (Fig. 4). The data of the two locations do not agree as to which parent had the highest proportion of dominant alleles (Fig. 3 and 4). Inbred A was consistently the most recessive parent and had the lowest husk leaf scores in both locations, while inbred F had the highest number of husk leaves in both locations and found to be the most dominant parent in one of the locations (location I). From these observations, dominance for greater husk leaf number and recessiveness for fewer husks leaves was deduced.

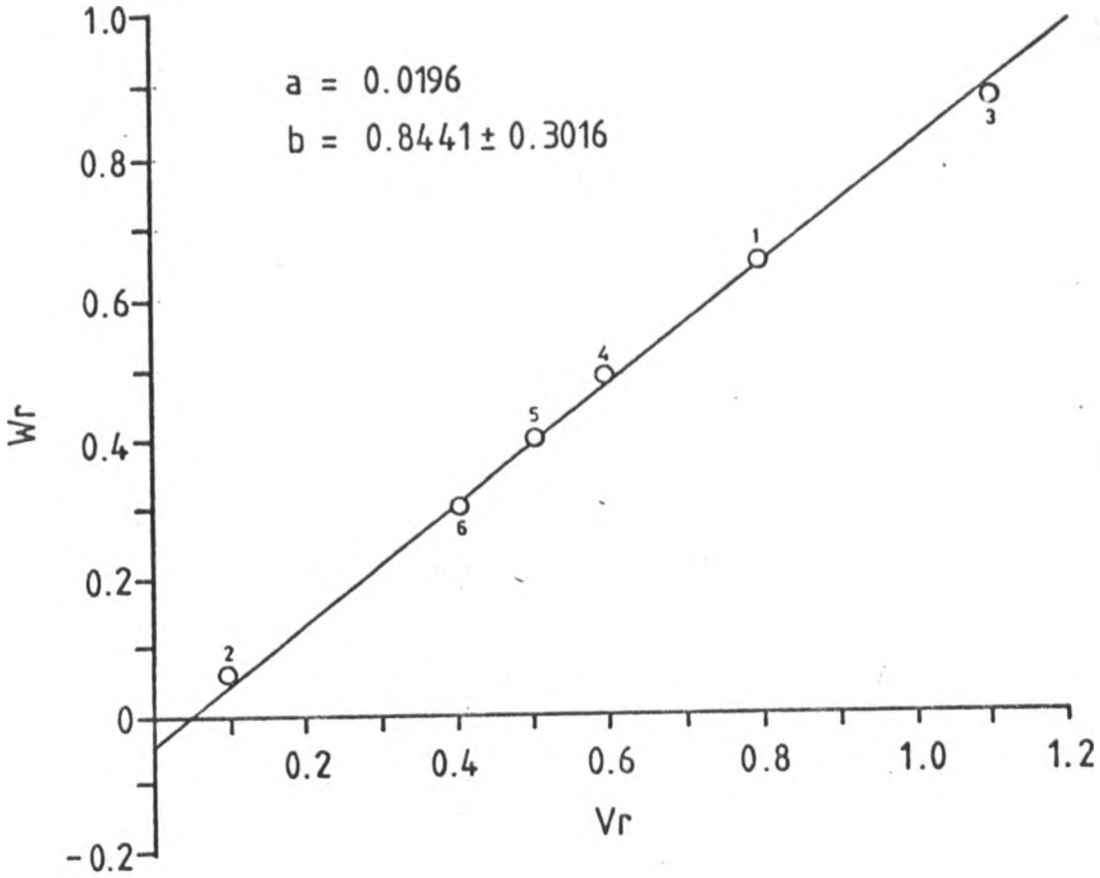

Fig. 3. Wr/Vr graph for Husk leaf number.
Location I (Sabwani), 1985.

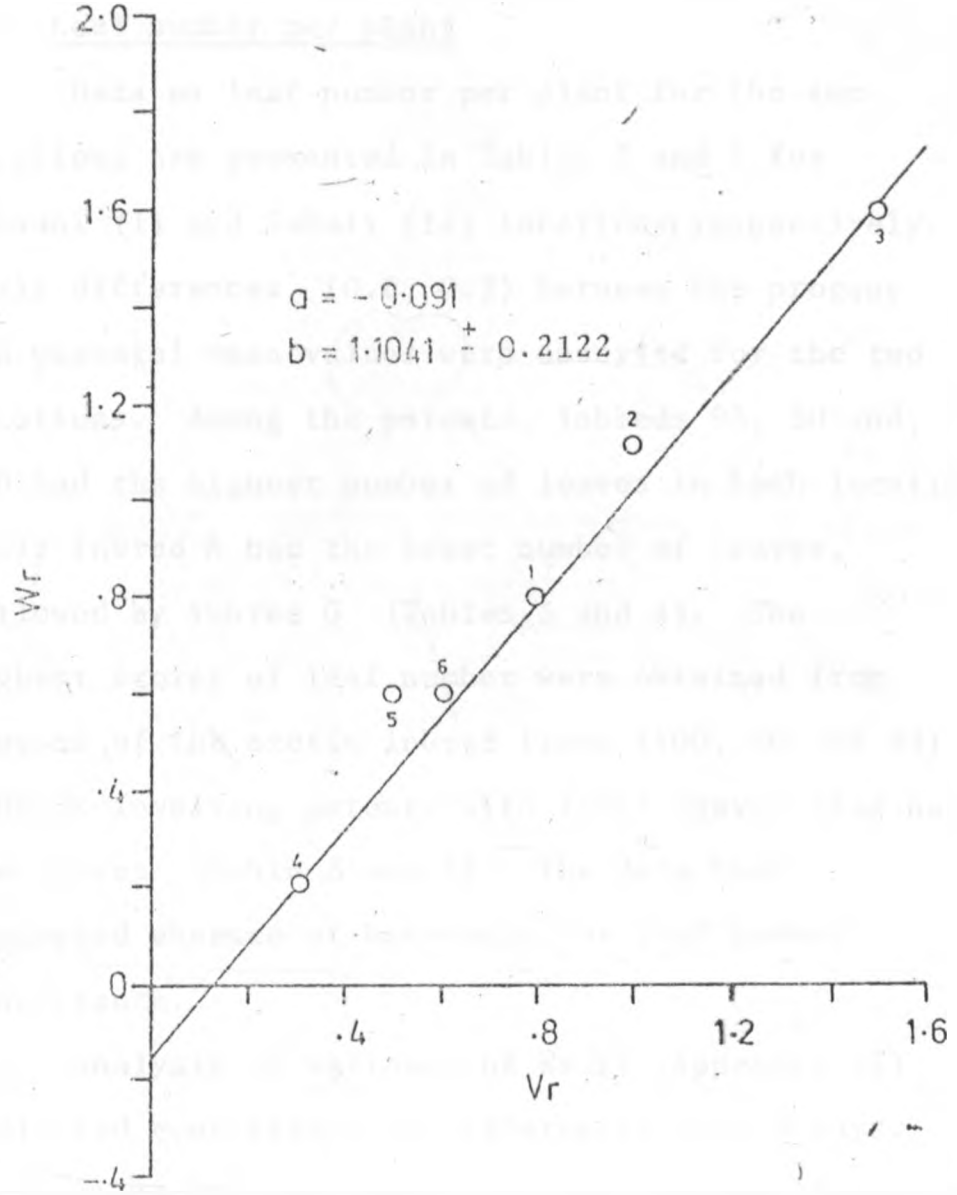

Fig. 4. Wr/Vr graph for Husk Leaf Number.
Location II (Jabali), 1985.

4:2 Leaf number per plant

Data on leaf number per plant for the two locations are presented in Tables 3 and 4 for Sabwani (I) and Jabali (II) locations, respectively. Small differences (0.6, 0.3) between the progeny and parental mean values were observed for the two locations. Among the parents, inbreds 93, 50 and 100 had the highest number of leaves in both locations, while inbred A had the least number of leaves, followed by inbred G (Tables 3 and 4). The highest scores of leaf number were obtained from crosses of the exotic inbred lines (100, 50 and 93). Hybrids involving parents with fewer leaves also had few leaves (Table 3 and 4). The data thus suggested absence of heterosis for leaf number inheritance.

Analysis of variance of Wr-Vr (Appendix II) indicated consistency of differences over arrays. The regression coefficient 'b' was not significantly different from unity. These indicated that the data on leaf number fitted the additive - dominance model. Bartlett's test (X^2 = 1.109, 2.141) of heterogeneity of variances was found to be nonsignificant so the pooled error term (Btr) together with individual block interaction error terms were used to test the

genetic components.

Both general and specific combining ability components were involved in the expression of leaf number. This was indicated by the significant a and b components (Table 13 and 14). Additive gene effects were however indicated by the data (D = 0.95, 1.47; H1 = 0.39, 0.44; H2 = 0.44, 0.28) to play a bigger role than dominance gene effects in the determination of leaf number.

Asymmetry of dominant and recessive allele distribution in the parents was suggested by H2/4H1 ratios, 0.28 and 0.16 for locations I and II, respectively. However the value H2/4H1, 0.28 was taken to be spurious since the maximum value should be 0.25. The b2 component for location I was significant indicating asymmetry of dominant and recessive allele distribution. This component in location II was however not significant suggesting the observed asymmetry (Table 16) was not significant. The suggested symmetry of allele distribution in Jabali (location II) was further supported by the ratio $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ which was close to unity (0.94) and the low value of F, 0.05, (Table 14).

The number of dominant genes or gene groups that controlled leaf number inheritance were very different

Table 13. Analysis of genetic variances for leaf number in location I (Sabwani) during 1985 season

Source of variation		Degrees of freedon (df)	Mean square	VR+	VR++
	a	5	4.39	33.3300**	45.7594**
	b1	1	3.09	42.1458	31.6094**
	b2	5	0.32	3.1095	3.2845*
	b3	9	0.05	0.6689	0.5302
	b	15	0.34	4.0083**	3.5198**
(Treatment)	tr	20	8.13		
(Blocks)	B	1	0.0021		
	Ba	5	0.132		
Error	Bb1	1	0.072		
Terms	Bb2	5	0.101		
	Bb3	9	0.076		
	Bb	15	0.084		
	Btr	20	0.096		

\+ Each item is tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

Table 14. Analysis of genetic variances for leaf number in location II (Jabali) during 1985 season.

Source of variation		Degree of freedom (df)	Mean square	VR+	VR++
a		5	6.27	93.5821**	78.3750**
b1		1	0.69	1.7647	8.6250**
b2		5	0.15	2.8302	1.8750
b3		9	0.10	1.4279	1.2500
b		15	2.32	27.6190**	29.0000**
(Treatments)	tr	20	1.68		
(Blocks)	B	1	0.086		
	Ba	5	0.067		
Error	Bb1	1	0.391		
Terms	Bb2	5	0.053		
	Bb3	9	0.068		
	Bb	15	0.084		
	Btr	20	0.080		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

for the two locations, to be of any reliability (Table 15 and 16). The estimate of the number of effective factors for the two locations was two (Table 15 and 16).

The ratio $(H1/D)^{0.5}$, 0.64, 0.55, indicated partial dominance for leaf number at the two locations.

High narrow and broad sense heritability values (NS: 73.2, 84.0), (BS: 87.6, 91.4) were obtained for this trait, for the two locations. The small differences between narrow and broad sense heritability values indicated presence of small nonfixable genetic variation and a large fixable genetic variation.

Inbred 93 (array 6) was indicated to possess the highest proportion of dominant alleles among the parents, while inbred A and G had the highest proportion of recessive alleles for leaf number (Figures 5 and 6). Inbreds F, 50, and 100 (arrays 2, 5 and 4) possessed more or less equal numbers of dominant and recessive alleles (Figures 5 and 6). Inbred G and A had the lowest leaf number scores while inbred 93 was among the inbreds with large leaf number scores. The data on leaf number suggested that dominant alleles increased leaf number while recessive alleles reduced leaf number per plant.

Table 15. Estimates of components of genetic variation for leaf number trait. in location I (Sabwani) during 1985 season

Genetic component	mean value
D	0.95 ± 0.071
H1	0.39 ± 0.179
H2	0.44 ± 0.160
h2	5.97 ± 0.108
F	-0.23 ± 0.172
E	0.09 ± 0.026
Derivatives	
$(H1/D)^{0.5}$	0.64
H2/4H1	0.28
h2/H2	13.57
K	2.39
$(4DH1)^{0.5} + F/(4DH1)^{0.5}-F$	0.69
Heritabilities	
+HNS	73.2
#HBS	87.2

\+ HNS - Narrow sense heritability

\# HBS - Broad sense heritability

Table 16. Estimates of components of genetic variation leaf number trait in location II (Jabali) during 1985 season.

Genetic component	Mean value
D	1.47 ± 0.108
H1	0.44 ± 0.274
H2	0.28 ± 0.245
h2	4214.36 ± 0.165
F	0.05 ± 0.264
E	0.08 ± 0.041
Derivatives	
$(H1/D)^{0.5}$	0.55
H2/4H1	0.16
h2/H2	15303.19
K	2.12
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	0.94
Heritabilities	
+ HNS	84.0
= HBS	91.4

+ HNS - Narrow sense heritability
= HBS - Broad sense heritability

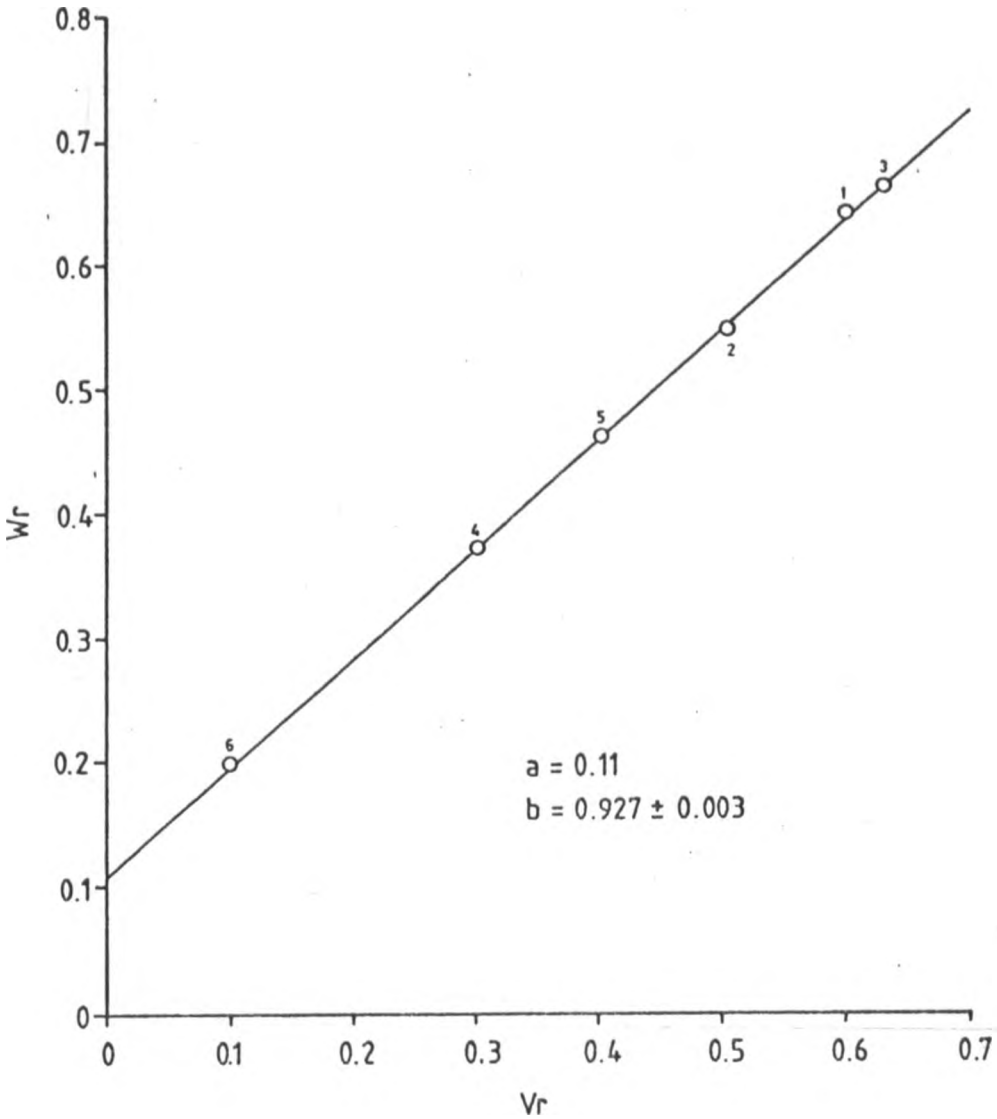

Fig. 5. Wr/Vr graph for Leaf number.
Location I (Sabwani), 1985.

