

**GENERAL AND SPECIFIC COMBINING ABILITY FOR GRAIN AND YIELD  
COMPONENTS IN A DIALLEL CROSS AMONG SELECTED NINE INBRED LINES  
OF MAIZE (*Zea mays* L)**

**BY**

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## **DECLARATION**

Declaration by the Candidate

This research thesis is my original work and has not been submitted to any other university by any other person for the award of any degree or diploma.

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## **DEDICATION**

To my mother Mary Wairimu, my husband Anthony Chelongo and daughter Antonellah Wairimu for their love, understanding and encouragement.

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## ABSTRACT

Analysis of combining ability plays an important role in identifying elite parents and crosses which can give best combinations based on the performances of their offspring. Hybrid variety production requires broad genetic base among the germplasm as materials to be used as parents because their increase heterosis which can be exploited. There is little knowledge on general and specific combining ability of inbred lines developed by Maseno University maize breeding programme which lead to development of inferior parent and crosses, also knowledge on inbred lines make breeding process more effective as save breeding cost and time. The general objective of this study was to identify parents and crosses with desirable combining ability in order to contribute to increased grain yield. The specific objectives were to analyze general and specific combining ability among selected maize inbred lines and their hybrids for grain yield and yield components among selected inbred lines and their hybrids, assessment of heterosis for F1 hybrids involving selected inbred lines of maize. The study was carried out in the Maseno University demonstration farm between 2019-2021 The study involved making crosses among nine inbred lines in half diallel method II model I to obtain 36 F1 hybrids and evaluating them. The nine inbred lines and their 36 hybrids were planted in randomized complete block design with three replications. The crosses were used to estimate general combining ability (GCA) and specific combining ability (SCA) effects on grain weight, yield related traits and assess heterosis for the F1 hybrids in order to select suitable parents for hybridization and identify superior and promising hybrids. The eight traits measured included days to 50% flowering, days to 50% silking, plant height, ear height, cob length, and cob width, number of rows per cob and grain weight. The data were subjected to Analysis of variance (ANOVA) and means separated using the Least Significant difference at  $p < 0.05$ . Mean squares for genotype, SCA and GCA were found to be significantly different. Inbred lines F620R, Cy441/2 and RC 9 were found to be good general combiners for most of the traits hence they can be useful for hybrids development. Crosses F620R X Ex 389, Ex614P X F620R, Ex614P X F-white, F-white X Cy441/2 and Cy441/2 X RC 9 had high positive and significant SCA for grain weight and most of yield related traits hence can be used to develop superior hybrids. Specific combining ability based on yield was used to indicate heterotic grouping of crosses. GCA: SCA ratio were high for days to 50% flowering, days to 50% silking, plant height and number of rows per cob while it was low for ear height, cob width, cob length and grain weight. This shows the importance of both GCA and SCA in inheritance of yield and yield related traits. Among 36 F1s all crosses exhibited high heterosis for grain yield except Ex 614P X Ex bear, Ex 614P X Ex 389, Ex 389 X Bear614 and F620R X Cy441/2 which exhibited low heterosis values. Identified parents and crosses with high GCA and low SCA values could be used in development of superior hybrids and synthetic varieties. There was significance difference in GCA, SCA and heterosis among genotypes hence they is genetic difference which can be exploited further.

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## **CHAPTER ONE**

### **INTRODUCTION**

#### **1.1 Background to the study**

Hybrid varieties of maize are preferred due to their high yielding capacity compared to unimproved maize varieties as they increase farmers` maize production and help to solve food insecurity problem in most developing countries (Hallauer *et al.*, 2010). The identification of the elite lines is important since such lines have desirable traits and can be used as parents for superior hybrid development (Elmyhun *et al.*, 2020; Karim *et al.*, 2018; Oakey *et al.*, 2006; Waburton *et al.*, 2002).

Knowledge on inheritance of quantitative traits and combining ability of parents is important in hybrid breeding programs (Chandel & Mankotia, 2014; Menkir *et al.*, 2003). Combining ability is an estimation of value of genotypes in relation to performances of their offspring using appropriate mating designs (Allard, 1960). General and specific combining ability was first introduced by (Sprague & Tatum, 1942) . General combining ability (GCA) is used to identify the average performance of a line in hybrid combinations while specific combining ability (SCA) is used to exhibit cases in which certain crosses combinations do better or worse than would be expected based on the average performance of lines involved (Ejigu *et al.*, 2017; Griffing, 1956). General and specific combining abilities are useful for characterization of inbred lines and their related crosses (Fasahat *et al.*, 2016). This concept was defined by Sprague and Tatum (1942). Griffing formulated mathematical expression model (Griffing, 1956), which also integrated GCA and SCA concept in diallel crosses. Combining ability concept is used to ‘test’ procedures that compare the relative performances of inbred lines in their respective hybrid combination.

Diallel mating design involves crossing among all parental lines in all possible combinations in order to identify the parents having best and poor combining ability in terms of GCA or SCA. Other procedures used in testing of combining ability include polycrosses, open pollination and top crosses (Frandsen, 1952; Hanson et al., 1956; Morrow et al., 1958). There are four methods of diallel cross, common two methods being half diallel and complete diallel method. Half diallel method involves making crosses excluding their reciprocal while complete diallel cross is a mating design in which a set of  $p$  inbred lines is selected and possible crosses are made including their reciprocal crosses (Griffing, 1956). Analysis of diallel crosses involves partitioning out the total genetic variation into GCA and SCA.

General and specific combining ability effects give an estimate of additive and non-additive gene variances respectively (Falconer, 1996). GCA is a result of gene action which is additive in their effects while SCA arises from the dominance and epistatic (non-additive) gene action (Griffing, 1956). GCA and SCA effects can be determined by making crosses among a set of selected parents and evaluating the performances of their progeny (Begna, 2021). Therefore, combining ability analysis helps in providing useful information on the nature of gene effects which mainly influence polygenic traits (Fasahat *et al.*, 2016). Maize improvement by crossbreeding largely depends on combining ability for set of parents. Combining ability analysis helps in selecting suitable parents which may have desirable traits such as high yield, disease resistance and drought tolerance (Ertiro *et al.*, 2017).

## **1.2. Problem statement**

In the Maseno University maize breeding programme, a number of inbred lines have been developed with the aim of making superior hybrid varieties. For the inbred lines to be useful in

hybrid variety development, adequate knowledge on their combining abilities is mandatory. There is little knowledge on a number of inbred lines developed in Maseno University maize breeding programme with regard to their general and specific combining abilities. Lack of adequate information on general and specific combining abilities usually leads to development of inappropriate and low yielding hybrid varieties; also lack of information on combining makes breeding process expensive, tiresome and is time consuming. Combining ability, especially specific combining ability is an indicator of exploitable genetic diversity among parental lines in a breeding program.

### **1.3. Objectives**

#### **1.3.1. General objective**

To determine combining ability for 36 F1 hybrids and nine maize inbred lines for grain and yield components to contribute increased to grain production in maize.

#### **1.3.2. Specific objectives**

1. To estimate general combining ability of selected maize inbred lines for grain and yield components
2. To estimate specific combining among 36 F1 hybrids involving the selected inbred lines.
3. To determine heterosis among F1 hybrids involving selected inbred lines of maize.

### **1.3 Null Hypotheses**

1. There are no significant differences in general combining ability among selected inbred lines for grain and yield components.
2. There are no significant differences in specific combining ability for yield components and grain yield among the F1 hybrids.

3. There are no significant differences in heterosis among F1 hybrids involving selected inbred lines.

#### **1.4. Justification**

Although there is big achievement that modern plant breeding has made towards improved food security in Kenya and world at large, it is important to continue developing and advancing plant breeding programs due to increasing grain food demand. Knowledge on combining ability is essential for the development of good hybrids in terms of adaptability, yield, and pest and disease resistant maize varieties. Combining ability is useful for selecting suitable parents and also providing information regarding nature of important gene effects that play roles in influencing quantitative traits in maize.

#### **1.5. Significance of the study**

This study is expected to generate information on general and specific combining ability of nine inbred lines and their 36 hybrid combinations. The study help identify maize parental lines with good combining ability which can be used in breeding programs in order to develop superior hybrids and synthetic varieties.

## **CHAPTER TWO**

### **LITERATURE REVIEW**

#### **2.1. Introduction**

Maize is staple food in most developing countries and world's most widely grown cereal crop (Olaniyan, 2015; Shifiona *et al.*, 2016). Maize is highly cross pollinating crop, making it possible to exploit heterosis in breeding programmes by developing high yielding hybrids, synthetics and composites (Pavan *et al.*, 2011). Maize was introduced in Africa from America (Smale & Jayne, 2003). Cultivation of maize requires less technical skills and capital compared to crops like cotton and tobacco. Maize gives higher yields under favorable environmental conditions unlike many indigenous crops like sorghum and millet ( Wang *et al.*, 2018).

#### **2.2 Maize (*Zea may L.*) breeding**

Ancient breeding that was done for many years by American Indians before European colonial era. Breeding procedures like crossing ear-to-row and mass selection were mainly used to develop and improve new varieties of the open pollinated crops in 1800s and 1900s before the technology of development of inbred lines for hybrid seed production had started (Hallauer *et al.*, 1988; Sass *et al.*, 1977). Hybrid development begun in early 1900s through the work of Shull 1909, among others (Lee & Tracy, 2009). Cross-pollinating nature of maize leads to exchange of genetic material as pollen flows among maize populations (Zhang *et al.*, 2018). In case random cross pollination is not required there will be need to prevent unwanted pollination so as to help maintain genetic purity in a crop (Saxena & Hingane, 2015). When self-pollination occurs in several generations the progenies tend to have undesirable traits while cross-fertilization leads to significant yield advantage of hybrids as compared to their parents (Smale & Jayne, 2003).

Modern maize breeding has led to development of varieties that have high yields, improved adaptability with disease and pest resistance (Yadav *et al.*, 2015). The process of making crosses and screening for producing hybrids with high performance and assessing heterosis is expensive, time consuming and tiresome, hence in a situation where heterosis can be predicted and superior combination identified before final hybridization the cost of hybrid production is reduced (Labroo *et al.*, 2021; Venkateswarlu *et al.*, 2011).

According to Duvick (2005) an average of 50% of the current maize grain yield increase is due to agronomic field management while the other 50% is as result of breeding. Due to hybrid breeding programmes sustained breeding efforts have led to continuous changes in hybrid characteristics over the years making them more resistant to abiotic and biotic stresses that affect maize production (Yadav *et al.*, 2015). Newly developed hybrids have higher grain yields, compared to the old hybrids due to the fact that one of the major goals of developing newer hybrids is to improve the ability of maize varieties to resist stress rather than increase grain yield per se (Duvick, 2005).

### **2.2.1 Inbred lines**

Inbred lines are important component of hybrid breeding programmes (Tamirat *et al.*, 2014). They show high degree of homogeneity, homozygosity and consistency and lack heterosis due to inbreeding through sibbing and selfing for many generations (Gayatonde *et al.*, 2021; Odiyo, 2013). The effective generations of inbreeding of inbred lines determine the degree of homozygosity (Crnokrak & Barrett, 2002) . For example 99.22% homozygosity can be achieved after seven generations of selfing is done (Tripodi, 2021). All inbred lines are developed and

maintained through many generations because the more it is selfed the more genetic integrity will be maintained (Hallauer *et al.*, 1988).

### **2.3 Maize heterosis**

Heterosis refers to genetic expression of the superior of hybrid in relation to its parents in terms of size, growth, fertility and yield (Birchler *et al.*, 2006; Rehman *et al.*, 2021). Heterosis is influenced by the genetic divergence of parental lines. For example hybridization between inbred lines that have been developed from closely related lines leads to small magnitude of heterosis (Barata & Carena, 2006). The phenomenon of heterosis in maize has been explained mainly by one of the two hypotheses which include the hypothesis of dominance and hypothesis of heterozygosis (Fujimoto *et al.*, 2018). The dominance hypothesis was proposed by Bruce (1910) and Keeble and Pellew (1910). This hypothesis suggests that the increase of vigor after hybridization is a result of combining different dominant alleles from each of the parents. On other hand heterozygosis hypothesis was first formulated by Shull (1911a, b) and East and Hayes (1912) is based on occurrence of different alleles at different loci (Bonneuil, 2008). Heterozygotes at the various loci combine in a complementary manner with consequent physiological activities leading to increase in vigor in the individual affected (Kaeppler, 2012).

