ANALYSIS OF FULL DIALLEL CROSS IN MAIZE (*Zea mays* L.)

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بِسْمِ اللَّهِ الرَّحْمَٰنِ الرَّحِيمِ

أَفَرَأَيْتُم مَّا تَحْرُثُونَ ﴿٦٣﴾
أَأَنتُمْ تَزْرَعُونَهُ أَمْ نَحْنُ
الزَّارِعُونَ ﴿٦٤﴾

صدق الله العظيم

الواقعة

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Dana

This Dissertation is dedicated to…

My Wife **Roshna**

My Daughter **Vena**

Dana

I certify that this dissertation was prepared under my supervision at the University of Sulaimani, Faculty of Agricultural Sciences as a partial requirement for the degree of *Philosophy Doctorate* in *Field Crops - Plant Breeding and Genetics.*

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SUMMARY

Full diallel cross design including reciprocals were carried out during autumn season 2009 to produce 20 single cross hybrids of maize (***Zea mays*** L.) using (5 x 5) system. The single diallel and reciprocal crosses with their parents were evaluated in the spring season 2010 at two locations in Sulaimani region, which were Kanipanka and Qlyasan, in a Completely Randomized Block Design (CRBD) with three replicates.

Significant differences were observed among genotypes (parents and their crosses) for all of the studied characters with the exception of the character cob length at Kanipanka location, and the characters cob length, cob width, No. of ear plant^{-1}, and No. of kernels row^{-1} at Qlyasan location.

At Kanipanka location, genetical analysis revealed that the mean squares due to general combining ability (GCA) were significant for the most of the characters except for plant height, cob length, 300- kernels weight, and kernel yield plant^{-1} which were found to be non significant. Significant mean squares due to specific combining ability (SCA) were observed for the characters plant height, ear height, cob weight, No. of ear plant^{-1}, kernel weight row^{-1}, kernel weight ear^{-1}, 300- kernels weight, and kernel yield plant^{-1}. Reciprocal combining abilities (RCA) were significant for the characters days to 50% tasseling, days to 50% silking, plant height, cob weight, cob width, No. of rows ear^{-1}, and 300- kernels weight.

Regarding Qlyasan location, the mean squares due to general combining ability (GCA) were significant for the characters days to 50% tasseling, days to 50% silking, plant height, ear height, cob weight, and cob width, No. of rows ear^{-1}, and 300- kernels weight. Whereas, the characters cob length, No. of ear plant^{-1}, No. of kernels row^{-1}, kernel weight ear^{-1}, kernel weight row^{-1}, and kernel yield plant^{-1} showed non-significant mean squares. Significant specific combining ability (SCA) were observed for the characters cob weight, No. of rows ear^{-1}, kernel weight ear^{-1}, and kernel yield plant^{-1}.

Significant mean squares due to reciprocal combining abilities (RCA) were noticed for the characters days to 50% tasseling, days to 50% silking, plant height, ear height, kernel weight row^{-1}, and kernel weight ear^{-1}, but not significant for the rest.

At Kanipanka location, the desirable values for the characters days to 50% tasseling, and cob length were produced by the cross (*ZP 434* x *MIS 43100*), days to 50% silking, and No. of kernels row^{-1} were produced by the cross (*ZP 434* x *5012*), plant height, cob weight were produced by the cross (*MIS 43100* x *MIS 4279*), ear height was produced by the cross (*5012* x *MIS 43100*), cob width was produced by the cross (*5012* x *MIS 4279*), kernels weight row^{-1} was produced by the cross (*MIS 4218* x *MIS 4279*), No. of rows ear^{-1} was produced by the cross (*ZP 434* x *MIS 4279*), No. of ears plant^{-1}, kernels weight ear^{-1} and kernels yield plant^{-1} were produced by the cross (*MIS 4279* x *MIS 4218*), and 300-kernels weight was produced by the cross (*MIS 4218* x *MIS 43100*).

At Qlyasan location, the desirable values for the characters days to 50% tasseling, cob weight and cob length were produced by the cross (*ZP 434* x *MIS 43100*), days to 50% silking was produced by the cross (*MIS 4279* x *ZP 434*), plant height was produced by the cross (*MIS 43100* x *5012*), ear height was produced by the cross (*MIS 4218* x *MIS 43100*), cob width and kernels yield plant^{-1} were produced by the cross (*5012* x *MIS 4279*), No. of ears plant^{-1} was produced by the cross (*ZP 434* x *5012*), No. of rowear^{-1} was produced by the cross (*5012* x *MIS 4218*), No. of kernels row^{-1} was produced by the cross (*MIS 4279* x *5012*), kernels weight row^{-1} was produced by the cross (*MIS 43100* x *MIS 4279*), kernels weight ear^{-1} was produced by the cross (*MIS 4218* x *5012*), and 300-kernels weight was produced by the cross (*MIS 43100* x *ZP 434*).

The ratio of $\sigma^2_{GCA}/\sigma^2_{SCA}$ was less than one in almost all of the characters at both locations, which indicates the importance of non-additive gene effect in the inheritance of these characters and the average degree of dominance were more than one in those characters with the exception of the characters days to 50 %

tasseling, day to 50 % silking, cob width, and No. of kernels row^{-1} at both locations, No. of rows ear^{-1} at Kanipanka location, and No. of ear plant^{-1}, and 300-kernel weight at Qlyasan location.

Heritability in broad sense were found to be moderate to high, which indicate that the large percentage of phenotypic variance of the character referred to the genetic variance. Heritability in narrow sense was low to moderate for almost all of the characters at both locations.

Kernels yield plant^{-1} had positive and significant correlation with No. of kernels row^{-1}, and kernels weight ear^{-1} at both locations, and with cob weight at Kanipanka location, while has no significant correlation with the other characters.

Path analysis indicated that kernel weight ear^{-1}, No. of ears plant^{-1}, and No. of kernels row^{-1} showed high direct effect on kernel yield plant^{-1} at Kanipanka location, while at Qlyasan location No. of kernel row^{-1}, 300-kernel weight, No. of ears plant^{-1} , and kernel weight ear^{-1} showed the high direct effect on kernel yield plant^{-1}, these traits can be considered as principal yield component and the breeder can be use these as selection criteria for kernel yield improvement.

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List of Abbreviations

$\sigma^2{}_P$	*Phenotypic variance.*
$\sigma^2{}_G$	*Genetic variance.*
σ^2e	*Mean squares of experimental error or (Environmental variance).*
$\sigma^2{}_A$	*Additive variance.*
$\sigma^2{}_D$	*Dominance variance.*
$\sigma^2{}_{Dr}$	*Dominance variance for reciprocal crosses.*
GCA	*General combining ability.*
SCA	*Specific combining ability for diallel crosses.*
RCA	*Specific combining ability for reciprocal crosses.*
$\sigma^2{}_{GCA}$	*The variance of general combining ability.*
$\sigma^2{}_{SCA}$	*The variance of specific combining ability for diallel crosses.*
$\sigma^2{}_{RCA}$	*The variance of specific combining ability for reciprocal crosses.*
$\hat{g}_{ii}$	*General combining ability effect.*
$\hat{s}_{ij}$	*Specific combining ability effect.*
$\acute{r}_{ij}$	*Reciprocal combining ability effect.*
$\bar{a}$	*Average degree of dominance.*
$\bar{a}_r$	*Average degree of dominance for reciprocals.*
$h^2{}_{b.s}$	*Heritability in broad sense.*
$h^2{}_{n.s}$	*Heritability in narrow sense.*
MSe'	*Revised mean squares of experimental error.*

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1. INTRODUCTION

Maize (***Zea mays* L.**) is the world's most widely grown cereal and is the primary staple food in many developing countries and ranks second to wheat in production with milled rice occupying the third position in the world (Downswell *et al.*, 1996, and Morris *et al.*, 1999). It is one of the most important grown plants in the world. Superior position of maize is due to his very wide and variety utilization. During the centuries maize plant was known for it's multifariously use. Maize is used like a human food, livestock feed, for producing alcohol and no alcohol drinks, built material, like a fuel, and like medical and ornamental plant (Bekric *et al.*, 2008).

The ultimate goal of plant breeding is to develop cultivars that have consistently good performance for the primary traits of interest. Primary traits will vary among crop species over time, but the ultimate goal remains the same. To attain this goal, it is essential that plant breeders use all of the information and techniques that are at their disposal. Many of the traits that are important in cultivar development are quantitative. Although progress had been made in cultivar development in most crop species sense the rediscovery of Mendelism, further genetic progress required more information on the inheritance of the primary traits and associations with other traits needed in improved cultivars. Quantitative geneticists believed they could enhance breeding methods if the inheritance of quantitative traits was better understood. Generally, the basic concepts were accepted and incorporated with the previously used breeding methods (Hallauer, 2007).

Because of very wide utilization of maize, the main goal of all maize breeding programs is to obtain new inbreds and hybrids that will outperform the existing hybrids with respect to a number of traits. In working towards this goal, particular attention is paid to grain yield as the most important agronomic characteristic (Zorana *et al.*, 2010).

By origin, maize is native to South America and it is a tropical crop and has adapted magnificently to temperate environments with much higher productivity. It is grown from latitude 58° N to 40° S, from sea level to higher than 3000 m altitudes and in areas receiving yearly rainfall of 250 mm to 5000 mm. Most of the area under this crop is, however, in the warmer parts of temperate regions and in humid subtropical climate. Highest production is in area having the warmest month isotherms from 21° to 27° C and a frost-free season of 120 to 180 days duration **(**Downswell *et al.*, 1996).

Maize is widely cultivated crop throughout the world. In 2010/2011, the world Area planted with maize was 162.72 million hectares, and the total maize production was 820.02 million tons with the average of 5.04 tons per hectares. The United States of America alone has the largest area under its cultivation with 32.96 million hectares producing 316.17 million tons with the average of 9.59 tons per hectares, followed by China with 32.45 million hectares producing 173.00 million tons with the average of 5.33 tons per hectares, Brazil with 13.30 million hectares producing 55.00 million tons with the average of 4.14 tons per hectares, India with 8.55 million hectares producing 20.50 million tons with the average of 2.40 tons per hectares, Nigeria with 4.90 million hectares producing 8.70 million tons with the average of 1.78 tons per hectares, Argentina with 3.20 million hectares producing 22.00 million tons with the average of 6.88 tons per hectares, Indonesia with 3.00 million hectares producing 6.75 million tons with the average of 2.25 tons per hectares, and others with 57.36 million hectares producing 197.00 million tons with the average of 3.43 tons per hectares (USDA, 2011).

The diallel mating scheme is probably the most frequently used mating design in plant research and is an excellent scheme to determine how parents perform in crosses. The diallel mating design has many useful purposes if analyzed and interpreted correctly (Hinkelmann, 1977, and Baker, 1978). As the name implies, n^2 crosses are produced between n parents, including reciprocals.

Because of the logistics in producing and evaluating the crosses between parents, the number of parents included in the diallel mating design usually includes less than 20 parents. Usually, the main emphasis is to estimate the relative general combining ability (GCA) effects of the parents in crosses and specific combining ability (SCA) effects for specific crosses of the parents (Hallauer, 2007).

The improvement of a new variety with high yield is the unique target of all Maize breeders. The first step in a successful breeding program is to select appropriate parents. Diallel analysis provides a systematic approach for the detection of appropriate parents and crosses superior in terms of the investigated traits. It also helps plant breeders to choose the most efficient selection method by allowing them to estimate several genetic parameters (Verhalen and Murray, 1967).

In applied breeding programs, the estimation of the GCA and SCA effects can be very informative in the evaluation of inbred lines in hybrids (Sprague and Tatum, 1942). Another instance of effective use of the diallel crossing designs is to evaluate cultivars in crosses to identify possible new heterotic groups (Kauff man *et al.*, 1982). The parents and crosses are evaluated to estimate GCA and SCA effects and heterosis of the parents vs. crosses (Gardner and Eberhart, 1966). Other combinations and analyses can be used depending crop species and objectives of the investigator. Estimates of genetic effects are appropriate for most diallel mating systems, but often investigators desire to extend estimation to include genetic components of variance and heritabilities (Hallauer, 2007).

The concept of GCA and SCA was introduced by Sprague and Tatum (1942) and its mathematical modeling was set about by Griffing (1956) in his classical paper in conjunction with the diallel crosses.

The value of any population depends on its potential *per se* and it’s combining ability in crosses (Vacaro *et al.*, 2002). The usefulness of these concepts for the characterization of an inbred in crosses have been increasingly popular among the maize breeders sense the last few decades.

Maize hybrids are cultivated on only a limited area in the developing countries in spite of their higher yield potential (Vasal *et al.*, 1994). A series of combining ability studies have been made by many workers from the International Maize and Wheat Improvement Center (CIMMYT) to establish heterotic patterns among several maize populations and gene pools, and to maximize their yield for hybrid development (Beck *et al.*, 1990, 1991; Crossa *et al.*, 1990, and Vasal *et al.*, 1992). Likewise, the variances of general and specific combining ability are related to the type of gene action involved. Variance for GCA includes additive portion while that of SCA includes non-additive portion of total variance arising largely from dominance and epistatic deviations (Rojas and Sprague, 1952).

Diallel crosses have been widely used in genetic research to investigate the inheritance of important traits among a set of genotypes. These were devised, specifically, to investigate the combining ability of the parental lines for the purpose of identification of superior parents for use in hybrid development programmes. Analysis of diallel data is usually conducted according to the methods of Griffing (1956) which partition the total variation of diallel data into GCA of the parents and SCA of the crosses (Yan and Hunt, 2002). A diallel is simple to manipulate in maize and supplies important information about the studied populations for various genetic parameters (Vacaro *et al.*, 2002). The analysis is also useful for the evaluation of populations *per se*.

The expression of heterosis in hybrids has been exploited in many different plant species (Coors and Pandey, 1999). Because of the interests in determining the types of genetic effects that are important in the expression of heterosis, topics related to heterosis have always been prominent in quantitative genetic and plant breeding literature and conferences. Empirical evidence of heterosis has been observed for the past two centuries. The intriguing question has been, and still is, what types of genetic effects are of major importance for the expression of heterosis ? (Hallauer, 2007). Similar to SCA, heterosis occurs when the crosses exceed the average of the parents because of non-additive genetic effects. Comparisons of crosses (hybrids) with their parents have been of interest in the plant kingdom sense the 18th century (Olby, 1985). The early hybridizers, however, were not in most instances studying crosses as a means to develop superior cultivars. Their interests primarily were in trying to determine how and to what extent the parental traits were transmitted to their hybrids. During the 20th century when the inbred-hybrid concept in maize became a functional and commercially viable method to develop improved yielding cultivars, greater emphasis was given the hybrid breeding methods. Initially, not all maize hybrids were superior to the better open-pollinated cultivars (Sprague, 1946; Hallauer, 1999).

The objective of this study was to evaluate the performance of five maize inbred lines, their diallel, and reciprocal crosses which were never appeared to be tested before for the following parameters:

1- Gene action controlling the inheritance of yield and its components, and other morphological traits.
2- Combining ability of parents and specific for diallel and reciprocal hybrids.
3- Heritability in broad and narrow sense.
4- Average degree of dominance.
5- Heterosis.
6- Correlation coefficient and path coefficient analysis.

2. LITERATURE REVIEW

The genetic improvement of crop plants through breeding depends, mainly, on the existence of variation within the species and knowledge about the genetic basis of the variation and nature of gene action involved in the manifestation of characters of interest. Information regarding general and specific combining abilities further helps the breeders in the selecting of parental lines to be used in hybridization. Diallel analysis is one of biometrical techniques that have been used extensively to gain combining abilities information in various crops (Iqbal, 2004).

2.1. Diallel Cross

The diallel is defined as making all possible crosses in a group of genotypes. It is the most popular method used by breeders to obtain information on value of varieties as parents, and to assess the gene action in various characters. This technique was developed by Jinks and Hayman (1953); Jinks (1954, 1956); Hayman (1954 a, b, 1957 and 1958), and Griffing (1956).

Different types of progenies can be produced with the diallel mating design. As a consequence, different analyses can be used. There are four methods of producing progenies:

a) Method I = n^2. It includes all possible crosses and parents.

b) Method II = $n (n+1) / 2$. This method is the most widely used and it includes one set of crosses and the parents (no reciprocals).

c) Method III = $n (n-1)$. It includes two sets of crosses without parents.

d) Method IV = $n (n-1) / 2$. It only includes one set of crosses with neither reciprocals nor parents.

The option will change depending on the material used. In maize, for pure lines the most logical choice would be to use one or two sets of crosses without parents. Otherwise, competition effects would be important. Contrarily, if we use synthetic varieties we can use diallel mating designs including not only crosses but also parents to compare mean performance and heterosis. Based on the previous information we can see that one limitation of the diallel design is the number of parents that can practically be included (Griffing, 1956).

In order to choose appropriate parents and crosses, and to determine the combining abilities of parents in the early generation, the diallel analysis method has been widely used by plant breeders. This method was applied to improve self- and cross-pollinated plants (Jinks and Hayman, 1953; Hayman, 1954; Jinks, 1956; Griffing, 1956; Hayman, 1960). It is one of the several biometrical techniques available to plant breeders for evaluating and characterizing genetic variability existing in a crop species is diallel analysis (Singh and Paroda, 1984).

Griffing's biometrical analysis has been widely used in plant improvement programs to identify superior parents for crossing and for characterizing general, specific, and reciprocal effects. This analysis is not hindered by the requirements of numerous genetic assumptions and interpretations from this evaluation are usually straightforward. However, several important factors must be considered when using the analysis (Shattuck *et al.*, 1993).

Diallel crosses have been widely used in genetic research to investigate the inheritance of important traits among a set of genotypes. These were devised, specifically, to investigate the combining ability of the parental lines for the purpose of identification of superior parents for use in hybrid development programs (Malik *et al.*, 2004).

Plant breeders frequently need overall information on average performance of individual inbred lines in crosses- known as general combining ability, for subsequent choosing the best amongst them for further breeding. For this purpose, diallel crossing techniques are employed (Himadri and Ashish, 2003).

Diallel mating designs provide the breeders with useful genetic information, such as general combining ability GCA and specific combining ability SCA, to help them devise appropriate breeding and selection strategies (Zhang *et al.*, 2005).

Diallel crossing schemes and analyses have been developed for parents that range from inbred lines to broad genetic base varieties. After the crosses are made, evaluated, and analyzed, inferences regarding the types of gene action can be made. It is important, however, that the assumptions and limitations of the diallel mating design are realized when one interprets the data. If correctly analyzed, the diallel mating design is very powerful, e.g., alternative heterotic patterns have been proposed (Hallauer *et al.*, 1988; Carena and Hallauer, 2001; Carena and Wicks III, 2006).

The mechanical procedures for making the diallel crosses will vary among crop species (self- vs. cross-pollinators) and within crop species (inbred vs. non-inbred parents). If the parents are relatively homozygous (inbred lines), the series of diallel crosses can be made by repeating each parent for each combination of crosses and making paired-row crosses; the only limitation to the number of plants included and cross-pollinated for each pair-row cross is the quantity of seed needed for testing the crosses. By use of paired-row crosses, seed produced on each parent can be bulked for each cross-combination or kept separate if each cross-permutation is desired (Hallauer *et al.*, 2010).

In diallel technique, if only a small number of inbreeds are tested, the estimates of combining ability tend to have a large sampling error. These difficulties have led to development of the concept of sampling of crosses produced by large number of inbreeds without affecting the efficiency of diallel technique, to achieve this goal, different approaches have been followed by various workers (Kempthorne and Curnow , 1961; Fyfe and Gilbert, 1963) .