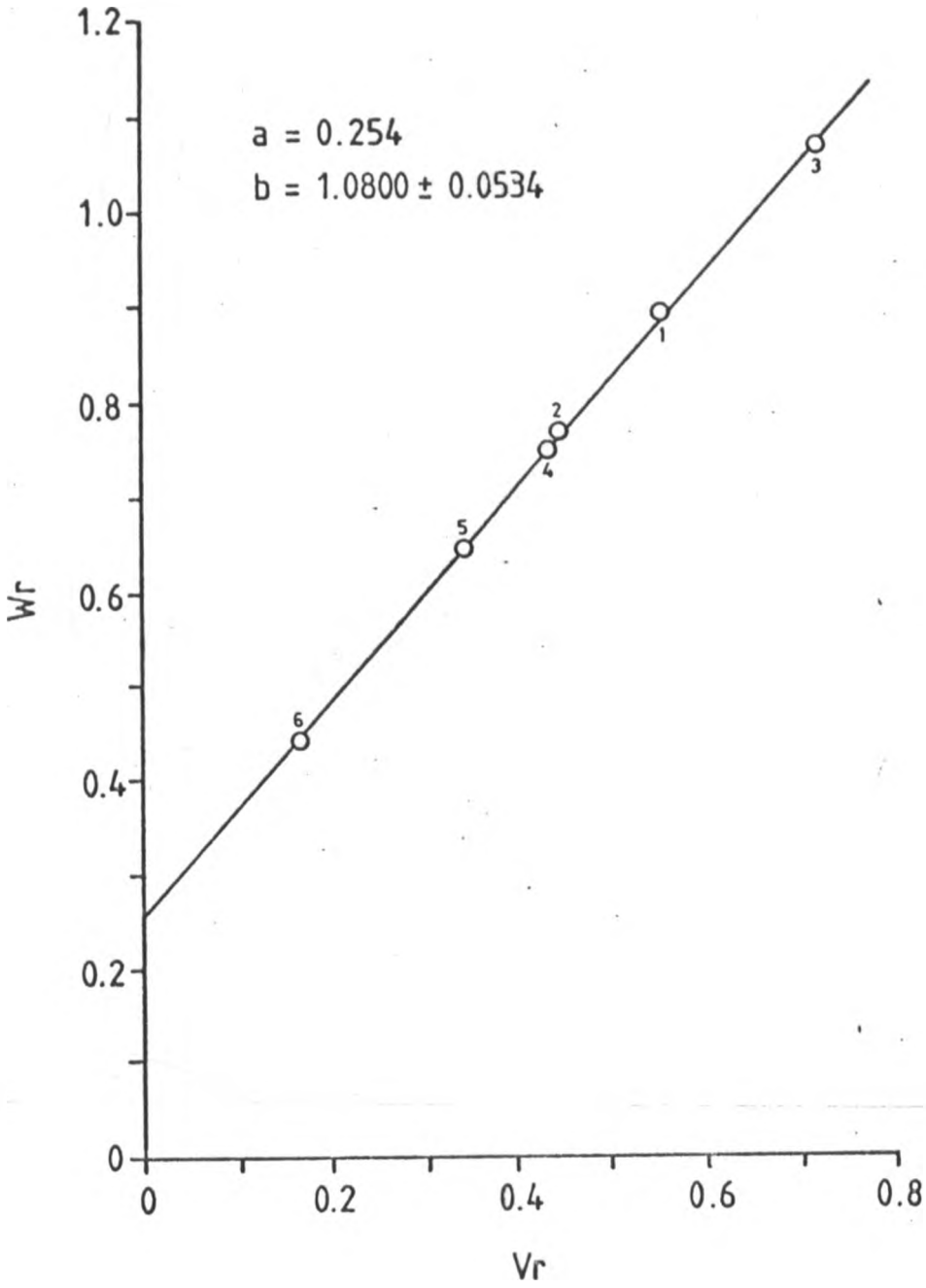

Fig. 6. Wr/Vr graph for Leaf Number.
Location II (Jabali), 1985.

4.3 Days from planting to pollen shed.

Mean values of days from planting to pollen shed of the parents were larger than the mean values of the crosses (Tables 3 and 4) implying that the hybrids were earlier in flowering than the parents. The range among the parents was 103.5 to 118 days (Table 3) and 102.0 to 115.5 days (Table 4) for locations I and II, respectively. In both locations, inbred A was the earliest to flower (103.5 and 102 days), (Table 3 and 4), followed closely by inbred F. The exotic lines (100, 50, 93) were all late flowering in both locations, while the local inbred lines (G, F and A) were early flowering. The range in flowering time among the hybrids was 100 to 113 days in location I (Table 3) and 98 to 115.5 days in location II (Tables 4). Heterosis of 7.3 and 6.7 per cent over the parental mean for early flowering among the hybrids was recorded (Tables 3 and 4) for locations I and II, respectively.

Regression coefficient (b = 0.960, 0.874), (Figures 7 and 8) and the analysis of Wr-Vr variance indicated that the data fitted the additive - dominance model.

Analysis of variance for the various genetic components is presented in Table 17 and 18 for location I and II, respectively. Bartlett's test

Table 17. Analysis of genetic variances for days to pollen shed trait in location I (Sabwani) during 1985 season.

Source of variation		Degree of freedon (df)	Mean square	VR+	VR++
a		5	156.82	66.3049**	50.6128**
b1		1	571.67	166.2740**	185.6905**
b2		5	5.02	6.1426*	15.4444**
b3		9	18.72	3.9834*	6.0814**
b		15	51.02	15.3600**	16.5714**
(Treatments)	tr	20	803.25		
(Blocks)	B	1	3.43		
	Ba	5	2.350		
	Bb1	1	3.438		
Error	Bb2	5	0.817		
Terms	Bb3	9	4.700		
	Bb	15	3.321		
	Btr	20	3.079		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

*,** Significant of 5% and 1% level respectively.

Table 18. Analysis of genetic variances for days to pollen shed trait, in location II (Jabali) during 1985 season.

Source of variation		Degree of freedon (df)	Mean square	VR+	VR++
a		5	143.00	204.2857**	149.4253**
b1		1	453.69	7706.6102**	475.1202**
b2		5	5.17	2.7691	5.4023**
b3		9	18.12	26.1095**	18.9342**
b		15	42.90	41.1314**	44.8276**
(Treatments)	tr	20	67.93		
(Blocks)	B	1	5.36		
	Ba	5	0.700		
Error	Bb1	1	0.059		
Terms	Bb2	5	0.867		
	Bb3	9	0.694		
	Bb	15	1.043		
	Btr	20	0.957		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

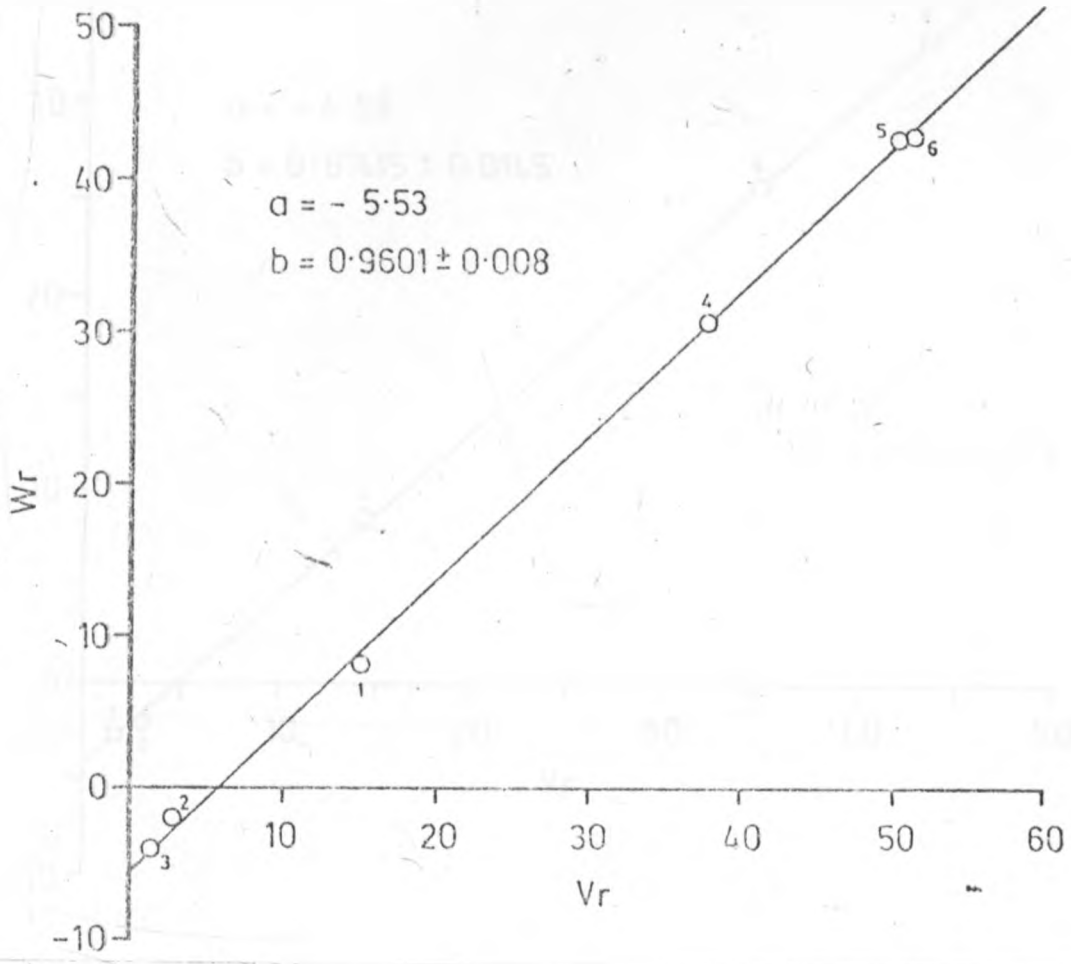

Fig. 7. Wr/Vr graph for Days from planting to pollen shed. Location I (Sabwani), 1985.

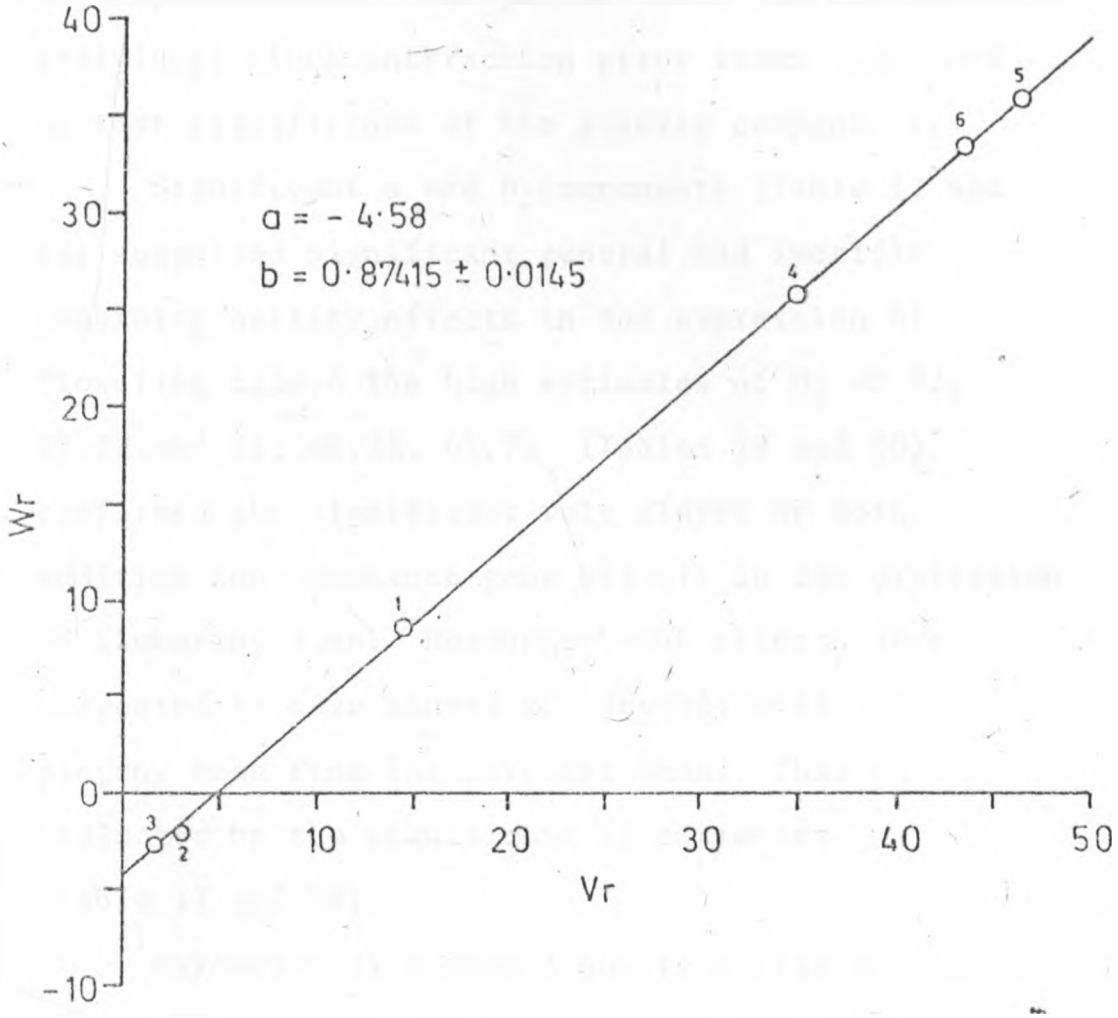

Fig. 8. Wr/Vr graph for Days to pollen Shed.
Location II (Jabali), 1985.

for heterogeneity of variances (X^2 = 2.0609, 2.0277) were not significant so that pooled error (Btr) as well as individual block interaction error terms were used to test significance of the genetic components.