Shull (1946, 1948) introduced the concept of overdominance which was thought to be the same as heterotic gene interaction. Another hypothesis was proposed by Brieger (1950) who suggested that the nature of the inter-allelic interaction may be of dominant complementary factors. Rasmusson (1933) also proposed the idea of quantitative gene interaction to explain heterosis. The concept of heterotic groups has also been used to explain heterotic patterns (Brieger, 1950). Heterotic groups refer to a group of unrelated genotypes from the same or different populations

which display heterosis and combining ability when crossed with genotypes from other genetically distinct germplasm groups (Begna, 2021; Xie *et al.*, 2014) .

Determination of heterotic pattern is important factor for exploitation of heterosis in order to maximize performance of the population crosses and developed hybrids (Eberhart & Russell, 1969). Heterotic patterns have a major influence on improvement of crops because they predetermine the type of germplasm that will be used in breeding process (Meena *et al.*, 2017; Melchinger & Gumber, 1998; Tracy & Chandler, 2006).

Heterotic grouping for maize germplasm is important for a plant breeder because it helps in maximum exploitation and utilization of heterosis for hybrid development. Assessing genetic diversity of germplasm is essential as it helps in formation of heterotic groups (Reif *et al.*, 2003). Crosses among unrelated heterotic groups of inbred lines yield better compared to those that belong to same heterotic groups (Barata & Carena, 2006; Hallauer *et al.*, 1988; Melchinger & Gumber, 1998). Genetic diversity and heterotic groupings are important features in hybrid development since it is useful to the breeder. Maize germplasm heterotic groups can fully be exploited for heterosis purpose if they are adequately diverse (Begna, 2021; Melchinger, 1999).

### **2.3.1 Establishment of heterotic patterns**

Heterotic patterns can be established based on two strategies, namely strategy proposed by Cress 1967 and another proposed by Melchinger and Gumber 1998 (Mitiku Abdeta, 2021). Cress 1967 strategy was reviewed in terms of simulation study and suggested that every genetic resource that will be inserted into long-term program of interpopulation improvement should be crossed into a synthetic population (Hallauer *et al.*, 2010). Melchinger and Gumber 1998 established criteria of identifying new heterotic patterns which are based on;

1. High mean performance and high genetic variability in hybrids,
2. High adaptability in hybrid populations.
3. Minimal inbreeding depression in the hybrids.

According to last strategy heterotic patterns can be established based on performance of related hybrid population.

### **2.3.2 Methods of developing heterotic groups**

#### **Pedigree method**

Reid and Lancasters heterotic groups were identified through pedigree evaluation of inbred lines that were used in the USA Corn Belt (Santiago *et al.*, 2013). This involved classifying inbred line into groups based on pedigree information and predicting heterotic patterns for increased efficiency of population improvement (Badu-Apraku *et al.*, 2021; Betrán *et al.*, 2003).

#### **Quantitative genetics analysis**

Quantitative genetics usually focus on the genetic basis that affects phenotypic variation among individuals (Mackay, 2014). Quantitative genetics analysis provides the bases for evaluating the genetic merit of potential parents (Johannes *et al.*, 2009). Quantitative genetics analysis focuses on the inheritance of traits between individual (Bijma, 2014; Roff, 2012). A study by Melchinger (1999) showed different ways to group and identify heterotic groups. Hallauer and Miranda (1988) used quantitative genetics to develop hybrid.

### **2.3.3 Heterotic grouping**

Heterotic grouping is important since it helps in identifying related and unrelated inbred lines which is very useful for exploiting heterosis (Begna, 2021). Heterotic grouping contribute to the

specific combining ability and also hybrid vigour of subsequent generation (Yu *et al.*, 2020). Inbred lines Ex614P, Hanang 4, Exbear, Ex389, and Bear614 belong to heterotic group A while F620R, F-White, Cy441/2 and RC 9 belongs to heterotic group B.

#### **2.4 General and specific combining ability**

Combining ability is parents' ability to combine well with each other during the crossing process so that favourable genes or traits can be transmitted to their offspring (Fasahat *et al.*, 2016). General combining ability (GCA) and specific combining ability (SCA) have influence on inbred line and hybrid combinations selection. GCA is the average performance of a genotype in hybrid combinations while SCA is defined in regard to when a hybrid combination performs better or poorer as compared to what is expected on basis of the average of parental inbred lines (Sprague & Tatum, 1942).

Good GCA is achieved when parents show high average combining ability in crosses while good SCA is achieved if parents' potential to combine well is related to a particular cross (Fasahat *et al.*, 2016). GCA is usually main additive effect and SCA is as considered non-additive interaction effect (Kulembeka *et al.*, 2012).

The diallel crosses are used to study the genetic control of traits and select parents to obtain either hybrids or synthetics in crops (Rodrigues *et al.*, 2006; Welcker *et al.*, 2005). GCA is useful in selection of suitable parents based on the performance of the offspring mostly in F1 but also in F2 and other generations as well. A low GCA value, which might be a positive or a negative value indicates that mean of a parent in crossing with the other parent does not vary largely from overall mean of their cross while a high GCA value indicates that the parental mean is inferior or superior to the overall mean of the crosses (Fasahat *et al.*, 2016). High GCA value suggests the

potential occurrence of desirable gene effects which can easily be transmitted from the parents to the progenies. It also gives information about existinse additive genes (Caixeta Franco *et al.*, 2001). A high GCA value is important since it indicates higher heritability of traits to the progenies with less environmental effects, with minimal gene interaction which make process of selection of desirable parents easy (Chigeza *et al.*, 2014; Topal *et al.*, 2004). Desirable parents should have good adaptability and produce superior hybrids when crosses are made, especially when selection for good cross combinations is done (Bao *et al.*, 2009). Information about GCA effects can help to utilize existing variability in germplasm resources in order to select a parent with desirable characteristic and distinguishes genotypes into heterotic groups (Lv *et al.*, 2012; Sprague & Tatum, 1942).

High SCA values obtained from crosses where both parents have good GCA may be as a result of additive x additive gene action (Dey *et al.*, 2014; Verma & Srivastava, 2004). Specific combining ability usually relates to dominance and epistatic effects of the genes. The SCA is useful to the breeder since it helps in determining heterotic patterns among inbred lines to find out the promising single crosses and put the genotypes into heterotic groups (Fasahat *et al.*, 2016; Menkir & Maziya-Dixon, 2004; Warburton *et al.*, 2005). GCA and SCA effects for a particular line are calculated only when GCA and SCA overall mean squares are significant Dabholkar, (1992).

Interaction between GCA and SCA play important role in plant breeding. In case in which GCA and SCA are not significant epistatic gene may be involved inheritance of traits (Farshadfar *et al.*, 2013). The ratio of combining ability mean square is mostly used to predict the type of gene action involved in expression of traits and also gives information on additive and non-additive

gene which resource that that be exploited in hybrid breeding (Fasahat *et al.*, 2016). When SCA mean squares exceed GCA mean square

#### **2.4.1 Combining ability for yield**

Grain yield is a quantitative trait and mostly it is dependent on other traits such as yield related trait (Peng *et al.*, 2019). Yield related traits include days to flowering, days to silking, and days to maturity, plant height, ear height, leaf length, leaf width cob length, cob width, number of row per cob and grain weight. Usually it is not effective to do selection based on grain yield data only, hence it is important to examine yield related components which influence yield production (Lawlor & Paul, 2014).

#### **2.5. Mating designs in plant breeding**

Mating designs are procedures of producing required progenies by a breeder. They are six mating design namely bi-parental progenies, polycrosses, topcross, line X tester, North Carolina (I,II,III) and Diallel (I,II,III,IV) (Acquaah, 2009; Griffing, 1956). Bi-parental mating is design in which a number of plants are paired off to give half sib families the parents are mated only once in pairs. Polycrosses mating is a cross in which the female parent is known but the male may belong to any of several available strains and which is used in the production of new line (Nduwumuremyi *et al.*, 2013). Topcross mating design occurs as result between superior male and inferior female to improve the average quality of the progeny (Witcombe & Virk, 2009). Line X tester is mating design where inbred lines are crossed to a common line. North Carolina design is a mating type each member of a group of parents is used as males is mated to a different group of parents used as females (Muthoni & Shimelis, 2020). Diallel is mating of selected parents are crossed in all possible combinations The choices of mating design to be used

depend on the objective of the study and availability of resources such as space (Nduwumuremyi *et al.*, 2013). Analysis of variance is used to estimate the components of variance.

## **2.6. Diallel design**

Diallel design was introduced by a Danish geneticist called Schmidt, 1919 while Griffing formulated mathematical expression model (Griffing, 1956), which also integrated GCA and SCA concept in diallel crosses (Bolboacă *et al.*, 2011). This design was first used in plant breeding in 1950's. In this mating design the parent genotypes are crossed in all possible combinations (Pospíšilová, 2010). The genetic analysis of a diallel design usually operates based on the following five assumptions.

1. There should be no epistasis and non-allelic interactions
2. Parents must be diploid and homozygous.
3. There should not be reciprocal differences
4. The genes are independently distributed between the two parents involved in the cross.
5. Should not have multiple alleles.

Diallel mating design is used mostly in recurrent selection. All diallel design mating methods described by (Griffing, 1956) are useful in estimating variability existing in the crosses and estimating GCA and SCA for quantitative traits (Christie & Shattuck, 2010). The reciprocal effects estimated in the diallel designs helps to quantify existing variation due to maternal effects of some traits (Fasahat *et al.*, 2016; Rashid *et al.*, 2007). The diallel mating designs use two models of analysis, namely, fixed and random models (Griffing, 1956). A random model is where parents are selected randomly in a random population and is important in estimating GCA and SCA variability (Nduwumuremyi *et al.*, 2013). Fixed model involves estimating the GCA effects

for each inbred line used as parents and SCA effects for each pair of inbred line used in hybrid combination (Makumbi *et al.*, 2011). Diallel mating which has selfed parents and reciprocals is not useful because selfing does contribute to recombination of genes between parents (Acquaah, 2009).

The fixed model in method III and IV diallel analysis is most suitable for obtaining unbiased estimates of GCA and SCA effects and also indicates gene action (Oliveira *et al.*, 2016). One shortcoming of diallel design is that it makes analysis of data complex. Apart from providing estimates for lines GCA, diallel analysis also tests GCA as well (Sharma, 2006). Relatively high GCA/SCA ratio shows importance of additive gene effects while a lower GCA/SCA variance ratio demonstrates occurrence of dominance or interaction effects (Christie & Shattuck, 2010; Nduwumuremyi *et al.*, 2013).

Diallel methods of Griffing are mostly used for multi-environment trials, one location trial and also can be used for one environment trial which are known to give genetic information that is more reliable (Fasahat *et al.*, 2016). The interpretation of the combining ability effects and variances is mostly dependent on the source of parents and diallel method used. The four different diallel procedures and their analyses given by (Griffing, 1956) are briefly described as below.

### **Method 1**

This is also referred to as full diallel design, and consists of parents, one set of F1's generation and reciprocal F1's. It gives  $p^2$  genotypes. Mathematical models for analysis of combining ability are random and fixed models as given by (Griffing, 1956). The number of crosses plus the parents is given by  $p^2$ , where  $p$  is numbers of parents

## **Method II**

Method II includes parents and a set of F1`s without reciprocals. The number of crosses obtained is determined by  $p(p + 1)/2$  where p is numbers of parents.

## **Method III**

Method III includes set of F1`s and their reciprocal F1`s. The parents are not included. Number of possible crosses is obtained  $p(p-1)$  genotypes where p is numbers of parents.

## **Method IV**

Method IV includes only one set of F1`s in analysis. Parents and reciprocal crosses are excluded. This method is suitable where there is no reciprocal effect where p is numbers of parents. The number of crosses obtained is.

$$\frac{p(p-1)}{2}$$

The above four methods are often used to study patterns of inheritance of quantitative traits in a crop of interest (Moterle *et al.*, 2012; Vieira *et al.*, 2012).