Diallel crosses among a set of maize populations are handled similarly to inbred lines, but the sampling of the population genotypes increases the number of individual plants included in the population crosses. Amount of seed usually is not a problem, but the number of crosses between different plants required to sample the populations increases the space and time needed. Several sets of pair-rows per cross are recommended to increase the sample size. Also, detasseling males after crossing can make the sample more representatives with the advantage of reducing future number of pollinations. Shootbags from males can also be removed. Crosses between 10 plants of inbred lines may be sufficient for seed needs, whereas many more are necessary to adequately sample the genotypes in a population (Hallauer *et al.*, 2010).

Griffing (1956) and Cockerham (1963) have discussed the diallel analysis in detail as well as the analysis of variance for fixed models (model I, where the parents are the genotypes under consideration) and random models (model II, where the parents are a sample of genotypes from a reference population). Model I estimates apply only to the genotypes included and cannot be extended to some hypothetical reference population. Model II estimates are interpreted relative to some reference population from which the genotypes included are an unselected sample. The use of model I or II depends on sample size and this will vary among species (e.g., we could represent the tobacco species with 5–10 lines and the diallel mating design could be useful. Although limited sample sizes in some crops do not allow the estimation of heritability, genetic gain, genetic correlations with model I, we can get as much information as model II (GCA, SCA effects).

In most instances, the reference population either is not adequately sampled or the parents included are not from the same population. Estimation of components of genetic variances requires an adequate sample of individuals (n > 100) from a reference population to obtain estimates with reasonable standard errors (Marquez-Sanchez and Hallauer, 1970). A group of pure-line cultivars may be included in diallel crosses that have different origins (in some instances origin may not be known) and the reference population for the interpretations of the components of genetic components would be nebulous, unless one considers that the estimates apply to the entire crop species. The expectations for GCA (covariance half-sibs) and SCA (covariance full-sibs minus two covariance half-sibs) include the covariances of relatives which have genetic components of variances. The options for use of the diallel mating design to estimate components of genetic variance would be either to include different sets of diallels whose parents are sampled from the same population and data are pooled over sets or use of the partial diallel where a greater number of parents can be included but not all possible crosses (Kempthorne and Curnow, 1961). If a cross classification mating design is preferred, then the North Carolina Design II would be a good option for estimation of components of variance (Cockerham, 1963); a greater number of parents is included to produce a fewer number of crosses, compared with a diallel mating design. The diallel mating systems are good designs. They have been used in plant research more frequently than any other mating design, but often genetic components of variance, genetic correlations, heritabilities, and predicted gains have been reported for instances of either inadequate sample sizes or parents were selected that did not represent a specific population. Estimates of GCA and SCA effects are appropriate and very useful genetic parameters of the parents and their crosses (Hallauer, 2007).

Before the experiments were conducted, an important decision was made about the parents included to make the crosses: Are the parents the reference genotypes or are the parent’s random genotypes from some reference population? Parents can be either the reference genotypes (model I or fixed model) or random genotypes from a reference population (model II or random model). This decision is made before analysis and the interpretation of the analysis changes depending on that decision. The answer to the former question has great implications in the interpretations made from the analysis of the diallel mating design, and it usually has been the basic feature in arguments for and against the utility of that design to provide the information desired by the researcher. Usually, the assumption made about the parents to be included, not how the experiment was conducted and analyzed, and causes difficulties in the interpretation of the estimated parameters (Hallauer *et al.*, 2010).

Various forms of diallel crosses play an important role in evaluating the breeding potential of genetic material in plant and animal breeding. Genetic properties of inbred lines in plant breeding experiments are investigated by carrying out diallel crosses. Complete diallel cross designs involve equal numbers of occurrences of each of the $p\ (p - 1)/2$ distinct crosses among p inbred lines (Das *et al.*, 1998).

Diallel mating designs have proved informative in determining the inheritance of quantitative traits of interest to plant breeders. Apart from the well-established analyses of a complete diallel, the two-way factorial data structure of this design lends itself to analysis by the additive-main-effects-and-multiplicative-interaction (AMMI) model (Ortiz *et al.*, 2001).

The choice of any of the several alternative breeding procedures to be adopted for amelioration of a crop, primarily depends upon the nature and magnitude of gene actions involved in the expression of different characters and mating flexibilities (Chaudhary *et al.*, 1977).

Diallel analysis is used to estimate general combining ability and specific combining ability effects and their implications in breeding (Makumbi, 2005).

2.2. Combining ability

Combining ability describes the breeding value of parental lines to produce hybrids. The concept of combining ability is becoming increasingly important in plant breeding. It is especially useful in connection with testing procedures, in which it is desired to study and compare the performances of lines in hybrid combination (Griffing, 1956; Basal and Turgut, 2003).

Sprague and Tatum (1942) introduced the concepts of GCA and SCA to distinguish between the average performance of parents in crosses (GCA) and the deviation of individual crosses from the average of the margins (SCA). The concepts of GCA and SCA are extensively used in plant breeding and have particular significance to the diallel mating design. Precisely such a system can be defined in terms of general and specific combining ability.

They defined that the term of GCA is used to designate the average performance of a line in hybrid combination. The term of SCA is used to designate those cases in which certain combinations do relatively better or worse than it would be expected on the basis of the average performance of the lines involved (Ahmed, 2003, and Chawdhary *et al.*, 1998). The ability of an inbred line or true breeding plant to transmit desirable performance to the hybrid progeny is referred to as their combining ability (Chawdhary *et al.*, 1998).

Combining ability analysis helps in identification of desirable parents and crosses for their further exploitation in breeding program (Verma *et al.*, 2007).

It has been indicated that both general and specific combining ability variances were important in controlling the inheritance of the traits studied. However, GCA variance was predominating; relatively higher magnitude of (GCA × Environments) interactions suggested a higher sensitivity of GCA to environment than that of SCA (Bhathagar and Sherma, 1977).

Significant GCA values indicate the importance of additive or additive × additive gene effects as reported previously (Griffing, 1956).

Breeding methods for improvement of allogamous crops should be based on the nature and magnitude of genetic variance controlling the inheritance of quantitative traits. Selection of crosses may be based on specific combining ability and per se performance linked with heterosis and inbreeding depression for cross exploitation (Pandey, 2007).

The importance of the concept of combining ability has been widely appreciated both in plant and animal breeding. The concept is especially significant in a breeding program where it is desired to use genotypes which would combine well in hybrid combinations (Hayes and Paroda, 1974).

The combining ability analyses are perhaps most helpful when making parental choices (Riggs and Hayter, 1972).

Combining ability analysis is important in identifying the best parents or parental combinations for a hybridization program. General combining ability GCA is associated to additive genetic effects while specific combining ability SCA is associated to non-additive genetic effects. GCA is the average performance of a line in hybrid combination and SCA is the deviation of crosses based on average performance of the lines involved (Makumbi, 2005).

Sense the 1960s, along with the progress in biometric methods (particularly those connected with diallel crossing systems), information on the general combining ability of parental genotypes seemed to be promising for solving this problem (Kuczyñska *et al.*, 2007).

2.3. Heterosis

Heterosis is a phenomenon not well understood but has been exploited extensively in breeding and commercially. Hybrid cultivars are used for commercial production in crops in which heterosis expression is important. The commercial use of hybrids is restricted to those crops in which the amount of heterosis is sufficient to justify the extra cost required to produce hybrid seed. Heterosis, or hybrid vigor, refers to the phenotypic superiority of a hybrid over its parents with respect to traits such as growth rate and reproductive success and plays significant role in evolution (Janick, 2008; Basal and Turgut, 2003).

Hybrid vigor in maize is manifested in the offspring of inbred lines with high specific combining ability (SCA). Heterosis was first applied by the purposed hybridization of complex hybrid mixtures made by farmers in the 1800s (Enfield, 1866; Leaming, 1883; Waldron, 1924, and Anderson and Brown, 1952).

However, public scientists East and Shull developed the concept of hybrid vigor or heterosis in maize independently in the early 1900s (East, 1936; Shull, 1952; Wallace and Brown, 1956; Hayes, 1963). It was realized that genetic divergence of parental crosses was important for hybrid vigor expression (Collins, 1910). However, the range of genetic divergence limited the expression of heterosis (Moll *et al.*, 1965). Heterosis can be inferred from heterotic patterns (Hallauer and Carena, 2009). A heterotic pattern is the cross between known genotypes that expresses a high level of heterosis (Carena and Hallauer, 2001).

Some earlier studies measured different traits at different stages of plant development in the parents and their crosses to determine when heterosis occurred in hybrids (Sprague, 1953). Different morphological and physiological traits were measured to determine if the observed heterosis could be attributed to specific morphological or physiological traits (Hallauer, 2007).

These types of approaches invariably showed that the hybrids were superior to the parents for any of the traits studied. The traits were, of course, under genetic control but usually no attempt was made to explain the superiority of the hybrid relative to types of genetic effects expressed in the hybrids. At the 1950 heterosis conference, selection and breeding methods were presented and Comstock and Robinson (1952) suggested mating designs to estimate level of dominance. Most of the discussion at the 1950 conference was directed at the question, what is the genetic basis of heterosis? Despite a great array of quantitative genetic studies, a definitive answer has been elusive. It is evident; however, that interactions of alleles at individual loci and interactions of allels between loci are involved. The difficulty is that we probably have different interactions of allels at individual loci and between loci for different hybrids. An extensive volume of literature is available to study the theories, methods used, and data available on heterosis studies for an array of plant species (Gowen, 1952; Sprague, 1953; Coors and Pandey, 1999; Lamkey and Edwards, 1999; Reif *et al.*, 2005; Troyer, 2006). More recent researches on the genetic basis of heterosis is being done at the DNA level (Coors and Pandey, 1999).

Heterotic patterns became established by relating the heterosis of crosses with the origin of the parents included in the crosses (Hallauer and Miranda Fo., 1988). This was a consequence of diallel crosses studies on performance based on pedigree relationships. The data suggested that hybrids of lines from different germplasm sources had greater yields than hybrids of lines from similar sources. More than 50 years were needed to identify hybrid combinations that provided the highest yielding corn hybrids. Predicting the best hybrid combination is a breeding process that needs good germplasm knowledge and extensive testing. Modern research approaches were based on biochemical assays (Smith *et al.*, 1985 a, b).

Even though heterosis is seen in plant species, its level of expression is usually variable, depending on the crop and its natural mode of reproduction as well as its natural level of heterozygosity. Heterosis can be expressed as mid parent heterosis (MPH) and high parent heterosis (HPH). MPH is the performance of the offspring compared with the average performance of the parents. HPH is the performance of the offspring compared with the best parent in the cross. Out of the two methods of measuring heterosis, the HPH is the most important to breeders. A better performance of hybrids, such as yield increase or number of seeds, is only meaningful if it has increased value over the better parent. Heterosis may decrease when diversity is excessively high (Makumbi, 2005; Mateo, 2006).

Application of heterosis (hybrid vigor) to agricultural production is a multi-billion dollar enterprise. It represents the single greatest applied achievement of the discipline of genetics (Griffing, 1990).

Identification of combinations with strong yield heterosis is the most important step in developing crop hybrids. Generally, parents with a higher general combining ability and long genetic distance can produce a hybrid with better yield performance (Shahnejat-Bushehri *et al.*, 2005).

The F_1 progeny of all parents showed marked heterosis for the expression of biological yield and economic yield (Khalifa, 1979).

The method of evaluation and the choice of varieties included for evaluation of heterosis also changed. Instead of crossing a group of varieties to a common tester variety, the diallel mating design was used to determine general performance of a variety in comparison with other varieties and specific performance of a particular pair of varieties. The latter information was important in the choice of varieties and/or improved populations for initiating reciprocal recurrent selection (RRS). Open-pollinated varieties were included in many of the diallel series of crosses, but synthetic varieties, composites, and varieties improved by selection also were often included. In most instances a measure of heterosis was desired among the variety crosses, but in some instances genetic information was obtained by selfing either the parental varieties or the variety crosses.

Two methods were proposed to actually measure the performance of a hybrid relative to its parents:

(1) Mid-parent (MP) heterosis (MPH): It is the performance of a hybrid relative to the average performance of its parents expressed in percentage.

(2) High-parent (HP) heterosis (HPH): It is the performance of a hybrid relative to the performance of its best parent expressed in percentage.

The HP heterosis method has been less used but it provides better and more accurate information (Hallauer *et al.*, 2010).

The manifestation of heterosis in crosses of maize varieties ranges from that of Morrow and Gardner (1893) to information evaluating effectiveness of recurrent selection. Because yield is the most important economic trait of maize, only the heterosis information on yield is given. This study included 611 varieties and 1394 variety crosses that were evaluated for yield heterosis. Heterosis relative to the average of the two parent varieties (mid-parent) and the high-parent variety is given for each reported study and averaged over all studies. Average mid-parent heterosis for the 1394 crosses weighted for the number of crosses in each study was 19.5%. Average mid-parent heterosis was evident in nearly all studies; the only exception was for some of the varieties and variety crosses reported by Noll (1916), which was − 0.5%. Mid-parent heterosis was the average for each study. Variety crosses that were either above or below the mid-parent also were studied. Except for the study by Noll (1916) a majority of variety crosses exceeded the mid-parent values. High-parent heterosis and frequency of variety crosses that exceeded the high parent varied considerably among the reported studies. High-parent heterosis for variety crosses evaluated before 1932 was generally quite small. Average high-parent heterosis ranged from − 9.9 % for the one variety cross reported by Garber and North (1931) to 43.0 % for 10 flint variety crosses reported by Troyer and Hallauer (1968). Average high-parent heterosis for the 1394 variety crosses was 8.2%.

Mid-parent (MP) and high-parent (HP) heterosis values were gathered for 71 improved populations in the 1980s. The average MP heterosis across improved population crosses was 19.5 %, while the average HP heterosis across the same population crosses was 8.2 %. One of the reasons variety crosses were not widely accepted is because choice of germplasm sources for inbred lines and their improve versions were not ideal. Weatherspoon (1973) suggested that in order for recurrent selection to be successful the initial germplasm pool should be the most elite material available. A more careful selection of improved germplasm after extensive testing can improve average values of mid- and high-parent heterosis to 38.9 and 28.2 %, respectively.

2.4. Heritability

Heritability is the proportion of the observed variation in a progeny that is inherited. If the genetic variation in a progeny is large in relation to the environmental variation, then heritability will be high; or if genetic variation is small in relation to the environmental variation, then heritability will be low. Selection is more effective when genetic variation in relation to environmental variation is high than when it is low (Poehlman and Sleper, 1995).

Lush (1945) defined heritability (h^2) either as the ratio of the additive genetic variance (σ^2_A) to the phenotypic variance (σ^2_P) or as the ratio of the total genetic variance (σ^2_G) to the σ^2_P. The ratio, σ^2_A/σ^2_P, was designated as h^2 in the narrow sense, whereas σ^2_G/σ^2_P was designated as h^2 in the broad sense. These definitions provided information for specific situations (e.g., mass selection) but they have limited generality in plant breeding. Because of the range of possible situations in different plant species, estimates of heritability are applicable for specific breeding methods (Hallauer, 2007).

Success of breeders in changing the characteristics of a population depends on the degree of correspondence between phenotypic and genotypic values. A quantitative measure, which provides information about the correspondence between genotypic variance and phenotypic variance, is heritability. The term heritability has been further divided into broad sense and narrow sense, depending whether it refers to the genotypic value or breeding value, respectively. The ratio of genetic variance to phenotypic variance (VG/VP) is called heritability in the broad sense or genetic determination. It expresses the extent to which individual phenotypes are determined by the genotypes (Gebre, 2005).

All estimates of heritability are specific for each population for the combination of genetic and phenotypic variance estimates (Hanson and Robinson, 1963; Nyquist, 1991; Holland *et al.*, 2003) have discussed the factors that are important in determining estimates of h^2 in plant populations. Estimates of h^2 can be obtained from mating designs imposed on a population that provide estimates of variances; these estimates can be used to calculate estimates of h^2 for different combinations of progenies and testing conditions. Estimates of h^2 also can be obtained from evaluation trials where progenies developed from a population that is under some type of recurrent selection (Hallauer, 2007).

The basic idea in the study of variation among observations arising out of crosses is its partitioning into components attributed to different causes like additive value, dominance deviation and epistatic deviation. The relative magnitude of these components determines the genetic properties of the population. One of such properties is heritability which is of paramount interest to plant breeders to understand the gene action on which depend the breeding policies. The relative importance of heredity in determining phenotypic values is called the heritability of a character in broad sense (Himadri and Ashish, 2003).

The phenotypic variation that the breeder must manipulate to produce improved genotypes typically contains contributions from both heritable and non-heritable sources as well as from interactions between them. In biometrical genetics the statistics that describe the phenotypic distributions are themselves completely described by heritable components based on the known types of gene action and interaction in combination with non-heritable components defined by the statistical properties of the experimental design (Jinks, 1981).

Broad sense and narrow sense heritability estimates generally were found to be high for the height and maturity characters but low for neck length (Thomas and Tapsell, 1983).

Heritability values of kernel weight ranged from 25.3 and 25.9% when measured by parent-progeny correlation to 43.1 and 46.0% when measured by variance of F_2 (broad sense) (Borthakur and Poehlman, 1970).

Heritability estimates using variance components were high for kernel plumpness, intermediate to high for plant height, low to intermediate for lodging, and slightly lower for yield (Nasr *et al.*, 1972).

2.5. Gene Action and Average Degree of Dominance

The understanding of gene action is of paramount importance to plant breeders. Alleles with a dominant, additive or deleterious phenotypic effect influence heritability differently depending on whether they are in homozygous or heterozygous condition (Tawfiq, 2004).

Epistatic effects are statistically defined as interactions between effects of alleles from two or more genetic loci (Fisher, 1918). Interactions, however, are simply deviations from additivity in a general linear model; as such, they are often treated as statistical errors. Epistasis is now considered as an important source of genetic variation for quantitative traits, because different components involve interactions of different numbers and different types of alleles (Xul and Jia, 2007).

Information on genetic determination of quantitative traits may be obtained by estimation of genetic parameters determining additive, dominance and epistatic (additive × additive, additive × dominance and dominance × dominance) gene effects. These genetic parameters have been defined as a sum of individual effects of all segregating loci, with the assumption of equal effect in each locus (Kaczmarek *et al.*, 2002).

2.6. Correlation of the Characters

Grain yield is a complex quantitative trait conditioned by the interaction of various growth and physiological processes throughout the life cycle. It’s within great influence of environmental conditions, has complex mode of inheritance and low heritability. Because of that during selection of grain yield, in order to select the best selection method, we need to know the nature and magnitude of correlation coefficient between kernel yield and the characters, because the appropriate knowledge of such interrelationships between kernel yield and its contributing components can significantly improve the efficiency of breeding program through the use of appropriate selection indices (Mohammadia *et al.*, 2003, and Zorana *et al.*, 2010).

The inter relationship of quantitative characters with yield determine the efficiency of detection in breeding programs. It merely indicates the intensity of correlation. Phenotypic correlation reflects the observed relationship, while genotypic correlation underline the true relationship among characters. Selection procedures could be varied depending on the relative contribution of each. The following paragraphs give review of literature on correlation in maize (Nadagoud, 2008). Relationships between two metric characters can be positive or negative, and the cause of correlation in crop plants can be genetic or environmental (Gebre, 2005).

Besides that, knowing the correlations between the traits is also of great importance for success in selections to be conducted in breeding programs, and analysis of correlation coefficient is the most widely used one among numerous methods that can be used (Yagdi and Suzen, 2009).

The nature of association between grain yield and its components determine the appropriate traits to be used in indirect selection for improvement in grain yield. The correlation studies simply measure the associations between yield and other traits. Path coefficient analysis permits the separation of correlation coefficient into direct and indirect effects (effects exerted through other variables). It is basically a standardized partial regression analysis and deals with a closed system of variables that are linearly related. Such information provides realistic basis for allocation of appropriate weight-age to various yield components (Rafiq *et al.*, 2010).