Significant a and b components (Table 17 and 18) suggested significant general and specific combining ability effects in the expression of flowering time. The high estimates of D; 42.92, 32.22 and H1; 69.33, 61.75 (Tables 19 and 20) confirmed the significant role played by both additive and dominance gene effects in the expression of flowering time. Dominance gene effects were suggested to have caused the deviation of the progeny mean from the parental mean. This was indicated by the significant b1 estimates (Table 17 and 18).

Asymmetry of dominant and recessive allele distribution in the parents was indicated by significant b2 genetic component estimates. This was true for both locations (Tables 17 and 18). H2/4H1 ratios and $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ ratio (Tables 19 and 20) however indicated that the suggested asymmetry was small, and thus the dominant and recessive alleles were about equal in proportion in the parents. Presence of extra

Table 19. Estimates of components of genetic variation for days to pollen shed trait in location I (Sabwani) during 1985 season.

Genetic component	Mean value
D	42.92 ± 3.693
H1	69.33 ± 9.375
H2	68.94 ± 8.374
h2	1141.61 ± 5.636
F	6.39 ± 9.022
E	3.23 ± 1.400
Derivatives	
$(H1/D)^{0.5}$)	1.27
H2/4H1	0.248
h2/H2	16.56
K	3.87
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.12
Heritabilities	
+ HNS	47.4
# HBs	91.7

+ HNS - Narrow sense heritability

HBS - Broad sense heritability

Table 20. Estimates of components of genetic variation for days to pollen shed trait in location II (Jabali) during 1985 season.

Genetic component	Mean value
D	32.22 ± 2.945
H1	61.75 ± 7.475
H2	59.29 ± 6.678
h2	107291.07 ± 15.810
F	-6.40 ± 7.193
E	0.96 ± 1.113
Derivatives	
$(H1/D)^{0.5}$	1.38
H2/4H1	0.24
h2/H2	1809.60
K	3.58
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	0.86
Heritabilities	
+ HNS	55.9
= HBS	97.3

+ HNS - Narrow sense heritability
= HBS - Broad sense heritability

dominance was suggested by significant b3 values (Table 17 and 18), for both locations.

Overdominance was suggested to influence flowering time by the $(H1/D)^{0.5}$ estimates which were 1.27 and 1.38, (Table 19 and 20) for location I and II, respectively. Negative 'a' intercept, (Figure 7 and 8) further supported the overdominant role in the expression of days to pollen shed. At least three effective factors (Tables 19 and 20) for both locations, were suggested to control the inheritance of days to pollen shed. The estimate of number of genes or gene groups (h2/H2) varied very much between the two locations that their reliability was questionable. As compared to narrow sense heritability values (Ns, 47.4, 55.9) broad sense heritability values (Bs, 91.7, 97.3), (Tables 19 and 20) were quite high in both locations. The data (Tables 19 and 20) indicated that about one half of the genetic variation for flowering time was due to interacting genetic effects.

Inbred 50 and 93 (arrays 5 and 6, Figures 7 and 8) possessed a higher proportion of recessive than dominant alleles. This was true for the two locations. These two inbreds were also late flowering. Inbreds F and A (arrays 2,3) had a higher proportion of dominant alleles relative to the

recessive alleles (Figures 7 and 8), in the two locations. These two inbreds were also early flowering. Inbreds G and 100 (array 1, 4) were intermediate between these two extremes (Figures 7 and 8), with inbred 100 having more of the recessive alleles than inbred G. The results on days to pollen shed indicated that earlines was caused by dominant alleles while lateness in flowering was due to recessive alleles.

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4:4 Plant height and ear height

4:4:1 Plant height

Mean values for plant height as presented in Tables 3 and 4 for locations I and II, respectively, indicated a wide range, particularly between the parents and their progeny. A difference of 159.5 cm and 145.0 cm (Tables 3 and 4) was recorded between the tallest and the shortest genotypes. Plant height among the parents ranged from 225.8 cm to 293.2 cm in Sabwani (I) (Table 3) and from 245.3 cm to 302.4 cm in Jabali (II), (Table 4). In both locations, the shortest and tallest inbreds were G and 100, respectively. Among the hybrids, a range of 321.3 cm to 385.3 cm was recorded in Sabwani (I) (Table 3) and 342.1 cm to 390.3 cm in Jabali (II) (Table 4). Heterosis of 132 per cent and 133 per cent in hybrids, relative to the parents was recorded for Sabwani (I) and Jabali (II), respectively, (Table 3 and 4). The crosses between unrelated inbred lines were taller than crosses of related inbred lines indicating a bigger heterotic response in hybrids of unrelated parents. This was true for both locations.

The data on plant height were found through the consistency of Wr-Vr variances over arrays, to fit the additive-dominance model. The regression

coefficient 'b' values which were not significantly different from unity (0.867, 0.845, Fig. 9 and 10) further indicated that the data fitted the model.

Pooled block interaction error (Btr) as well as the individual block interaction error terms were used to test the significance of the various genetic components, after the Bartlett's test (X^2 = 3.969, 1.423) of heterogeneity of variances was found to be nonsignificant.

General and specific combining ability were suggested to play a significant role in the expression of plant height, in both locations, as indicated by significant values of a and b (Table 21 and 22). The relative values of D; 645.56, 562.79 and H1; 6134.98, 6879.53, (Table 21 and 22) however indicated dominance gene effects to play a bigger role than additive gene effects in the expression of this trait. The predominant dominance gene effects role in the expression of this trait was further supported by the wide range between narrow and broad sense heritability values (NS; 5.6, 1.1%; BS; 87.4, 96.2%). A high proportion of nonfixable genetic variation (dominance) was thus suggested by the data. For both locations, bl genetic component was

Table 21. Analysis of genetic variance for plant height trait in location I (Sabwani) during 1985 season.

Source of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	1351.99	14.0163**	5.8990**
b1		1	62137.60	383.1093**	271.1188**
b2		5	304.18	0.6109	1.3272
b3		9	828.37	5.1427*	3.6143**
b		15	4740.92	17.3385**	20.6856**
(treatments)	tr	20	69363.06		
(Blocks)	B	1	192.857		
	Ba	5	96.459		
	Bb1	1	162.193		
Error	Bb2	5	497.923		
Terms	Bb3	9	161.077		
	Bb	15	273.433		
	Btr	20	229.189		

Table 22. Analysis of genetic variances for plant height trait in location II (Jabali) during 1985 season.

Sourse of variation		Degrees of freedom (df)	Mean square	VR+	VR++
	a	5	756.92	11.3597**	11.1381**
	b1	1	71639.32	1321.2955**	1054.1705**
	b2	5	506.16	9.3775**	7.4481**
	b3	9	736.18	9.3341**	10.8321**
	b	15	5386.35	78.1480**	79.2600**
(Treatments)	tr	20	2028.99		
Blocks	B	1	1498.28		
	Ba	5	65.05		
	Bb1	1	54.219		
Error	Bb2	5	53.976		
Terms	Bb3	9	78.865		
	Bb	15	68.925		
	Btr	20	67.958		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

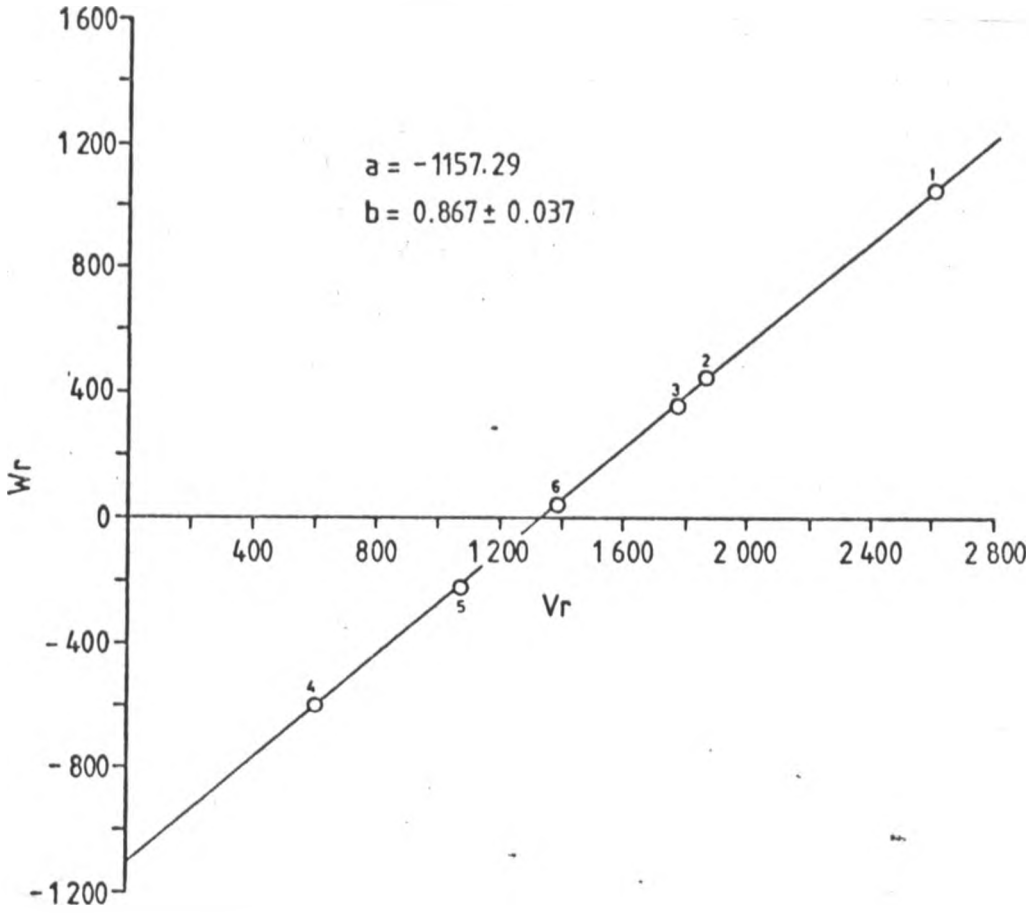

Fig. 9. Wr/Vr graph for Plant Height, Location I (Sabwani), 1985.

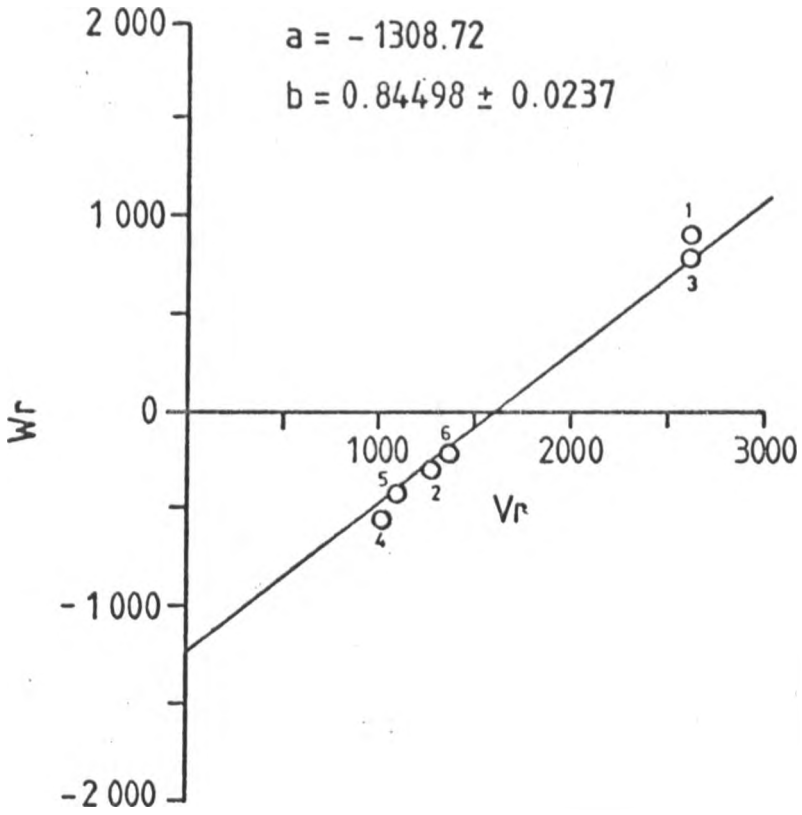

Fig. 10. Wr/Vr graph for Plant Height.
Location II (Jabali), 1985.

significant indicating a significant involvement of dominance gene effects in the deviation of the progeny mean from the parental mean (Tables 21 and 22).

Symmetry of dominant and recessive allele distribution in the parents was indicated by the nonsignificant b2 genetic component. This was true for location I. Asymmetry of dominant and recessive allele distribution in the parents was however indicated in location II (Table 22). The values of F and $(4DH1)^{0.5} + F / (4DH1)^{0.5} - F$ (Table 24) suggested presence of more dominant than recessive alleles in the parents in Jabali location.

In location I, a minimum of four effective factors were suggested while in location II, a minimum of five effective factors were estimated (Table 23 and 24). An estimate of 44 and 55 genes or gene groups for plant height trait were obtained for location I and II, respectively, (Table 23 and 24).

Due to the large values of H1, relative to D, overdominance gene effects $(H1/D)^{0.5}$ (3.08, 3.50) were implicated in the expression of plant height. Negative intercept of Wr ('a' = -1157.29, -1308.72), (Figures 9 and 10) further supported this apparent

Table 23. Estimates of components of genetic variation for plant height in location I (Sabwani) during 1985 season.

Genetic component	Mean value
D	645.56 ± 288.750
H1	6134.98 ± 733.006
H2	5931.82 ± 654.81
h2	262609.67 ± 440.733
F	645.31 ± 408
E	229.19 ± 109.146
Derivatives	
$(H1/D)^{0.5}$	3.08
H2/4H1	0.24
h2/H2	44.27
K	4.89
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.39
Heritabilities	
+ HNS	5.6
# HBS	87.4

+ HNS - Narrow sense heritability

HBS - Broad sense heritability

Table 24. Estimates of components of genetic variation for plant height in location II (Jabali)during 1985 season.

Genetic component	Mean value
D	562.79 ± 157.877
H1	6879.53 ± 400.778
H2	6656.88 ± 358.025
h2	364820.45 ± 240.974
F	677.29 ± 385.688
E	67.96 ± 59.77
Derivatives	
$(H1/D)^{0.5}$	3.50
H2/4H1	0.24
h2/H2	55.05
K	5.07
$(4DH1)^{0.5} + F/(4DH1)^{0.5}-F$	1.42
Heritabilities	
+ HNS	1.1
≠ HBS	96.2

+ HNS - Narrow sense heritability

≠ HBS - Broad sense heritability

overdominance for plant height.