### **2.7. Stability of combining ability effects in maize hybrids**

Stability of yield in a genotype refers to the ability of a variety to have uniformity in terms of yield environmental effects (Chemeli, 2016). Stability in combining ability estimates differs among hybrids depending on environment in which the cross progenies are tested (Oliveira *et al.*, 2009; Ribeiro *et al.*, 2000).

Studies by Machado (2008) and Aguiar (2003) suggest the presence of interaction between hybrids and environmental conditions, hence, it is important to identify hybrids that have wide

adaptation to different environments and are highly stable (Aguilar et al., 2003; J. C. Machado et al., 2008). Maize varieties with wide adaptability are useful in stabilizing yields under favorable environmental conditions. According to Plesisis, (2003) cultivars with a higher stability make it easier to predict yield ability of a crop (Du Plessis, 2003).

A study by Eberhart and Russel (1966) indicated that there were differences in GCA and SCA stability among populations assessed and that double-crosses obtained from the parents show higher stability as compared to single crosses. GCA and SCA stability parameters are mostly estimated using the method by Eberhart & Russel (1966).

## **CHAPTER THREE**

### **MATERIALS AND METHOD**

#### **3.1. Experimental site**

The experiment was conducted at Maseno University farm. The site lies along the Equator at latitude  $0^{\circ} 7' E$  and longitude  $34^{\circ} 30' S$  and elevation of 1515 m above sea. The area receives annual rainfall of about 1510-1750 mm per annum and mean precipitation of about 1618.44 mm per annum. The rainfall distribution is bimodal with, first season between March and June and second season is between August and October. The two seasons are separated with dry season. The ambient temperature is  $21.50^{\circ} C$ , ranging between a minimum of  $12.57^{\circ} C$  and a maximum of  $29.05^{\circ} C$  annually, (FAO, 2018).

#### **3.2. Plant material**

The materials used in the experiment were forty five genotypes which consist of 36  $F_1$  hybrids and nine inbred lines of maize developed by Prof Dida of Maseno University. The nine selected inbred lines were Ex 614P, F620R, Hanang 4, Ex bear, Ex 389, Bear614, F-white, Cy441\2 and RC 9. These nine inbred lines of maize which had morphological traits were crossed in a half diallel mating design method II proposed by (Griffing, 1956) to form 36  $F_1$  single crosses excluding reciprocals. Method II which includes parents and a set of  $F_1$ 's without reciprocals was used to calculate the number of genotypes that were to be used in experiment using the formula by Griffing 1956

$$\text{Genotypes} = p(p + 1)/2 = \frac{9(9+1)}{2} = 45 \text{ genotypes}$$

P= number of parents

### 3.3 Inbred line used and their pedigree

Most of inbred lines had related pedigree while others had unrelated pedigree shown Table 1 below which influences their combining ability.

**Table 1: Nine inbred lines used in experiment and their pedigree**

No.	Inbred line	Pedigree information
1.	Ex 614P	Is an inbred line developed from hybrid 614D.
2.	F620R	It is an inbred line developed from Ababario open pollinated variety.
3.	Hanang 4	It is an inbred line developed from a cross between 614 and a collection of Hanang from Tanzania.
4.	Exbear	It is an inbred line derived a cross between Hanang collection and an inbred line derived from hybrid 614D.
5.	Ex 389	It is an inbred line derived from a cross of inbred line hybrid 614 and cml 389.
6.	Bear614	It is an inbred line from a cross between Hanang collection derived line and an inbred line developed from hybrid 614D.
7.	F-white	It is an inbred line developed from Ababario collection in Maseno.
8.	Cy441/2	It is an inbred line derived from CIMMYT line Cy034 and Ex 441/2 inbred line.
9.	RC 9	It is an inbred line derived from Ababario open pollinated variety from Maseno.

Crossing was done April and May 2019 Table 2. Below show crosses made and evaluated in two seasons that experiment was done.

**Table 2: The list of 36 F generated through half diallel cross and their parental lines**

No.	Cross	Female parent	Male parent
1.	Ex 614P X Hanang 4	Ex 614 P	Hanang 4
2.	Ex 614P X F620R	Ex 614P	F620R
3.	Ex 614P X Ex bear	Ex 614P	Exbear
4.	Ex 614P X Ex 389	Ex 614P	Ex 389
5.	Ex 614P X Bear614	Ex 614P	Bear614
6.	Ex 614P X F-white	Ex 614P	F-white
7.	Ex 614P X Cy441\2	Ex 614P	Cy441/2
8.	Ex 614P X RC 9	Ex 614P	RC 9
9.	Hanang 4 X F620R	Hanang 4	F620R
10.	Hanang 4 X Ex bear	Hanang 4	Exbear
11.	Hanang 4 X Ex 389	Hanang 4	Ex 389
12.	Hanang 4 X Bear614	Hanang 4	Bear614
13.	Hanang 4 X F-white	Hanang 4	F-white
14.	Hanang 4 X Cy441\2	Hanang 4	Cy441/2
15.	Hanang 4 X RC 9	Hanang 4	RC 9
16.	F620R X Ex bear	F620R	Exbear
17.	F620R X Ex389	F620R	Ex 389
18.	F620R X Bear614	F620R	Bear614
19.	F620R X F-white	F620R	F-white
20.	F620R X Cy441\2	F620R	Cy441/2
21.	F620R X RC 9	F620R	RC 9
22.	Ex bear X Ex 389	Ex bear	Ex 389
23.	Ex bear X Bear614	Ex bear	Bear614
24.	Ex bear X F-white	Ex bear	F-white
25.	Ex bear X Cy441\2	Ex bear	Cy441/2
26.	Ex bear X RC 9	Ex bear	RC 9
27.	Ex 389 X Bear614	Ex 389	Bear614
28.	Ex 389 X F-white	Ex 389	F-white
29.	Ex 389 X Cy 441\2	Ex 389	Cy441/2
30.	Ex 389 X RC 9	Ex 389	RC 9
31.	Bear614 X F-white	Bear614	F-white
32.	Bear614 X Cy 441\2	Bear614	Cy441/2
33.	Bear614 X RC 9	Bear614	RC 9
34.	F-white X Cy441\2	F-white	Cy441/2
35.	F-white X RC 9	F-white	RC 9
36.	Cy441\2 X RC 9	Cy441/2	RC 9

### **3.4. Experimental design**

The experiment was laid out in randomized complete block design (RCBD) with forty five genotypes consisting of thirty six crosses and nine inbred lines. The forty five genotypes were replicated three times giving 135 experimental units in each season. Each genotype was planted in a single row plot of 3 meters long and a spacing of 75cm between rows 30 cm between plants within the row. Five seeds was planted per hill and then thinned to two plants per hill after three weeks of planting; a row had six hills, giving 12 plants per row. One guard row was planted surrounding experimental materials. The experiment was done in two seasons, that is, between August and December 2019 and April and December 2021 in Maseno University demonstration farm.

### **3.5. Data collection**

Data were collected for plant height, ear height, days to 50% flowering, days to 50% silking, cob length, cob width, and number of rows per cob, and grain weight. Five plants were randomly sampled per replicate for each genotype for data collection; this because five plants was close to half population of each plot which will give unbiased data (Hope *et al.*, 2003). Method used for data collection was same GCA, SCA and heterosis because only mean values were taken for each trait. Heterosis was estimated for the same traits as those of GCA and SCA.

- Plant height was measured using meter rule. The meter rule was placed at the base of a stem up to the shoot apex at flag leaf. Plant height was taken upon physiological maturity that a unit of measurement was in centimeter.
- Ear height was measured using a meter rule from the ground to the ear placement of plant using a meter rule upon physiological maturity in centimeter.

- Days to 50% flowering was taken on the day, half plants in a plot showed pollen. Days to flowering were calculated by getting difference between flowering day and planting day.
- Days to 50% silking was taken on the day half of the plants in plot shown silk. Silking days were recorded following number of days from planting until 50 % of plants show silk.
- Cob length was determined on five randomly selected plants at harvesting time by use of meter ruler at average mean was taken of five cobs.
- Number of rows per cob was determined on five randomly selected plants by counting rows in each selected plant and calculating average of each genotype.
- Grain weight was obtained by directly weighing the grains, after drying and shelling of grain in each five randomly selected cob in a replicate. one cob was collected data on per plant sample.

### **3.6. Data analysis**

Analysis of variance was computed for the grain yield and yield component traits measured as indicated above. AGD-R (Analysis of Genetic Designs) package in R Software was used for the analysis of variance of GCA and SCA values. The genotypes were considered fixed effect while environment was random effects. Significant means were separated by use of Least Significant Differences (LSD). Mean values of 36 F<sub>1</sub> crosses and nine inbred line were used to calculate GCA, SCA and was used to assess the heterosis the hybrid in the study. General combining ability for each parent was estimated as the mean of all crosses involving that inbred line minus the overall mean. Specific combining ability was estimated as deviation of population mean and corrected GCA values (Malik *et al.*, 2004). The Griffing method was used because it gives

unbiased analyses inbred lines and crosses as compared line X tester which gives analysis based on tester alone (Nduwumuremyi, *et al.*, 2013). Estimates of GCA and SCA were calculated and their significance was determined by use *t* test.

Interaction between general combining ability and specific combining ability play major role in identifying which gene of action is predominant and influence inheritance of traits in offspring. It was determined based on the ratio of mean square due general combining and specific combining.

Griffing (1956 b) method II model 1 was used for combining ability analysis as described by.

The linear model for this analysis is

$$Y = \mu + g_i + g_j + s_{ij} + y_k + r + e_{ijk} \dots \dots \dots (1)$$

Where,

Y= the mean phenotypic value of cross ij in replicate l in year k

$y_k$ = the effect of  $k^{th}$  year (season)

$\mu$  =the population mean;

$g_i$  = the general combining ability effect of the  $i^{th}$  parent.

$g_j$ = the general combing ability effects of the  $j$ th parents;

$s_{ij}$ = the specific combining ability effect of the cross between  $i^{th}$  and  $j^{th}$  parents.

$r_l$ =effect of replicate l in  $k^{th}$  year.

$e_{ijk}$  = the environmental effect associated with  $i, j, k^{\text{th}}$  observation.

$p$  = number of parent lines.

Population mean is the average value of certain genotype was obtained as

$$\mu = \frac{2}{p(p+1)} X_{..}$$

$\mu$  = the population mean

$p$  = number of parent lines

$X_{..}$  = overall mean

**Table 3: Equations for computation of components of ANOVA in method II diallel design**

Source of variation	Degree of freedom	Mean square	Expected means square
<b>Year</b>	$y - 1$	$MS_y$	
<b>Reps</b>	$r - 1$	$MS_R$	
<b>Genotypes</b>	$\frac{p(p+1)}{2} - 1$	$MS_G$	$\delta^2 e + ryc^2$
<b>GCA</b>	$p - 1$	$MS_{Gca}$	$\delta^2 e + \frac{p+1}{p-1} \sum g_i^2$
<b>SCA</b>	$\frac{(p-1)}{2}$	$MS_{sca}$	$\delta^2 e + \frac{2}{p(p-1)} \sum s_{ij}^2$
<b>Error</b>	$x$	$MS_e$	$\delta^2 e$
<b>Total</b>			

Source: Griffing (1956b)

$$\text{Error df. } x = \left( \frac{p(p+1)}{2} - 1 \right) - (p - 1) - \left( \frac{p(p-1)}{2} \right)$$

The GCA and SCA effects are estimated according to the analysis of Griffing 1956 as follows

Estimation of GCA for each parent was obtained as:

$$\text{GCA effects} \quad g_i = \frac{1}{p+2} [(X_{i.} + X_{.i}) - \frac{2}{p} X_{..}] \dots\dots\dots (2)$$

Estimation of SCA for each of 36 crosses was obtained as follows

$$\text{SCA effects} \quad s_{ij} = \frac{1}{p+2} (X_{i.} + X_{.i} + X_{ij} + X_{ji}) + \frac{2}{(p+1)(p+2)} X_{..} \dots\dots\dots (3)$$

Where

$X_i$  = total for means of the crosses involving the  $i^{\text{th}}$  parent.