Earlier workers Devi *et al.* (2001); El-Shouny *et al.* (2005); Mohan *et al.* (2002), and Tollenaar *et al.* (2004) identified different traits like ear length, ear diameter, kernels row^{-1}, ears plant^{-1}, 100-seed weight and rows ear^{-1} as potential selection criteria in breeding programs aiming at higher yield.

The efficiency of a breeding program depends mainly on the direction and magnitude of the association between yield and its components and also the relative importance of each factor involved in contributing to grain yield.

According to Annapurna *et al.* (1998) kernels yield plant^{-1} was positively and significantly correlated with plant height, No. of kernels row^{-1}, No. of rows ear^{-1}, No. of kernels.ear^{-1}.

In another study, Khatun *et al.* (1999) found that kernels yield plant^{-1} was positively and significantly correlated with 300-kernels weight, and No. of kernels ear^{-1}.

Gautam *et al.* (1999 a) found that kernel yield was positively correlated with No. of rows ear^{-1}, 300-kernels weight, plant height and ear height. Rather *et al.* (1999) estimated positive correlation between days to 50% silking and ear height and kernels yield plant height had no association with kernels yield.

The genotypic correlation between kernels per row and grain yield per plant and direct effect of kernels per row were both positive and almost equal in magnitude. Therefore, selection for more No. of kernels row^{-1} will definitely increase kernel yield plant^{-1} (Mahajan *et al.*, 1990; Singh and Singh, 1993; Kumar and Mishra, 1995; Singh *et al.*, 1995; Agrama, 1996; Annapurna *et al.*, 1998; Arias *et al.*, 1999; Gautam *et al.*, 1999 b; Khatun *et al.*, 1999; Mani *et al.*, 1999; Geetha and Jayaraman, 2000, and Kumar and Kumar, 2000).

According to Appadurai and Nagarajan (1975), kernel weight row^{-1} and No. of kernel row^{-1} had little effect on yield, while ear length has positive correlation with yield.

Kim (1975) reported that 1000-kernels weight was negatively correlated with days to silking and days to tasseling. Sharma *et al.* (1982) reported that kernel yield was positively correlated with kernels ear^{-1}, 100- kernel weight, plant height and ear height. Ei-Nagouly *et al.* (1983) concluded that phenotypic and genotypic correlation between yield and days to 50 % silking and ear height was positive and highly significant.

Saha and Mukherjee (1985) observed that kernel yield plant^{-1} was significantly correlated with kernels ear^{-1} and 100-kernel weight. Malhotra and Khehra (1986) recorded positive correlation between kernel yield and yield components like ear length, No. of rows ear^{-1}, 100-kernel weight, days to silking, ear height and plant height.

Tyagi *et al.* (1988) opined that kernel yield was influenced more by ear weight, ear length, plant height, kernels row^{-1} and 100-kernel weight. Maha rajan *et al.* (1990) concluded that kernel yield was positively correlated with ear length, No. of kernels row^{-1} and plant height. Singh *et al.* (1991) noticed that kernel yield plant^{-1} had significant positive correlations with plant height and ear weight. Debnath and Khan (1991) revealed that days to silking, plant height, No. of kernels row^{-1} and 1000-kernel weight had strong positive contributions to kernel yield.

Dash *et al.* (1992) reported that maturity traits showed a negative correlation with yield plant^{-1}. Boraneog and Duara (1993) observed that plant height and ear height were found to be significant and positively correlated with yield.

Saha and Mukherjee (1993) reported positive significant correlations between kernel yield plant^{-1} with 100-kernel weight, ear length, No. of rows ear^{-1} and No. of kernels row^{-1}.

According to Satyanarayana and Saikumar (1996) grain yield was positively correlated with rows ear^{-1}, ear length, and 300-kernel weight. Kumar and Kumar (1997) found that the values of genotypes correlation were slightly higher than the corresponding phenotypic values.

Nadagoud (2008) found that the mean of 181 inbred lines for No. of kernels row^{-1} recorded was 23.55 with a range observed was 8.00 to 36.33, for checks the mean value recorded was 35.13, with a range of 32.67 to 38.33. The average 100- kernel weight of 181 inbred lines and 5 checks observed was 22.16 and 33.61 respectively, while range observed for lines was 10.40 to 41.83, but for checks, it was 29.90 to 39.47. The 181 lines had recorded mean 60.93 for kernel yield plant^{-1} with a range 11.00 to 137.31, but for checks mean observed was 161.42 with a range of 127.40 to 212.30.

2.7. Path Coefficient Analysis

Assuming yield is a contribution of several characters which are correlated among themselves and to the yield. Path coefficient analysis was sugested by Wright (1921) and described Dewey and Lu (1959) wich was calculated to detect the relative importance of characters contributing to grain yield (Selvaraja and Nagarajan, 2011).

Unlike the correlation coefficient which measures the extent of relationship, path coefficient measures the magnitude of direct and indirect contribution of a component character to a complex character and it has been defined as a standardized regression coefficient which splits the correlation coefficient into direct and indirect effects (Nadagoud, 2008).

Because correlation coefficient measures the mutual association only between a pair of variables, when more than two variables are involved, the correlations per se may not provide a clear picture of the importance of each component in determining grain yield. Path coefficient analysis provides more information among variables than do correlation coefficients sense this analysis provides the direct effects of specific yield components on yield, and indirect effects via other yield components (Garcia *et al.*, 2003).

Mani *et al.* (1999) suggested that Number of kernels row^{-1} were the best direct contributor to kernels yield plant^{-1}. Hence, maize breeders should give more importance to kernels row^{-1} as selection criteria for yield improvement.

Kumar and Kumar (2000) put emphasis on plant height with greater ear weight, No. of rows ear^{-1} and No. of kernels row^{-1} for better kernels yield plant^{-1}.

Probecky (1976) reported that yield depends primarily on the No. of kernels plant^{-1}, which in turn depended mainly on the No. of kernels in the rows.

A positive direct effect of cob length for kernel yield was indicated by Tyagi *et al.* (1988); Dash *et al.* (1992); Kumar *et al.* (1999); Gautam *et al.* (1999 a), and Nemati *et al.* (2009). Ear height had a positive direct effect on kernels yield as indicated by El-Nagouly *et al.* (1983); Tyagi *et al.* (1988), and Rahman *et al.* (1995). Favorable influence of No. of rows ear^{-1} on kernels yield was noticed by Singh and Singh (1993); Manivannan (1998), and Arais *et al.* (1999). Selvaraja and Nagarajan (2011) recorded that plant height, days to tasseling, ear height, cob width, No. of kernels row^{-1}, and No. of kernels.ear^{-1} recorded negative direct on kernels yield plant^{-1} even though genotypic correlation on kernel yield were positive. Singh *et al.* (1999) indicated that the highest positive direct effect on yield was exhibited by kernel rows ear^{-1}, followed by plant height and ear diameter. Vaezi *et al.* (2000) showed that 300-kernels weight had the highest positive effect on kernel yield whereas ear diameter had a negative indirect effect on kernel yield through some traits. Geetha and Jayaraman (2000) observed that No. of kernel row^{-1} exerted a maximum direct effect on kernel yield.

300-kernels weight had a positive direct effect of 0.734 on kernel yield plant^{-1}. Their was also positive and significant genotypic correlation coefficient between the traits. Therefore, direct path and correlation explain the true association between the two traits and selection for heavier kernel will improve kernel yield (Parh *et al.*, 1986; Dash *et al.*, 1992; Rahman *et al.*, 1995, and Khatun *et al.*, 1999).

Guang Cheng *et al.* (2002) showed that importance of eight yield components to kernel yield and suggested that more attention should be paid to cob length, cob width. Anees and Saleem (2003) reported that vegetative phase had the highest positive direct contribution to kernel yield plant^{-1} followed by days to tasseling. Venugopal *et al.* (2003) indicated that number of kernels row^{-1} followed by 300-kernel weight, days to 50 % tasseling, and plant height contributed directly towards kernels yield plant^{-1}.

Sharma *et al.* (1982) reported that path analysis showed that yield was directly influenced by ear height and indirectly affected by days to 50 % silking via ear height. Viola *et al.* (2003) revealed that early silking, greater plant height, cob length, cob weight, ear height and No. of ear plant^{-1} directly contributed to increased ear yield.

Bao Heping *et al.* (2004) reported that maize yield was mainly influenced by cob length, followed by No. of kernels row^{-1}, cob width, No. of rows ear^{-1}, and 300-kernels weight. Arun and Singh (2004 a) reported that days to 50 % silking and cob length had the maximum positive direct effect on kernel yield. Whereas, days to 50 % tasseling had the maximum negative effect on kernel yield.

Shelake *et al.* (2005) reported that the path analysis revealed high magnitude of direct effects for all characters at the genotypic level and days to 50 % tasseling and days to 50 % silking showed higher genotypic direct effect.

Wang Dachun (2006) reported that kernel weight row^{-1} mainly affected by cob length and cob width and the cob length played an important role on kernel weight ear^{-1} in high yielding combinations. Kumar *et al.* (2006) observed that day to 50 % tasseling, ear height and 300-kernel weight had highest direct effect on kernel yield. The days to 50 % silking exhibited negative direct effect on kernel yield. Abirami *et al.* (2007) showed that weight of the cob contributed to the maximum direct effect to kernel yield. Sofi and Rather (2007) indicated that

300-kernel weight had the greatest direct effect on kernel yield followed by No. of kernels row^{-1}, No. of rows ear^{-1}, cob length and cob width.

Xie *et al.* (2007) showed that kernels plant^{-1} was arranged for the top position among the many agronomic traits that contributed to the yield enhancement of a single plant and was followed by No. of kernels row^{-1}, 300-kernels weight. Akbar *et al.* (2008) showed that all traits exerted positive direct effectt on kernel yield plant^{-1} except days to 50 % silking.

Path coefficient analysis revealed that No. of kernels ear^{-1} had the greatest direct effect on kernels yield plant^{-1}, plant height, days to 50 % silking and cob length also influenced the yield indirectly via No. of kernels ear^{-1}.

Khatun *et al.* (1999) found that path analysis showed that 300-kernels weight and No. of kernels ear^{-1} were the most important components determining kernel yield.

The direct effects of plant height and ear height towards kernel yield were small, similar to that of days to silking, indicating the possibility of developing high yielding plant types with short plant height, medium ear height (Gautam *et al.*, 1999 a).

In another study on popcorn, Gautam *et al.* (1999 b) reported that No. of kernels row^{-1} imparted maximum positive direct effect towards kernels yield plant^{-1} followed by plant height.

The direct and indirect effects of different quantitative traits on kernels yield were studied in 90 hybrids by Geetha and Jayaraman (2000) and they reported that No. of kernels row^{-1} exerted a maximum direct effect on kernel yield. Hence, selection for No. of kernels row^{-1} will be highly effective for improvement of kernels yield plant^{-1}.

A quantitative trait expresses itself in close association with many other traits. Alteration in the expression of one trait is usually associated with a change in the expression of other traits. Therefore, a plant breeder has to study the degree of characters association. The genotypic correlation coefficient was significant and positive between two traits, but the direct effect of plant height was negative and low on yield. The indirect positive effect through 300-kernels weight is the possible cause of positive correlation between plant height and kernel yield plant^{-1}. Therefore, these traits must be considered if selection is made through plant height (Parh *et al.*, 1986)

The magnitude of direct effect of ear height on kernel yield plant^{-1} was very small, while the genotypic correlation was positive and statistically significant between ear height and kernel yield plant^{-1}. Therefore, if selection is made through ear height then the traits such as 300-kernels weight should also be considered simultaneously as indirect effects through them were high and positive (Gautam *et al.*, 1999 a).

There was significant and positive genotypic correlation coefficient between No. of rows ear^{-1} and kernel yield plant^{-1}. The direct effect on kernel yield plant^{-1} was also positive and greater in magnitude than that of genotypic correlation. Therefore, correlation explains the true relationship between the two traits (Trifunovic, 1988; Ivakhnenko and Klimov, 1991; Singh and Singh, 1993; Singh *et al.*, 1995). Kumar and Kumar (2000) suggested the effectiveness of indirect selection for kernel yield through No. of rows ear^{-1}.

Tyagi *et al.* (1988) reported that 50 % silking had a direct correlation with yield and so, early maturing genotypes had relatively low yield. Dash *et al.* (1992) reported that path coefficient analysis revealed that cob width, plant height, cob length and 300-kernels weight were the major factors contributing to yield. Packiaraj (1995) observed direct positive correlation between kernel yield and No. of kernels row^{-1}.

Rahman *et al.* (1995) reported that kernel yield was significantly and positively correlated with plant height, ear height, No. of kernels ear^{-1} and 300-kernels weight. Path analysis revealed that ear height, plant height and 300-kernels weight were the main contributors for kernel yield.

3. MATERIAL AND METHODS

This study was conducted at two locations in Sulaimani region, Kanipanka Nursery Station, Sulaimani Agricultural Directorate, Ministry of Agriculture (Lat 35^o 22' ; N, Long 45^o 43' ; E, 550 masl) in Shahrazoor valley 35 Km east of Sulaimani city and Qlyasan Agricultural Research Station, College of Agriculture, University of Sulaimani (Lat 35^o 34' 307" ; N, Long 45^o 21' 992" ; E, 765 masl), 2 Km north west of Sulaimani city during the autumn and spring growing season of 2009 – 2010 (Townsend and Guest , 1966).

Appendices (1 and 2) show the metrological data, soil physical & chemical properties of both location's respectively.

Five maize lines (MIS 4218, MIS 4279, MIS 43100, ZP 434, and 5012) were crossed in the spring of the year 2009, in a diallel mating design including reciprocals to form 25 F_1 hybrids (Table 1 and Figure 1). Each ear was obtained by cross fertilization to one tassel only and no tassel was used to pollinate more than two ear shoots. The ears were harvested, dried and shelled manually, they were kept in the controlled environment to be used in the trials next growing season.

All the F_1 hybrids along with their parental lines were grown in the following growing season. Trials were irrigated throughout the growing season cultural operations, fertilization, and weed control were accomplished according to normal field practices. Hills were overplanted and thinned after emergence for a final plant density of about 55,000 plants ha^{-1}. Each cross was planted in one raw, 0.75 m apart and 5 m long with 0.25 m between plants (Figure 2). Samples were harvested by hand, for yield assessment.

Table 1. Studied Breeding Materials

No.	Diallel, Reciprocal Crosses, and Parental No.	Parentage
1	1 x 2	MIS 4218 x MIS 4279
2	2 x 1	MIS 4279 x MIS 4218
3	1 x 3	MIS 4218 x MIS 43100
4	3 x 1	MIS 43100 x MIS 4218
5	1 x 4	MIS 4218 x ZP 434
6	4 x 1	ZP 434 x MIS 4218
7	1 x 5	MIS 4218 x 5012
8	5 x 1	5012 x MIS 4218
9	2 x 3	MIS 4279 x MIS 43100
10	3 x 2	MIS 43100 x MIS 4279
11	2 x 4	MIS 4279 x ZP 434
12	4 x 2	ZP 434 x MIS 4279
13	2 x 5	MIS 4279 x 5012
14	5 x 2	5012 x MIS 4279
15	3 x 4	MIS 43100 x ZP 434
16	4 x 3	ZP 434 x MIS 43100
17	3 x 5	MIS 43100 x 5012
18	5 x 3	5012 x MIS 43100
19	4 x 5	ZP 434 x 5012
20	5 x 4	5012 x ZP 434
21	1	MIS 4218
22	2	MIS 4279
23	3	MIS 43100
24	4	ZP 434
25	5	5012

3.1. Data Collection

Five plants were tagged randomly for recording observations for each entry for all the quantitative characters except for days to 50 % tasseling and silking. Mean of five plants for each entry in each replication was worked out for each character at each location and used for statistical analysis.

3.2. Recorded Observations

Observations on the following quantitative characters were recorded at appropriate stages of plant growth.

3.2.1. Days to 50% tasseling

The number of days from sowing upto the day on which 50 % of the plants showed tassel emergence was recorded as days to 50 % tasseling.

3.2.2. Days to 50% silking

The number of days from sowing upto the day on which 50 % of plants showed silk emergence was recorded as days to 50 % silking.

3.2.3. Plant height (cm)

Height of the plant from ground level upto the base of fully opened flag leaf was recorded in centimeters as plant height when plants were mature.

3.2.4. Ear height (cm)

Height from ground level upto the base of the upper most bearing internode was recorded as ear height in centimeters.

3.2.5. Cob weight (g)

Weight of the ear was measured and recorded in grams at the time of harvest as its total weight.

3.2.6. Cob length (cm)

Length of the ear was measured and recorded in centimeters - from the base to the tip of the ear - at the time of harvest as its total length.

3.2.7. Cob width (cm)

Cob width was measured and recorded in centimeters - at the middle of the ear - as the thickness of the ear.

3.2.8. No. of ears plant^{-1}

Number of ears per plant was counted and average was recorded.

3.2.9. No. of rows ear^{-1}

Number of kernel rows per ear was counted and recorded.

3.2.10. No. of kernels row^{-1}

Number of kernels per row was counted and average was recorded as number of kernels per row.

3.2.11. Kernels weight row^{-1} (g)

The weight of kernel of five rows was average and recorded.

3.2.12. Kernels weight ear^{-1} (g)

The weight of kernels of five ears was average and recorded.

3.2.13. 300-kernels weight (g)

The weight of sun dried 300-grain samples were recorded in grams at 15 % moisture content.

3.2.14. Kernels yield plant^{-1} (g)

Kernel yield per plant expressed in grams was recorded by weighing the grains obtained after shelling of cobs from individual plant.

3.3. Genetic Parameters

3.3.1. General Combining Ability (GCA) and its variance
3.3.2. Specific Combining Ability (SCA) and its variance
3.3.3. Heterosis %
3.3.4. Reciprocal Effect %
3.3.5. Heritability in Broad Sense
3.3.6. Heritability in Narrow Sense
3.3.7. Average Degree of Dominance (ā)

3.4. Analysis of Variance

A range of statistical analysis was conducted for each character; A Completely Randomized Block Design (CRBD) with three replications was implemented according to the following linear modeling (Al-Mohammad and Al-Yonis, 2000).

$$Y_{ij} = \mu + \tau_i + \rho_j + \varepsilon_{ij} \quad \begin{Bmatrix} i = 1, 2, ..., t \\ j = 1, 2, ..., r \end{Bmatrix}$$

Where:

Y_{ij} : The value of observation belongs to the experimental unit designated

μ : The general mean value,

τ_i : The value of the actual effect of the treatment " i ",

ρ_j : The value of actual effect of the block " j ", and

ε_{ij} : The value of the actual effect of the experimental error belongs to the observation designated as treatment " i " in the block " j ".

ε_{ij} ~ IND (0, σ^2)

3.5. Combining Ability Analysis

Griffing (1956) designed two main models and four methods for the analysis of diallel data. In the present study, analysis of the combining ability for each character was done following Griffing's method I, where parents, F_1s and reciprocals were included. The data was analyzed using a fixed model. If the fixed effects model is used, the sampling error becomes the effective residual for testing combining ability mean squares and estimating variance components and standard errors. It should be noted here that the replication values are actually the means of plot over individual observations i.e., c.

Thus, we obtained data from a table that containing $\frac{1}{bc}\sum\sum Y_{ijk} = Y_{ij}$ values. Obviously Y_{ij} is the mean of *(i x j)*th genotype over *k* and *l*.

The (GCA) and (SCA) were estimated using the general linear model for the analysis which takes the formula of Singh and Chaudhary (1985).