In both locations, inbred 100 (array 4) was found to possess the highest proportion of dominant alleles among the parents. The same inbred was also the tallest parent (Tables 3 and 4). In location I (Figure 9) inbred G (array 1) was indicated to carry the highest proportion of recessive alleles, relative to the other inbreds, while in location II (Figure 10) both inbred G and A (arrays 1, 3) possessed the highest proportion of recessive alleles. These two inbreds were also the shortest of the parents (Table 3 and 4). The data thus, suggested dominance gene effects for greater plant height and recessiveness for lower plant height.

4:4:2 Ear height

A big difference (56.9 cm, 53.1 cm) was recorded between the progeny and parental means in locations I and II, respectively, (Table 3 and 4). Inbreds G, F and A (local inbreds) had lower ear placement than the exotic inbreds (100, 50 and 93), (Table 3 and 4). On average, crosses between unrelated inbred lines had larger ear height scores than those crosses derived from related inbred lines

(Tables 3 and 4). Heterosis for greater ear height was thus recorded. Ear height was 39% and 34% higher in the crosses than in the parents for location I and II, respectively, (Tables 3 and 4).

The data on ear height fitted the additive - dominance model as was established by the analysis of Wr-Vr variance (Appendix II). The adequacy of the additive-dominance model was further suggested by the regression coefficient ('b': 0.869, 0.952; Figures 11 and 12) estimates which did not differ significantly from unity.

Analysis of variance was carried out on the ear height data and presented in Table 25 and 26. Nonsignificant Bartlett's test (X^2 = 3.4853, 2.8560) allowed for the use of pooled error term (Btr) to test the genetic components.

As depicted in Tables 25 and 26, general and specific combining ability contributed significantly to the expression of ear height as shown by significant a and b genetic components. This was found to be true for both Sabwani (I) and Jabali (II) locations. The deviation of the progeny values from the parental values (Tables 25 and 26) was attributed to dominance gene effects as indicated by significant b1 genetic component. Dominance gene

Table 25. Analysis of genetic variances for ear height in location I (Sabwani) during 1985 season.

Source of viariation		Degrees of freedom (df)	Mean square	VR+	VR++
	a	5	1329.94	20.8575**	14.1470**
	b1	1	27786.72	116.0348	295.5761**
	b2	5	175.17	1.0139	1.8633
	b3	9	601.86	11.8243**	6.4022**
	b	15	2271.96	21.8267**	24.1645**
(Treatments)	tr	20	32165.65		
(Blocks)	B	1	321.19		
	Ba	5	63.763		
Error	Bb1	1	239.469		
Terms	Bb2	5	172.758		
	Bb3	9	50.900		
	Bb	15	104.091		
	Btr	20	94.009		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

Table 26. Analysis of genetic variances for ear height in location II (Jabali) during 1985 season.

Source of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	1552.85	20.5175**	12.5536**
b1		1	24155.95	271.2445*	195.2817**
b2		5	1238.85	8.1864*	10.0151**
b3		9	4122.14	29.8366**	33.3242**
b		15	1967.80	14.0856**	15.9081**
(Treatments)	tr	20	1864.06		
(Blocks)	B	1	74.93		
	Ba	5	75.684		
	Bb1	1	89.056		
Error	Bb2	5	151.330		
Terms	Bb3	9	138.869		
	Bb	15	139.703		
	Btr	20	123.698		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

*,** Significant at 5% and 1% levels respectively.

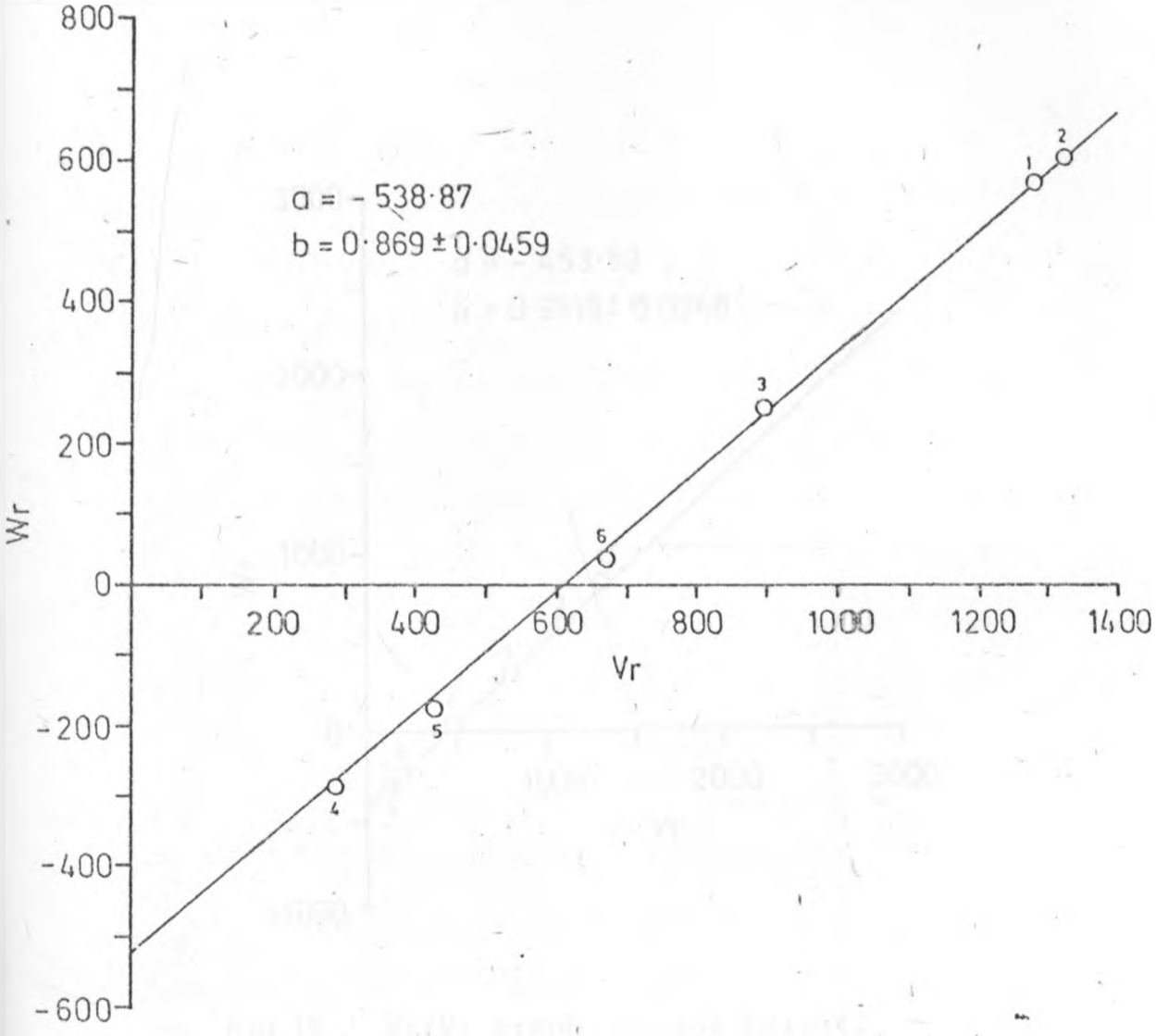

Fig. 11. Wr/Vr graph for Ear height.
Location I (Sabwani), 1985.

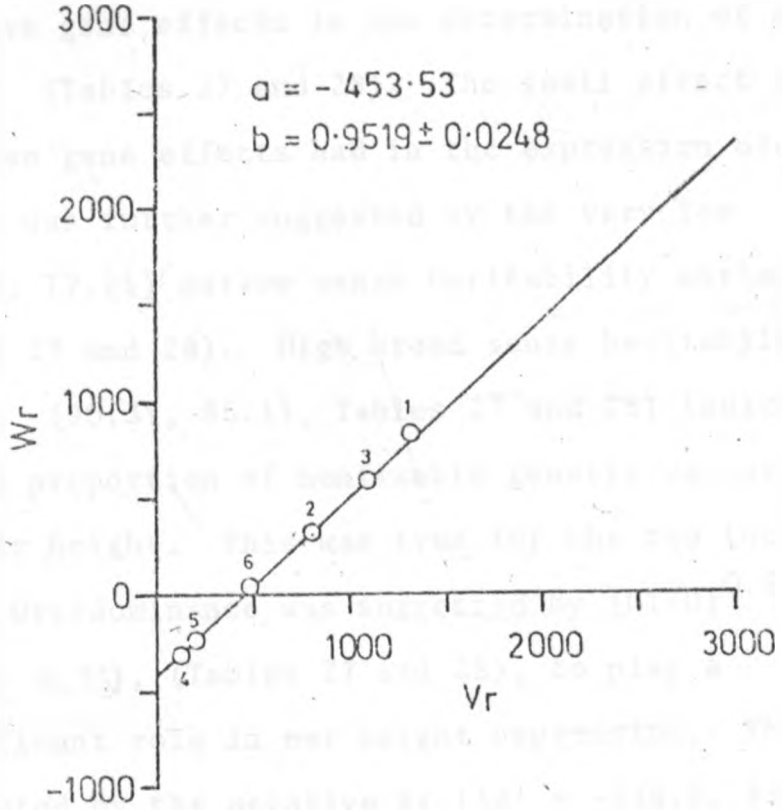

Fig.12. Wr/Vr graph for Ear Height.
Location II (Jabali), 1985.

effects were suggested by larger H1 (3021.6, 11045.2) and H2 (2929.8, 2510.8) values relative to D (448.5, 583.8) values, to play a bigger role than additive gene effects in the determination of ear height (Tables 27 and 28). The small effect that additive gene effects had in the expression of ear height was further suggested by the very low (15.0%, 17.9%) narrow sense heritability estimates (Table 27 and 28). High broad sense heritability values (90.3%, 86.1%, Tables 27 and 28) indicated a high proportion of nonfixable genetic variation for ear height. This was true for the two locations.

Overdominance was suggested by $(H1/D)^{0.5}$ ratio (2.60, 4.35), (Tables 27 and 28), to play a significant role in ear height expression. This was supported by the negative Wr ('a' = -538.9, 453.5), (Figures 11 and 12) intercept of the regression line.

Asymmetry of positive and negative alleles was suggested by the values of H2/4H1 (0.24, 0.15) for both locations and significant b2 genetic component (only in Jabali II location, Table 26), while b2 genetic component in location I (Table 25) indicated that the observed asymmetry was not significant. An excess of dominant to recessive alleles was implied by the positive estimates of F and the $(4DH1)^{0.5}$ +

Table 27. Estimates of components of genetic variation for ear height in location I (Sabwani) during 1985 season.

Genetic component	Mean value
D	448.49 ± 170.027
H1	3021.61 ± 431.622
H2	2929.78 ± 385.579
h2	54443.17 ± 259.175
F	249.26 ± 415.371
E	94.01 ± 64.270
Derivatives	
$(H1/D)^{0.5}$	2.60
H2/4H1	0.24
h2/H2	18.58
K	4.42
$(4DH1)^{0.5} + F/(4DH1)^{0.5}-F$	1.24
Heritabilities	
+ HBS	15.0
* HBS	90.3

+ HNS - Narrow sense heritability.

* HBS - Broad sense heritability.

Table 28. Estimates of components of genetic variation for ear height in location II, (Jabali) during 1985 season.

Genetic component	Mean value
D	583.80 ± 454.639
H1	11045.24 ± 1154.126
H2	2510.80 ± 1031.011
h2	147873.38 ± 693.917
F	8787.07 ± 1110.672
E	123.70 ± 171.853
Derivatives	
$(H1/D)^{0.5}$	4.35
H2/4H1	0.15
h2/H2	58.90
K	3.28
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.89
Heritabilities	
+ HNS	17.9
= HBS	86.1

+ HNS - Narrow sense heritability

= HBS - Broad sense heritability

Table 28. Estimates of components of genetic variation for ear height in location II, (Jabali) during 1985 season.

Genetic component	Mean value
D	583.80 ± 454.639
H1	11045.24 ± 1154.126
H2	2510.80 ± 1031.011
h2	147873.38 ± 693.917
F	8787.07 ± 1110.672
E	123.70 ± 171.853
Derivatives	
$(H1/D)^{0.5}$	3.75
H2/4H1	0.15
h2/H2	59.12
K	3.28
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.89
Heritabilities	
+ HNS	17.9
= HBS	86.1

+ HNS - Narrow sense heritability

= HBS - Broad sense heritability

$F/(4DH1)^{0.5}$ -F ratio, (Tables 27 and 28).

In Figure 11 (Sabwani (I) location) the parents with the highest proportion of recessive alleles; inbreds G and F (arrays 1,2) had the lowest ear height scores. The parents with the highest number of dominant alleles (inbreds 100 and 50; arrays 4 and 5) were also found to have the highest ear height scores among the parents. Inbred 100 however had more dominant alleles than inbred 50 and it correspondingly had a higher ear height score (Table 4). As was the case in location I, inbreds 100 and 50 were also found to possess the highest proportion of dominant alleles among the parents in location II (Figure 12). Inbreds G and A (arrays 1, 3; Figure 12) possessed the highest number of recessive alleles in location II, while inbred F (array 2) which was the second most recessive parent in Sabwani (location I) ranked third. From the data of the two locations, it was deduced that dominant alleles favoured greater ear height, while recessive alleles were responsible for lower ear height.

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4:5 Kernel Weight and Grain yield

4:5:1 Kernel weight

The progeny mean exceeded the parental mean by 8.42 g and 15.02 g (Tables 3 and 4) in location I and II, respectively. Among the parents, inbred F had the heaviest kernels followed by inbred A. Inbreds G, 50 and 93 had the lightest kernels in both locations, while inbred 100 was intermediate in kernel weight. Among the crosses, hybrid 50 x 93 in location I had the lowest kernel weight while in location II it had the fourth lowest kernel weight (Tables 3 and 4). Hybrids F x 93, A x 100 and F x A in that order, had the heaviest kernels in location I (Table 3), while hybrids F x A, F x 100 and F x 93 had the heaviest kernels in location II (Table 4). Most of these hybrids had inbred F as one of the parents. The data suggested that to obtain hybrids with heavy kernels, one or both parents should have heavy kernels.

The consistency of Wr-Vr differences over arrays (Appendix II) and the regression coefficient 'b' values (0.963, 0.962, Figures 13 and 14), that were close to one suggested that the data adequately fitted the additive-dominance model.

Partitioned genetic components are presented in Tables 29, 30, 31 and 32. Since Bartlett's test for heterogeneity of variances (X^2 = 4.1872, 0.3753) was not significant, pooled error term (Btr) as well as the individual block interaction error terms were used to test the significance of the genetic components.

General and specific combining abilities contributed significantly to the expression of kernel weight. This was indicated by the significant values of a and b genetic components (Tables 29 and 30). The variation of the progeny mean from the parental mean was not significant as indicated by the nonsignificant b1 genetic component (Table 29). In Jabali (II), a significant b1 component of variation was obtained which indicated involvement of dominance gene effects in the deviation of progeny mean from the parental mean (Table 30).