$X_j$  = total for means of the crosses involving the  $j^{\text{th}}$  parents.

$X_{..}$  = overall mean;

$p$  = number of parent lines.

### 3.6 Estimation of heterosis

Heterosis was calculated from the midparent values for each character as follows:

$$\text{Heterosis} = \frac{F_1 - MP}{MP} * 100 \dots\dots\dots (4)$$

Where  $F_1$  = the hybrid mean

$MP$  = the midparent value

$$MP = \frac{(\text{mean parent 1} + \text{mean parent 2})}{2}$$

The differences in the mean values of  $F_1$  for all thirty six crosses and mid-parent of their related inbred lines was tested for significance of heterosis for eight traits taken in this study using ‘t’ value formula from Wynne, (1970) as follows:

$$t_{ij} = \frac{F_{ij} - MP}{\sqrt{1/2(EMS)}}$$

$F_{ij}$ - means performance of  $F_1$  both of parent  $i^{\text{th}}$  and  $j^{\text{th}}$

MP- means values of the parent (P1 and P2) of the cross

EMS- Error mean square

Calculated t-value is compared to tabulated t-value at 0.05(1.96) and for 0.01(2.57).

## CHAPTER FOUR

### RESULTS

#### 4.1 Single season analysis during short rains seasons 2019

The mean squares for general and specific combining abilities for eight traits in the study indicates significant differences for GCA and SCA effects in Table 4 below. GCA/SCA ratio was high for days to 50% flowering, days to 50% silking, plant height, ear height and cob length but ratio was less than one grain weight, cob width and number of rows per cob.

Mean values are important in analysis of GCA, SCA and heterosis values. Table 5 and Table 7 shows mean values in 2019 and 2021 of nine inbred line and thirty six F1 crosses.

**Table 4: Mean squares due to general and specific combining ability for eight traits in 2019**

Source of Variation	df	Plant height	Ear height	Days Flowering	Days Silking	Cob length	Cob width	Number of row	Grain Weight
Rep	2	5504.24*	2527.53*	108.40*	137.64*	4.28	0.30	2.60	0.74
Genotype	44	3543.80*	1144.13*	61.42*	72.58*	23.65*	1.22*	7.29*	8.67*
GCA	8	2544.26*	1012.30*	52.13*	67.19*	8.15*	1.98*	22.20*	12.67*
SCA	36	3770.84*	1179.81*	63.79*	73.95*	27.46*	1.06*	4.24*	7.82*
Error	88	619.50	306.98	14.94	16.96	3.07	0.11	2.13	0.65
GCA:SCA		1.5	1.2	1.2	1.1	3.4	0.5	0.2	0.6

\* indicate at 5% level of significance; GCA, General combining ability; SCA, Specific combining ability; Rep, Replicate; Df, degree of freedom.

#### 4.1.2. Mean values during short rains season 2019

**Table 5: Mean values of yield and yield component traits for 36 crosses and 9 inbred lines of maize for eight traits.**

Crosses/ Inbred line	Plant height (cm)	Ear height (cm)	Day to Floweri ng	Days to Silking	Cob length (cm)	Cob width (cm)	Numbe r of row	Grain weight (t/ha)
<b>P1 (Ex614P)</b>	170.3	99.0	91	95	10.0	2.2	8	0.7
<b>P2 (HANANG4)</b>	140.0	70.0	81	86	12.4	3.4	12	1.0
<b>P3 (F620R)</b>	157.7	81.9	83	88	8.6	3.5	11	1.0
<b>P4 (Exbear)</b>	158.3	95.7	88	91	10.9	3.5	10	1.7
<b>P5 (Ex389)</b>	117.3	58.3	92	98	11.7	3.1	10	1.4
<b>P6 (Bear614)</b>	155.3	86.0	92	96	10.4	3.1	12	0.9
<b>P7(F-white)</b>	153.3	73.7	88	91	10.4	3.4	11	1.3
<b>P8(Cy441/2)</b>	106.0	54.7	88	93	9.6	3.4	12	1.8
<b>P9 (RC 9)</b>	146.3	88.3	84	88	11.1	3.6	11	1.6
<b>Ex614 P X Hanang 4</b>	206.0	117.0	81	85	15.7	3.5	11	2.6
<b>Ex614P X F620R</b>	251.7	139.0	75	78	18.0	4.8	12	5.3
<b>Ex614P X Exbear</b>	194.0	95.0	82	87	14.0	3.7	10	2.3
<b>Ex614P X Ex389</b>	206.3	104.3	82	87	13.7	3.3	10	2.0
<b>Ex614P X Bear614</b>	221.0	120.7	81	85	15.7	3.6	10	1.9
<b>Ex614P X F-white</b>	245.3	131.0	75	79	17.3	4.2	13	4.7
<b>Ex614P X Cy441/2</b>	194.7	102.0	81	85	17.3	4.5	12	3.8
<b>Ex614P X RC 9</b>	224.0	118.0	80	83	17.0	4.1	11	3.7
<b>Hanang4 X F620R</b>	234.0	131.3	77	80	16.3	4.7	14	5.3
<b>Hanang 4 X Exbear</b>	200.3	63.7	83	86	16.0	3.9	12	3.1
<b>Hanang 4 X Ex389</b>	206.3	110.7	80	84	14.7	3.8	11	3.0
<b>Hanang 4 X Bear614</b>	235.3	128.7	77	81	16.3	3.9	11	3.2
<b>Hanang 4 X F-white</b>	234.0	124.7	78	80	16.7	4.3	12	4.4
<b>Hanang4 X Cy441/2</b>	185.3	94.7	78	81	18.7	4.1	14	4.5
<b>Hanang4 X RC9</b>	205.3	105.7	77	80	16.3	3.9	12	3.6
<b>F620R X Exbear</b>	239.3	126.3	81	85	17.3	4.6	13	4.4
<b>F620RX Ex389</b>	222.3	121.3	76	79	16.3	4.9	13	4.0
<b>F620R X Bear614</b>	236.0	133.0	76	79	16.0	4.8	13	4.7
<b>F620R X F-white</b>	211.7	103.0	76	80	16.0	4.7	14	4.0
<b>F620R X Cy441/2</b>	212.3	118.3	81	84	19.0	5.3	15	5.6
<b>F620R X RC9</b>	219.0	111.0	75	78	16.3	4.9	14	4.4
<b>Exbear X Ex389</b>	212.7	107.7	81	85	16.3	3.8	12	3.2
<b>Exbear X Bear614</b>	209.3	116.3	79	83	14.3	3.8	12	2.7
<b>Exbear X F-white</b>	242.0	129.7	78	81	17.3	4.3	13	4.0
<b>Exbear X Cy441/2</b>	197.7	92.7	78	81	20.0	4.7	14	7.1
<b>Exbear X RC9</b>	223.3	125.7	80	83	17.3	4.3	12	4.9
<b>Ex389 X Bear614</b>	207.7	109.0	82	85	14.0	3.8	11	2.4

<b>Ex389 X F-white</b>	236.0	121.3	76	80	16.3	4.2	12	3.7
<b>Ex389 X Cy441/2</b>	220.3	121.3	77	81	17.0	4.7	13	5.6
<b>Ex389 X RC9</b>	214.0	107.3	80	85	16.0	4.0	11	4.7
<b>Bear614 X F-white</b>	240.7	118.0	74	78	18.3	4.4	13	4.8
<b>Bear614 X Cy441/2</b>	193.7	101.2	77	81	16.7	4.4	13	5.6
<b>Bear614 X RC9</b>	231.7	128.3	77	80	17.7	4.4	12	5.0
<b>F-white X Cy441/2</b>	205.0	104.3	80	82	16.0	4.9	16	6.6
<b>F-white X RC9</b>	218.0	109.3	78	81	16.7	4.6	15	5.1
<b>Cy441/2 X RC9</b>	223.3	120.3	77	80	19.3	5.1	15	7.1
<b>MEAN</b>	203.6	107.0	80.3	83.9	15.4	4.1	12.2	3.6
<b>LSD (5%)</b>	40.4	30.0	6.4	6.8	2.8	0.5	1.2	1.3
<b>C.V%</b>	12.2	17.3	4.9	5.0	11.2	7.9	11.8	22.3

LSD, Least significant difference; C.V, Coefficient of variations

50% to days flowering ranged from 81 (Hanang 4) to 85 (Ex 389) and (Bear614) for inbred lines and 74 (Bear614 X F-white) to 83 (Hanang 4 X Exbear) for crosses. The mean for days to 50% flowering was 80. Days to 50% silking ranged from 86 (Hanang 4) to 98(Ex 389) days for inbred lines and 78 (Ex 614P X F620R, F620R X RC 9 and (Bear614 X F-white) to 87 (Ex 614P X Ex 389) and Ex 614P X Bear614) days for crosses with the mean of silking was 84 days.

Plant height for inbred lines ranged from 106cm (Cy441/2) to 170.3cm (Ex 614 P) and 185.3 cm (Hanang 4 X Cy441/2) to 251.7cm (Ex 614P X F620R) for the crosses with a mean of 203.6cm. Ear height ranged 54.7cm (Cy441/2) to 99.0cm (Ex 614 P) among the inbred lines and from 63.7cm (Hanang 4 X Exbear) to 139.0cm (Ex 614P X F620R) for the crosses with a mean 113.6 cm. Grain weight for inbred line ranged from 0.7 t/ha (Ex 614P) to 1.8 t/ha (Cy441/2) and for crosses it ranged from 2.0 t/ha (Ex614P X Bear614) to 7.1 t/ha (Exbear X Cy441/2) and (Cy441/2 X RC 9) with mean of 3.6t/ha.

Cob length for inbred lines ranged from 8.6cm (F620R) to 12.4cm (Hanang 4) and for the crosses it ranged from 13.7cm (Ex614P X Ex389) to 20.0cm (Ex bear X Cy441/2), with overall mean of 15.4cm. Cob width for inbred lines ranged 2.2cm (Ex 614P) to 3.6cm (RC 9) and for the

crosses it ranged from 3.3cm (Ex 614P X Ex 389) to 5.3cm (F620R X Cy441/2), with mean of 4.1cm.

Number of rows for inbred lines ranged from 8 (Ex 614P) to 12 (Hanang 4, Bear614 and Cy441/2) and for the crosses it ranged from 10 (Ex 614P X Ex bear, Ex 614P X Ex 389 and Ex 614P X Bear614) to 16 (F-white X Cy441/2), with mean of 12.2 rows.

#### 4.2. Means squares analysis of variance GCA and SCA during long season 2021

All the traits were significantly different for traits studied. The GCA/SCA ratio was less than 1 or equal to 1 for days to 50% flowering, days to 50% silking, plant height, ear height, cob width and number of rows, but higher than 1.0 for grain weight and cob width data shown in Table 6.

**Table 6: Means squares of analysis of variance of GCA and SCA for eight traits 2021**

Source of variation	Df	Plant height	Ear height	Days Flowering	Days to silking	cob length	cob width	Number of rows	Grain weight
Rep	2	23.57	60.66	5.12	7.46	0.29	0.03	0.54	1.34
Genotype	44	3960.05*	1367.76*	45.00*	67.03*	38.52*	1.16*	7.09*	42.51*
GCA	8	4651.36*	1512.76*	78.64*	98.25*	14.83*	1.72*	24.91*	28.18*
SCA	36	3822.35*	1367.63*	37.83*	60.07*	43.79*	1.03*	3.27*	45.72*
Error	88	263.24	163.85	5.29	4.05	1.83	0.06	0.42	1.63
GCA:SCA		0.8	0.9	0.5	0.6	3.0	0.6	0.1	1.6

\* indicated at 5% level of significance; GCA, General combining ability; SCA, Specific combining ability; Rep, Replicate; Df, degree of freedom.

#### 4.2.1 Mean values during long rains 2021 for eight traits.

Mean values during long rains of 2021 are given in Table 7. Days to 50% flowering ranged from 72 (Ex 614P) to 84(RC 9) for inbred lines and 70 (Hanang 4 X F-white, Exbear X Bear614 , Ex 389 X RC 9, Bear614 X Cy441/2) to 80 (Ex 614P X Bear614 ) for crosses with the mean days to 50% flowering being 74.2. Days to 50% silking ranged from 76 (RC 9) to 88 (F-white and Cy441/2 ) days for inbred lines and 72(Hanang X F-white, F620R X Bear614 , F620R X F-white, Exbear X Bear614 , Ex389 X RC 9, and Bear614 X RC 9) to 82 (Ex 614P X Bear614 ) for crosses. The mean of silking was 76.3 days.