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + R_{ij} + r_k + \frac{1}{bc}\sum\sum \varepsilon_{ijk}$$

Where: Y_{ijk} : observed value of the experimental unit,

μ : populations mean,

g_i : general combining ability (GCA) effect for the ith parent,

g_j : general combining ability (GCA) for the jth parent,

s_{ij} : specific combining ability (SCA) for the diallel crosses involving parents i and j,

R_{ij} : specific combining ability (RCA) for the reciprocal crosses involving parents i and j,

r_k : replication (block) effect, and

$\frac{1}{bc}\sum\sum \varepsilon_{ijk}$: means error effect.

3.6. Estimation of General and Specific Combining Ability Effect

(Singh and Chaudhary, 1985).

$$\hat{g}_{ii} = \frac{1}{2P}\left(Y_{i.} + Y_{.j}\right) - \frac{1}{P^2}Y_{..}$$

$$\hat{s}_{ij} = \frac{1}{2}\left(Y_{ij} + Y_{ji}\right) - \frac{1}{2P}\left(Y_{i.} + Y_{.i} + Y_{j.} + Y_{.j}\right) + \frac{1}{P^2}Y_{..}$$

$$\hat{r}_{ij} = \frac{1}{2}\left(Y_{ij} - Y_{ji}\right)$$

$\hat{g}_{ii}$ *:* Effect of general combining ability for parent “ i ”,

$\hat{s}_{ij}$*:* Effect of expected specific combining ability for single diallel crosses ij when i = j,

$\hat{r}_{ij}$ *:* Effect of specific combining ability for single reciprocal crosses ij when i = j,

Y_{ij}*:* F$_1$s mean as a result of crossing parent “ i ” with parent “ j ”,

$Y_{..}$: Sum of the means of all parents and F$_1$s hybrids non-reciprocal,

P: Parent's number.

3.7. Estimation of components of variance for both General and Specific Combining Abilities (Singh and Chaudhary, 1985).

$$\sigma^2 \hat{g}_{ii} = (g_{ii})^2 - \frac{MS'e}{p^2}$$

$$\sigma^2 \hat{\mathrm{s}}_{\mathrm{ij}} = \frac{1}{\mathrm{p-2}} \sum \hat{\mathrm{s}}_{\mathrm{ij}}^{\ 2} - \frac{MS'e(p^2 - 2p + 2)}{2p^2}$$

$$\sigma^2 \hat{\mathrm{r}}_{\mathrm{ij}} = \frac{1}{\mathrm{p-2}} \sum \hat{\mathrm{r}}_{\mathrm{ij}}^{\ 2} - \frac{MS'e}{2}$$

$\sigma^2 \hat{g}_{ii}$: Variance of expected effect of general combining ability of the parent i,

$\sigma^2 \hat{\mathrm{s}}_{\mathrm{ij}}$: Variance of expected effect of specific combining ability for diallel crosses of parent i, and

$\sigma^2 \hat{\mathrm{r}}_{\mathrm{ij}}$: Variance of expected effect of specific combining ability for reciprocal crosses of parent i.

3.8. Estimation of standard error for the differences between the effects of the general combining ability of two parents (Singh and Chaudhary, 1985).

$$S.E._{(g_i - g_j)} = \sqrt{\frac{MS'e}{p}}$$

3.9. Estimation of standard error for the differences between the effects of two diallel crosses (Singh and Chaudhary, 1985).

$$S.E._{(S_{ij} - S_{ik})} = \sqrt{\frac{(p-1)MS'e}{p}}$$

3.10. Estimation of standard error for the differences between the effects of two reciprocal crosses (Singh and Chaudhary, 1985).

$$S.E._{(r_{ij} - r_{ik})} = \sqrt{MS'e}$$

3.11. Heterosis

It was estimated as the percentage deviation of F_1s hybrid from mid parental value (AGB301, 2004).

$$Heterosis\ \left(H\right)\% = \frac{\overline{F}_1 - \overline{M}.P}{\overline{M}.P} \times 100$$

Where: $\overline{F}_1$ *:* Mean of hybrid,

$\overline{M}.P$ *:* Mid Parental value.

Where: $\overline{M}.P = \frac{P_1 + P_2}{2}$

P_1: Parent No. 1,

P_2: Parent No. 2.

3.12. Heritability

Heritability in broad and narrow sense was estimated depending on the variance of general and specific combining abilities, and on the variance of experimental error according to Singh and Chaudhary (1985), and as follows:

$$h^2{}_{b.s} = \frac{\sigma^2{}_G}{\sigma^2{}_P} = \frac{\sigma^2{}_A + \sigma^2{}_D}{\sigma^2{}_A + \sigma^2{}_D + \sigma^2 e} = \frac{2\sigma^2{}_{GCA} + \sigma^2{}_{SCA}}{2\sigma^2{}_{GCA} + \sigma^2{}_{SCA} + \sigma^2 e}$$

$$h^2{}_{n.s} = \frac{\sigma^2{}_A}{\sigma^2{}_P} = \frac{\sigma^2{}_A}{\sigma^2{}_A + \sigma^2{}_D + \sigma^2 e} = \frac{2\sigma^2{}_{GCA}}{2\sigma^2{}_{GCA} + \sigma^2{}_{SCA} + \sigma^2 e}$$

Where: $h^2{}_{b.s}$: Heritability in broad sense,

$h^2{}_{n.s}$: Heritability in narrow sense,

$\sigma^2{}_{GCA}$: The variance of general combining ability,

$\sigma^2{}_{SCA}$: The variance of specific combining ability,

$\sigma^2\ e$: The variance of experimental error i.e. environmental variance,

$\sigma^2{}_A$: Additive genetic variance,

$\sigma^2{}_D$: Non-additive (dominance and epistasis) genetic variance,

$\sigma^2{}_G$: Total genetic variance, and

$\sigma^2{}_P$: Phenotypic variance (genetic and environmental variance).

3.13. The Average Degree of Dominance (ā)

The degree of dominance mean for all traits was estimated as follows:

$$\bar{a} = \sqrt{\frac{2\sigma^2{}_D}{\sigma^2{}_A}} = \sqrt{\frac{2\sigma^2{}_{SCA}}{2\sigma^2{}_{GCA}}} = \sqrt{\frac{\sigma^2{}_{SCA}}{\sigma^2{}_{GCA}}}$$

If $\bar{a} = 0$ indicates no dominance

If $\bar{a} < 1$ indicates partial dominance

If $\bar{a} = 1$ indicates complete dominance

If $\bar{a} > 1$ indicates over dominance

3.14. The Reciprocal Effects

$$\text{Re}\mathit{ciprocal\ \ Effect}\ \ (R.E)\% = \frac{(\bar{F}_{1r} - \bar{F}_1)}{\bar{F}_1} \times 100$$

Where: $\bar{F}_1$: The average of diallel hybrid

$\bar{F}_{1r}$: The average of reciprocal hybrid

3.15. Correlation Analysis

The correlation coefficients were calculated to determine the degree of association of characters with yield and also among the yield components themselves in each environment.

Phenotypic correlations were computed by using the formula given by Webber and Moorthy (1952) and Singh and Chaudhary (1985).

$$r = \frac{\sum XY - \frac{(\sum X)(\sum Y)}{n}}{\sqrt{\left(\sum X^2 - \frac{(\sum X)^2}{n}\right)\left(\sum Y^2 - \frac{(\sum Y)^2}{n}\right)}}$$

$$t_{(r)Cal.} = \frac{r}{\sqrt{1 - r^2 / n - 2}}$$

Where: n : Number of the treatments,

r : Correlation factor value.

The significance of r value was tested according to *t-test* at *n-2* degree of freedom.

Analysis of Variance for Full Diallel Cross According to Griffing 1956, Method I, Model I (Parents, Diallel Crosses, and Reciprocal Crosses) (Singh and Chaudhary, 1985).

S.O.V	d.f	SS	MS	E(M.S)
Blocks	$(b-1)=2$	$SS_B=\frac{\sum Y_{..k}^2}{p^2}-\frac{Y^2..}{bp^2}$	MS_B	
Genotypes	$(p^2-1)=24$	$SS_G=\frac{\sum Y_{ij.}^2}{b}-\frac{Y^2..}{bp^2}$	MS_G	
GCA	$(p-1)=4$	$SS_{GCA}=\frac{1}{2p}\sum_i\left(Y_{i.}+Y_{.j}\right)^2-\frac{2}{p^2}Y_{..}^2$	MS_{GCA}	$\sigma_{GCA}^2=\sigma^2e+\frac{2P}{p-1}\sum g_i^2=\frac{MS_{GCA}-MS'e}{2p}$
SCA	$\frac{p(p-1)}{2}=10$	$SS_{SCA}=\frac{1}{2P}\sum_i\sum_j Y_{ij}\left(Y_{ij}-Y_{ji}\right)-\frac{1}{2}\sum_i\left(Y_{.i}+Y_{i.}\right)^2+\frac{1}{p^2}Y_{..}^2$	MS_{SCA}	$\sigma_{SCA}^2=\sigma^2e+\frac{2}{p(p-1)}\sum\sum s_{ij}^2=\left(MS_{SCA}-MS'e\right)$
RCA	$\frac{p(p-1)}{2}=10$	$SS_{RCA}=\frac{1}{2}\sum_i\sum_j\left(Y_{ij}-Y_{ji}\right)^2$	MS_{RCA}	$\sigma_{RCA}^2=\sigma^2e+\frac{2}{p(p-1)}\sum\sum r_{ij}^2=\left(MS_{RCA}-MS'e\right)/2$
Error	$(b-1)(p^2-1)=48$	$SS_e=SS_T-SS_B-SS_G$	MS'_e	σ^2e
Total	$bp^2-1=74$	$SS_{Total}=\sum Y_{ijk}^2-\frac{Y^2..}{bp^2}$		

Path Coefficient Analysis

The path coefficient techniques involve partitioning of correlation coefficient to determine direct (unidirectional path way `P') and indirect effects through alternate path ways (Path way `P' X correlation coefficient `r') of various variables and kernel yield per plant. Kernel yield was considered as the resultant variable and the others as causal variables.

The path coefficient analysis was carried out as suggested by Dewey and Lu (1959), Soomro (2010), Singh and Chaudhary (1985), and Arbuckle (2009), through (Analysis of Moment Structures) AMOS Ver. 18 Software.

4. RESULTS AND DISCUSSION

4.1. Days to 50 % tasseling

At Kanipanka location, analysis of variance as shown in Appendix (3) revealed that there were highly significant differences between genotypes as presented in Table (2) for number of days to 50 % tasseling. Parent 4 was the earliest with 69.333 days to 50 % tasseling, while parent 3 was the latest with 72 days to 50 % tasseling. The differences in parent’s day to 50 % tasseling caused also the differences in their hybrids. Regarding the diallel hybrids, the hybrids 2×4 and 4×5 with 69.333 days were the earliest and it was earlier than the parents, but the diallel hybrid 2×5 with 71.667 days was the latest. The reciprocal hybrid 4×3 with 68.667 days had the shortest, while 3×1 with 71.667 had the longest period to 50 % tasseling, also the analysis of variance as shown in Appendix (4) showed highly significant differences between genotypes at Qlyasan location as presented in the same table. Parent 4 also was the earliest with 69.000 days, while parent 3 was the latest with 72.667 days. The diallel hybrids 2×4 with 69.000 days was the earliest, but the diallel hybrid 1×2 with 73.333 days was the latest. The reciprocal hybrid 4×3 with 68.667 days had the shortest, while 3×1 with 75.000 had the longest period to 50 % tasseling.

El-Baroudiy (1999); Malik *et al.* (2004), and Mohammad (2005) recorded significant differences between genotypes.

Significant positive and negative heterosis over the mid-parental values at both locations were calculated in Table (3). The highest positive heterosis values were 1.415 % for diallel cross 2×5, and 2.326 % for the cross 1×2 at Kanipanka and Qlyasan respectively, while the lowest negative values were - 1.402 % for the hybrid 2×3 and -1.429 % for the hybrid 2×4 at Kanipanka and Qlyasan respectively. Concerning the reciprocal crosses, the highest positive heterosis value was 0.952 % shown by the hybrid 5×4 and 3.448 % for the hybrid 3×1 at Kanipanka and Qlyasan respectively, while the value -2.830 % for the hybrid

Table 2. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Days to 50 % tasseling at both locations.

Kanipanka Location					
Parents	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)
MSI 4218 (1)	70.333	70.667	70.667	70.333	70.667
MSI 4279 (2)	70.000	70.667	70.333	69.333	71.667
MSI 43100(3)	71.667	70.000	72.000	70.667	71.333
ZP 434 (4)	69.333	70.000	68.667	69.333	69.333
5012 (5)	70.000	70.000	71.000	70.667	70.667

Parental Mean	Diallel Mean	Reciprocal Mean	General Mean	l.s.d ($p \le 0.05$) for genotypes
70.600	70.500	70.133	70.373	1.363

Qlyasan Location					
Parents	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)
MSI 4218 (1)	72.333	73.333	72.000	70.667	70.333
MSI 4279 (2)	72.000	71.000	71.333	69.000	70.333
MSI 43100 (3)	75.000	73.000	72.667	71.333	73.000
ZP 434 (4)	69.000	69.667	68.667	69.000	70.000
5012 (5)	72.000	70.000	72.000	69.333	71.333

Parental Mean	Diallel Mean	Reciprocal Mean	General Mean	l.s.d ($p \le 0.05$) for genotypes
71.267	71.133	71.067	71.133	2.139

4×3 and also the value -3.059 % for the hybrid 4×3 showed a desirable negative heterosis at Kanipanka and Qlyasan respectively. Positive and negative heterosis values were also exhibited by Al-Zawbaey (2001); Al-Azawy (2002); Al-Falahy (2002); Al-Janaby (2003), and Mohammad (2005). The differences between diallel and reciprocal crosses in their heterosis values may be due to the presence of maternal effect, which were reported previously by Singh and Singh (1962); Hunter and Gamble (1968); Rao and Fleming (1980); Nawar (1984), and Griffing (1990).

Table 3. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Days to 50 % tasseling at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		0.236	- 0.703	0.716	0.236	0.273
MSI 4279 (2)	- 0.709		- 1.402	- 0.952	1.415	
MSI 43100 (3)	0.703	- 1.869		0.000	0.000	
ZP 434 (4)	- 0.716	0.000	- 2.830		- 0.952	
5012 (5)	- 0.709	- 0.943	- 0.467	0.952		
S.E	0.353					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		2.326	- 0.690	0.000	- 2.088	0.425
MSI 4279 (2)	0.465		- 0.696	- 1.429	- 1.171	
MSI 43100 (3)	3.448	1.624		0.706	1.389	
ZP 434 (4)	- 2.358	- 0.476	- 3.059		- 0.238	
5012 (5)	0.232	- 1.639	0.000	- 1.188		
S.E	0.607					

Table (4) shows the effects of reciprocal crosses, which found to be significant at both locations. These effects reached 1.923 % for a cross 5×4, and 4.167 % for the cross 3×1 at Kanipanka and Qlyasan respectively, while the lowest negative values were -2.830 % for the hybrid 4×3 and -3.738 for the hybrid 4×3 at Kanipanka and Qlyasan respectively. The positive values exhibited the predominance of reciprocal hybrids over its diallel hybrids. These results indicated the presence of maternal effects (Cytoplasmic effects). Similar results reported by Mohammad (2005).

Table 4. Reciprocal effect value percentages for the character Days to 50 % tasseling at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 0.943				
MSI 43100 (3)	1.415	- 0.474			
ZP 434 (4)	- 1.422	0.962	- 2.830		
5012 (5)	- 0.943	- 2.326	- 0.467	1.923	
S.E	0.491				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 1.818				
MSI 43100 (3)	4.167	2.336			
ZP 434 (4)	- 2.358	0.966	- 3.738		
5012 (5)	2.370	- 0.474	- 1.370	- 0.952	
S.E	0.783				

The effects of GCA, SCA and RCA were show in Table (5); results of genetic analysis gave high significant mean squares for GCA, but not significant for SCA and significant mean squares for RCA concerning number of days to 50 % tasseling at both locations (Appendices 3 and 4). Similar results were shown previously by El-Baroudiy (1999) and Mohammad (2005).

The highest positive values of $\hat{g}ii$ were 0.460 and 1.033 in parent 3 at Kanipanka and Qlyasan respectively, these values indicated the high contribution of this parent in increasing the number of days to 50 % tasseling in its hybrids, while parent 4 gave the lowest negative value of $\hat{g}ii$ reaching - 0.673 and -1.567 at Kanipanka and Qlyasan respectively, indicating the contribution of this parent in reducing number of days to 50 % tasseling in their hybrids. Concerning the SCA effect of the hybrids, the maximum SCA effect values were 0.673 and 1.700 in the diallel hybrid 1×3 at Kanipanka and Qlyasan respectively followed by the reciprocal hybrid 4×3 with the effect value of $\hat{r}ij$ of 1.000 and 1.333 at Kanipanka and Qlyasan respectively. These positive effects of SCA indicated the increase of this character in these hybrids compared with their parents.

The highest variances of GCA effect were 0.453 and 2.454 in parent 4 at Kanipanka and Qlyasan respectively, which signifies the large contribution of this parent in transferring this trait to its hybrids. The highest values due to the variance of SCA effect were 0.337 for parent 4 and 1.193 for the parent 1 at Kanipanka and Qlyasan respectively, pointing out the contribution of these parents in transferring this trait to one or a few numbers of its hybrids, while the lowest values of this variance were 0.099 for parent 3 and 0.146 for parent 2 at Kanipanka and Qlyasan respectively, which meant that the contribution of these parents to transferring this trait to most of its hybrids was not quite high. Regarding $\sigma^2\hat{r}ij$, parent 3 gave the maximum values with 0.625 and 1.641 at Kanipanka and Qlyasan respectively.

Table 5. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Days to 50 % tasseling at both locations.

Kanipanka Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	0.027	- 0.027	0.673	0.107	- 0.293	- 0.008	0.106	0.126
MSI 4279 (2)	0.333	- 0.040	- 0.627	0.007	0.273	0.002	0.115	0.278
MSI 43100 (3)	- 0.500	0.167	0.460	- 0.493	0.107	0.212	0.099	0.625
ZP 434 (4)	0.500	- 0.333	1.000	- 0.673	0.073	0.453	0.377	0.233
5012 (5)	0.333	0.833	0.167	- 0.667	0.227	0.051	0.348	0.059
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					
	0.214	0.429	0.479					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.230	0.157	0.031	5.064	0.313	0.188
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.444	0.600	0.546	1.095	0.686	0.429

Qlyasan Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	0.767	0.833	1.700	- 0.500	- 0.567	0.565	1.193	1.078
MSI 4279 (2)	0.667	- 0.067	0.067	- 0.167	- 0.733	0.004	0.146	0.509
MSI43100 (3)	- 1.500	- 0.833	1.033	- 0.600	0.500	1.068	0.992	1.641
ZP 434 (4)	0.833	- 0.333	1.333	- 1.567	0.267	2.454	0.692	0.250
5012 (5)	- 0.833	0.167	0.500	0.333	- 0.167	0.028	0.169	0.393
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					
	0.336	0.673	0.752					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.566	0.979	0.170	5.758	1.958	0.423
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.416	0.790	0.727	0.657	0.808	0.665

Table (5) also describes some genetic parameters for number of days to 50 % tasseling. The variance component due to GCA was much greater than the variance component due to SCA, making the ratio of $\sigma^2_{GCA} / \sigma^2_{SCA}$ value more than one (5.064 and 5.758) at Kanipanka and Qlyasan respectively which confirmed the large contribution of additive gene action in the inheritance of this character, while previous workers confirmed the importance of non additive gene effect in controlling this character El-Baroudiy (1999) and Mohammad (2005). This was reflected on the average degree of dominance values for diallel crosses by giving less than one (0.444 and 0.416) at Kanipanka and Qlyasan respectively, but there were 1.095 and 0.657 for reciprocal crosses at Kanipanka and Qlyasan respectively. Previously it was indicated that the average degree of dominance value was more than one, confirming the importance of non additive gene effect (Baktash, 1979; Yousif, 1997; El-Baroudiy,1999, and Mohammad, 2005).