In location II, the b2 genetic component was significant when tested against both interaction error terms, while in location I this genetic component was significant only when tested against its own block interaction error term (Table 29 and 30). Asymmetric distribution of dominant and recessive alleles in the parents was indicated by the

Table 29. Analysis of genetic variances for kernel weight in location I (Sabwani) during 1985 season.

Source of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	1616.04	55.1305**	23.3346**
b1		1	607.20	357.1765*	8.7676
b2		5	163.08	5.9544**	2.3548
b3		9	280.39	2.0677	4.0487
b		15	263.07	3.1861*	3.7986**
(Treatments)	tr	20	580.93		
(Blocks)	B	1	12.60		
	Ba	5	29.313		
	Bb1	1	1.700		
Error	Bb2	5	27.388		
Terms	Bb3	9	135.605		
	Bb	15	82.569		
	Btr	20	69.255		

+ Each item tested against its own block interaction

++ All items tested against pooled block interaction (Btr).

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

Table 30. Analysis of genetic variances for kernel weight in location II (Jabalil) during 1985 season.

Sourse of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	3426.66	45.6486**	110.7518**
b1		1	1932.86	203.6948*	62.4712**
b2		5	107.57	8.0589*	3.4767*
b3		9	359.84	19.3691**	11.6303**
b		15	308.58	19.0141**	9.9735**
(Treatments)	tr	20	1142.10		
(Blocks)	B	1	84.40		
	Ba	5	75.066		
Error	Bb1	1	9.489		
Terms	Bb2	5	13.348		
	Bb3	9	18.578		
	Bb	15	16.229		
	Btr	20	30.940		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

*,** Significant at 5% and 1% respectively.

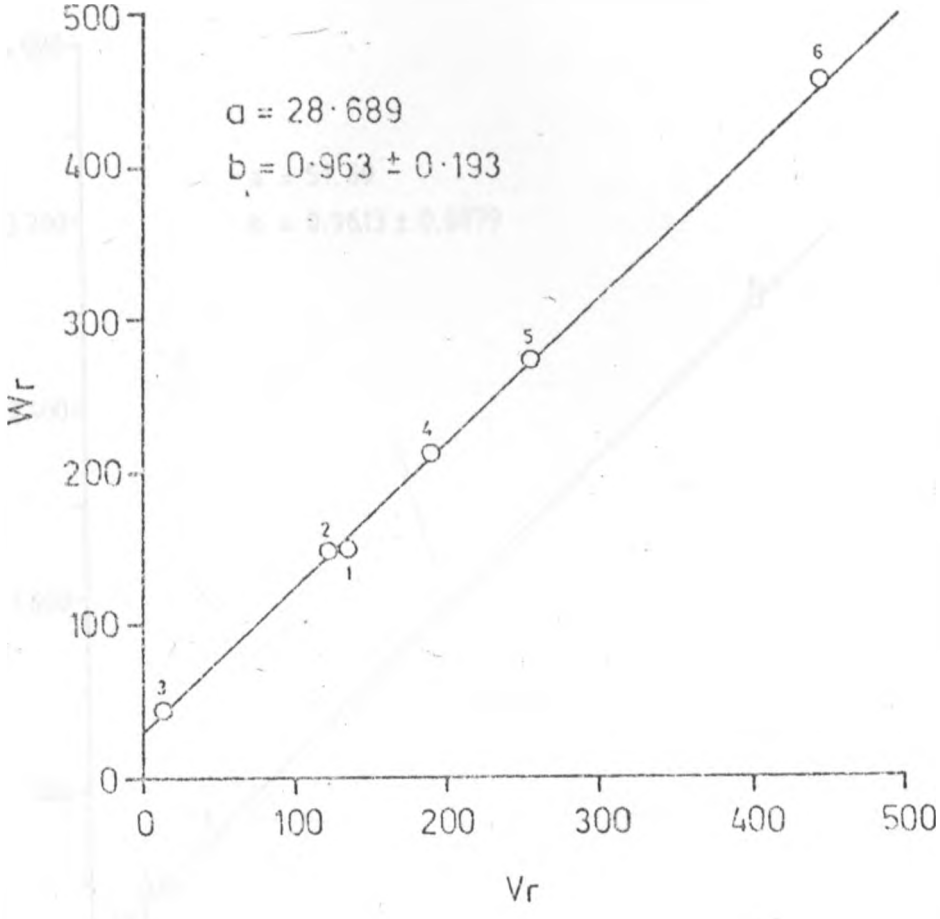

Fig. 13. Wr/Vr graph for Kernel Weight.
Location I (Sabwani), 1985.

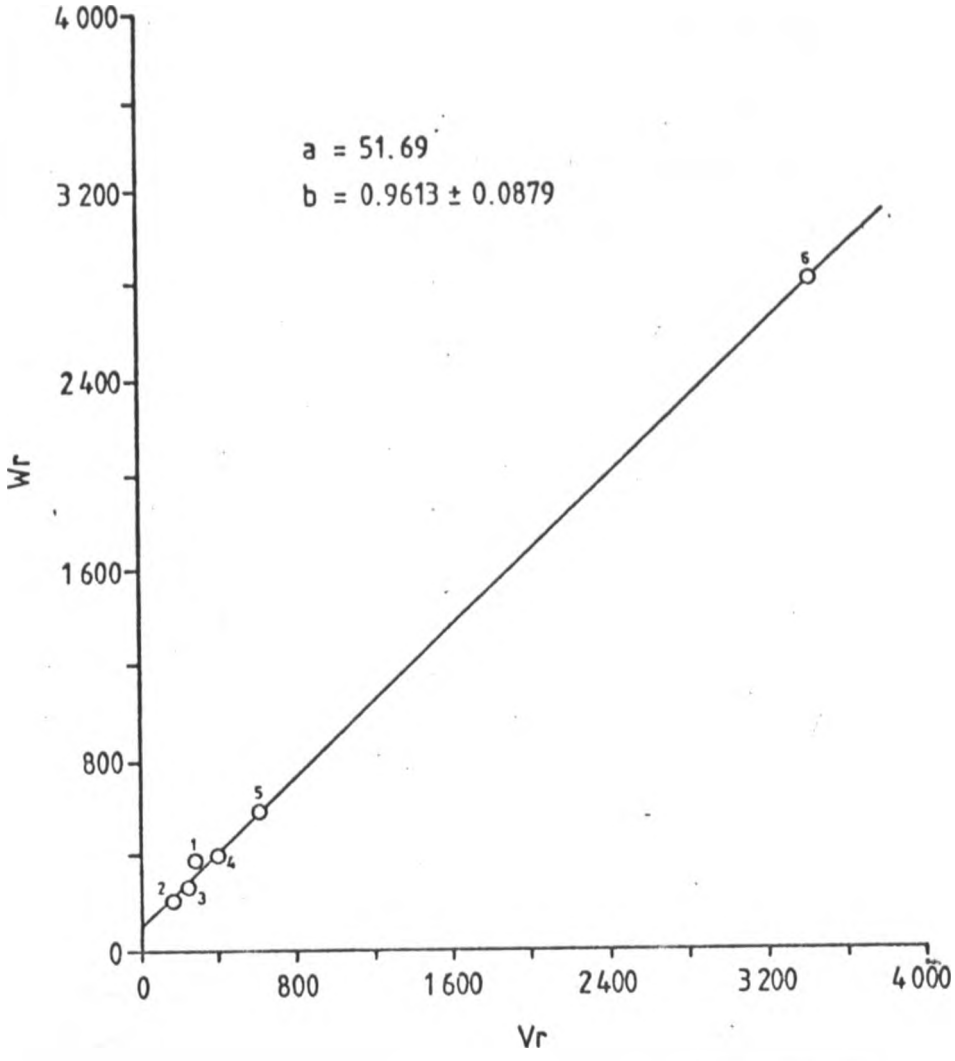

Fig. 14. Wr/Vr graph for Kernel Weight.
Location II (Jabali), 1985.

significant b2 genetic component. This was further supported by the $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ ratio (1.51, 0.93, (Tables 31 and 32) for location I and II, respectively. The F value obtained from location I (Sabwani) data (Table 31) indicated presence of more dominant than recessive alleles in the parents, while the opposite was true for location II (Jabali), (Table 32), hence no conclusion could be deduced from these observations.

High estimates of D (508.5, 810.6), H1 (452.1, 629.7) and H2 (421.5, 595.9), (Tables 31 and 32) were obtained in both locations. These estimates indicated that both additive and dominance gene effects were important in the determination of kernel weight.

The ratio $(H1/D)^{0.5}$ (0.94, 0.89) in Tables 31 and 32 indicated partial dominance gene action in the control of kernel weight inheritance. The positive 'a' intercepts ('a' = 28.7, 51.7; Figures 13 and 14) confirmed partial dominance gene action for kernel weight inheritance.

At least three genes or gene groups and a minimum of one effective factor were estimated to be involved in the expression of kernel weight, in location I (Table 31). In location II, at least

Table 31. Estimates of components of genetic variation for kernel weight in location I (Sabwani) during 1985 season.

Genetic component	Mean value
D	508.50 ± 57.778
H1	452.05 ± 146.671
H2	421.49 ± 131.025
h2	1134.13 ± 88.188
F	184.16 ± 141.148
E	69.26 ± 21.927
Derivatives	
$(H1/D)^{0.5}$	0.94
H2/4H1	0.24
h2/H2	2.69
K	0.68
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.51
Heritabilities	
+ HNS	50.4
# HBS	80.3

+ HNS - Narrow sense heritability

HBS - Broad sense heritability

Table 32. Estimates of components of genetic variation for kernel weight in location II (Jabali) during 1985 season.

Genetic component	Mean value
D	810.61 ± 67.079
H1	629.70 ± 170.272
H2	595.92 ± 152.108
h2	130379.21 ± 102.378
F	-46.15 ± 163.861
E	30.94 ± 25.354
Derivatives	
$(H1/D)^{0.5}$	0.89
H2/4H1	0.24
h2/H2	217.87
K	1.53
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	0.93
Heritabilities	
+ HNS	70.9
# HBS	95.0

+ HNS - Narrow sense heritability

HBS - Broad sense heritability

two effective factors and 217 genes or gene groups were estimated for kernel weight inheritance, (Table 32).

High narrow sense heritability values (NS; 50.4%, 70.9%) were obtained for kernel weight in location I and II, respectively, (Table 31 and 32). Phenotypic selection for heavier kernels would be possible, because of the high proportion of additive gene effect involvement in the inheritance of this trait. The difference between narrow and broad sense heritability values for the two sites indicated a small proportion of nonfixable genetic variation for kernel weight (Tables 31 and 32).

Results of location I (Figure 13) indicated inbred A to possess the highest proportion of dominant alleles while inbred 93 was indicated to carry the largest number of recessive alleles. The other inbred lines had intermediate frequencies of dominant and recessive alleles, with inbred F and G carrying proportionately more dominant than recessive alleles, while inbred 100 and 50 tended to have more of the recessive alleles (Figure 13). Inbred 93 was also indicated by the results of location II to carry the highest proportion of

recessive alleles (Figure 14). The rest of the inbreds; G, F, A,100 and 50 were close to the origin (Figure 14) indicating that these inbreds had more of dominant than recessive alleles, with inbreds A and F being the most dominant parents. The results on kernel weight suggested dominant alleles favoured greater weight while recessive alleles favoured low kernel weight.

4:5:2 Grain yield

Results on grain yield are presented in Table 3 and 4. Large differences between the progeny and parental yields were recorded in both locations. Yields among the parents ranged from 1481.5 kg ha^{-1} to 4074.0 kg ha^{-1} in location I (Sabwani, Table 3). The yields among the hybrids ranged from 4074.0 kg ha^{-1} to 7407.3 kg ha^{-1}. The highest yielding parent, inbred 100 yielded as much as the lowest yielding hybrid, 50 x 93, (Table 3). Mean yield of the hybrids exceeded the mean yield of the parents by as much as 188%. Heterosis for higher yields in the crosses was revealed by the large differences between the yields of the parents and their hybrids. In location II (Jabali) the yields of the parents ranged between 1481.5 kg ha^{-1}

and 4814.8 kg ha $^{-1}$ while those of the hybrids ranged between 4814.8 ha^{-1} to 12.222.1 kg ha^{-1}, Table 4). The highest yielding parents in location II were inbreds 100 and F (4814.8 kg ha^{-1}, Table 4) while inbred G was the lowest yielding parent in the same location. For both locations, the highest parental yields were equivalent to the lowest yielding hybrids (Tables 3 and 4). The hybrids in location II outyielded the parents by 113%, heterosis for higher yields was thus indicated by the results, (Table 4). The highest yielding hybrids were F x 93 and G x 93 for locations I and II, respectively. Both hybrids had inbred 93 as one of the parents indicating this inbred to have a high specific combining ability. On average, the crosses of related inbreds yielded less than the hybrids of unrelated inbred lines (Tables 3 and 4), indicating greater heterosis response in hybrids of unrelated parents.

Conformity of the data to the additive-dominance model with independent gene distribution was indicated by the consistency of Wr-Vr differences over arrays (Appendix II), and the regression coefficient 'b' values (0.448, 0.0699), which were not significantly different from unity (Figures 15 and 16).

Table 33. Analysis of genetic variances for grain yield in location I (Sahwani) during 1985 season.

Source of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	0.045	0.4240	0.4393
b1		1	7.900	72.8055	77.2935**
b2		5	0.077	1.4612	0.7564
b3		9	0.163	1.2840	1.5920
b		15	0.650	6.4420	6.3601**
(Treatments)	tr	20	8.84		
(Blocks)	B	1	0.009		
	Ba	5	0.1059		
Error	Bb1	1	0.1085		
Terms	Bb2	5	0.0529		
	Bb3	9	0.1267		
	Bb	15	0.1009		
	Btr	20	0.1022		

+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

Table 34. Analysis of genetic variances for grain yield in location II (Jabalia) during 1985 season.

Sourse of variation		Degrees of freedom (df)	Mean square	VR+	VR++
a		5	0.17	1.8478	1.6346
b1		1	10.98	447.3913*	105.5769**
b2		5	0.39	3.6449	3.7500*
b3		9	0.59	4.9580*	5.6731**
b		15	1.22	11.2963**	11.7308**
(Treatments)	tr	20	0.96		
(Blocks)	B	1	0.26		
	Ba	5	0.092		
	Bb1	1	0.023		
Error	Bb2	5	0.107		
Terms	Bb3	9	0.119		
	Bb	15	0.108		
	Btr	20	0.104		

\+ Each item tested against its own block interaction.

++ All items tested against pooled block interaction (Btr).