Plant height for inbred lines ranged from 143.3cm (Cy441/2) to 236.3cm (Hanang 4) for inbred lines and 234.7cm (Ex 389 X Bear614) to 312.7cm (Ex614P X F-white) for the crosses with a mean of 258.9cm. Ear height also ranged 73.7cm (Cy441/2) to 127.0cm (Hanang 4) for inbred lines and 95.0cm (Ex614P X Bear614) to 178.7cm (Ex614P X F620R) for the crosses with a mean 135.7 cm. Grain weight for inbred lines ranged from 1.6t/ha (Ex 614P) to 3.7 t/ha (RC 9) and for crosses it ranged from 3.1t/ha (Ex 389 X Bear614) to 13.8t/ha (F620R X Ex 389). The mean for the grain was 8.5t/ha.

**Table 7: Mean values of yield and yield component traits for 36 crosses and 9 inbred lines of maize for eight traits during long rains season 2021.**

CROSSES	Plant height (cm)	Ear height (cm)	Day to Flowering	Days to Silking	Cob length (cm)	Cob width (cm)	Number of rows	Grain weight (t/ha)
P1 (Ex 614P)	211.0	119.3	84	86	12.1	2.7	12	1.6
P2 (Hanang4)	236.3	127.0	77	78	15.2	3.9	13	3.6
P3 (F620R)	212.7	110.7	78	80	14.6	4.9	15	3.1
P4 (Exbear)	214.7	116.0	78	80	14.9	4.0	10	3.4
P5 (Ex 389)	195.0	107.3	82	86	12.6	3.5	10	2.4
P6 (Bear614)	223.7	124.0	80	83	13.4	4.0	12	3.0

P7(F-White)	178.0	87.3	82	88	8.9	3.4	10	1.8
P8(Cy441/2	143.3	73.7	81	88	12.3	3.5	13	2.5
P9 (RC 9)	215.7	95.0	72	76	12.9	4.4	12	3.7
Ex614 P X Hanang 4	308.7	157.7	72	73	20.2	4.5	12	9.5
Ex614P X F620R	309.7	178.7	74	75	22.1	5.2	11	11.6
Ex614P X Exbear	279.0	153.0	75	76	19.0	4.3	11	4.9
Ex614P X Ex 389	242.0	136.7	77	80	16.6	3.9	10	4.8
Ex614P X Bear614	248.3	95.0	80	82	18.4	4.3	11	4.6
Ex614P X F-white	312.7	172.0	73	74	23.2	5.1	12	11.3
Ex614P X Cy441/2	248.0	140.3	75	77	21.6	4.8	13	11.6
Ex614P X RC 9	298.7	161.0	72	74	22.1	4.7	12	11.4
Hanang4 X F620R	274.7	143.0	71	74	20.8	5.1	13	10.3
Hanang4X Exbear	268.3	142.0	71	73	20.1	4.5	13	8.6
Hanang4 X Ex 389	258.3	142.7	73	77	18.4	4.1	12	6.2
Hanang4 X Bear614	276.3	135.3	73	75	20.1	4.8	13	11.0
Hanang4 X F-white	278.0	138.7	70	72	20.9	5.0	14	11.5
Hanang4 X Cy441/2	244.7	127.0	72	73	22.9	4.7	14	12.6
Hanang4 X RC9	288.3	138.0	71	72	22.1	4.9	16	10.0
F620R X Exbear	300.0	160.3	71	73	22.2	5.1	13	11.8
F620RX Ex 389	300.7	153.3	72	73	23.5	5.3	12	13.8
F620R X Bear614	289.7	158.3	71	72	21.9	5.3	14	12.3
F620R X F-white	269.0	130.3	71	72	19.5	5.1	15	8.2
F620R X Cy441/2	235.7	120.0	72	73	21.5	5.3	16	11.0
F620R X RC9	289.7	153.7	72	74	19.5	5.2	14	9.5
Exbear X Ex 389	262.0	132.0	79	81	18.0	4.3	11	5.5
Exbear X Bear614	258.0	130.7	70	72	18.3	4.7	12	9.0
Exbear X F-white	277.3	139.0	73	75	19.6	4.7	13	8.1
Exbear X Cy441/2	244.7	127.3	74	73	21.6	4.5	15	11.2
Exbear X RC9	290.3	149.3	71	73	20.1	4.8	12	11.2
Ex 389 X Bear614	234.7	113.3	79	81	15.4	3.3	10	3.1
Ex 389 X F-white	292.7	158.0	74	75	20.5	4.8	13	11.1
Ex 389 X Cy441/2	242.7	125.0	77	78	17.0	4.4	14	9.4
Ex 389 X RC9	286.7	158.3	70	72	20.9	4.7	12	10.4
Bear614 X F-white	285.3	158.0	72	73	22.5	4.8	12	11.4
Bear614 X Cy441/2	254.7	125.0	73	74	21.7	4.9	14	12.1
Bear614 X RC9	284.3	158.3	70	72	21.0	4.9	12	11.6
F-white X Cy441/2	256.7	130.0	73	74	22.3	5.3	16	13.5
F-white X RC9	264.7	122.3	73	73	16.8	4.7	13	7.2
Cy441/2 X RC9	266.3	146.7	72	76	22.3	5.2	16	13.0
<b>MEAN</b>	258.9	135.7	74.2	76.3	18.9	4.6	12.6	8.5
<b>LSD (5%)</b>	26.4	21.1	3.7	3.4	2.2	0.4	1.1	2.0
<b>C.V(% )</b>	6.3	9.6	3.0	2.7	7.1	5.8	5.3	14.6

LSD, Least significant differences; C.V, Coefficient of variations

Cob length for inbred lines ranged from 8.9cm (F-white) to 15.2cm (Hanang 4) and for the crosses it ranged from 15.4cm (Ex 389 X Bear614) to 23.5cm (F620R X Ex 389), with overall mean of 18.9cm. Cob width for inbred lines ranged 2.7cm (Ex 614P) to 4.9cm (F620R) and for the crosses it ranged from 3.3cm ( (Ex 389 X Bear614) to 5.3cm (F620R X Ex 389), F620R X Bear614P , F620R X Cy441/2 , F-white X Cy441/2), cob width had mean of 4.6cm. Number of rows for inbred lines ranged from 10 (Exbear, Ex 389 and F-white) to 15(F620R) and for the crosses it ranged from 10 (Ex 614P X Ex 389) to 16 (Hanang 4 X RC 9, F620R X Cy441/2, F-white X Cy441/2 and Cy441/2 X RC9) with a mean of 12.6 rows.

#### **4.3 General combining ability during short rains season 2019**

The estimates of general combining ability effects are presented in Table 8. There was variability for all the traits in relation to GCA effects and also among the inbred lines. In this season days to 50% flowering, days to 50% silking, plant height and ear height with significant and negative GCA effects were considered to have good general combining ability while cob length, number of row, grain yield and cob width with significant and positive GCA effects were considered to have a good general combining ability. F620R showed significant negative GCA effects for days to 50% flowering and days to 50% silking. For plant height Cy441/2 had significant negative GCA effects and for ear height inbred lines Ex 389 and Cy441/2 had significant negative GCA effects. Ex 389, Cy 441/2 and RC 9 had significant positive GCA for grain weight. Inbred line Cy441/2 had positive GCA values for cob length. F620R, Ex389 and Exbear had positive GCA effects for cob width. Cy441/2, F620R and RC 9 had significant positive GCA effects for number of rows.

**Table 8: Estimates of General combining ability effects for eight traits during 2019**

<b>Parents</b>								
	<b>Plant Height</b>	<b>Ear height</b>	<b>Days to Flowering</b>	<b>Days to Silking</b>	<b>Cob length</b>	<b>Cob width</b>	<b>Number of rows</b>	<b>Grain weight</b>
<b>Ex 614P</b>	4.48	3.87	1.52*	1.76*	-0.49	-0.10	-1.46*	-0.80*
<b>Hanang4</b>	-5.02	-2.68	-1.14	-1.07	0.01	0.11	-0.15	-0.89*
<b>F620R</b>	9.72*	6.38	-1.72*	-1.84*	-0.10	0.27*	0.66*	0.31*
<b>Exbear</b>	0.50	1.47	1.38	1.26	-0.13	0.13*	-0.19	-0.09
<b>Ex 389</b>	-7.97	-6.95*	1.28	1.85*	-0.76*	0.35*	-0.64*	0.49*
<b>Bear614</b>	4.57	4.63	0.46	0.39	-0.32	-0.00	-0.34	-0.38*
<b>F-white</b>	9.5*	1.11	-1.08	-1.39	0.19	-0.42*	0.60*	0.27
<b>Cy441/2</b>	-17.31*	-10.19*	-1.02	0.25	0.88*	-0.20*	1.36*	1.18*
<b>RC 9</b>	1.51	2.35	-1.02	-1.21	0.47	-0.15*	0.15	0.49

\* indicated at 5% level of significance

#### **4.3.2 Estimates of General combining ability values during long rains 2021**

Cy441/2 was significant different from other parents for most traits expect for day to 50% flowering. Ex 614 P had the highest GCA values for day to 50% flowering, days to 50% silking and ear height. F620R had the highest GCA estimate for grain weight, cob length and cob width. RC 9 had the highest GCA estimates for plant height, days to 50% flowering. GCA estimates are shown in Table 9.

**Table 9: Estimates of general combining ability values of the inbred lines in 2021 for eight traits**

Parents	Plant height	Ear height	Days Flowering	Days Silking	Cob length	Cob width	Number of rows	Grain weight
<b>Ex 614P</b>	7.11*	9.51*	2.24*	2.43*	-0.14	-0.02	-0.89*	-1.05*
<b>Hanang 4</b>	8.12*	3.40	-1.61*	-1.37*	0.57*	-0.2*	0.28*	0.20
<b>F620R</b>	9.14*	5.45*	-1.01*	-1.48*	1.00*	0.26*	0.96*	0.97*
<b>Exbear</b>	0.97	0.28	-0.10	-0.64	-0.09	-0.02	-0.53*	-0.77*
<b>Ex 389</b>	-5.77	-0.73	1.87*	2.43*	-1.22*	0.28*	-1.19*	-1.30*
<b>Bear614</b>	-1.11	-0.49	0.63	0.40	-0.28	-0.04	-0.47*	-0.31
<b>F-white</b>	0.14	-4.21	-0.10	-0.06	-0.55*	0.34*	0.2	0.24
<b>Cy441/2</b>	-28.26*	-14.64*	0.57	0.79*	0.59*	-0.34*	1.50*	1.38*
<b>RC 9</b>	9.68*	1.42	2.49*	-2.60*	0.13	-0.02	0.14	0.64*

\* indicated at 5% level of significance

#### **4.4. Specific combining ability during long rains season 2019**

Table 10 shows SCA effects during 2019. For plant height ten crosses had positive significant SCA estimate. Seven crosses were positive and significant SCA estimates for ear height. Five and six crosses showed negative and significant SCA values for days to 50% flowering and days to 50% silking respectively. For cob width eleven crosses showed positive and significant value. For cob width eleven crosses showed positive and significant SCA values. For Grain weight twelve crosses had positive and significant SCA values. For number of rows one crosses had positive and significant values.