Heritability estimates in broad sense for diallel was 0.600 and 0.790 at Kanipanka and Qlyasan respectively, while in narrow sense was 0.546 and 0.727 at Kanipanka and Qlyasan respectively, but the heritability estimates in broad senses for reciprocal crosses were 0.686 and 0.808 at Kanipanka and Qlyasan respectively, while in narrow sense was 0.429 and 0.665 at Kanipanka and Qlyasan respectively. Similar results were obtained by the researchers Warner (1952); Gyanendra *et al.* (1995); Al- Jumaely (1996); El-Baroudiy (1999); Choudhary and Chaudhari (2002); Sumathi *et al.*(2005); Om prakash *et al.* (2006); Akbar *et al.* (2008). Nevertheless, low estimates of heritability were recorded previously for the diallel crosses by Satyanaraya and Saikumar (1996); Mohammad (2005); Pradeep and Satyanarana (2001), and Salami *et al.* (2007).

4.2. Days to 50 % silking

Analysis of variance in Appendices (3 and 4) revealed that there were highly significant differences between genotypes as presented in Table (6) for days to 50 % silking at Kanipanka and Qlyasan locations. At Kanipanka parents 4 and 5 were the earliest with 73.333 days to 50 % silking, while parent 3 was the latest with 77.333 days to 50 % silking. The differences in parent’s day to 50 % silking caused also the differences in their hybrids. Regarding the diallel hybrids, the hybrid 4×5 with 73.333 days was the earliest, but the diallel hybrids 1×2 and 2×3 with 76.333 days were the latest. The reciprocal hybrids 4×1and 5×1 with 74.000 days were the shortest, while 3×1, 5×2, 5×3, and 5×4 with 77.000 gave the longest period to 50 % silking. At Qlyasan location, parent 4 was the earliest with 74.000 days, while parent 3 was the latest with 78.000 days. The diallel hybrids 2×4 with 73.000 days was the earliest, but the diallel hybrid 3×5 with 76.333 days was the latest. The reciprocal hybrid 4×1 with 74.000 days had the shortest, while 3×1 with 79.667 had the longest period to 50 % silking. Significant differences were also reported previously by Al-Zawbaey (2001); Al-Azawy (2002); Al-Janaby (2003), and Mohammad (2005).

The estimation of heterosis percentage as the F_1s deviation from mid parental values for days to 50 % silking were represented in Table (7) for both diallel and reciprocal crosses in both locations. At Kanipanka location, all heterosis due to diallel crosses showed negative values with the exception of the cross 1×2 with a positive value 0.659 %, while the negative heterosis values restricted between -2.632 % and -0.219 % for both hybrids 1×5 and 2×5 respectively. Regarding the reciprocal crosses in the same location, it was observed that half of the crosses gave a negative values which restricted between -2.632 % and - 0.433 % for both crosses 4×3 and 5×1 respectively, while maximum positive heterosis values recorded by 3×1 which was 2.796 %. Previous workers recorded high heterosis percentage values due to diallel crosses, confirming the effect of over dominance gene effect toward delaying of

Table 6. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Days to 50 % silking at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	75.667	76.333	75.333	74.333	74.000
MSI 4279 (2)	75.667	76.000	76.333	74.333	76.000
MSI 43100 (3)	77.000	75.667	77.333	75.000	75.667
ZP 434 (4)	74.000	74.667	74.333	73.333	73.333
5012 (5)	74.000	77.000	77.000	77.000	76.333

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
75.733	75.067	75.633	75.427	2.020

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	77.000	75.667	75.333	75.000	75.333
MSI 4279 (2)	77.000	74.667	75.667	73.000	75.333
MSI 43100 (3)	79.667	76.667	78.000	75.000	76.333
ZP 434 (4)	74.000	74.333	74.000	74.000	74.000
5012 (5)	76.667	75.333	76.000	75.000	77.000

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
76.133	75.067	75.867	75.600	1.968

silking (Al-Zawbaey, 2001; Al-Falahy, 2002; Al-Azawy, 2002; Al-Janaby, 2003, and Mohammad, 2005).

Table 7. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Days to 50 % silking at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		0.659	- 1.525	- 0.224	- 2.632	0.316
MSI 4279 (2)	- 0.220		- 0.435	- 0.446	- 0.219	
MSI 43100 (3)	0.654	- 1.304		- 0.442	- 1.518	
ZP 434 (4)	- 0.671	0.000	- 1.327		- 2.004	
5012 (5)	- 2.632	1.094	0.217	2.895		
S.E	0.480					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 0.220	- 2.796	- 0.662	- 2.165	0.254
MSI 4279 (2)	1.538		- 0.873	- 1.794	- 0.659	
MSI 43100 (3)	2.796	0.437		- 1.316	- 1.505	
ZP 434 (4)	- 1.987	0.000	- 2.632		- 1.987	
5012 (5)	- 0.433	- 0.659	- 1.935	- 0.662		
S.E	0.525					

Table (8) explains the reciprocal effect for days to 50 % silking at both locations. The maximum positive effect value at Kanipanka recorded by the reciprocal cross 5×4 with 5.000 %, while maximum negative effect value was -0.889 % recorded by the reciprocal cross of 4×3. At Qlyasan location, positive and negative effects were noticed, the maximum effect was 5.752 % recorded by the cross 3x1, while maximum negative effect was -1.333 exhibited by the reciprocal crosses 4×l and 4×3 respectively. Similar results reported by Al-Jumaely (1996); El-Baroudiy (1999), and Mohammad (2005).

It is obvious from Appendices (3 and 4), the presence of highly significant differences in the mean squares of genotypes for this character, which confirmed the necessity of genetic analysis at both locations (Table 9). At Kanipanka location, the parents 1 and 4 recorded the negative effects of general combining ability with -0.227 and -1.060 respectively, indicating the ability of these parents in reducing days to 50 % silking. Nevertheless, the parents 2, 3 and 5 exhibited positive GCA effects value with 0.373, 0.673 and 0.240 respectively which also confirmed the ability of these parents towards delaying the silking dates in combining ability effects for the diallel crosses. The maximum positive SCA effect was 5.560 recorded by the hybrid 4×5, indicating the ability of this hybrid to increase the days to 50 % silking, while maximum negative value of SCA effect was -1.440 produced by the hybrid 1×5, indicating the ability of this hybrid in reducing days to 50 % silking compared to their parents. Regarding the specific combing effect of reciprocal crosses, it was observed that the hybrids 2×1, 3×2 and 4×3 showed maximum positive values for this effect which was 0.333, while maximum negative value recorded by the reciprocal cross 5×4 with -1.833. The negative effects of SCA indicated the reduction of this character in these hybrids compared to their parents. The maximum variance of GCA effect was 1.124 in parent 4, which signified the large contribution of this parent in transferring this trait to its hybrids. El-Baroudiy (1999) observed significant mean squares due to GCA and SCA, while Mohammad (2005) found significant mean squares due to GCA only.

Regarding the variance of SCA effect of diallel crosses, the maximum value of this variance was exhibited by parent 5, which was 1.180. Maximum $\sigma^2\hat{r}ij$ was recorded by the parent 4 with 1.186. Table (9) also describes same genetic parameters for Days to 50 % silking. The variance component due to GCA was much higher than the variance component due to SCA, making the ratio of $\sigma^2_{GCA} / \sigma^2_{SCA}$ value becomes more than one (1.600) confirming the large contribution of additive gene effect in the inheritance of this character. The average degree of dominance value for diallel crosses were less than one (0.791), while the average degree of dominance for reciprocal crosses was 0.803. These results were in agreement with the results of the previous

Table 8. Reciprocal effect value percentages for the character Days to 50 % silking at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 0.873				
MSI 43100 (3)	2.212	- 0.873			
ZP 434 (4)	- 0.448	0.448	- 0.889		
5012 (5)	0.000	1.316	1.762	5.000	
S.E	0.592				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	1.762				
MSI 43100 (3)	5.752	1.322			
ZP 434 (4)	- 1.333	1.826	- 1.333		
5012 (5)	1.770	0.000	- 0.437	1.351	
S.E	0.655				

researchers Baktash (1979); Nawar (1981); Cross and Nevado (1990); Beck *et al*. (1991);Vassal *et al.* (1992); Mahajan *et al.*(1997), and Sanviceute *et al.* (1998).

At Kanipanka location, heritability estimates in broad sense were 0.678 and 0.680, while in narrow sense were 0.517 and 0.514 for diallel and reciprocal crosses respectively, these results confirmed suitability of both selection and hybridization methods to improve this character.

At Qlyasan location, Parent 3 showed the highest positive effects of $\hat{g}ii$ which was 0.867, this indicated a high contribution of this parent to increase days to 50 % silking, while parent 2 and 4 showed maximum negative value of this effect with -0.367 and -1.367, indicating the contribution of these parents in reducing days to 50 % silking.

Table 9. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Days to 50 % silking at both locations.

Kanipanka Location

$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.227	0.427	0.527	0.027	- 1.440	0.031	0.673	0.025
MSI 4279 (2)	0.333	0.373	- 0.473	- 0.240	0.460	0.139	0.030	0.190
MSI 43100 (3)	- 0.833	0.333	0.673	- 0.373	- 0.007	0.453	0.143	0.352
ZP 434 (4)	0.167	- 0.167	0.333	- 1.060	0.560	1.124	- 0.012	1.186
5012 (5)	0.000	- 0.500	- 0.667	- 1.833	0.240	0.058	1.180	0.866
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	0.318	0.635	0.711					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.505	0.406	0.254	1.600	0.812	0.261
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.791	0.678	0.517	0.803	0.680	0.514

Qlyasan Location

$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	0.667	0.433	1.367	- 0.400	- 0.467	0.425	0.648	1.705
MSI 4279 (2)	- 0.667	- 0.367	0.067	- 0.200	- 0.100	0.134	0.003	0.294
MSI 43100 (3)	- 2.167	- 0.500	0.867	- 0.600	- 0.500	0.751	1.689	0.717
ZP 434 (4)	0.500	- 0.667	0.500	- 1.367	0.067	1.868	0.153	0.270
5012 (5)	- 0.667	0.000	0.167	- 0.500	0.200	0.040	0.078	0.161
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	0.309	0.619	0.692					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.479	0.762	0.072	10.545	1.523	0.466
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.308	0.769	0.734	0.782	0.806	0.617

The estimation of $\hat{s}ij$ revealed that most diallel hybrids had a negative effects ranged between -0.600 to -0.100 for both diallel crosses 3×4 and 2×5 respectively , while the positive values of this effect were restricted between 0.067 for both diallel crosses 2×3 and 4×5 to 1.367 for the cross 1×3 respectively. Regarding the reciprocal crosses the negative values for $\hat{r}ij$ were restricted between -2.167 recorded by the reciprocal cross of 3×1 and - 0.500 for both reciprocal crosses 3×2 and 5×4, but the positive values for this effect restricted between 0.167 for the reciprocal cross 5×3 and 0.500 for both crosses 4×1 and 4×3. Parent 4 showed maximum variance of $\hat{g}ii$ with 1.868, indicating the large contribution of this parent in the inheritance of these characters to the hybrids shared by them. Regarding the variance of $\hat{s}ij$, the maximum value recorded by the parent 3 with 1.689. Maximum value for the variance of $\hat{r}ij$ recorded by parent 1 which was 1.705, indicating the ability of this parent to transfer this character to a few number of its hybrids.

Some genetic parameters due to this character represented in the same table, also indicated the large value of the variance component due to GCA 0.762 compare to the variance component due to SCA which was 0.072, making the ratio of $\sigma^2_{GCA}/\sigma^2_{SCA}$ more than one (10.545). The average degree of dominance for the diallel crosses was 0.308 which confirmed the importance of additive gene effect in the inheritance of this character, while it was 0.782 for the reciprocal crosses. Our results at both locations were in agreement with the results of the previous researchers Baktash (1979); Nawar (1981); Cross and Nevada (1990); Beck *et al.* (1991);Vasal (1992); Mahajan (1997), Sanviceute (1998).

Heritability estimates in broad sense were 0.769 and 0.806, while in narrow sense were 0.734 and 0.617 for diallel and reciprocal crosses respectively, considering that the selection method is more efficient to improve this character. High heritability estimations were obtained previously by the researchers Mani and Bisht (1996); Gyanendra *et al.* (1995); Al- Jumaely

(1996); El-Baroudiy (1999); Jha and Ghosh (2001); Satyanarayana *et al.* (2005); Sumathi *et al.*(2005); Om prakash *et al.* (2006), and Akbar *et al.* (2008). But low estimates of heritability recorded for diallel crosses previously by Reddy and Agarwal (1992); Satyanarana and Saikumar (1996); Pradeep and Satyanarana (2001), and Salami *et al.* (2007).

4.3. Plant height (cm)

Table (10) and Appendix (3) reveal the presence of highly significant differences between genotypes in plant heigh at Kanipanka location. Parent 5 gave maximum plant heigh with 195.000 cm and followed by parent 3 and 1 with 186.667 and 185.333 cm respectively, while parent 4 exhibited minimum plant heigh, which was 175.000 cm. These differences between parental values in this character reflected significantly on both diallel and reciprocal crosses.

Regarding the diallel crosses, it was observed that the values were restricted between 179.667 to 226.667cm for both crosses 1×4 and 2×3 respectively, while the reciprocal crosses values ranged between 175.667 to 234.000 cm for both reciprocal crosses 3×1 and 3×2 respectively. Concerning Qlyasan location, it was noticed in the same table and Appendix (4) that there were highly significant differences between genotypes in plant heigh. Maximum plant heigh exhibited by parent 5 with 204.333 cm, while parent 4 with 190.000 cm produced minimum plant heigh. The diallel crosses values for this character were restricted between 172.667 cm for the diallel cross 3×4 and 209.667 cm for the diallel cross 3×5, while the reciprocal crosses values ranged between 183.667 to 208.667 cm for both reciprocal crosses 4×2 and 5×3 respectively. Similar results were recorded previously by El-Baroudiy (1999) and Mohammad (2005).

Table 10. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character plant height at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	185.333	199.667	197.333	179.667	186.000
MSI 4279 (2)	200.667	181.333	226.667	182.000	181.333
MSI 43100(3)	175.667	234.000	186.667	214.000	198.000
ZP 434 (4)	197.000	178.667	182.333	175.000	188.000
5012 (5)	216.333	223.333	193.000	198.667	195.000

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
184.667	195.267	199.967	195.027	29.709

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	195.333	194.333	201.667	200.667	205.333
MSI 4279 (2)	195.667	197.333	198.000	202.667	198.667
MSI 43100(3)	200.333	200.333	197.333	172.667	209.667
ZP 434 (4)	201.333	183.667	203.667	190.000	190.667
5012 (5)	194.333	206.667	208.667	191.000	204.333

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
196.867	197.433	198.567	197.773	15.391

Highly significant differences among parental values due to this character resulted in the presence of significant heterosis estimated as the F_1s deviation from mid parental values at both locations. Table (11) explains the heterosis values at both locations. At Kanipanka location most diallel hybrids showed positive heterosis values which were restricted between 1.622 % to 23.188 % for both diallel crosses 4×5 and 2×3 respectively, while the diallel cross 2×5 showed maximum negative heterosis value which was -3.632 %. All reciprocal crosses showed positive heterosis values with the exception the cross 3×1 with a negative value -5.556 %, while the positive heterosis values ranged between 0.281 % to 27.174 % for both reciprocal crosses 4×2 and 3×2 respectively.

Table 11. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character plant height at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		8.909	6.093	- 0.278	- 2.191	2.777
MSI 4279 (2)	9.455		23.188	2.152	- 3.632	
MSI 43100(3)	- 5.556	27.174		18.341	3.755	
ZP 434 (4)	9.343	0.281	0.829		1.622	
5012 (5)	13.760	18.689	1.135	7.387		
S.E	3.092					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 1.019	2.716	4.152	2.752	1.502
MSI 4279 (2)	- 0.340		0.338	4.647	- 1.079	
MSI 43100(3)	2.037	1.520		- 10.843	4.398	
ZP 434 (4)	4.498	- 5.164	5.164		- 3.297	
5012 (5)	- 2.752	2.905	3.900	- 3.128		
S.E	1.124					

The heterosis values for Qlyasan location were represented in Table (11) also. Maximum positive value due to diallel crosses exhibited by the cross 2×4 with 4.647 % while minimum positive heterosis value was 0.338 % produced by the cross 2×3. The diallel cross 3×4 showed maximum heterosis, which was -10.843 %. Regarding the reciprocal crosses at Qlyasan location, maximum positive heterosis was 5.164 % recorded by the cross 4×3, whereas the maximum negative heterosis value was -5.164 % showed by the reciprocal 4×2. Positive and negative heterosis values previously were reported by Yousif (1995); Al – Jumaely (1996), and Malik *et al.* (2004).

Data in Table (12) explains the percentage of reciprocal effect, which estimated as the F_1s diallel hybrids from their reciprocal hybrids at both locations for plant heigh. At Kanipanka location, maximum reciprocal was

Table 12. Reciprocal effect value percentages for the character plant height at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	0.501				
MSI 43100 (3)	- 10.980	3.235			
ZP 434 (4)	9.647	-1.832	- 14.798		
5012 (5)	16.308	23.162	- 2.525	5.674	
S.E	3.662				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	0.686				
MSI 43100 (3)	- 0.661	1.178			
ZP 434 (4)	0.332	- 9.375	17.954		
5012 (5)	- 5.357	4.027	- 0.477	0.175	
S.E	2.238				

23.162 produced by the reciprocal cross 5×2, while maximum value recorded at Qlyasan was 17.954 % exhibited by the reciprocal cross 4×3. Combining ability analysis confirmed highly significant SCA mean squares, and significant reciprocal mean squares, while GCA mean squares was found to be not significant at Kanipanka location (Appendix 3), while at Qlyasan location the GCA and SCA mean squares were found to be significant but was not significant for SCA mean square (Appendix 4). The estimations of general and specific combining ability effects were represented in Table (13) for both locations. Maximum positive GCA effect at Kanipanka location was 4.407 recorded by parent 3 and followed by parent 2 with 3.873, indicating the heigh contribution of these parents in the inheritance of this character to their hybrids. Maximum negative $\hat{g}ii$ value was -7.993 recorded by parent 4, indicating the ability of this parent in reducing plant heigh in its crosses, maximum positive effect value was 27.027 recorded by the cross 2×3, while the maximum negative effect was -10.573 showed by the diallel cross 2×4. Regarding the SCA effect for reciprocal crosses as represented in the same table, the maximum positive effect was 15.833 exhibited by the reciprocal cross 4×3 , in which the maximum negative effect was -21.000 recorded by the cross 5×2. The highest variance of GCA effect recorded at Kanipanka location showed by parent 4 was 63.893 indicating the large contribution of this parent in its hybrids in the inheritance of this character. Parent 2 showed maximum variance due to $\hat{s}ij$ with 244.041 and followed by parent 5 with 198.125. This means the high ability of these parents to transfer this character to some of their hybrids without others, while the lowest value was 1.774 recorded by parent 1, indicating the high ability of this parent to transfer this character to most of its hybrids. Maximum variance due to RCA was 343.531 exhibited by parent 3. Significant reciprocal effects were obtained previously by Goma and Shaheen (1994); El-Baroudiy (1999); Malik *et al.* (2004), and Mohammad (2005) for this character also.

Some genetic parameters for this character at Kanipanka location were also represented in Table (13). The variance components due to SCA were higher than variance components due to GCA, making $\sigma^2_{GCA}/\sigma^2_{SCA}$ to be less than one (0.087), confirming the great role of non-additive gene effect in the inheritance of this character. The average degree of dominance recorded at Kanipanka location were 3.399 and 1.908 for both diallel and reciprocal crosses respectively, indicating the over dominance gene effect as controlled the inheritance in this character. Heritabilities in broad sense were 0.679 and 0.468, while the values were 0.100 and 0.166 in narrow sense for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character.