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

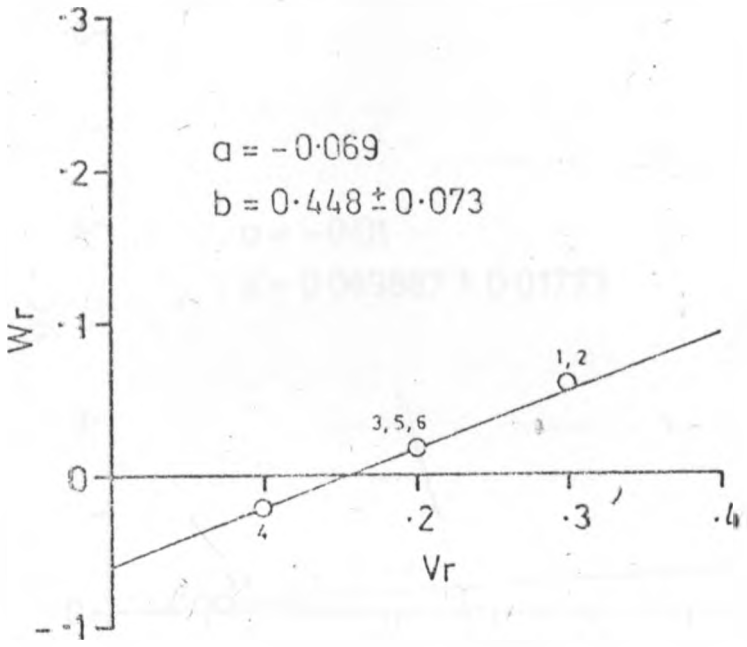

Fig. 15. Wv/Vr graph for Grain yield.
Location I (Sabwani), 1985.

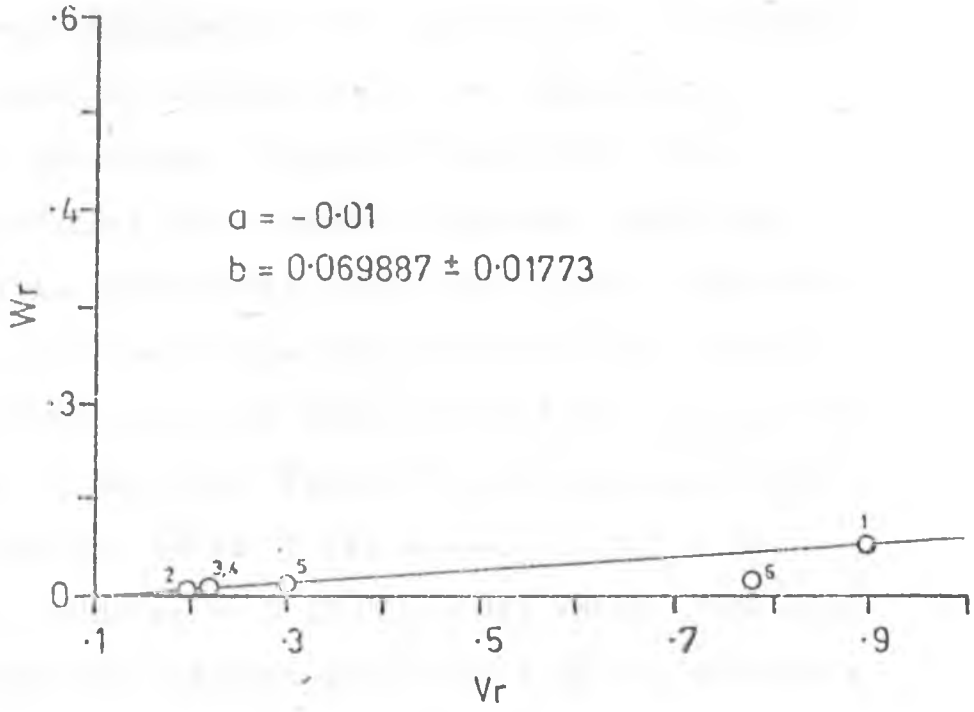

Fig. 16. Wr/Vr graph for Grain yield.
Location II (Jabali(, 1985.

General combining ability for yield as estimated by a played a nonsignificant role in the two locations, while specific combining ability for yield was indicated by the significant b component, to account for virtually all the significant genetic variation (Tables 33 and 34). The nonsignificant role played by general combining ability in determining yield was further indicated by the very low narrow sense heritability values (2.6%, Table 35, 6.1% Table 36) and the very low D values (0.06, 0.07, Tables 35 and 36, respectively). The large H1 (0.82, 1.88) and H2, (0.83, 1.73) values, relative to D (0.06, 0.08) values indicated a predominant dominant gene effect in the determination of yield. Significant deviation of progeny mean from the parental mean as a result of dominance effects was suggested by the significant b1 genetic component (Tables 33 and 34).

In location I, (Sabwani) asymmetry of dominant and recessive allele distribution in the parents was suggested by $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ ratio (1.31), F value (0.06) and the nonsignificant b2 component (Tables 35 and 36). The data obtained from location II (Jabali), (Tables 34 and 36)

Table 35. Estimates of components of genetic variation for grain yield in location I (Sabwani) during 1985 season.

Genetic component	Mean value
D	0.06 ± 0.068
H1	0.82 ± 0.175
H2	0.83 ± 0.156
h2	15.15 ± 0.105
F	0.06 ± 0.164
E	0.09 ± 0.026
Dereivatives	
$(H1/D)^{0.5}$	3.70
H2/4H1	0.25
h2/H2	18.25
K	6.16
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.31
Heritabilities	
+ HNS	2.6
= HBS	67.9

+ HNS - Narrow sense heritability.
= HBS - Broad sense heritability.

Table 36. Estimates of components of genetic variation for grain yield in location II (Jabali) during 1985 season.

Genetic component	Mean value
D	0.07 ± 0.281
H1	1.88 ± 0.714
H2	1.73 ± 0.638
h2	0.16 ± 0.306
F	0.16 ± 0.687
E	0.10 ± 0.106
Derivatives	
$(H1/D)^{0.5}$	5.18
H2/4H1	0.23
h2/H2	0.09
K	2.98
$(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$	1.55
Heritabilities	
+ HNS	6.1
= HBS	82.3

+ HNS - Narrow sense heritability.
= HBS - Broad sense heritability.

also indicated asymmetry in dominant and recessive allele distribution in the parents. The ratio $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$, (1.55); the F value (0.16), and the significant b2 components, all indicated asymmetry in allele distribution in the parents. The positive F value indicated an excess of dominant alleles over the recessive alleles in the parents.

The estimates of $(H1/D)^{0.5}$ 3.70, 5.18; Tables 35 and 36) were much greater than 1.0 and indicated that overdominance was involved in the determination of grain yield. Negative 'a' intercept (-0.01, -0.07, Figures 15 and 16, respectively) further indicated overdominant gene involvement in the expression of yield.

Nineteen genes or gene groups, with dominance effects were suggested by h2/H2 ratio in location I (Sabwani). The same estimate in location II (Jabali) was too low (0.09), considering earlier indications of a predominant dominant role in the expression of grain yield. A minimum of six and three effective factors for grain yield were estimated for location I and II, respectively.

The wide range between narrow and broad sense

heritability values, 2.6%, 6.1% versus 67.9, 82.3, respectively, (Tables 35 and 36) indicated that much of the genetic variation for grain yield was largely nonfixable.

Inbreds G and F (arrays 1,2) were indicated to carry the highest proportion of recessive alleles, while inbred 100 (array 4) was suggested to possess the highest proportion of dominant alleles, among the parents in location I (Figure 15). Inbreds A, 50 and 93 possessed intermediate values of dominant and recessive alleles. In location II, (Figure 16) inbred G had the highest proportion of recessive alleles among the parents, while inbred 93 was the second most recessive parent. The rest of the inbreds (F, A, 100 and 50) were indicated to have more of dominant than recessive alleles. Considering the relative positions of the arrays (Figures 15 and 16) and the relative yields among the parents (Tables 3 and 4), it was deduced that dominant alleles increased grain yield while the recessive alleles were responsible for low yields.

CHAPTER 5

DISCUSSION

The results reported in this study were obtained from an evaluation of six maize inbred lines and their F1 hybrids at two locations in one season. Genetic components and their possible contributions in the inheritance of the plant traits under consideration were estimated. Although the results ruled out the role of inter-allelic gene interactions in the expression of the traits considered, it must be pointed out that interallelic interactions often influence the estimation of genetic effects (Allard 1956, Jana 1975). Gene linkages in the repulsion phase are another source of possible bias in the estimation of some of the genetic parameters (Robinson et al.,1949, and Gardner et al., 1953), while seasonal and environmental differences have been reported to influence the genetic expression of certain traits (Allard, 1956; Paroda and Hayes, 1971; and Riggs and Hayter, 1972). The results of this study must thus, be considered in the light of these possible limitations.

5:1 Bare tip trait and ear husk leaf number

5:1:1 Bare tip

The results obtained at the two locations indicated heterosis for bare tip trait in those crosses with inbred G as one parent (Tables 3 and 4). Only one hybrid among the crosses involving inbred F; (F x 93) showed heterosis over the parental value in both locations. The rest of the hybrids showed little or no heterosis for greater bare tip numbers.

Both general and specific combining abilities (indicated by a and b genetic components. Tables 5 and 6) were important in the inheritance of bare tip. The much higher values of dominance effects, H1, H2 than additive effects, D values (Tables 7 and 8) suggested that dominance played a greater role than additive effects in the inheritance of this trait. The significant role of dominance gene effects in the expression of this trait was further indicated by the significant b1 genetic component, which suggested that dominance accounted for the significant deviation of progeny mean from the parental mean. Significant b3 component indicated presence of dominant gene effects, unaccounted for

by the b1 and b2 dominance effects. Asymmetry in distribution of dominant and recessive alleles in the parents was suggested by the significant b2 component in the two locations (Tables 5 and 6) and confirmed by H2/4H1 ratio (Tables 7 and 8). Presence of excess recessive alleles over dominant alleles in the parents was indicated by the negative F values and the $(4DH1)^{0.5} + F/(4DH1)^{0.5}-F$ ratio (Tables 7 and 8). Results reported herein suggested that recessive alleles were responsible for husk leaf extension (complete husk cover). The higher frequency of recessive alleles in the parents for this trait could have resulted through selection for complete husk cover in the population stocks from which these inbred lines were extracted.

Overdominance was suggested by $(H1/D)^{0.5}$ ratio (Tables 7 and 8) and the negative Wr intercept of Wr/Vr graph (Figures 1 and 2), to influence the expression of this trait. In contrast, Robinson et al. (949) suggested complete dominance for husk extension. Robinson et al. (1949) pointed out that tight linkage of certain genes controlling a given trait in the F1 generation could result in apparent overdominant gene effects for that trait. Overdominance could also result from

complementary interaction of genes, confounded in the estimation of average degree of dominance (Allard, 1956), or from multiplicative effects of individual components that contribute to the trait under consideration (Duarte and Adams, 1963). There is need therefore to investigate the genetic effects controlling this trait beyond the F1 generation.

At least one effective factor was suggested to control the expression of bare tip trait, for both locations (Tables 7 and 8). The two locations differed in the estimation of number of genes or gene groups that control the trait. In location I (Sabwani) this estimate was five while in location II (Jabali) the estimate tended to zero. Perhaps genotypic-environmental interactions could have caused the large differences between the two locations. Interactions of genotype - environment variances when specific combining ability is important are usually larger requiring more sites and seasons for evaluation in order to obtain a better approximation (Sprague, 1955). The effective factors and the number of genes or gene groups refer only to those genes or factors which have dominant gene action.

Genetic variability accounted for a high proportion of the total variance for this trait, in both locations. This was indicated by the high broad sense heritability values (Tables 7 and 8). Of the total genetic variation, a high proportion was accounted for by additive variance indicating possible rapid progress in selection for complete husk cover. High heritability values reported by Robinson et al. (1949) support the results recorded in this study.

In figures 1 and 2, the results suggested inbred G possessed the highest number of dominant alleles among the parents, and from the mean values of bare tip scores (Tables 3 and 4) it was observed that this inbred line had the highest number of ears with bare tips. Hybrids which had inbred G as one of the parents also had high scores of bare tip ears (Tables 3 and 4). Inbred 93 was suggestd by the results to carry the highest proportion of recessive alleles (Figures 1 and 2) and it was one of the two inbreds with the least bare tip scores (Tables 3 and 4). These results suggested that dominant alleles were responsible for the expression of bare tip trait while recessive alleles were responsible for complete husk cover of the ear.

For adequate protection of the ear against adverse effects of pests, pathogens and weathering extension of husks to cover the tip of the ear is a prerequisite, before selection for husk compression against the tip of the ear is considered. Starks and McMillian (1967) suggested extension of husk leaves to cover the tip of the ear was necessary. Douglas (1947) suggested a three inch extension of husk leaves beyond the ear tip to adequately confer resistance against earworm damage. Results obtained in this study suggested that selection for complete husk cover is possible. Selection for earworm resistance was effective in two maize synthetics, as reported by Zuber et al. (1971). The resistance was attributed to husk cover. Collins and Kempton (1917) demonstrated that characters for resistance to earworm damage were associated with husk extension and husk numbers and they were able to transfer these traits from field corn to sweet corn.

5:1:2 Ear husk leaf number

Half of the F1 progenies had ear husk numbers that were intermediate between those of

their parents, in both locations (Table 3 and 4). Five and seven hybrids in location I and II respectively had values greater than that of the better parent, two and one hybrid in location I and II respectively had same values as the better parent. Only one hybrid in location I had a value lower than that of the lower parent.

Both general and specific combining abilities (indicated by a and b components) were significant for both locations (Tables 9 and 10) indicating their involvement in the expression of husk leaf number. Brewbaker and Kim (1979) found a predominant general combining ability involvement in the expression of husk leaf number, with specific combining ability playing a small role, and associated mainly with tropical inbred lines. The additive component D was smaller than the dominance H1 genetic component in location I (Table 11) while in location II the estimate of D was larger than that of H1 (Table 12). The results indicate overdominance and complete dominance for the expression of husk leaf number in location I and II, respectively. The results of this study indicated that both additive and dominance effects were important in the inheritance of this trait, while

the results presented by Brewbaker and Kim (1979) indicated additive gene effects in the determination of husk leaf number. That dominant gene effects had a significant role in the expression of husk leaf number was further indicated by b1 genetic component in location I (Table 9). The deviation of the progeny mean from the parental mean was attributed to dominance effects. The results of location II (Table 10), (significant b2 component) indicated asymmetry of dominant and recessive allele distribution in the parents. This asymmetry was further supported by the estimate of H2/4H1 ratio (Table 12). Asymmetry of dominant and recessive allele distribution in the parents was suggested by H2/4H1 ratio in location I (Table 11). A nonsignificant b2 component (Table 9) however indicated that the observed asymmetry was not significant. Positive F value for the two locations (Tables 11 and 12) indicated that there were more dominant than recessive alleles in the parents for this trait.

The results of location I (Table 11) suggested overdominance (1.18) to have determined the inheritance of husk leaf number, while the data of location II, (Table 12) suggested complete

dominance for the inheritance of husk leaf number. The observed overdominance could be a true presentation of allelic mode of action. It could also have resulted from gene interactions. Allard (1956) pointed out that overdominance could result from complementary gene interactions which increase variance (Vr) values relative to the covariance (Wr) values. Tight linkage of loci in repulsion phase could also have caused the observed overdominance (Robinson et al., 1949; Gardner et al., 1953).