**Table 10: Estimation of specific combining ability during short rains season 2019**

Crosses	Plant height	Ear height	Days Flowerin g	Day Silking	Cob length	Cob width	Number of rows	Grain weight
Ex614 P X Hanang 4	3.40	8.16	0.12	0.45	0.77	0.68*	-0.22	0.23
Ex614P X F620R	33.44*	21.10*	-5.30*	-5.78*	2.95*	-0.52*	0.96	2.21*
Ex614P X Exbear	-14.45	-17.98	-1.06	-0.11	-1.10	-0.87*	0.13	-0.40
Ex614P X Ex389	6.36	-6.23	-0.63	-0.48	-0.66	-0.77*	-0.07	-0.39
Ex614P X bear614	8.48	4.52	-0.81	-1.35	1.12	0.24	-0.38	-0.55
Ex614P X F-white	27.87*	18.37	-5.27*	-5.23*	2.45*	0.97*	1.35	1.56*
Ex614P X Cy441/2	4.02	0.68	-0.99	-0.54	1.68	0.26	0.26	-0.26
Ex614P X RC 9	14.54	4.13	-0.99	-1.75	1.71	0.77*	0.47	0.36
Hanang4 X F620R	25.82*	19.98*	-0.30	-0.61	1.27	-0.65*	0.99	1.88*
Hanang 4 X Exbear	6.24	1.56	2.00	2.14	0.41	-0.33	0.17	0.11
Hanang 4 X Ex389	3.52	-1.02	-3.30	-3.64	-1.81	-0.18	-1.38	0.06
Hanang 4 X Bear614	32.31*	19.07*	-2.48	-2.52	1.16	-0.12	-0.35	0.39
Hanang 4 X F-white	26.03	18.37	0.06	-1.07	0.88	0.12	-0.28	0.54
Hanang4 X Cy441/2	4.19	-0.11	-1.67	-2.04	2.38*	0.61*	0.62	0.14
Hanang4 X RC9	5.36	-1.65	-1.33	-1.25	0.65	0.76*	0.17	0.02
F620R X Exbear	27.20*	10.83	1.18	1.39	2.28*	0.17	0.35	0.59
F620R X Ex389	30.72*	14.25	-3.39	-4.54*	1.81	0.56*	1.13	0.53
F620R X Bear614	19.72*	14.35	-3.23	-3.08	1.44	0.54*	0.50	1.12*
F620R X F-white	-11.04	-12.14	-1.02	-0.96	0.37	-0.15	0.23	-0.24
F620R X Cy441/2	16.44	14.50	2.25	1.74	2.71*	-0.36*	0.81	0.50
F620R X RC9	4.29	-5.38	-2.75	-3.14	0.35	0.07	0.68	-0.07
Exbear X Ex389	16.67	5.50	-1.48	-1.98	1.44	-0.29	0.99	0.53
Exbear X Bear614	0.79	2.59	-3.33	-2.52	-0.65	-0.42*	0.35	-0.43
Exbear XF-white	28.52*	19.43*	-2.45	-3.07	1.89*	0.46*	0.41	0.17
Exbear X Cy441/2	11.00	-6.26	-3.51	-4.04	3.76*	0.64*	0.98	2.37*
Exbear X RC9	17.85	14.19	-0.85	-1.25	1.11	-0.09	0.20	0.89*
Ex389 X Bear614	-2.42	3.67	-0.24	-1.11	-0.21	-0.03	0.14	-0.38
Ex389 X F-white	30.99*	19.53*	-4.69*	-4.65*	1.58	0.39*	0.20	0.26
Ex389 X Cy441/2	42.14*	30.83*	-4.42*	-5.29*	1.63	0.71*	0.44	1.27*
Ex389 X RC9	16.99	4.28	-0.42	0.16	1.11	0.29	-0.35	1.07*
Bear614 X F-white	23.11	10.18	-5.20*	-4.87*	2.89*	-1.41*	0.23	1.31*
Bear614 X Cy441/2	2.93	-0.75	-3.60	-3.51	0.49	-0.50*	0.14	1.16*
Bear614 X RC9	22.11	13.71	-2.93	-3.05	2.26*	0.51*	-0.32	1.29*
F-white X Cy441/2	9.32	5.77	-0.39	-0.38	-0.22	-0.30	1.53	1.53*
F-white X RC9	3.51	-1.78	-0.39	-0.26	0.54	-0.45*	1.75*	0.71
Cy441/2 X RC9	35.67*	20.53*	-2.11	-2.57	2.53*	-0.41*	0.98	1.77*

\* indicated at 5% level of significance

#### **4.4.1 Specific combining ability during long rains season 2021**

Table 11: shows SCA effects for long rains season 2021. Eleven and nineteen crosses showed negative and significant SCA values for days to 50% flowering and days to 50% silking respectively. For plant height fourteen crosses had positive significant SCA estimates and two crosses had negative significant SCA estimates. Twelve crosses were positive while two crosses had negative and significant SCA estimates for ear height. For Grain weight twenty one crosses had positive SCA effects while two crosses had negative for SCA effects. For cob width fourteen crosses showed positive while seven had negative and significant SCA estimates. For cob length eighteen crosses showed positive and significant SCA values while two crosses had negative and significant SCA values. For number of rows seven crosses had positive estimates while four crosses had negative and significant SCA values.

**Table 11: Estimates of specific combining ability during long rains season 2021 for eight traits**

Crosses								
	Plant height	Ear height	Days Flowerin g	Days silking	Cob width	Cob length	Number of rows	Grain weight
Ex614 P X Hanang 4	34.36*	8.81	-3.16*	-4.12*	0.35*	0.90	0.33	1.88*
Ex614P X F620R	34.34*	27.77*	-1.10	-2.00	-0.64*	2.33*	-1.68*	3.21*
Ex614P X Exbear	11.84	7.27	-1.67	-2.52*	-0.71*	0.30	-0.19	-1.68*
Ex614P X Ex389	-18.42*	-8.05	-0.98	-1.58	-0.83*	-0.85	-0.20	1.29
Ex614P X bear614	-16.75	-18.96*	2.93*	2.78*	-0.50*	-0.08	-0.26	-2.52*
Ex614P X F-white	46.34*	30.77*	-3.68*	-4.55*	0.51*	4.99*	0.42	3.70*
Ex614P X Cy441/2	10.07	9.52	-1.69	-2.28*	0.48*	2.29*	-0.56	2.84*
Ex614P X RC 9	22.80*	14.13*	-1.95	-2.55*	0.56*	3.19*	-0.20	3.33*
Hanang4 X F620R	-1.67	-1.46	-0.59	-0.12	-0.95*	0.35	-0.52	0.71
Hanang 4 X Exbear	-7.37	-0.82	-0.50	0.21	0.09	0.06	0.24	-0.44
Hanang 4 X Ex389	14.57	21.39*	-3.47*	0.54	-0.02	0.18	-0.70	-0.15
Hanang 4 X Bear614	10.24	0.48	0.11	-0.09	0.03	0.87	-0.90*	2.69*
Hanang 4X F-white	10.66	3.54	-2.83*	-3.43*	0.41*	1.98*	0.90*	2.61*
Hanang 4 X Cy441/2	5.72	2.30	-1.50	-2.49*	0.67*	2.85*	-0.73	2.54*
Hanang 4 X RC9	11.45	-2.76	0.56	-0.09	0.49*	2.46*	0.63	0.71
F620R X Exbear	30.81*	18.66*	-2.43	-1.61	0.34*	2.41*	-0.04	3.16*
F620RX Ex389	38.22*	12.68	-3.41*	-4.34*	0.26*	4.79*	-0.04	5.69*
F620R X Bear614	22.55*	17.43*	-2.50*	-2.98*	0.41*	2.23*	0.56	3.19*
F620R X F-white	0.64	-6.84	-2.10	-2.64*	-0.11	0.18	0.90*	-0.42
F620RX Cy441/2	-4.30	-6.75	-1.77	-2.49*	0.15	0.99	0.59	0.21
F620R X RC9	8.77	10.86	1.62	2.02	-0.07	-0.55	-0.04	-0.52
Exbear X Ex389	7.72	-3.49	3.35*	2.48*	-0.01	0.40	0.45	-0.91
Exbear X Bear614	-0.94	-5.06	-5.07*	-3.81*	1.22*	-0.27	0.05	-1.60*
Exbear X F-white	17.14	6.99	-1.01	-1.15	0.65*	1.31	0.72	0.22
Exbear X Cy441/2	12.88	5.75	-1.01	-3.21*	0.17	2.22*	1.08*	2.18*
Exbear X RC9	20.60*	11.69	-0.28	-0.15	0.12	1.16	0.11	2.88*
Ex 389 X Bear614	-17.54*	-21.39*	2.29	2.11	0.12	-2.00*	-0.95*	-3.74*
Ex 389 X F-white	39.22*	27.01*	-2.32	-3.55*	0.44*	3.36*	1.05*	3.71*
Ex 389 X Cy441/2	17.61*	4.43	0.02	-1.28	0.88*	-1.27	1.08*	0.91
Ex 389 X RC9	23.68*	21.71*	-3.59*	0.16	-0.20	3.07*	0.44	2.58*
Bear614 X F-white	27.22*	16.77*	-3.07*	-4.19*	-1.45*	4.40*	-0.68	2.98*
Bear614 X Cy441/2	24.95*	13.86	-2.41	-3.58*	-0.28*	2.47*	0.35	2.59*
Bear614 X RC9	16.68	18.80*	-2.01	-1.86	0.39*	2.26*	0.05	2.78*
F-white X Cy441/2	25.71*	12.92	-1.67	-2.92*	-0.39*	3.30*	2.02*	1.53*
F-white X RC9	-4.23	-10.81	0.05	-0.52	0.25	-1.71*	0.05	-2.09*
Cy441/2 X RC9	25.83*	23.95*	-0.62	-1.25	0.42*	2.61*	1.41*	2.57*

\* indicated at 5% level of significance

#### **4.5. Heterosis values during short rains season 2019**

There was variation in heterosis estimates among the F1's in 2019. Results for heterosis in season one is presented Table 12. Heterosis for days to 50% flowering in crosses had negative values which ranged from -17.3% (Bear614 X F-white) to -1.4% (Hanang 4 X Exbear). All crosses had negative values for days to 50% silking ranging from -16.6% (Bear614 X F-white) to -2.5% (Hanang 4 X Exbear).

Heterosis for plant height among crosses ranged from 18.1% (Ex 614P X Exbear) to 97.3% (Ex 389 X Cy441/2). Heterosis for ear height ranged from -2.4% (Ex 614P X Exbear) to 114.7% (Ex 389 X Cy441/2). Apart from cross Ex6 14P X Ex bear, all crosses had positive heterosis.

For grain weight heterosis estimates were positive and significant expect two crosses (Ex 614P X Ex 389) and (EX 614P X Bear614). Heterosis ranged from 548.2% (Ex 614P X F620R) to 89.1% (Ex 614P X Ex 389). For cob length heterosis estimates ranged from 26.3% (Ex 614P X Ex 389) to 108.8% (F620R X Cy441/2), with all the crosses having positive and significant values for heterosis. Heterosis for cob width ranged from 11.7% (Hanang 4X RC 9) to 67.5% (Ex 614P X F620R) with all crosses showing positive and significant heterosis except one (Hanang X RC 9). Heterosis for the number of rows ranged from -1.5% (Hanang 4 X Bear614 ) to 38.2% (F-white X Cy441/2 ). Eighteen out of thirty six crosses exhibited positive and significant heterosis values for this trait.