Table 13. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character plant height at both locations.

Kanipanka Location								
$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 2.727	3.993	- 6.573	4.027	6.427	3.068	1.774	86.334
MSI 4279 (2)	- 0.500	3.873	27.027	- 10.573	0.993	15.003	244.041	157.723
MSI43100 (3)	10.833	- 3.667	4.407	6.727	- 6.373	19.419	35.108	343.531
ZP 434 (4)	- 8.667	1.667	15.833	- 7.993	3.860	63.893	77.378	67.234
5012 (5)	- 15.167	- 21.000	2.500	- 5.333	2.440	5.954	198.125	32.603
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	4.673	9.3452	10.448					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
109.165	17.009	196.458	0.087	34.018	61.953
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
3.399	0.679	0.100	1.908	0.468	0.166

Qlyasan Location								
$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	0.660	- 3.127	0.173	7.707	- 2.193	- 0.736	14.709	- 4.232
MSI 4279 (2)	- 0.667	- 0.307	0.507	0.840	1.607	0.094	- 8.632	39.129
MSI43100 (3)	0.667	- 1.167	1.193	- 5.660	6.607	1.424	15.868	80.262
ZP 434 (4)	- 0.333	9.500	- 15.500	- 5.140	- 5.393	26.420	109.938	30.721
5012 (5)	5.500	- 4.000	0.500	- 0.167	3.593	12.912	5.548	26.709
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	2.421	4.8413	5.4127					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
29.298	7.392	10.422	0.709	14.783	23.290
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
1.187	0.462	0.271	1.775	0.565	0.219

Regarding the Qlyasan location, maximum positive GCA effect was 3.593 recorded by parent 5 and followed by parent 3 with 1.193 indicating the high contribution of these parents in the inheritance of this character to their hybrids, while maximum negative $\hat{g}ii$ value was -5.140 recorded by parent 4 indicating the ability of this parent in reducing this character in its hybrid. Concerning $\hat{s}ij$ values, maximum effect was 7.707 recorded by the cross 1×4, while maximum negative value for this effect was -5.660 exhibited by the cross 3×4. Regarding the reciprocal crosses the highest value for $\hat{r}ij$ was 9.500 showed by the reciprocal cross 4×2 , but maximum negative value was -15.500 produced by the cross 4×3. Parent 4 showed maximum variance due to $\hat{g}ii$ which was 26.420, indicating the large contribution of this parent in the inheritance of this character in its hybrids. Regarding the variance $\hat{s}ij$, parent 4 with 109.938 showed maximum value, confirming the high ability of this parent to transfer this character to some of its hybrids without others. The variance of $\hat{r}ij$ for reciprocal crosses reached 80.262 in parent 3. Some genetic parameters for this character at Qlyasan location were represented in the same table. The variance components due to SCA were larger than the variance components due to GCA and the ratio of $\sigma^2_{GCA} / \sigma^2_{SCA}$ was less than one (0.709), indicating the importance of non additive gene effect in the inheritance of this character. The average degree of dominance was 1.187 and 1.775 for both diallel and reciprocal crosses respectively. Previous workers found this ratio to be more than one indicating the importance of additive gene effect, controlling this character El-Baroudiy (1999); Malik *et al.* (2004), and Mohammad (2005).

Heritability values in board sense were 0.462 and 0.565, while the values were 0.271 and 0.219 for narrow sense for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character. Similar results were recorded by El-Baroudiy (1999) and Mohammad (2005), while high heritability values were reported previously by Reddy and

Agarwal (1992); Robin and Subramanian (1994); Gyanendra *et al.* (1995); Mani and Bisht (1996), and Jha and Ghosh (2001).

4.4. Ear height (cm)

Data in Table (14) and Appendices (3 and 4), show highly significant differences between genotypes on the character ear height at both locations. Regarding Kanipanka location maximum ear heigh was 52.987 cm recorded by parent 3. The diallel hybrids values for this character were restricted between 56.512 cm to 74.150 cm for the hybrids 2×5 and 3×5 respectively, while the reciprocal crosses values ranged between 49.310 to 85.267cm for both reciprocal crosses 3×1 and 5×3 respectively. Concerning the Qlyasan location the parental values due to this character were restricted between 70.093 recorded by parent 2 to 88.877 showed by parent 5. The differences between parental values had significant effect on their diallel and reciprocal values in ear height. The diallel crosses values were restricted between 62.350 to 89.807 cm for both 2×3 and 1×3 respectively, while the reciprocal cross values ranged between 63.380 to 85.650 cm for both cross 4×1 and 5×1 respectively. Similar results were recorded previously by El-Baroudiy (1999); Malik *et al.* (2004), and Mohammad (2005).

The estimations of heterosis percentage as the F_1s deviation from parental values were represented in Table (15) for both locations. Regarding Kanipanka location, the maximum positive diallel heterosis value was 29.269 % recorded by the cross 1×3, while maximum negative value was -15.612 % recorded by the cross 2×5. The heterosis percentages due to reciprocal crosses at the same location represented in the same table, maximum positive value was 33.69 % exhibited by the cross 5×3, while the cross 3×1 showed maximum negative value with -7.431 % . In the second location maximum positive heterosis value due to diallel crosses was 16.903 % exhibited by the cross 1×3, while the

Table 14. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Ear height at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	53.550	60.558	68.858	70.200	60.413
MSI 4279 (2)	60.377	59.367	58.072	59.373	56.512
MSI 43100 (3)	49.310	56.220	52.987	62.888	74.150
ZP 434 (4)	58.310	63.477	58.610	59.017	64.100
5012 (5)	59.888	68.503	85.267	68.500	74.567

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
59.897	63.513	62.846	62.523	13.173

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	79.660	79.790	89.807	71.680	86.913
MSI 4279 (2)	63.990	70.093	62.350	76.607	67.673
MSI 43100 (3)	77.750	73.867	73.983	68.390	75.483
ZP 434 (4)	63.380	72.333	84.717	72.027	76.277
5012 (5)	85.650	82.387	73.440	69.500	88.877

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
76.928	75.497	74.701	75.465	13.867

Table 15. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Ear height at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		7.262	29.267	24.726	- 5.690	4.442
MSI 4279 (2)	6.940		3.373	0.307	- 15.612	
MSI 43100(3)	- 7.431	0.077		12.297	16.265	
ZP 434 (4)	3.601	7.239	4.658		- 4.030	
5012 (5)	- 6.510	2.295	33.696	2.558		
S.E	3.587					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		6.562	16.903	- 5.489	3.139	3.195
MSI 4279 (2)	- 14.539		- 13.449	7.806	- 14.860	
MSI 43100(3)	1.208	2.538		- 6.321	- 7.303	
ZP 434 (4)	- 16.433	1.792	16.042		- 5.189	
5012 (5)	1.640	3.651	- 9.812	- 13.613		
S.E	3.286					

maximum negative value was -14.860 % showed by the cross 2×5. Previously positive and negative heterosis values were recorded by Michelini and Hallauer (1993); Goma and Shaheen (1994); El-Baroudiy (1999); Al-Zawbaey (2001); Al-Falahy (2002); Malik *et al.* (2004), and Mohammad (2005). Regarding the reciprocal crosses, maximum positive heterosis value was 16.042 % recorded by the cross 4×3, while the cross 4×1 produced maximum negative value with -16.433 %.

Data in Table (16) explains the reciprocal effect values at both locations, estimated as the F_1s diallel crosses deviation from their reciprocal crosses. Maximum positive effect value was 21.220 % for the cross 5×2 and 23.873 % for the cross 4×3 for both locations respectively, while maximum negative effect

Table 16. Reciprocal effect value percentages for the character Ear height at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 0.300				
MSI 43100 (3)	- 28.389	- 3.189			
ZP 434 (4)	- 16.937	6.911	- 6.803		
5012 (5)	- 0.869	21.220	14.992	6.864	
S.E	4.614				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 19.802				
MSI 43100 (3)	- 13.425	18.471			
ZP 434 (4)	- 11.579	- 5.578	23.873		
5012 (5)	- 1.454	21.742	- 2.707	- 8.884	
S.E	4.955				

values were -28.389 % recorded by the cross 3×1 and -19.802 % recorded by the cross 2×1 for both locations respectively.

Similar results were noticed by the researchers Singh and Singh (1962); Hunter and Gamble (1968); Kalsy and Sharma (1972); El-Baroudiy (1999), and Mohammad (2005).

The estimations of general and specific combining abilities effects and their variances for the character ear height, represented in Table (17). Results of genetic analysis confirmed highly significant mean squares due to GCA and SCA for both locations, while it was significant for RCA in the first location only (Appendices 3 and 4). In the first location the parent 5 with 6.124 showed positive GCA effect, while negative GCA effect exhibited by the rest, maximum negative $\hat{g}ii$ value showed by parent 1 with -3.021. The maximum positive SCA effect due to diallel crosses was 11.650 exhibited by the cross 3×5, while the

Table 17. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Ear height at both locations.

Kanipanka Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^{2}\hat{g}ii$	$\sigma^{2}\hat{s}ij$	$\sigma^{2}\hat{r}ij$
MSI 4218 (1)	- 3.021	3.306	0.356	4.927	- 5.474	8.271	14.472	32.920
MSI 4279 (2)	0.091	- 2.340	- 2.449	1.416	- 3.799	5.478	0.183	17.316
MSI 43100 (3)	9.774	0.926	- 0.588	- 1.012	11.650	0.346	70.414	13.865
ZP 434 (4)	5.945	- 2.052	2.139	- 0.174	- 2.173	0.030	8.986	10.716
5012 (5)	0.263	- 5.996	- 5.558	- 2.200	6.124	37.500	16.621	61.613
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	2.072	4.1437	4.6328					

Mse´	σ^{2}_{GCA}	$\sigma^{2}_{SCA} = \sigma^{2}_{D}$	$\sigma^{2}_{GCA}/\sigma^{2}_{SCA}$	σ^{2}_{A}	$\sigma^{2}_{RCA} = \sigma^{2}_{Dr}$
21.462	10.974	33.440	0.328	21.949	10.497
$\bar{a}$	$h^{2}b.s$	$h^{2}n.s$	$\bar{a}_{r}$	$h^{2}b.s_{r}$	$h^{2}n.s_{r}$
1.746	0.721	0.286	0.978	0.602	0.407

Qlyasan Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^{2}\hat{g}ii$	$\sigma^{2}\hat{s}ij$	$\sigma^{2}\hat{r}ij$
MSI 4218 (1)	2.363	- 2.391	8.914	- 7.527	4.411	4.633	45.678	26.900
MSI 4279 (2)	7.900	- 3.547	- 3.722	5.323	- 0.931	12.578	27.069	32.521
MSI 43100 (3)	6.028	- 5.758	- 0.088	3.948	- 4.958	0.008	28.469	53.667
ZP 434 (4)	4.150	2.137	- 8.163	- 2.771	- 3.848	7.680	26.326	37.350
5012 (5)	0.632	- 7.357	1.022	3.388	4.043	16.344	14.262	19.904
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	2.181	4.362	4.877					

Mse´	σ^{2}_{GCA}	$\sigma^{2}_{SCA} = \sigma^{2}_{D}$	$\sigma^{2}_{GCA}/\sigma^{2}_{SCA}$	σ^{2}_{A}	$\sigma^{2}_{RCA} = \sigma^{2}_{Dr}$
23.782	8.170	23.256	0.351	16.341	16.847
$\bar{a}$	$h^{2}b.s$	$h^{2}n.s$	$\bar{a}_{r}$	$h^{2}b.s_{r}$	$h^{2}n.s_{r}$
1.687	0.625	0.258	1.436	0.583	0.287

cross 1×5 with -5.474 produced maximum negative $\hat{s}ij$. Maximum positive $\hat{r}ij$ recorded by the reciprocal cross 3×1 with 9.774 , but the cross 5×3 with -5.558 showed maximum negative value for RCA effect. Parent 5 with 37.500 showed maximum variance due to GCA effect , while maximum variance due to SCA effect was 70.414 exhibited by parent 3, while parent 5 also showed maximum variance due to $\hat{r}ij$ with 61.613.

Some genetic parameters due to ear height for the first location represented in the same table. The variance component due to SCA was larger than GCA, making $\sigma^2_{GCA}/\sigma^2_{SCA}$ less than one (0.328). The average degree of dominance for diallel and reciprocal crosses were 1.746 and 0.978 respectively, showing the importance of both additive and non-additive gene effect as controlled the inheritance of this character. Heritability in broad sense were 0.721 and 0.602, while it was 0.286 and 0.407 in narrow sense for diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character.

Regarding the second location maximum positive $\hat{g}ii$ value recorded by parent 5 with 4.043 and followed by parent 1 with 2.363, while maximum negative effect due to GCA exhibited by parent 2 with -3.547.The cross 1×3 with 8.914 showed maximum positive SCA effect, while the cross 1×4 with -7.527 showed maximum negative SCA effect. Regarding reciprocal crosses maximum $\hat{r}ij$ value was 7.900 produced by the cross 2×1, but maximum negative value for this effect was -8.163 recorded by the reciprocal cross 4×3. Parent 5 with 16.344 produced maximum variance due to GCA effect, while parent 1 showed maximum variance due to SCA effect with 45.678 and parent 3 with 53.667 showed the highest variance value due to $\hat{r}ij$.

Some genetic parameters for ear heigh in the second location also represented in Table (17). The variance component due to SCA was larger than GCA producing $\sigma^2_{GCA}/\sigma^2_{SCA}$ less than one (0.351).The average degree of dominance values were 1.687 and 1.436 for both diallel and reciprocal crosses respectively confirming the importance of non-additive gene effect in controlling ear heigh. Similar results were obtained by El-Baroudiy (1999); Malik *et al.* (2004), and Mohammad (2005).

Heritability in broad sense were 0.625 and 0.583, while the values were 0.258 and 0.287 for narrow sense due to both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character. High values of heritability in broad sense recorded previously by Reddy and Agarwal (1992); Mani and Bisht (1996); Chaudhary and Chaudhari (2002); Satyanarayana *et al.* (2005), and Om prakash *et al.* (2006) which is similar to our results, while low heritability in broad sense were recorded by Pradeep and Satyanarayana (2001); Salami *et al.*(2007), and Akbar *et al.* (2008).

4.5. Cob weight (g)

Data concerning the character cob weight were represented in Table (18) for both locations. From Appendix (3), it noticed that there were highly significant differences between genotypes at Kanipanka location. Parent 4 with 63.607 g, showed maximum cob weight and followed by parent 2 with 60.350 g. Nevertheless, parent 5 recorded minimum cob weights with 41.700 g. These differences between parental values affected significantly on their diallel and reciprocal crosses. The diallel crosses values restricted between 39.527 to 64.077 g for both crosses 2×5 and 2×4 respectively. The reciprocal crosses value ranged between 40.713 to 74.327g for both crosses 3×1 and 3×2 respectively.

Data on this character recorded at Qlyasan location exhibited significant differences between genotypes (Appendix 4). Parent 1 with 45.940 g gave maximum cob weight and followed by parent 4 and 2 with 43.147 and 41.429 g respectively. The diallel crosses in this location restricted between 35.135 g to 51.248 g for both crosses 1×4 and 2×4 respectively. The reciprocal crosses value ranged between 27.934 to 53.069 g for both reciprocal crosses 3×1 and 4×3 respectively.

Table 18. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Cob weight at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	55.487	49.240	46.680	48.650	39.680
MSI 4279 (2)	55.073	60.350	58.877	64.077	39.527
MSI 43100 (3)	40.713	74.327	42.897	44.577	56.493
ZP 434 (4)	66.337	55.950	51.530	63.607	54.087
5012 (5)	59.320	42.490	51.830	49.483	41.700

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
52.808	50.189	54.705	52.519	13.243

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	45.940	38.433	40.532	35.135	40.930
MSI 4279 (2)	37.755	41.429	42.473	51.248	35.437
MSI 43100 (3)	27.934	38.302	29.252	45.522	46.613
ZP 434 (4)	38.834	47.624	53.069	43.147	42.386
5012 (5)	43.329	52.383	38.091	47.543	35.004

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
38.954	41.871	42.487	41.534	13.045

The estimations of heterosis values as F_1s deviation from mid parental values for both diallel and reciprocal crosses and for both locations represented in Table (19). Regarding the first location maximum positive heterosis values were 33.559 % and 43.979 % for both diallel cross 3×5 and reciprocal cross 3×2 respectively. In the second location the diallel cross 3×5 showed maximum positive value with 45.08 %, while maximum positive heterosis value due to the reciprocal crosses recorded by the cross 4×3 with 46.601 %.

Table 19. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Cob weight at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 14.984	- 5.106	- 18.299	- 18.343	5.640
MSI 4279 (2)	- 4.912		14.050	3.386	- 22.535	
MSI 43100 (3)	- 17.235	43.979		- 16.291	33.559	
ZP 434 (4)	11.403	- 9.727	- 3.233		2.722	
5012 (5)	22.074	- 16.727	22.534	- 6.021		
S.E	6.346					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 12.020	7.809	- 21.121	1.131	6.266
MSI 4279 (2)	- 13.572		20.184	21.188	- 7.274	
MSI 43100 (3)	- 25.699	8.380		25.755	45.086	
ZP 434 (4)	- 12.817	12.620	46.601		8.471	
5012 (5)	7.058	37.070	18.560	21.670		
S.E	7.188					

The percentage of reciprocal effect for the character cob weight represented in Table (20), deviation from their diallel crosses for locations. Maximum positive reciprocal crosses deviation from their diallel crosses for both locations. Maximum positive reciprocal effect value recorded by 5×1 with 49.496 %, while maximum negative reciprocal was -12.782% recorded by the cross 3×1 in the first location. Regarding the second location, maximum positive value for this effect showed by the cross 5×2 with 47.822 %. Nevertheless, maximum negative value recorded by 3×1 with -31.081%.

Table 20. Reciprocal effect value percentages for the character Cob weight at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	11.847				
MSI 43100 (3)	- 12.782	26.241			
ZP 434 (4)	36.355	- 12.683	15.599		
5012 (5)	49.496	7.497	- 8.255	- 8.511	
S.E	6.885				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 1.764				
MSI 43100 (3)	- 31.081	- 9.821			
ZP 434 (4)	10.528	- 7.070	16.577		
5012 (5)	5.860	47.822	- 18.283	12.168	
S.E	6.866				

Regarding the genetic analysis for this character as represented in Table (21), it observed that the mean squares due to GCA and SCA were highly significant, while it was only significant due to RCA in the first location (Appendix 3). Parent 2 and 4 showed positive $\hat{g}_{ii}$ value with 3.507 and 3.671 respectively, while maximum negative GCA effect recorded by parent 5 with -4.888. The SCA effect for diallel crosses as represented in the same table and the first location showed positive and negative values. Maximum positive $\hat{s}_{ij}$ value recorded by the cross 2×3 with 12.013, while the cross 2×5 showed maximum negative $\hat{s}_{ij}$ value with -10.129. Regarding the $\hat{r}_{ij}$ values due to the reciprocal crosses in the first location maximum positive effect value was found to be 4.063 recorded by the cross 4×2, while the cross 5×1 gave maximum negative $\hat{r}_{ij}$ value with -9.820.

Table 21. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Cob weight at both locations.