A minimum of four effective factors were estimated by location I results, to control the inheritance of husk leaf number. This value is however at variance with the estimated value in location II, which was estimated to be one (Tables 11 and 12). The estimated values of genes or gene groups also differed between the two locations (Tables 11 and 12). The approximate value for this trait however cannot be discerned from these results; more locations and seasons may be required to approximate the genes or gene groups for this trait.

Moderately high narrow sense heritability

values (51.7%, 46.6%; Tables 11 and 12) for husk leaf number were obtained in this study. Brewbaker and Kim (1979) obtained similar results (52% and 47%) for this trait. These results suggest that progress through selection for this trait is possible.

The relative positions of the inbred lines (arrays) along the Wr/Vr regression line are presented in Figures 3 and 4. In both locations inbred A (array 3) (Figures 3 and 4) was indicated to have the largest proportion of recessive alleles. This inbred also had the least number of husk leaves in both locations (Tables 3 and 4). Inbred F (array 2) was indicated to be the most dominant parent in location I (Figure 3) but not in location II (Figure 4). This inbred had the highest score of husk leaves in both locations (Tables 3 and 4). From these results, it was deduced that dominant alleles caused an increase in the number of husk leaves while recessive alleles decreased this number. The results of this study seem to indicate no association between bare tip trait and the number of husk leaves. Inbred A, with the least number of husk leaves had less bare tip ears than inbred F which had the largest number of husk leaves. Inbred

G had the highest number of bare tip ears among the parents but did not have the least number of husk leaves. Collins and Kempton (1917) reported resistance to earworm attacks was associated with husk leave extension and husk leaf numbers.

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5:2 Leaf number per plant

Results of this study indicated that both additive and dominance gene effects were important in the inheritance of leaf number. Higher values of additive, a and D components, relative to dominance effects, b,H1,H2 components (Tables 13, 14, 15 and 16) suggested that additive gene effects played a bigger role than dominance effects in the inheritance of leaf number. Similar results were reported by Bonaparte (1977) and Rood and Major (1981). General combining ability played a bigger role than specific combining ability in the inheritance of leaf number Russel and Stuber (1985). Mean values of F1 hybrids were intermediate between parental values for leaf number, in many instances (Tables 3 and 4) and a few F1 values exceeded the parent with higher leaf number score. High narrow sense heritability values (73.2, 84.0) obtained and the small differences between these values and broad sense heritability values (87.6, 91.4) confirmed the major role that additive gene action had in the expression of leaf number. High narrow and broad sense heritability values were reported by Bonaparte (1977), and Rood and Major, (1981). Considering the significant role of additive gene effects and the high heritability values obtained,

leaf number was considered a highly heritable trait and progress through selection for it would be effective.

Partial dominance (0.64, 0.55; Tables 15 and 16) was indicated by $(H1/D)^{0.5}$ ratio and confirmed by the positive Wr intercept (Figures 5 and 6). Partial dominance for leaf number was also reported by Leng (1951), Bonaparte (1977) and Rood and Major (1981). The role of dominance gene effects in determining leaf number, though smaller than additive gene effects, was significant. This was indicated by the significant b1 gene components (Tables 13 and 14), similar results were reported by Bonaparte (1977).

Asymmetry in the distribution of dominant and recessive alleles in the parents was suggested by H2/4H1 ratio (Tables 15 and 16) and b2 component (Table 15). Bonaparte (1977) and Rood and Major (1981) reported similar findings. The results of F1 (negative values) and $(4DH1)^{0.5}$ +F/ $(4DH1)^{0.5}$ -F ratio indicated the presence of more recessive than dominant alleles in the parents. Bonaparte (1977) reported presence of more dominant than recessive alleles in the material he studied.

At least two effective factors (K) were suggested by the results to control this trait in the two locations (Tables 15 and 16). The estimation of the number of genes or gene groups that control the expression of this trait for location I and II were too varied (Tables 15 and 16) to be relied on. The estimation of the effective factors and the genes or gene groups pertains only to those loci that exhibit some degree of dominance in the control of the trait under consideration (Hayman, 1954b; Jinks, 1954). A minimum of one effective factor was reported to govern leaf number inheritance Bonaparte (1977).

The most dominant parent, inbred 93 had the highest leaf number score in location I (Table 3) and was among the inbreds with the highest score in location II (Table 4). Inbreds G and A were the most recessive parents. Inbred A had the least number of leaves per plant, while inbred G had the second lowest score. The relative positions of the arrays along the Wr/Vr line and the mean leaf number estimates indicated partial dominance gene effects for greater leaf number.

5.3 Days from planting to pollen shed.

Results obtained in this study indicated the presence of heterosis for earlines. The F1 mean was much lower than the parental mean for days to pollen shed. Some of the hybrids flowered earlier than the earliest parent. Heterosis for earlines was also reported by Yang (1949), Leng (1951) and Rood and Major (1980). The Wr/Vr graph for days to pollen shed indicated that dominant alleles favoured earliness while the recessive alleles caused lateness in flowering. Rood and Major (1980) reported similar results. The three late flowering inbreds; 100, 50 and 93 also had the highest proportion of recessive alleles. The opposite was true for the three early flowering inbreds, G, A, and F.

Diallel analysis showed that both additive and dominance gene effects were involved in the inheritance of days to pollen shed (Tables 17 and 18). Similar findings were reported by Bonaparte (1977), in maize. In sorghum, Chiang and Smith (1967) found both additive and dominance gene effects to be involved in the expression of days to bloom.

Estimation of average degree of dominance $(H1/D)^{0.5}$ indicated overdominance involvement in

the expression of flowering time. Overdominance was reported by Chiang and Smith (1967) to be involved in the expression of flowering time in sorghum. In contrast to the results of this study, Giesbrecht (1959) and Rood and Major, (1980) reported partial dominance for early flowering in maize. Although overdominance gene effects were suggested for flowering time in this study, other factors such as gene linkage in the repulsion phase could have caused the observed overdominance (Robinson et al., 1949; Gardner et al., 1953). Epistasis though ruled out by the model could have been the cause of overdominance (Allard, 1956; Jana, 1975). Giesbrecht (1959), by carrying out analysis beyond the F1 found epistasis effects for earliness in maize.

Dominance was observed to be involved in the expression of flowering time in this study. Yang (1949), Mohamed (1959) and Bonaparte (1977) have reported similar results in maize. Extra dominance deviation not accounted for by b1 and b2 components was indicated by the significant b3 component.

Asymmetry of dominant and recessive alleles at loci showing dominance for earliness was

indicated by b2 and H2/4H1 values. Similar results were obtained by several workers; (Chiang and Smith, 1967 ; Phul et al., 1970; Paroda and Hayes, 1971; Riggs and Hayter, 1972; Bonaparte, 1977). There were more dominant than recessive alleles in the parents for this trait, as suggested by the positive F values and the $(4DH1)^{0.5} + F/(4DH1)^{0.5}-F$ ratio. In support of these results were the findings reported by Bonaparte (1977).

At least four effective factors were estimated for flowering time in this study. Five four, and three effective factors for flowering time in maize were reported by Giesbrecht (1959) Mohamed (1959) and Bonaparte (1977), respectively. The estimates of the number of genes or gene groups for earliness for the two locations were too variable for an approximate number to be deduced.

Moderately high narrow sense heritability values (47.4%, 55.9%) were obtained for flowering time in the present study. These resuts indicated possible progress in selection for earliness. The heritability values obtained for flowering time in this study were lower than those reported by Giesbrecht (1959) and Rood and Major (1981), in maize experiments. Much higher heribatility values were reported in sorghum experiments by Phul et al. (1970), Ibrahim et al. (1985).

5:4 Plant height and ear height

5:4:1 Plant height

Heterosis for greater plant height was indicated by the results obtained in this study. Both additive and dominance gene effects were suggested to be involved in the inheritance of plant height (Tables 21 and 22). Additive and dominance gene action were reported to be involved in the expression of plant height in sorghum by Chiang and Smith (1967).

Dominance, H1 and H2 components of genetic variation exceeded the additive component D, indicating dominance gene effects played a bigger role than additive gene effects in the control of plant height. Similar results in maize experiments were reported by Darrah and Hallauer (1972) and Rood and Major (1981). The smaller role played by additive gene effects in the expression of this trait was further indicated by the low narrow sense heritability values, 5.6%, 1.1%. Whereas narrow sense heritability values were low, very high broad sense heritability values (87.4%, 96.2%) were obtained, showing a high proportion of

genetic variability which was largely nonfixable. Rood and Major (1981) reported results that support the findings of this study. Low narrow sense heritability values were reported for plant height in sorghum by Chiang and Smith (1967). In contrast to the results of the present study, high narrow sense heritability values were reported for plant height in maize by Robinson et al. (1949). The predominant dominant gene effects for plant height reported in this study were at variance with the additive gene effects reported by Castro et al. (1968); Russell and Eberhart (1970) and Cornelius and Dudley (1976) to play a bigger role when compared to other forms of gene action, in determining plant height. The results of these workers do not support the findings of this study. Additive and dominant gene effects were equally important in the determination of plant height as observed by Moreno-Gonzalez and Dudley (1981) in Maize.

Overdominance for plant height was suggested by $(H1/D)^{0.5}$ ratios, which were far in excess of 1.0, the value for complete dominance. Negative Wr intercept in the Wr/Vr graph supported the observed overdominance. Results similar to those obtained

in this study were reported by other workers; (Bauman, 1959; Rood and Majar, 1981; in maize and Chiang and Smith, 1967) in Sorghum.

Partial dominance for plant height was reported by Robinson et al. (1949) and Gamble (1962b). Yang, (1949) reported dominance gene effects, while Gardner et al. (1953) reported partial to complete dominance gene effects for plant height in maize. Partial to complete dominance gene effects for plant height in maize, reported by these workers do not support the findings of this study. Overdominance gene effects reported for plant height in maize by Rood and Major (1981)were attributed to overdominance in one of the components of plant height; internode length. It was pointed out by (Duarte and Adams, 1963 / and Sinha and Khanna, 1975) that apparent overdominance for a given trait could actually result from multiplicative effects of components that individually show partial or complete dominance. Other workers have suggested possible causes of apparent overdominance observed for various traits. Allard (1956) suggested possible confounding of complementary gene interaction in the estimation of $(H1/D)^{0.5}$. Tight linkage of certain genes in repulsion phase was advanced by

Robinson et al. (1949) and Gardner et al. (1953) to be a possible cause of apparent overdominance for plant height in maize.

Slight asymmetry of dominant and recessive alleles was suggested by H2/4H1 ratio (0.24, Tables 23 and 24). Positive F values and $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ ratio (Tables 23 and 24) indicated an excess of dominant alleles over recessive alleles in the parents. Symmetry of allele distribution in the parents, in maize was reported by Rood and Major (1981). Extra dominance deviation in the present study was suggested by significant b3 component. Chiang and Smith (1967) in sorghum studies reported significant b3 component.

Fourty four and fifty five genes or gene groups were estimated in location I and II, respectively, for this trait. Four and five effective factors in location I and II, respectively, were estimated for the same trait.

Inbred G was indicated by the Wr/Vr graph (Figures 9 and 10) to be the most recessive parent while inbred 100 was the most dominant parent. Inbreds 93, 50, F and A had intermediate values of dominant and recessive alleles. The results of the relative positions of the inbred lines (arrays)

along the Wr/Vr line and those of Tables 3 and 4 indicated dominance for greater plant height. The most dominant parents, inbreds 100 and 50 in that order, were the tallest parents while the most recessive parent, inbred G was the shortest parent.

5:4:2 Ear height

Heterosis for greater ear height was indicated by the results presented in Tables 3 and 4. The progeny mean exceeded the parental mean and F1 hybrid values exceeded that of the parent with higher ear placement. Heterosis for higher ear placement was reported by Giesbrecht, (1961).

Both dominance and additive gene effects significantly contributed to the inheritance of ear height, (Table 25 and 26), however, higher dominance; H1 and H2 estimates, (Tables 27 and 28) indicated that dominance played a major role in the expression of this trait. Dominance for greater ear height in maize was reported by Kimani and Drolson (in press). Partial to complete dominance for ear height was reported Gardner et al., (1953) while Robinson et al., (1949) found no dominance for ear height. Ear height was largely determined by additive gene effects in maize, (Castro et al., 1968; Cornelius and Dudley, (1976).

These observations did not support the results obtained in this study. Both dominance and additive gene effects were found by Thompson et al.,(1971) to be important in the inheritance of ear height in maize, although the dominant effects were several times greater than the additive effects. These observations are similar to those obtained in the present study.

Overdominance was suggested by $(H1/D)^{0.5}$ and the negative Wr intercept, to control ear height inheritance. These results were not in agreement with the results reported by Gardner et al., (1953) and Giesbrecht, (1961). The possibility that the estimates of the degree of dominance, $(H1/D)^{0.5}$ for ear height could have been influenced by gene linkages,(Robinson et al., 1949; Gardner et al., 1953) and complementary gene interaction, (Allard, 1956) cannot be ruled out. Epistatic gene effects were found by Thompson et al., (1971) to significantly influence ear height expression in some of the maize hybrids he studied.

Nonsignificant asymmetry of allele distribution was indicated by the b2 genetic component in location I, (Table 25) while in location II, this asymmetry was significant. For both locations, F and $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$

estimates indicated more dominant than recessive alleles in the parents for this trait.

Eighteen and fifty nine genes or gene groups which exhibited some dominance in the control of this trait were estimated for location I and II, respectively. Four and three effective factors for the trait were estimated in location I and II, respectively. Between four and seven effective factors were reported by Giesbrecht (1961) to control the expression of ear height in maize.

As indicated by high broad sense heritability values (Tables 27 and 28), genetic variability accounted for much of the total variation. Narrow sense heritability was found to account for a small (17.9%, 15.0%) proportion of the total genetic variation. The results suggested a slow but possible phenotypic selection for ear height. In contrast to the results of this study, Robinson et al. (1949) Giebrecht (1961) and Moll et al. (1975) reported high narrow sense heritability values for ear height in maize.

Dominance for higher ear height and recessiveness for lower ear height was suggested by the results of Tables 3 and 4 and the relative

distribution of parents along the Wr/Vr regression line (Figures 11 and 12). The parents with the highest proportion of dominant alleles; inbreds 100 and 50 had the highest ear placement, while the opposite was found to be true for inbreds G and F. Inbred 93 carried a greater number of dominant alleles than inbread A and accordingly, it had a high ear placement than inbred A.

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5:5 Kernel weight and Grain yield

5:5:1 Kernel weight

Over sixty per cent of the F1 hybrids had mean kernel weight values intermediate between those of their parents (Tables 3 and 4). Four and five hybrids in location I and II, respectively, had higher values than the higher parent while one hybrid in location I had a mean kernel weight lower than that of the lower parent. Partial dominance atmost seemed to govern the inheritance of kernel weight.