**Table 12: Heterosis values during short rains season 2019**

CROSSES									
	Plant height%	Ear height%	Days flowering %	Days silking%	Cob length %	Cob width%	Number of rows %	Grain weight %	
<b>Ex614 P X Hanang 4</b>	33.0**	38.5**	-6.2	-5.9	39.7**	24.4**	3.3	209.7**	
<b>Ex614P X F620R</b>	53.5**	53.9**	-14.0**	-14.4**	92.5**	67.5**	32.1**	548.2**	
<b>Ex614P X Exbear</b>	18.1	-2.4	-8.0**	-6.28*	32.8**	31.9**	18.5	95.1*	
<b>Ex614P X Ex 389</b>	43.5**	25.0	-9.9**	-9.84**	26.3*	20.8*	9.1	89.1	
<b>Ex614P X Bear614</b>	35.7**	30.5*	-11.0**	-11.0**	54.0**	32.6**	3.4	138.8	
<b>Ex614P X F-white</b>	51.6**	51.7**	-15.5**	-15.1**	71.5**	50.5**	31.0**	386.5**	
<b>Ex614P X Cy441/2</b>	40.9**	32.8*	-9.3**	-8.9**	78.7**	62.0**	23.3*	209.8**	
<b>Ex614P X RC 9</b>	41.5**	36.5*	-8.8**	-9.5**	62.1**	38.9**	21.4*	229.5**	
<b>Hanang 4 X F620R</b>	57.2**	73.2**	-6.3	-7.5*	57.2**	34.7**	20.6*	437.9**	
<b>Hanang 4 X Exbear</b>	34.3**	22.7	-1.4	-2.5	36.7**	13.6*	12.1	129.9**	
<b>Hanang 4 X Ex 389</b>	60.4**	72.5*	-8.1*	-8.5**	22.7*	17.3*	-1.5	152.1**	
<b>Hanang 4X Bear614</b>	59.4**	65.0**	-11.2**	-11.2**	41.2**	18.2*	-2.9	228.2**	
<b>Hanang 4 X F-white</b>	59.5**	73.5**	-7.7*	-9.2**	42.7**	27.1**	8.8	251.4**	
<b>Hanang4 X Cy441/2</b>	50.7**	51.9**	-8.3*	-9.3**	68.4**	21.2**	16.7*	224.3**	
<b>Hanang4 X RC9</b>	43.4**	33.5*	-7.3*	-7.7*	39.4**	11.7	8.8	184.4**	
<b>F620R X Exbear</b>	51.5**	42.5**	-5.1	-5.2	80.9**	34.2**	25.8**	226.5**	
<b>F620R X Ex 389</b>	61.7**	73.3**	-12.8**	-14.7**	63.9**	46.2**	27.0**	233.5**	
<b>F620R X Bear614</b>	50.8**	58.6**	-13.5**	-13.5**	72.8**	47.5**	18.2*	389.6**	
<b>F620R X F-white</b>	36.1**	32.6*	-10.6**	-11.0**	66.0**	36.7**	28.1**	254.6**	
<b>F620R X Cy441/2</b>	61.1**	73.6**	-5.3	-6.8*	108.0**	55.3**	32.4**	309.6**	
<b>F620R X RC9</b>	44.1**	30.6*	-10.6**	-11.6**	63.5**	39.6**	28.1**	241.2**	
<b>Exbear X Ex 389</b>	54.3**	39.8*	-9.5**	-10.2**	44.4**	15.8*	21.3*	102.9**	
<b>Exbear X Bear614</b>	33.5**	28.1*	-12.4**	-11.1**	35.3**	17.5*	12.5	105.7**	
<b>Exbear X F-white</b>	55.3**	53.1**	-11.0**	-11.5**	63.2**	26.2**	25.8**	166.6**	
<b>Exbear X Cy441/2</b>	49.6**	23.3	-10.8**	-11.4**	95.3**	39.4**	30.3**	306.6**	
<b>Exbear X RC9</b>	46.6**	36.6**	-7.2*	-7.6*	54.1**	22.4**	19.4*	198.2**	
<b>Ex389 X Bear614</b>	51.6**	51.0**	-11.2**	-12.4**	28.8*	23.0**	4.6	104.6**	
<b>Ex 389X F-white</b>	74.4**	83.8**	-15.8**	-16.0**	49.4**	31.1**	17.5	176.8**	
<b>Ex 389 X Cy441/2</b>	97.3**	114.7**	-14.1**	-15.5**	63.0**	43.7**	19.4*	254.0**	
<b>Ex 389 X RC9</b>	62.3**	46.4**	-9.1**	-9.1**	43.7**	18.6**	7.9	216.7**	
<b>Bear614 X F-white</b>	55.9**	78.8**	-17.3**	-16.6**	72.9**	38.3**	15.2	344.2**	
<b>Bear614 X Cy441/2</b>	48.2**	44.1*	-14.1**	-14.0**	63.7**	37.6**	21.2*	316.7**	
<b>Bear614 X RC9</b>	53.6**	47.2**	-12.9**	-12.9**	64.8**	32.8**	6.1	303.4**	
<b>F-white X Cy441/2</b>	58.1**	62.6**	-10.1*	-10.5**	61.0**	47.2**	38.2**	339.6**	
<b>F-white X RC9</b>	45.5**	35.0*	-9.5**	-9.7**	52.9**	31.6**	37.5**	261.7**	
<b>Cy441/2 X RC9</b>	77.8**	68.3**	-10.8**	-11.1**	85.5**	49.0**	29.4**	325.0**	

#### **4.5.1 Heterosis values during long rain season 2021 for eight traits**

Results for heterosis during 2021 presented Table 13. All crosses exhibited negative heterosis values on days to 50% flowering which ranged from -12.8% (Ex 614P X F-white) to -1.0% (Ex bear X Ex 389). All crosses had negative values for days to 50% silking which ranged from -16.3% (Ex 614P X F-white) to -3.0% (Ex bear X Ex 389).

Heterosis for plant height ranged from 12.1% (Ex 389 X Bear614) to 60.8% (Ex 614 P X F-white), with all the crosses showing positive values of heterosis. Heterosis for ear height ranged from -2.0% (Ex 389 X Bear614) to 73.9.7% (Cy441/2 X RC 9). With all crosses having positive heterosis except (Ex 614P X Exbear). Heterosis for grain weight in all crosses exhibited positive and significant values. Heterosis for grain weight ranged from 13.4% (Ex 389 X Bear614) to 560.2% (Ex 614 P X F-white). For cob length heterosis ranged from 18.4% (Ex 389 X Bear614) to 121.2% (Ex 614 P X F-white). All the crosses for cob length exhibited positive and significant values for heterosis. Heterosis for cob width ranged from -12.3% (Ex 389 X Bear614P) to 65.7% (Ex 614 P X F-white), with all crosses showing positive and significant heterosis estimates except one cross, (Hanang 4 x RC 9). Heterosis for the number of rows ranged from -17.5% (Ex614P X F620R) to 40.0% (F-white X Cy441/2). One cross (F-white X Cy441/2) showed positive and significant heterosis values for this trait. Heterosis on number of rows for the crosses ranged from -17.5% (Ex 614P X F620R) to 40% (F-white X Cy441/2). Nineteen out thirty six crosses exhibited positive and significant

**Table 13: Heterosis values during long rains season of 2021 for eight traits.**

CROSSES	Plant height%	Ear height%	Days to flowering %	Days to silking%	Cob length %	Cob width %	Number of rows %	Grain weight%
	<b>Ex614 P X Hanang 4</b>	38.0**	28.0**	-11.0**	-12.7**	48.2**	7.6	0.0
<b>Ex614P X F620R</b>	46.2**	55.4**	-8.6**	-11.4**	65.8**	-0.9	-17.5**	429.8**
<b>Ex614P X Exbear</b>	31.1**	95.0**	-8.2**	-10.8**	40.4**	25.3**	-1.5	97.3**
<b>Ex614P X Ex 389</b>	19.2**	20.6*	-7.0**	-9.5**	35.1**	23.8**	-4.6	138.0**
<b>Ex614P X bear614</b>	14.3**	3.6	-2.8	-5.0**	44.3**	29.3**	-7.0	97.1**
<b>Ex614P XF-white</b>	60.8**	66.5**	-12.8**	-16.3**	121.1**	65.7**	10.4	560.2**
<b>Ex614P X Cy441/2</b>	40.0**	45.4**	-8.7**	-12.8**	77.1**	51.7**	1.3	461.3**
<b>Ex614P X RC 9</b>	40.0**	50.2**	-8.1**	-10.9**	76.6**	33.4**	-1.4	328.9**
<b>Hanang4 X F620R</b>	22.3**	20.6**	-8.4**	-7.1**	39.9**	16.8**	3.9	225.9**
<b>Hanang4X Exbear</b>	19.0**	16.9*	-8.8**	-7.8**	33.5**	13.1**	13.0	146.9**
<b>Hanang4 X Ex389</b>	19.8**	21.8**	-8.0**	-6.1**	32.5**	10.5*	4.5	87.9**
<b>Hanang4 X Bear614</b>	20.1**	11.0	-6.6**	-6.6**	40.2**	23.3**	9.6	234.3**
<b>Hanang4X F-white</b>	34.2**	29.4**	-12.4**	-13.8**	73.4**	39.1**	21.7	325.9**
<b>Hanang4 X Cy441/2</b>	28.9**	26.6**	-8.9**	-11.6**	66.3**	28.2**	0.0	312.0**
<b>Hanang4 X RC9</b>	27.6**	24.3**	-5.1*	-6.1**	56.8**	17.5**	12.3	175.2**
<b>F620R X Exbear</b>	40.4**	41.5**	-9.8**	-9.4**	50.8**	14.6**	4.0	282.7**
<b>F620R X Ex 389</b>	47.5**	40.7**	-10.6**	-12.4**	72.9**	24.5**	1.4	430.8**
<b>F620R X Bear614</b>	32.8**	34.9**	-10.1**	-11.4**	56.4**	21.3**	3.8	324.1**
<b>F620R X F-white</b>	37.7**	31.6**	-11.6**	-14.1**	66.6**	24.4**	17.3	301.4**
<b>F620R X Cy441/2</b>	32.4**	30.2**	-9.4**	-12.7**	59.8**	26.8**	13.3	315.1**
<b>F620R X RC9</b>	33.9**	49.4**	-4.0**	-4.7**	41.8**	12.0**	3.8	194.8**
<b>Exbear X Ex 389</b>	27.9**	18.2*	-1.0	-3.0	30.7**	16.8**	13.3	87.4**

<b>Exbear X Bear614</b>	17.7**	8.9	-12.2**	-11.2**	28.9**	16.5**	6.1	178.8**
<b>Exbear X F-white</b>	41.3**	36.7**	-9.1**	-11.1**	64.3**	29.0*	21.9	210.8**
<b>Exbear X Cy441/2</b>	36.7**	34.3**	-7.3**	-12.5**	58.6**	28.2**	25.7	278.7**
<b>Exbear X RC9</b>	34.9**	41.5**	-5.3**	-6.2**	44.3**	15.5**	12.1	558.8**
<b>Ex 389 X Bear614</b>	12.1*	-2.0	-2.7	-3.9*	18.4*	-12.3**	-6.2	13.4
<b>Ex 389 X F-white</b>	56.9**	62.3**	-10.3**	-13.6**	90.5**	41.7**	11.8	420.3**
<b>Ex 389 X Cy441/2</b>	43.4**	38.1**	-5.7**	-10.0**	36.3**	24.5**	23.5	279.9**
<b>Ex 389 X RC9</b>	39.6**	56.5**	-9.3**	-11.5**	63.5**	18.2**	12.5	238.0**
<b>Bear614 X F-white</b>	42.1**	40.1**	-11.9**	-15.0**	101.5**	30.8**	6.1	367.1**
<b>Bear614 X Cy441/2</b>	38.8**	36.3**	-9.3**	-13.3**	68.4**	30.8**	13.5	334.7**
<b>Bear614 X RC9</b>	29.4**	42.2**	-7.9**	-8.8**	59.6**	18.5**	5.7	525.2**
<b>F-white X Cy441/2</b>	59.8**	61.5	-10.4**	-15.4**	109.4**	56.1**	40.0**	519.8**
<b>F-white X RC9</b>	34.5**	34.2	-7.3**	-10.4**	27.4**	19.8**	18.2	161.4**
<b>Cy441/2 X RC9</b>	48.4**	73.9**	-6.3**	-10.2**	75.9**	32.1**	27.0	318.2**

. \* indicated at 5% level of significance

\*\* indicated at 1% level of significance

## CHAPTER FIVE

### DISCUSSION

#### 5.1 Introduction.

The study produced 36 F1 hybrids of maize in half diallel mating design, which showed great variability among crosses and the nine inbred lines, this indicated potential of the genotypes in maize improvement through breeding. Similar results were obtained by Begum *et al.*, (2018); Carena, (2005); Hemada *et al.*, (2020); Mogesse *et al.*, (2020) who they found significant difference between their genotypes, GCA and heterosis values in their studies. Hybrids performed better compared to their respective parental inbred lines since hybrids were more vigorous, larger and taller plants due to heterosis which result in development of superior crosses (Hochholdinger & Baldauf, 2018).

Mean values that had negative and significant values for ear height, days to 50% flowering and days to 50% silking were considered desirable since such genotypes tend to lower ear placement and are early maturing while positive and significant is considerable for cob length, cob width, number of rows per cob and grain weight (Khodarahmpour & Hamidi, 2012) .Crosses with desirable traits are as a result genetic diversity between the inbred lines (Sharma, 2006).