Kanipanka Location

$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.853	- 3.017	- 8.422	2.156	2.722	- 0.141	23.323	53.169
MSI 4279 (2)	- 2.917	3.507	12.013	0.316	-10.129	12.298	77.799	29.161
MSI 43100 (3)	2.983	- 7.725	- 1.437	- 6.700	7.968	2.066	51.609	77.590
ZP 434 (4)	- 8.843	4.063	- 3.477	3.671	0.483	13.477	28.304	18.310
5012 (5)	- 9.820	- 1.482	2.332	2.302	- 4.888	23.894	29.079	57.911
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	2.083	4.166	4.657					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_{D}$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{A}	$\sigma^2_{RCA} = \sigma^2_{Dr}$
21.690	10.946	70.515	0.155	21.893	18.479
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
2.538	0.810	0.192	1.299	0.651	0.353

Qlyasan Location

$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 2.058	- 2.499	- 4.885	- 5.723	2.515	3.392	15.907	4.359
MSI 4279 (2)	0.339	1.117	0.166	3.553	1.120	1.249	- 2.482	28.559
MSI 43100 (3)	6.299	2.086	- 2.430	6.960	3.110	5.904	26.889	18.762
ZP 434 (4)	- 1.850	1.812	- 3.773	3.232	0.061	10.443	- 0.175	33.489
5012 (5)	- 1.199	- 8.473	4.261	- 2.579	0.138	0.019	25.525	5.752
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	2.052	4.103	4.588					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_{D}$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{A}	$\sigma^2_{RCA} = \sigma^2_{Dr}$
21.048	3.357	24.307	0.138	6.715	5.788
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
2.691	0.596	0.129	1.313	0.373	0.200

Parent 5 with 23.894 showed maximum variance due to $\hat{g}ii$, while maximum variance for $\hat{s}ij$ recorded by parent 2 with 77.799. The maximum variance due to $\hat{r}ij$ was 77.590 recorded by parent 3.

Some genetic parameters for cob weight represented in the same table. The variance components due to SCA were larger than GCA, making the ratio of $\sigma^2_{GCA}/\sigma^2_{SCA}$, to be less than one (0.155), confirming the importance of non-additive gene effect in controlling the inheritance of this character. The average degree of dominance values were 2.538 and 1.299 for both diallel and reciprocal crosses respectively in the first location.

Heritability in broad sense were 0.810 and 0.651 while in narrow sense the values were 0.192 and 0.353 for both diallel and reciprocal crosses respectively.

Regarding the second location the studied parameters represented in Table (21) and Appendix (4), confirming the presence of significant mean squares due to GCA and SCA , while no significant mean squares observed due to RCA for cob weight. Parent 4 with 3.232 showed maximum positive GCA effect, while maximum negative value exhibited by parent 3 with -2.430. The diallel cross 3×4 showed maximum positive RCA effect showed by the reciprocal cross 3×1 with 6.299. Parent 4 with 10.443 and 33.489 produced maximum variance due to GCA and RCA effect respectively whereas parent 3 with 26.889 exhibited the highest variance due to SCA effect. From the same table, it was observed that the variance components due to SCA were higher than GCA that affected the value of $\sigma^2_{GCA}/\sigma^2_{SCA}$ be less than one (0.138). The average degrees of dominance for both diallel and reciprocal crosses found to be more than one (2.691 and 1.313) respectively, indicating the importance of non-additive gene effect in controlling the inheritance of cob weight.

Heritability in broad sense were 0.596 and 0.373, while the values were 0.129 and 0.200 in narrow sense for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character.

4.6. Cob length (cm)

Data in Table (22) and Appendices (3 and 4) showed not significant differences between genotypes at both locations, while highly significant difference were recorded previously by Mohammad (2005) for cob length. Regarding the first location parent 5 with 20.933 cm showed maximum cob length, while parent 2 exhibited minimum cob length with 19.200 cm. The diallel cross 4×5 produced the longest cob with 23.000 cm, while the cross 1×3 with 18.667 cm showed minimum cob length. Regarding the reciprocal crosses maximum cob length was 23.167 cm exhibited by the cross 4×3, while the cross 5×1 with 18.600 cm showed minimum cob length. Regarding the second location it observed that parent 5 with 22.533 cm showed maximum cob length, while minimum value was 19.167 cm exhibited by parent 2. Maximum values for this character due to both diallel and reciprocal crosses were 22.933 and 24.000 cm respectively, while minimum values were 18.333 and 19.833 cm for both diallel and reciprocal crosses respectively.

The percentage of heterosis estimated as the F_1s deviation from mid parental values for cob length and both locations represented in Table (23). At Kanipanka location, maximum positive heterosis percentage were 9.960 and 12.187 % for both diallel and reciprocal crosses respectively, while in the second location maximum positive heterosis values were 10.301 % and 15.431 % for both diallel and reciprocal crosses respectively. Previously similar results were estimated by Altinbas (1995); Tradovic (1996), and Mohammad (2005).

Table (24) explains the reciprocal effect estimated as the percentage of diallel cross deviation from their reciprocal crosses for both locations, maximum positive effect were 14.876 % and 27.727 % for both locations respectively. Similar results were reported previously by Fleming (1960); Hunter (1966), and Kalsy and Sharma (1972).

Table 22. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Cob length at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	20.400	20.433	18.667	19.667	19.167
MSI 4279 (2)	21.667	19.200	20.333	20.833	21.000
MSI 43100 (3)	19.500	21.500	20.400	20.167	20.667
ZP 434 (4)	19.167	21.100	23.167	20.900	23.000
5012 (5)	18.600	20.500	20.267	20.333	20.933

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
20.367	20.393	20.580	20.463	2.722

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	20.667	20.400	19.300	18.800	21.167
MSI 4279 (2)	21.533	19.167	20.083	21.767	18.333
MSI 43100 (3)	20.367	20.817	19.917	22.933	19.667
ZP 434 (4)	23.650	21.650	24.000	21.667	20.333
5012 (5)	22.583	23.417	19.833	21.000	22.533

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
20.790	20.278	21.885	21.023	3.643

Table 23. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Cob length at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		3.199	- 8.497	- 4.762	- 7.258	1.845
MSI 4279 (2)	9.428		2.694	3.907	4.651	
MSI 43100(3)	- 4.412	8.586		- 2.341	0.000	
ZP 434 (4)	- 7.183	5.237	12.187		9.960	
5012 (5)	- 10.000	2.159	- 1.935	- 2.789		
S.E	2.388					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		2.427	- 4.887	- 11.181	- 2.006	2.416
MSI 4279 (2)	8.117		2.772	6.612	- 12.070	
MSI 43100(3)	0.370	6.525		10.301	- 7.342	
ZP 434 (4)	11.732	6.041	15.431		- 7.994	
5012 (5)	4.552	12.310	- 6.557	- 4.977		
S.E	2.295					

It was observed from Table (25) and Appendix (3), the presence of highly significant mean squares due to GCA effect, while the mean squares due to SCA and RCA effects were not significant at the first location. Maximum positive GCA effect was 0.461 produced by parent 4 for this character, indicating the high contribution of this parent to increasing cob length in its hybrids. Maximum negative value for GCA effect was - 0.696 exhibited by parent 1 indicating the contribution of this parent in reducing the cob length in its hybrids. Concerning the SCA and RCA effect of the hybrids maximum values found to be 1.169 and 1.333 for the hybrids 1×2 and 5×4 respectively, indicating the increase of this character in these hybrids compared to their parents.

The variance of general of specific combining ability effects for both diallel and reciprocal crosses represented in the same table. Parent 1 showed

Table 24. Reciprocal effect value percentages for the character Cob length at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	6.036				
MSI 43100 (3)	4.464	5.738			
ZP 434 (4)	- 2.542	1.280	14.876		
5012 (5)	- 2.957	- 2.381	- 1.935	- 11.594	
S.E	2.259				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	5.556				
MSI 43100 (3)	5.527	3.651			
ZP 434 (4)	25.798	- 0.536	4.651		
5012 (5)	6.693	27.727	0.847	3.279	
S.E	3.154				

maximum variance due to $\sigma^2 \hat{g}ii$ with 0.448, whereas the maximum variances for SCA effect was 0.888 recorded by parent 1. Maximum variance for $\hat{r}ij$ was 1.010 showed by parent 3. These results confirmed the ability of parent 3 to transfer this character to some of their hybrids without others.

The analysis of some genetic parameters for the first location were also represented in Table (25). The variance components due to SCA effect was larger than GCA effect, and the ratio of $\sigma^2_{GCA} / \sigma^2_{SCA}$ was less than one (0.207), while the average degrees of dominance values for both diallel and reciprocal crosses was 2.196 and 0.830 respectively.

Heritability in broad sense were 0.395 and 0.205, while in narrow sense were 0.116 and 0.152 for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character.

Table 25. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Cob length at both locations.

Kanipanka Location								
$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.696	1.169	- 0.807	- 0.811	- 0.961	0.448	0.888	- 0.226
MSI 4279 (2)	- 0.617	0.114	0.296	- 0.071	0.096	0.013	- 0.151	0.596
MSI 43100 (3)	- 0.417	- 0.583	0.044	0.699	- 0.117	0.002	0.027	1.010
ZP 434 (4)	0.250	- 0.133	- 1.500	0.461	0.666	0.212	0.613	0.976
5012 (5)	0.283	0.250	0.200	1.333	0.077	0.006	0.342	0.463
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	0.428	0.856	0.957					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.916	0.088	0.423	0.207	0.176	0.060
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
2.196	0.395	0.116	0.830	0.205	0.152

Qlyasan Location								
$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.110	0.443	- 0.458	- 0.412	0.845	- 0.054	- 0.128	1.509
MSI 4279 (2)	- 0.567	- 0.390	0.157	0.352	0.125	0.152	- 0.396	2.265
MSI 43100 (3)	- 0.533	- 0.367	- 0.340	2.060	- 1.050	0.116	1.364	0.175
ZP 434 (4)	- 2.425	0.058	- 0.533	0.723	- 1.197	0.523	1.975	1.549
5012 (5)	- 0.708	- 2.542	- 0.083	- 0.333	0.117	0.014	1.802	1.088
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	0.573	1.146	1.281					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
1.642	0.040	0.436	0.092	0.080	0.578
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
3.301	0.239	0.037	3.802	0.286	0.035

The genetic analysis for the Qlyasan location, indicating that the parent 4 with 0.723 showed maximum GCA effect value, indicating the high contribution of this parent in increasing this character in its hybrid, while parent 2 and 3 showed maximum negative $\hat{g}ii$ value with -0.390 and -0.340 respectively, confirming the contribution of these parents to produce this character in their hybrids. Maximum positive SCA effect value was 0.845 exhibited by the cross 1×5, while only the reciprocal cross 4×2 with 0.058 showed positive effect value. Parent 4 showed maximum variance for $\hat{g}ii$ and $\hat{s}ij$ with 0.523 and 1.975 respectively, while parent 2 with 2.265 showed maximum variance for $\hat{r}ij$.

Some genetic parameters for the second location also represented in the same table. The variance component due to SCA was larger than GCA, resulted in decreasing $\sigma^2_{GCA} / \sigma^2_{SCA}$ ratio, which was 0.092. Mohammad (2005) found the same result. The average degree of dominance values for both diallel and reciprocal crosses was 3.301 and 3.802 respectively, confirming the importance of non-additive gene effect controlling the inheritance of this character. These results were in agreement with the results of Al-Jumaely (1996); Tradovic (1996); Ali (1999); Wolf *et al.* (2000); Al-Zawbaey (2001); Al-Azawy (2002); Al-Falahy (2002), and Mohammad (2005).

Heritability in broad sense was 0.239 and 0.286, while in narrow sense it was 0.037 and 0.035 for both diallel and reciprocal crosses. These results confirmed the importance of hybridization method to improve this character. Heritability estimated previously were 0.69, 0.37, 0.47, 0.06, and 0.97 which obtained by the researchers Robin and Subramanian (1994); Mani and Bisht (1996); Pradeep and Satyanarana (2001); Choudhary and Chaudhari (2002), and Om prakash *et al.* (2006).

4.7. Cob width (cm)

Data recorded on cob width represented in Table (26) for both locations. Regarding the first location significant differences exhibited between genotypes (Appendix 3). Maximum cob width was 2.317 cm exhibited by parent 5, while the minimum cob width showed by parent 3 with 1.967cm showed minimum cob width. These differences between parental values had significant effect on their diallel and reciprocal crosses.

The diallel crosses values ranged between 1.967 to and 2.333 cm for both crosses 1×2 and 3×5 respectively, but ranged between 1.933 to 2.433 cm for both reciprocal crosses 4×1 and 5×2 respectively. Concerning the second location there were no significant differences between genotypes (Appendix 4). Parent 5 with 2.300 cm gave maximum cob width, while minimum cob width recorded by parent 3 with 2.000 cm. The diallel cross 1×5 showed maximum cob width with 2.383 cm, while the cross 1×3 recorded minimum cob width with 2.467 cm gave maximum value, while the minimum value for reciprocal crosses showed by the cross 4×3 with 2.067 cm .

The heterosis value for cob width estimated as the percentage of F_1s deviation from mid parental values for both locations represented in Table (27). Maximum positive heterosis value due to diallel crosses in the first location recorded by the cross 2×3 with 10.744 %, while for the reciprocal crosses it was 13.821 % recorded by 2×1 . In the second location maximum positive value for diallel crosses was 11.811% recorded by the cross 3×4, while for the reciprocal crosses maximum positive value was 11.628 % showed by the cross 5×3.

Table 26. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Cob width at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	2.033	1.967	2.100	2.067	2.267
MSI 4279 (2)	2.333	2.067	2.233	2.267	2.217
MSI 43100 (3)	2.067	2.250	1.967	2.100	2.333
ZP 434 (4)	1.933	2.100	2.133	2.067	2.133
5012 (5)	2.167	2.433	2.167	2.100	2.317

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \le 0.05$) for genotypes*
2.090	2.168	2.168	2.153	0.249

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	2.133	2.133	2.083	2.133	2.383
MSI 4279 (2)	2.033	2.233	2.333	2.250	2.367
MSI 43100 (3)	2.233	2.250	2.000	2.367	2.200
ZP 434 (4)	2.100	2.167	2.067	2.233	2.300
5012 (5)	2.267	2.467	2.400	2.167	2.300

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \le 0.05$) for genotypes*
2.180	2.255	2.215	2.224	0.281

Table 27. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Cob width at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 4.065	5.000	0.813	4.215	1.601
MSI 4279 (2)	13.821		10.744	9.677	1.141	
MSI 43100 (3)	3.333	11.570		4.132	8.949	
ZP 434 (4)	- 5.691	1.613	5.785		- 2.662	
5012 (5)	- 0.383	11.027	1.167	- 4.183		
S.E	2.109					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 2.290	0.806	- 2.290	7.519	1.559
MSI 4279 (2)	- 6.870		10.236	0.746	4.412	
MSI 43100 (3)	8.065	6.299		11.811	2.326	
ZP 434 (4)	- 3.817	- 2.985	- 2.362		1.471	
5012 (5)	2.256	8.824	11.628	- 4.412		
S.E	2.084					

Data in Table (28) explains the percentage of reciprocal effect estimated as F_1s diallel crosses deviation from their reciprocal crosses for both locations. Maximum positive effect exhibited by the reciprocal positive effect exhibited by the reciprocal cross 2×1 with 18.644 % at the first location, while at the second location was 9.09 % recorded by the cross 5×3.

Table 28. Reciprocal effect value percentages for the character Cob width at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	18.644				
MSI 43100 (3)	- 1.587	0.746			
ZP 434 (4)	- 6.452	- 7.353	1.587		
5012 (5)	- 4.412	9.774	- 7.143	- 1.562	
S.E	2.618				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 4.688				
MSI 43100 (3)	7.200	- 3.571			
ZP 434 (4)	- 1.562	- 3.704	- 12.676		
5012 (5)	- 4.895	4.225	9.091	- 5.797	
S.E	2.094				

From Table (29) and Appendix (3), it observed that the mean square due to GCA for this character was highly significant, while it was not significant for SCA and RCA in the first location. Parent 5 showed maximum positive value due to $\hat{g}ii$ with 0.092, indicating the high contribution of this parent to increase this character in its hybrids, while maximum negative value recorded by parent 1 and 4 both with -0.056, indicating the contribution of these parents to reduce this character in their hybrids Concerning the SCA effect of the hybrids. Maximum effect value was 0.069 in the diallel cross 2×3, indicating the increase of this character in this cross compared with its parents. Regarding the reciprocal crosses maximum positive $\hat{r}ij$ value was 0.083 for both crosses 4×2 and 5×3, while maximum negative $\hat{r}ij$ value was - 0.183 exhibited by the reciprocal cross 2×1.

Table 29. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Cob width at both locations.

Kanipanka Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.056	0.013	- 0.032	- 0.041	0.028	0.003	- 0.001	0.010
MSI 4279 (2)	- 0.183	0.041	0.069	0.046	0.039	0.002	0.011	0.006
MSI 43100 (3)	0.017	- 0.008	- 0.021	0.041	0.026	0.0004	- 0.002	0.004
ZP 434 (4)	0.067	0.083	- 0.017	- 0.056	- 0.072	0.003	0.003	0.002
5012 (5)	0.050	- 0.108	0.083	0.017	0.092	0.009	0.005	0.003
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	0.039	0.078	0.088					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.008	0.003	0.001	3.301	0.007	0.003
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.550	0.509	0.442	0.911	0.560	0.396

Qlyasan Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.061	- 0.103	0.009	- 0.024	0.071	0.003	0.002	- 0.001
MSI 4279 (2)	0.050	0.023	0.076	- 0.016	0.079	0.001	0.002	0.006
MSI 43100 (3)	- 0.075	0.042	- 0.031	0.046	0.016	0.001	-0.0001	0.013
ZP 434 (4)	0.017	0.042	0.150	- 0.022	- 0.059	0.0005	0.006	0.002
5012 (5)	0.058	- 0.050	- 0.100	0.067	0.091	0.008	0.003	0.005
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	0.044	0.088	0.099					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.010	0.003	0.002	1.646	0.005	0.001
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.780	0.402	0.308	0.491	0.366	0.326

The variance of general and specific effect for both diallel and reciprocal crosses represented in Table (29). Maximum variance for $\hat{g}ii$ was 0.009 recorded by parent 5, while the maximum values due to the variance for $\hat{s}ij$ and $\hat{r}ij$ were 0.011 and 0.006 recorded by parent 2.

Some genetic parameters for this character in the first location represented in the same table. The variance component due to GCA was larger than SCA, making the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ be larger than one (3.301). The average degrees of dominance for both diallel and reciprocal crosses were 0.550 and 0.911 receptively, indicating the importance of additive gene effect in controlling the inheritance of these characters. Heritability in broad sense was 0.509 and 0.560, while it was 0.442 and 0.396 for both diallel and reciprocal crosses respectively.

Regarding the second location, it observed from Appendix (4) that the mean square due to GCA was significant only. Parent 5 with 0.091 gave maximum positive $\hat{g}ii$ value, while parent 1 with -0.061 showed maximum positive SCA effect, while the reciprocal cross 5x4 showed maximum positive $\hat{r}ij$ value with 0.067. The variance of GCA effect due to parent 5 was 0.008, which was maximum value, however, the maximum variance value due to $\hat{s}ij$ was 0.002 recorded by both parents 1 and 2. Parent 3 with 0.013 gave maximum variance due to $\hat{r}ij$.

Some genetic parameters on this character for the second location also represented in Table (29) that indicated to the high variance component due to GCA in compare to SCA. The ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ were larger than one (1.646). The average degree of dominance for both diallel and reciprocal crosses was 0.780 and 0.491 respectively, indicating the submission of this character under the additive gene action in the inheritance of this character.

Heritability in broad sense was 0.402 and 0.366, while it was 0.308 and 0.326 in narrow sense for both diallel and reciprocal crosses respectively. These results indicated the ability of improving this character via selection method.