Both additive and dominance gene effects were suggested to contribute significantly to the inheritance of kernel weight (Tables 29 and 30) although additive gene effects were found to play a bigger role than dominance gene effects in determining kernel weight. Similar results were reported for kernel weight in maize by other workers; (Russell and Eberhart, 1970; Helms et al., 1971; Johnson, 1973; Cornelius and Dudley, 1976; Kimani and Drolsom, in press). Additive and dominance gene effects were found to contribute more or less equally in the expression of kernel weight in maize (Darrah and Hallauer, 1972).

Partial dominance for greater kernel weight was suggested by the results obtained in this study. Cornelius and Dudley (1976) reported complete dominance for kernel weight in maize, while Hallauer and Russell (1962) reported partial dominance for greater kernel weight in maize.

Asymmetry of dominant and recessive allele distribution as indicated by b2 and $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ values was obtained in this study. The observed asymmetry was due to the presence of more dominant (positive F values) than recessive alleles in the parents. Chiang and Smith (1967) reported asymmetry of allele distribution in the parents in sorghum. The observed asymmetry in the sorghum experiment was due to more recessive than dominant alleles in the parents.

One and two effective factors (K) were estimated in location I and II, respectively. While these values (K) were not very different from one another, there was a big difference between the estimates of the number of genes or gene groups that exhibit dominance in the expression of kernel weight in the two locations. The approximate number of these genes or groups of genes could not therefore be deduced from the results of these two locations.

High narrow sense heritability values (Tables 31 and 32) for kernel weight were obtained in this study. These values indicated the possibility of progress through selection for heavier kernels.

Inbred A and F were the most dominant parents. They also had the heaviest kernels. Inbred 93 on the other hand was the most recessive parent and had the lightest kernels. Inbreds 50 and 100 ranked second and third most recessive parents, respectively. Their kernel weight scores conformed to the relative proportions of dominant alleles each parent carried. It was observed that dominant alleles increased kernel weight while low kernel weight was due to recessive alleles.

5:5:2 Grain yield

Heterosis for higher yield was suggested by the results of this study. The lowest yielding hybrid, 50 x 93 yielded as much as the highest yielding parent, inbred 100. Heterosis for higher grain yield in maize was reported by Robinson and Cockerham (1961); Moll et al. (1962); Hallauer and Eberhart (1966); Castro et al. (1968); Troyer and Hallauer (1968) and Gerrish (1983). The results obtained in this study indicated a higher

heterotic response for higher yields in crosses of unrelated parents. Crosses of related parents had lower heterotic responses for higher yields than crosses of unrelated parents. Similar findings were reported by Moll et al. (1962) and Moreno-Gonzalez and Dudley (1981).

General combining ability as estimated by a genetic component played an insignificant role in the determination of yield. Essentially, dominance gene effects accounted for all the significant genetic variability for grain yield in this study. The significant b1 genetic component further supported the predominant role played by dominance gene effects in determining grain yield. Similar results were reported by Gamble (1962a); Russell and Eberhart (1970); Darrah and Hallauer (1972); Johnson (1973); Cornelius and Dudley (1976) and Moreno-Gonzalez and Dudley (1981). Results reported by Mason and Zuber (1976) and Kimani and Drolsom (in press), which indicated a predominant additive role in the expression of grain yield were in contrast to the findings of this study. Very low narrow sense heritability values (6.1% and 2.6%) for grain yield were obtained in this study. These results supported the insignificant role played by

additive gene effects in the determination of grain yield. Low narrow sense heritability values (20.1%) for grain yield in maize was obtained by Robinson et al. (1949).

Overdominance gene effects for grain yield were obtained in the present study. Overdominance for grain yield in maize was also reported by Robinson et al. (1949); Gardner et al. (1953) and Gardner and Lonnquist (1959). Values for average degree of dominance $(H1/D)^{0.5}$ ranging from complete dominance to overdominance were reported by Hallauer (1970) for grain yield in maize. Partial dominance for grain yield reported by Lonnquist (1953) did not support the results obtained in this study. Overdominance gene effects were reported to influence the expression of grain yield in maize, although it was suspected to have resulted from linked loci which otherwise show partial to complete dominance gene action (Robinson et al., 1949; Cornelius and Dudley, 1976). Gardner and Lonnquist (1959) reported the presence of overdominance in F2 and larger additive effects in F8 than in F2 indicating possible gene linkage as the cause of the observed overdominance. Grafius (1960) pointed out that

there may not be any genes for yield as a single component but its components and the observed overdominance could be the "geometry of the situation". Gardner and Lonnquist (1959) found no evidence of overdominance in the components of yield. Allard (1956) suggested complementary gene interaction to be a possible cause of overdominance.

Symmetry of dominant and recessive allele distribution in the parents was suggested by the data of location I; (b2 and H2/4H1) while asymmetry was suggested by the results of location II. An excess of dominant over recessive alleles was indicated by $(4DH1)^{0.5} + F/(4DH1)^{0.5} - F$ ratio and the estimate of F in location II. Genotype - environmental interactions could have caused the recorded difference in allele distribution between the two locations.

Six and three effective factors (K) were estimated for location I and II, respectively. There was a large difference in the estimates of the genes or gene groups between the two locations. The value obtained in location II was too low and it was assumed to be a spurious estimate.

Inbred 100 was indicated to carry the highest

proportion of dominant alleles and it was also found to be the highest yielder among the parents. Inbred G was the most recessive parent and had the lowest grain yield. The results of this study indicated that dominant alleles increased grain yield while recessive alleles were responsible for low grain yield.

CONCLUSION

1. Both additive and dominance gene effects contributed to the inheritance of bare tip and husk leaf number traits. Dominance was however indicated to play a major role. High heritability values were obtained for both traits.

2. Leaf number inheritance was largely controlled by additive effects. Partial dominance for greater leaf number was indicated. High heritability values were obtained for this trait.

3. Additive and dominance gene effects were involved in the expression of days from planting to pollen shed. Overdominance for earliness was suggested and high heritability values were obtained.

4. Dominance and additive gene effects were suggested to be involved in the inheritance of plant height and ear height. Dominance gene effects however played a greater role than the additive gene effects. Narrow sense heritability values were low for both traits, while broad sense heritability values were high.

5. Additive gene effects were nonsignificant

for grain yield and dominance gene effects accounted for all the significant genetic variability, while both additive and dominance gene effects contributed significantly to the inheritance of kernel weight. Additive gene effects were more important than dominance gene effects for this trait. Partial dominance gene effects for greater kernel weight was suggested while overdominance for higher yields was suggested for grain yield. Very low and very high narrow sense heritability values for grain yield and kernel weight respectively were obtained.

On the basis of information obtained in this study for various characters of six maize inbred lines and all possible F1 hybrids, it may be suggested that better maize hybrids could be obtained taking into consideration the type of gene action involved for various characters, for example, a hybrid which is comparatively more suitable to Kitale conditions, i.e fully covered ears, tall with high number of leaves and greater grain yield could be obtained using suitable hybrid combinations. Hybrids such as A x 50 and F x 100 would combine high grain yields and low bare tip scores.

Similar types of gene action may also be involved in the expression of characters under

for grain yield and dominance gene effects accounted for all the significant genetic variability, while both additive and dominance gene effects contributed significantly to the inheritance of kernel weight. Additive gene effects were more important than dominance gene effects for this trait. Partial dominance gene effects for greater kernel weight was suggested while overdominance for higher yields was suggested for grain yield. Very low and very high narrow sense heritability values for grain yield and kernel weight respectively were obtained.

On the basis of information obtained in this study for various characters of six maize inbred lines and all possible F1 hybrids, it may be suggested that better maize hybrids could be obtained taking into consideration the type of gene action involved for various characters, for example, a hybrid which is comparatively more suitable to Kitale conditions, i.e fully covered ears, tall with high number of leaves and greater grain yield could be obtained using suitable hybrid combinations. Hybrids such as A x 50 and F x 100 would combine high grain yields and low bare tip scores.

Similar types of gene action may also be involved in the expression of characters under

consideration, in other maize inbred lines maintained at Kitale and possibly Embu. Thus the results obtained in the present study may have a wider application than limited to these six inbred lines, used in this study.

In population improvement for a given trait or traits, reciprocal recurrent selection would be useful when both additive and dominance effects are important. When dominance gene effects are of major importance for a given trait, recurrent selection for specific combining ability would be useful. Recurrent selection for general combining ability would be effective for those traits which are controlled primarily by additive gene effects.

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APPENDIX 1. Analysis of variance of data obtained in 1985 season at two locations, on eight maize traits.

Trait				
Bare tip				Location
Source of variation	df	Ms	F ratio	
Total	41	18.585		Sabwani
Replications	1	9.500	6.2295*	
Treatments	20	36.100	23.6721**	
Error	20	1.525		
Total	41	19.215		
Replications	1	1.170	1.625	Jabali
Treatments	20	38.615	53.6319**	
Error	20	0.720		

APPENDIX 1. Cont.

Source of variation	Trait: Husk leaf number df	Ms	F ratio	Location
Total	41	1.032		
Replications	1	0.009	0.2247	Sabwani
Treatments	20	1.710	4.2697**	
Error	20	0.401		
Total	41	1.176		
Replications	1	0.004	0.0167	Jabali
Treatments	20	2.169	9.0075**	
Error	20	0.241		

APPENDIX 1. Cont.

Trait				
	Leaf number			Location
Source of variation	df	Ms	F ratio	
Total	41	0.707		
Replications	1	0.020	0.200	Sabwani
Treatments	20	1.350	13.5000**	
Error	20	0.100		
Total	41	0.860		
Replications	1	0.009	0.1125	Jabali
Treatments	20	1.683	21.0375**	
Error	20	0.080		

APPENDIX 1 cont.

Trait				
	Days to pollen shed			Location
Source of variation	df	Ms	F ratio	
Total	41	39.250		
Replications	1	4.100	0.2435	Sabwani
Treatments	20	77.220	25.3200**	
Error	20	3.050		
Total	41	33.733		
Replications	1	5.356	5.5967*	Jabali
Treatments	20	67.929	70.9812**	
Error	20	0.957		

APPENDIX 1, Cont.

Trait				
	Plant height			Location
Source of variation	df	Ms	F ratio	
Total	41	2015.900		
Replications	1	192.900	0.8416	Sabwani
Treatments	20	3893.700	16.9882**	
Error	20	229.200		
Total	41	2124.824		
Replications	1	1220.400	18.5260**	Jabali
Treatments	20	4228.995	64.1973**	
Error	20	65.875		

APPENDIX 1. Cont.

	Trait			
	Ear height			Location
Source of variation	df	Ms	F ratio	
Total	41	1045.276		
Replications	1	247.238	2.5302	Sabwani
Treatments	20	2032.750	20.8066**	
Error	20	97.705		
Total	41	971.466		
Replications	1	75.000	0.606	Jabali
Treatments	20	1864.060	15.0700**	
Error	20	123.695		

APPENDIX 1. Cont.

Trait				
	Kernel weight			Location
Source of variation	df	Ms	F ratio	
Total	41	316.900		
Replications	1	12.600	0.1837	Sabwani
Treatments	20	580.595	8.4629**	
Error	20	68.605		
Total	41	573.200		
Replications	1	48.400	1.5643	Jabali
Treatments	20	1142.100	36.9134**	
Error	20	30.940		

APPENDIX 1, Cont.

Trait				
	Grain yield			Location
Source of variation	df	Ms	F ratio	
Total	41	0.2902		
Replications	1	0.0090	0.0947	Sabwani
Treatments	20	0.5000	5.2632**	
Error	20	0.0950		
Total	41	0.5243		
Replications	1	0.2593	2.4861	Jabali
Treatments	20	0.9577	9.1822**	
Error	20	0.1043		

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

APPENDIX II. Analysis of variance of Wr-Vr over arrays, 1985 season data at two locations.

Trait	Location	Source of variation	df	Ms	F ratio
Bare tip	Sabwani	Total	11	40.06	
		Replications	1	23.00	0.8606
		Lines	5	58.82	2.1257
		Error	5	26.72	
	Jabali	Total	11	28.22	
		Replications	1	0.30	0.0128
		Lines	5	38.56	1.6436
		Error	5	23.46	

APPENDIX II. Cont.

Trait	Location	Source of variation	df	Ms	F ratio
Husk leaf number	Sabwani	Total	11	0.16	
		Replications	1	0.17	1.1972
		Lines	5	0.17	1.2113
		Error	5	0.14	
	Jabali	Total	11	0.19	
		Replications	1	0.87	3.6802
		Lines	5	0.15	0.6176
		Error	5	0.24	

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APPENDIX II. Cont.

Trait	Location	Source of variation	df	Ms	F ratio
Leaf number	Sabwani	Total	11	0.006	
		Replications	1	0.008	0.001
		Lines	5	0.005	0.625
		Error	5	0.008	
	Jabali	Total	11	0.022	
		Replications	1	0.001	0.0384
		Lines	5	0.028	1.3196
		Error	5	0.021	

APPENDIX II. Cont.

Trait	Location	Source of variation	df	Ms	F ratio
Days to pollen shed	Sabwani	Total	11	24.16	
		Replications	1	14.70	0.9620
		Lines	5	32.74	2.1427
		Error	5	15.28	
	Jabali	Total	11	17.72	
		Replications	1	41.80	3.7664
		Lines	5	19.53	1.7598
		Error	5	11.10	

APPENDIX II. Cont.

Trait	Location	Source of variation	df	Ms	F ratio
Plant height	Sabwani	Total	11	169969.7	
		Replications	1	253693.7	1.4651
		Lines	5	150033.7	0.8664
		Error	5	173160.9	
	Jabali	Total	11	53752.9	
		Replication	1	125706.0	8.4430
		Lines	5	78226.4	5.2541
		Error	5	14888.8	

APPENDIX II. Cont.

Trait	Location	Sourse of variation	df	Ms	F ratio
Ear height	Sabwani	Total	11	666.0	
		Replications	1	224352.0	11.9100**
		Lines	5	82819.5	4.3966
		Error	5	18837.3	
	Jabali	Total	11	6223290.5	
		Replications	1	59647598.0	62.1511**
		Lines	5	802000.8	0.8357
		Error	5	959718.8	

APPENDIX II. Cont.

Trait	Location	Source of variation	df	Ms	F ratio
Kernel weight	Sahwani	Total	11	8451.6	
		Replications	1	30120.1	4.3404
		Lines	5	5630.1	0.8113
		Error	5	6939.4	
	Jahali	Total	11	7554.7	
		Replications	1	5949.7	1.6511
		Lines	5	11827.0	3.2821
		Error	5	3603.5	

APPENDIX II. Cont.

Trait	Location	Source of variation	df	Ms	F ratio
Grain yield	Sabwani	Total	11	0.01	
		Replications	1	0.02	1.4286
		Lines	5	0.004	0.2857
		Error	5	0.014	
	Jabali	Total	11	0.134	
		Replications	1	0.000	
		Lines	5	0.247	
		Error	5	0.047	5.2553

** Significant at 1% level.