#### 5.2 The general combining ability of inbred lines.

There were significant differences among the two seasons and analyses of variance showed significant difference for both GCA and SCA effects ( $p < 0.05$ ). Chemeli (2016) and Gissa *et al.*, (2007) reported similar results of significant differences in GCA and SCA values. A low GCA value, which might be a positive or a negative value indicates that mean of a parent in crossing with the other parent does not vary largely from overall mean of their cross while a high GCA

value indicates that the parental mean is inferior or superior to the overall mean of the crosses (Fasahat *et al.*, 2016). High GCA value suggests the potential occurrence of desirable gene effects which can easily be transmitted from the parents to the progenies (Cameron *et al.*, 2008). GCA effect indicates additive nature of gene action and is transferred to their respective hybrids. The GCA effects differ in nature and magnitude depending upon character involved (Sharma, 2006). Negative and significant GCA effects for days to 50% flowering and days to 50% silking is desirable since it can be used to develop early maturing maize genotypes. Inbred lines F620R and RC 9 were considered good general combiners for days to 50% silking and days to 50% flowering. Negative and significant GCA and SCA effects for ear height are desirable because this helps to select genes for dwarfness for development of low ear height varieties in order to minimize lodging Bello & Olawuyi, (2015) who found that values of ear height to be negative and significant. Inbred line Cy441/2 showed negative and significant GCA effects for this trait can be used in maize breeding to minimize lodging due to high ear placement. Inbred lines Ex614P and Ex 389 had desired for plant height with a positive and significant GCA effects. The parental lines showing positive and significant, mean values, GCA effects for grain weight, cob length, cob width and number of rows are considered good general combiners (Begum *et al.*, 2018). Inbred lines Cy441/2, F620R and RC9 were considered as good general combiners for development high yielding crosses similar results were reported by Aslam *et al.*, (2017) and Gissa *et al.*, (2007) they found that positive and significant was desirable for most yield related traits.

### 5.3 Specific combining ability of crosses.

High specific combining ability for grain weight can occur as result of interaction between parents having high GCA, between parents with low GCA and high GCA and between parents having low GCA and low GCA value (Madić *et al.*, 2014). Cross F620R X Ex 389 involving inbred line F620R with high GCA values and inbred Ex 389 with low GCA values for grain yield this may be as result of interaction between additive and dominance gene of action. Cross Ex 389 X F-white having high SCA value was obtain from inbred lines having low GCA values Ex389 and inbred line F-white having average GCA values this may also be as result interaction between non-additive gene of action.

The hybrid Cy441/2 X RC 9 with high SCA value was obtained from inbred lines Cy441/2 and RC 9 both having high GCA values for grain yield this may be as result of additive and additive gene of action, similar were obtained and interpreted by Chemeli (2016) , Karim *et al.*, (2018) and Gissa *et al.*, (2020) the found that high SCA values may as result of high, average and low GCA values from the parents. Mean performance together with GCA effects is used as a guide to select elite parent (Pavan *et al.*, 2011; Sharma, 2006).

SCA reflects the role of non-additive gene action in expression of traits since such effects results from the dominance and epistatic gene action. High SCA effects result to increase in performance of a specific cross combination (Sharma, 2006). Positive SCA effects suggest that parents of an inbred line belong to different heterotic groups while negative SCA shows inbred lines used in breeding are in same heterotic group (Bidhendi *et al.*, 2012; Nyombayire *et al.*, 2021). Negative and significant SCA for days to 50% silking and days to 50% silking was considered desirable since those crosses tend to mature early than other crosses. Crosses Ex 614P

X F620R, Ex 389 X F-white, F620R X Ex 389 and F-white X Cy441/2 can be selected as early maturing hybrids. Negative and significant SCA effects for ear height are desirable because this helps to select genes for Shortness for development of low ear height placement varieties in order to minimize lodging. Cross Ex 389 X Bear614 showed desired low ear placement this trait can be used in maize breeding to minimize lodging due to high ear placement. Also Plant height reflects plant vigor which contributes positively to grain yield ( Machado *et al.*, 2002) maize with strong roots high biomass and low ear placement they rarely lodge. Crosses Ex614P X F-white and Ex389 X F-white had positive and significant SCA values for plant height. These results are in contrast with those of Gissa *et al.*, (2007) who suggested that negative and significant GCA and SCA values for plant height is desirable since they are useful in developing varieties with reduces stature maize. The crosses showing positive and significant, mean values, SCA effects for grain weight, cob length, cob width and number of rows are considered good general combiners. Crosses that were high yielding were F620R X Ex 389, EX 614P X F620R, Ex 389 X F-white and F-white X Cy441/2 and Cy441/2 X RC 9. High yielding crosses are usually results of respective line belonging to different heterotic group hence genetic diversity for maximum heterosis .This result is comparable with finding of Mogesse *et al.*, (2020) and Gissa *et al.*, (2007) who found that crossing unrelated inbred lines leads to development of high yielding hybrids.

#### **5.4 The interaction between general and specific combining ability.**

Presence of significant variation among the parents and their related crosses suggested potential differences among the inbred lines used that can be transmit to the subsequent progenies. There was variation in terms of GCA / SCA ratio for all studied traits during all the seasons .This may

be due to differences in combining ability or complex interaction of genes and variations among genotypes across the seasons (Aslam *et al.*, 2017). Significance of GCA / SCA mean square ratios show relative importance of additive and non-additive genes in controlling the expression of the characters studied (Derera *et al.*, 2007; Mogesse *et al.*, 2020; Sharma, 2006) they found that both GCA and SCA effects are important inheritances of traits.

The interaction between GCA and SCA has a significant role in selection of parents. Parental lines that have high GCA values, high mean values and their related crosses having low SCA values is considered in selection of component of synthetic variety (Fasahat *et al.*, 2016). Cross between F620R X Cy441/2 has high GCA values for the inbred line and high mean performance with the cross having low SCA values these crosses can be used to develop synthetic varieties (Aslam *et al.*, 2017; Sharma, 2006) Low SCA value is mostly an indication that the two parents involved in crossing belong to same heterotic group (Melani & Carena, 2005) cross Ex 389 X bear614 had low SCA values this may be due the fact that the two inbred lines may belong to same heterotic group.

### **5.5 Heterosis assessment of the crosses.**

Negative and significant heterosis is desirable for days to flowering, days to silking and ear height. Positive and significant heterosis is desirable for plant height, grain weight, cob length, cob width and number of row (Azad *et al.*, 2014). According to Shrestha *et al.*, (2018) heterosis of 0.4 and above is a good value that can be commercially exploited. Most of crosses showed heterosis above 0.4 for grain weight in this experiment. Positive and significant heterosis is desirable for plant height, grain weight, cob length, cob width and number of row while negative and significant heterosis is desirable for days to 50% flowering, days to 50% silking and ear

height. Crosses Ex 614P X F-white was having high heterosis value for days to 50% flowering, days to 50% silking, cob length and cob width. Cross Ex 389 X F-white was having high heterosis value for tall plant and ear height, cross Ex 389 X Bear614 was having low heterosis value for plant and ear height hence it can be used to develop plants with reduced stature. Crosses Ex 614P X F620R had high heterosis value for grain weight this may be due the fact inbred lines belong to different heterotic group. Ndhlela *et al.*,( 2015); Oyetunde *et al.*, (2020) and Wang *et al.*, (2016) reported similar results of high and significant heterosis which was associated with different heterotic group of inbred line used.

Most crosses generated from this study had heterosis above 100% of grain weight; this is a result low performance of the inbred lines this could be as result high level of homogeneity due to successive inbreeding hence they lack hybrid vigour. Heterosis data obtained in this study are similar to those obtained by Hammadi & Abed, (2018) who found heterosis values of above 100%. Crosses Ex 614P X Exbear, Ex 614P X Ex 389, Ex 389 X Bear614 and F620R X Cy441/2 which exhibited low heterosis values probably because they belong to same heterotic groups.

Heterotic grouping is important it helps in identifying related and unrelated inbred lines which are very useful for exploitation of heterosis (Larièpe *et al.*, 2017). In this study hybrids made using members of opposite heterotic groups performed better than those from same heterotic group probably because they had greater divergence, hence maximum exploitation of heterosis (Meena *et al.*, 2017). Inbred lines Ex614P, Hanang 4, Exbear, Ex389, and Bear614 belong to heterotic group A while F620R, F-White, Cy441/2 and RC 9 belongs to heterotic group B.

## **CHAPTER SIX**

### **CONCLUSION**

Analyses of variance showed significant differences between the genotypes, for SCA and GCA effects at ( $p < 0.05$ ) in all the eight traits study. Genetic diversity and environmental effects had significant effects on GCA, SCA and heterosis as suggested by significant by seasons X genotype interactions. All the genotypes in this study showed variability in all the traits measured indicating the potential of genotype to be exploited for hybrid development. Mean square ratio of general combining ability to specific combining ability showed GCA effects were predominant in days to 50% flowering, days to 50% silking, plant height and number of rows per cob while SCA effects were predominant for ear height, cob length, cob width and grain weight. This suggested importance of both additive and non-additive inherited traits for yield development for the materials used in the study.

General combining was high for inbred line F620R for days to 50% flowering and days to 50% silking, Ex 614P had high GCA values for plant height while Ex 389 had high GCA values for cob width. Inbred line Cy441/2 had high GCA values for ear height, cob length and number of row per cob. Inbred lines F620R, F-white, RC 9 and Cy441/2 were found to be good general combiner for most yields and yield related traits.

Specific combining ability for cross between F620R X Ex 389 had highest SCA values for days to 50% flowering, days to 50% silking, cob length and grain weight. Cross between Ex 389 X F-white had highest SCA value for plant height and ear height while Cross Ex 389 X Bear614 had

desirable SCA values for ear height. Cross Ex 389 X Cy441/2 had highest SCA values for cob width. Cross between F-white and Cy441/2 had highest SCA estimates for number of rows per cob. Crosses F620R X Ex 389, F-white X Cy441/2 and Cy441/2 X RC 9 were highest yielding; hence they can be used to develop high yielding hybrid varieties. Most of crosses exhibited high heterosis values for all the traits except the crosses Ex614P X Ex bear, Ex 614P X Ex 389, Ex 389 X Bear614 and Exbear X Ex 389, which exhibited low SCA and low heterosis values for most traits because their parental inbred lines belonged to the same heterotic grouping.

In conclusion there was significant differences in general combining ability of nine selected inbred lines for grain and yield components. There was also specific combining ability among the 36 F<sub>1</sub> crosses and also there were significant differences in heterosis among the 36 F<sub>1</sub> crosses. Hence maximum exploitation of the parental line and crosses can be done.

Combining ability studies play an important role in identification of superior inbred lines which can transmit favourable gene to other lines and crosses which useful in hybrid breeding and also specific combining ability enable breeders to make superior crosses which are high yielding. In this study many hybrids yield more than 10 t/ha which a good to improve food security

### **6.1 Recommendation from the study**

Inbred lines F620R, Cy441/2 and RC 9 were found to be good general combiner for most the traits. F620R was a good general combiner for days to 50% flowering and days to 50% silking, Cy441/2 was a good general combiner for grain weight and can be used in breeding to develop high yielding hybrids. Crosses F620R X Ex 389, F-white X Cy441/2 and Cy441/2 X RC 9 can be improved and used as high yielding hybrids since they had high specific combining ability and mean value for grain weight. Inbred line Cy441/2 was found to combine well with other

lines. This line may be used to develop varieties with reduced plant, ear height and higher grain yield.

### **6.3 Recommendation for further research**

Further research can be done to determine how many genes conditioning additive and non-additive gene of action that influence inheritance of traits that which can contribute to grain yield. Also divergence study of inbred lines can be done on the basis of genetic marker to evaluate the how diverse of the genotypes in terms origin.

Further research can be done on general and specific combining ability in relation to maize disease and lodging response of newly crossed thirty six hybrids using diallel method.

Other methods such as line by tester may be used to confirm the potential of the lines for hybrid seed production.

Further research may be carried out to assess how the crosses perform at different sites and their stability for grain yield.

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