4.8. No. of ears plant^{-1}

Data recorded on No. of ears plant^{-1} represented in Table (30) and Appendices (3 and 4), confirm the presence highly significant differences between genotypes At Kanipanka location. Mohammad (2005) obtained similar results, while it was not significant at Qlyasan location. Regarding the first location maximum No. of ears plant^{-1} exhibited by parent 1 with 1.883, and followed by parent 2 with 1.880. The differences between parental values resulted in the presence of high differences between their diallel and reciprocal crosses. The diallel cross values restricted between 1.44 ears plant^{-1} for both crosses 3×4 and 4×5 to 2.44 ears plant^{-1} for the cross 1×2. The reciprocal crosses values were ranged between 1.44 to 2.717ears plant for both crosses 3×1 and 2×1 respectively. Regarding the second location parent 4 with 1.633 showed maximum ears number, and followed by parent 1 with 1.417, while minimum number produced by parent 5 with 1.067 ears. Maximum value due to diallel crosses showed by the cross 4×5 with 1.667 ears, while minimum ears number was 1.117 ears exhibited by the cross 1×5. Concerning the reciprocal crosses value maximum ears number was 1.550 produced by the cross 5×2, but minimum number was 1.000 ear recorded by the cross 3×1.

The estimation of the percentage of heterosis values as F_1s deviation from mid parental values represented in Table (31) for both diallel and reciprocal crosses and for both locations. Maximum positive value due to diallel crosses in the first location was 30.011 % exhibited by the cross 3×5 and followed by 29.672 % for the cross 1×2, while maximum negative heterosis value was -14.793 % for the cross 3×4. Regarding the heterosis values for reciprocal crosses in the first location, maximum positive value recorded by the cross 2×1 with 44.376 %, while maximum negative value recorded by the cross 3×1 with -21.240 %. In the second location the diallel cross 3×5 with 36.232 % recorded maximum positive value, and followed by 23.457 % for the cross 4×5, while

Table 30. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character No. of ears plant^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	1.883	2.440	1.887	1.773	1.553
MSI 4279 (2)	2.717	1.880	2.220	1.667	1.663
MSI 43100 (3)	1.440	1.773	1.773	1.440	2.000
ZP 434 (4)	2.333	1.887	1.550	1.607	1.440
5012 (5)	1.663	1.887	1.773	1.777	1.303

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
1.689	1.808	1.880	1.813	0.613

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	1.417	1.533	1.417	1.233	1.117
MSI 4279 (2)	1.217	1.333	1.353	1.317	1.233
MSI 43100 (3)	1.000	1.193	1.233	1.333	1.567
ZP 434 (4)	1.333	1.333	1.350	1.633	1.667
5012 (5)	1.367	1.550	1.200	1.450	1.067

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
1.337	1.377	1.299	1.338	0.431

maximum negative heterosis value due to diallel cross was -19.126 % produced by the cross 1×4, regarding to the reciprocal crosses in the second location, maximum positive value was 29.167 % recorded by the cross 5×2, whereas maximum negative value was -24.528 % showed by the cross 3×1. These results were in accordance with the results of previous workers Mohammad (2005). Positive heterosis values were recorded by Nawar (1984); Goma and Shaheen (1994); Yousif (1997); Ali (1999); Al-Zawbaey (2001), and Al-Falahy (2002), whereas negative values were recorded by Baktash (1979), and Al- Jumaely (1996).

Table 31. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character No. of ears plant^{-1} at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		29.672	3.191	1.624	- 2.510	4.789
MSI 4279 (2)	44.376		21.533	- 4.398	4.503	
MSI 43100 (3)	- 21.240	- 2.920		- 14.793	30.011	
ZP 434 (4)	33.715	8.222	- 8.284		- 1.031	
5012 (5)	4.393	18.534	15.276	22.108		
S.E	6.221					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		11.515	6.918	- 19.126	- 10.067	5.345
MSI 4279 (2)	- 11.515		5.455	- 11.236	2.778	
MSI 43100 (3)	- 24.528	- 7.013		- 6.977	36.232	
ZP 434 (4)	- 12.568	- 10.112	- 5.814		23.457	
5012 (5)	10.067	29.167	4.348	7.407		
S.E	4.785					

Table (32) shows the reciprocal effects estimated as F_1s diallel cross deviated from their reciprocal crosses values. Maximum positive effect at the first location was 31.579 % recorded by the cross 4×1, while maximum negative effect was -23.675 % produced by the cross 3×1. At the second location the reciprocal cross 5×2 with 25.676 % recorded maximum positive effect , while maximum negative effect value was -29.412 % exhibited by the cross 3×1.

Table 32. Reciprocal effect value percentages for the character No. of ears plant^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	11.339				
MSI 43100 (3)	- 23.675	- 20.120			
ZP 434 (4)	31.579	3.200	7.639		
5012 (5)	7.082	13.427	- 11.333	23.380	
S.E	5.728				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 20.652				
MSI 43100 (3)	- 29.412	- 11.823			
ZP 434 (4)	8.108	1.266	1.250		
5012 (5)	22.388	25.676	- 23.404	- 13.000	
S.E	5.982				

The estimation of genetic analysis for general and specific combining abilities effect and their variances for both locations represented in Table (33). Regarding the first location the mean squares due to GCA found to be highly significant, while it was significant for SCA, but it was not significant for RCA (Appendix 3). The parents 1 and 2 showed positive GCA effect value with 0.144 and 0.188 respectively indicating clearly to a high contribution of these parents to increase ear number in their hybrids, while the other parents 3, 4 and 5 showed negative effect of GCA indicating that the contribution of these parents reduced the No. of ears plant^{-1} in their crosses. Maximum positive SCA effect value recorded by the cross 1×2 with 0.433, while the cross 1×3 with -0.416 showed maximum negative SCA effect. Regarding the reciprocal crosses maximum positive RCA effect was 0.223 for both crosses 3×1 and 3×2, while the maximum negative value for this effect was -0.280 recorded by the cross

4×1. Parent 2 produced maximum variance for GCA effect with 0.035, followed by parent 5 with 0.031. The maximum variance for SCA effect recorded by parent 1 with 0.128. Parent 2 with 0.087 recorded maximum variance due to RCA effect and followed by parent 3 with 0.064.

Some genetic parameters on this character for the first location represented in the same table. The variance component due to SCA was larger than GCA, confirming the importance of non-additive gene effect in controlling the inheritance of this character. The ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ were less than one (0.330). Similar results recorded by Mohammad (2005). The average degree of dominance value was 1.740 for the diallel crosses. Similar results were reported by Yousif (1997); Ali (1999); Al-Zawbaey (2000); Al-Azawy (2002), and Al-Falahy (2002), and it was not agreed with El-Zeir (1990), and Wolf *et al.* (2000), and it was 0.424 for the reciprocal crosses.

Heritability in broad sense was 0.691 and 0.492, while it was 0.275 and 0.451 for both diallel and reciprocal crosses respectively, confirming the contribution of hybridization method to improve this character.

Regarding the second location the genetic analysis for this character represented also in the same table. Parent 4 with 0.090 showed maximum positive effect value due to GCA, while parent 3 produced maximum negative effect value with -0.050. The maximum SCA effect value for diallel crosses was 0.140 recorded by the cross 4×5, while the cross 1×4 with -0.112 showed maximum SCA effect value. The reciprocal cross 3×1 showed maximum effect of RCA with 0.208, while maximum negative effect was - 0.158 showed by the cross 5×2. Parent 4 showed maximum variance for GCA effect 0.008, while the maximum variances for SCA effect recorded by parent 5 with 0.021. Parent 1 with 0.017 showed the highest value due to $\hat{r}ij$.

Table 33. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character No. of ears plant^{-1} at both locations.

Kanipanka Location

$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	0.144	0.433	- 0.416	0.201	- 0.172	0.019	0.128	0.027
MSI 4279 (2)	- 0.138	0.188	0.046	- 0.119	- 0.049	0.035	- 0.003	0.087
MSI 43100 (3)	0.223	0.223	- 0.050	- 0.163	0.301	0.003	0.056	0.064
ZP 434 (4)	- 0.280	- 0.110	- 0.055	- 0.105	0.077	0.011	0.017	0.037
5012 (5)	- 0.055	- 0.112	0.113	- 0.168	- 0.177	0.031	0.003	0.043
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					
	0.096	0.193	0.215					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.046	0.021	0.062	0.330	0.041	0.004
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
1.740	0.691	0.275	0.424	0.492	0.451

Qlyasan Location

$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.033	0.068	- 0.059	- 0.112	- 0.054	0.000161	0.0001	0.017
MSI 4279 (2)	0.158	0.002	- 0.016	- 0.105	0.062	0.000003	0.006	0.012
MSI 43100 (3)	0.208	0.080	- 0.050	- 0.037	0.105	0.002487	0.013	0.012
ZP 434 (4)	- 0.050	- 0.008	- 0.008	0.090	0.140	0.008184	- 0.0004	0.012
5012 (5)	- 0.125	- 0.158	0.183	0.108	- 0.010	0.000091	0.021	0.012
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					
	0.068	0.136	0.152					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.023	0.001	0.001	1.034	0.001	0.005
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.983	0.079	0.053	2.708	0.212	0.046

Some genetic parameters at the second location were also represented in Table (33) also, the variance component due to GCA was almost equal to SCA that was 0.001, making the ratio $\sigma^2_{GCA} / \sigma^2_{SCA}$ to be closer to one (1.034). The average degree of dominance were 0.983 and 2.708 for both diallel and reciprocal crosses respectively.

Heritability in broad sense were 0.079 and 0.212, while the values were 0.053 and 0.046 for narrow sense for both diallel and reciprocal crosses respectively. Similar results were obtained by Mohammad (2005).

4.9. No. of rows ear^{-1}

Data in Table (34) and Appendices (3 and 4) indicate to the presence of highly significant differences between the genotypes for character No. of rows ear^{-1} for both locations. Similar results were obtained by El-Baroudiy (1999), and Muhammad. Regarding the first location, parent 5 with 16.700 rows ear^{-1} showed maximum value for this character, while parent 1 with 11.233 gave minimum value. The differences between parental values affected significantly on their diallel and reciprocal crosses. The diallel cross values were restricted between 10.500 for the cross 1×2 to 15.667 for the cross 1×5, but the reciprocal crosses values ranged between 11.667 to 17.833 rows ear^{-1} for both crosses 3×1 and 5×4 respectively. Concerning the Qlyasan location the parental values restricted between 12.600 to19.500 rows ear^{-1} for both parents1 and 2 respectively. These differences between parental values resulted in the presence of significant differences between their diallel and reciprocal crosses for this character. The diallel cross values were restricted between 14.500 to 16.500 for both 3×5 and 1×5 respectively, while for reciprocal crosses the values were restricted between 13.667 to 17.667 for both 2×1 and 5×1 crosses respectively.

Table (35) explain the percentage of heterosis values estimated as F_1s deviation from mid parental values for both locations. Maximum positive heterosis value for diallel crosses in the first location was 23.944 % for the cross

Table 34. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character No. of rows ear^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	11.233	10.500	14.667	14.000	15.667
MSI 4279 (2)	14.667	15.900	14.500	14.333	14.500
MSI 43100 (3)	11.667	14.500	12.433	14.667	15.000
ZP 434 (4)	12.000	17.000	12.667	14.867	15.500
5012 (5)	16.667	16.333	15.667	17.833	16.700

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
14.227	14.333	14.900	14.539	2.568

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	12.600	15.167	15.833	14.667	16.500
MSI 4279 (2)	13.667	19.500	15.500	15.667	16.333
MSI 43100 (3)	15.667	15.833	14.000	15.500	14.500
ZP 434 (4)	14.833	14.500	15.667	15.333	15.333
5012 (5)	17.667	15.833	17.500	16.500	17.333

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
15.753	15.500	15.767	15.657	2.464

1×3, while maximum negative heterosis value was found to be -22.604 % for the cross 1×2. Regarding the heterosis values due to the reciprocal crosses in the first location , maximum positive value was 19.332% for the cross 5×1, while maximum negative value was -8.046 % for the cross 4×1. Concerning the second location the highest positive heterosis value for diallel crosses was 19.048 % for the cross 1×3, while the cross 2×5 gave maximum negative heterosis value which was -11.312 %. Concerning the heterosis value due to the reciprocal crosses in the second location maximum positive value was 18.040 % for the cross 5×1, while the cross 4×2 gave maximum negative value which was -16.746 %. Positive and negative heterosis values were recorded previously by

Table 35. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character No. of rows ear^{-1} at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 22.604	23.944	7.280	12.172	4.093
MSI 4279 (2)	8.108		2.353	- 6.826	- 11.043	
MSI 43100 (3)	- 1.408	2.353		7.448	2.975	
ZP 434 (4)	- 8.046	10.509	- 7.204		- 1.795	
5012 (5)	19.332	0.204	7.551	12.988		
S.E	2.794					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 5.504	19.048	5.012	10.245	3.209
MSI 4279 (2)	- 14.849		- 7.463	- 10.048	- 11.312	
MSI 43100 (3)	17.794	- 5.473		5.682	- 7.447	
ZP 434 (4)	6.205	- 16.746	6.818		- 6.122	
5012 (5)	18.040	- 14.027	11.702	1.020		
S.E	4.192					

Goma and Shaheen (1994); Altinbas (1995); Al- Jumaely (1996); El-Baroudiy (1999); Al-Azawy (2002), and Al-Falahy (2002).

Table (36) explain the reciprocal effect (maternal effect) of reciprocal crosses estimated as the percentage of the deviation of F_1s diallel crosses from their reciprocal crosses for both locations. Maximum positive effect value was 39.683, for the cross 2×1 and 20.690 % for the cross 5×3, while maximum negative values was -20.455% for the cross 3×1 and -9.890 % for the cross 2×1 for both locations respectively. Significant reciprocal effect were reported also by Mohammad (2005).

Table 36. Reciprocal effect value percentages values for the character No. of rows ear^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	39.683				
MSI 43100 (3)	- 20.455	0.000			
ZP 434 (4)	- 14.286	18.605	- 13.636		
5012 (5)	6.383	12.644	4.444	15.054	
S.E	5.717				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 9.890				
MSI 43100 (3)	- 1.053	2.151			
ZP 434 (4)	1.136	- 7.447	1.075		
5012 (5)	7.071	- 3.061	20.690	7.609	
S.E	2.735				

The genetic analysis due to the character No. of rows ear^{-1} were represented in Table (37) for both locations. Appendix (3) confirmed that the mean squares due to GCA and RCA were highly significant, while it was not significant for SCA in the first location. In the second location, the Appendix (4) indicated to the presence of highly significant mean squares due to GCA and SCA, while it was not significant for RCA. Significant mean square due to GCA and SCA also recorded by El-Baroudiy (1999). Concerning the first location parent 5 with 1.518 showed maximum positive GCA effect confirming the large contribution of this parent to increase rows number.ear^{-1} in its hybrids. However, parent 1 gave maximum negative effect value with -1.309, which signified the large contribution of this parent to reduce this character in its hybrids. The estimation of $\hat{s}ij$ revealed that half of diallel crosses have a positive value, which restricted between 0.092 for the cross 1×3 and 1.419 for the

Table 37. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character No. of rows ear^{-1} at both locations.

Kanipanka Location

$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 1.309	- 0.921	0.092	- 0.465	1.419	1.680	0.751	2.206
MSI 4279 (2)	- 2.083	0.275	0.405	0.619	- 0.915	0.075	1.631	1.156
MSI 43100 (3)	1.500	0.000	- 0.719	- 0.388	- 0.005	0.516	0.523	0.428
ZP 434 (4)	1.000	- 1.333	1.000	0.235	0.375	0.055	1.029	0.703
5012 (5)	- 0.500	- 0.917	- 0.333	- 1.167	1.518	2.304	0.577	0.997
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.815	1.084	0.457	2.371	2.169	0.885
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.649	0.763	0.630	0.904	0.789	0.560

Qlyasan Location

$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.737	- 0.996	0.571	0.154	1.337	0.514	0.788	- 0.070
MSI 4279 (2)	0.750	0.493	- 0.226	- 0.743	- 0.893	0.243	0.399	0.474
MSI 43100 (3)	0.083	- 0.167	- 0.257	0.507	- 0.226	0.066	- 0.141	0.878
ZP 434 (4)	- 0.083	0.583	- 0.083	- 0.324	- 0.243	0.105	- 0.118	0.391
5012 (5)	- 0.583	0.250	- 1.500	- 0.583	0.826	0.682	0.742	0.898
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					
	0.388	0.775	0.867					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.751	0.335	1.608	0.208	0.670	0.019
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
2.191	0.752	0.221	0.237	0.478	0.465

cross 1×5, while most of the reciprocal crosses showed a negative value for RCA effect. Maximum positive RCA effect was 1.500 for the cross 3×1, but the crosses 2×1 showed maximum negative effect with -2.083. The highest the variance of GCA effect was 2.304 in parent 5, which signified the large contribution of this parent in transferring this character to its hybrids. The highest value for the variance SCA effect was 1.613 for parent 2, pointing out the contribution of this parent in transferring this character to one or a few number of its hybrids. Parent 1 gave maximum value for the variance of $\hat{r}ij$ exhibited by parent 1 with 2.206.

Some genetic parameters for this character in the first location were represented in Table (37) also, which confirming that the variance component due to GCA was larger than SCA, and the ratio of $\sigma^2_{GCA}/\sigma^2_{SCA}$ was more than one (2.371). This reflected in the value of the average degree of dominance which was less than one (0.649 and 0.904) for both diallel and reciprocal crosses respectively. These results were in accordance with the results of El-Baroudy (1999), which confirmed the importance of additive gene effect in the inheritance of these characters in the first location.

Heritability in broad sense were 0.763 and 0.789, while in narrow sense the values were 0.630 and 0.560 for both diallel and reciprocal crosses respectively. These results suggest that both selection and hybridization methods were suitable in the improvement of this character.

Regarding the second location some genetic parameters due to this character represented in the same table. Parent 5 gave maximum positive GCA effect with 0.826, confirming the high contribution of this parent to increase this character in its hybrids, while parent 1 with -0.737 showed maximum negative value for $\hat{g}ii$, indicating the contribution of this parent to reduce this character in its hybrids. Maximum effect value of SCA recorded by the diallel crosses 1×3 with 0.571, while the reciprocal crosses 2×1 showed maximum effect value of $\hat{r}ij$. Parent 5 with 0.682 produced maximum variance due to $\hat{g}ii$, while parent 1 with 0.788 produced maximum variance due to $\hat{s}ij$. Parent 5 with 0.898 recorded maximum variance for $\hat{r}ij$. The variance component due to SCA effect was larger than GCA effect, and the ratio of $\sigma^2_{GCA}/\sigma^2_{SCA}$ was less than one (0.208). The average degree of dominance for both and reciprocal crosses were 2.191 and 0.237 respectively. These results are in accordance with the results of Mohammad (2005).

Heritability in broad sense were 0.752 and 0.478, while they were 0.221 and 0.465 in narrow sense for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character in the second location. High heritability values were obtained by Sumathi *et al.* (2005), and Om prakash *et al.* (2006), while low values were reported previously by Mani and Bisht (1996); Pradeep and Satyanarana (2001), and Choudhary and Chaudhari (2002).

4.10. No. of kernels row^{-1}

The averages of kernels number.row^{-1} represented in Table (38) for both locations. The differences between genotypes were significant in the first location (Appendix 3), while they were not significant in the second location (Appendix 4), previously significant differences between genotypes observed by El-Baroudiy (1999). Regarding the first location parent 5 with 33.367 kernels row^{-1} showed maximum value, while parent 2 with 24.300 kernels exhibited minimum number. These differences between parental numbers effected significantly on the values of their diallel and reciprocal crosses. The diallel crosses values were ranged between 18.293 to 39.267 kernels for the crosses 1×2 and 4×5 respectively, while the reciprocal crosses were ranged between 18.000 to 36.167 kernels for both crosses 3×1 and 5×3 respectively. Concerning the second location parent 5 gave maximum number with 41.833 kernel but parent 2 with 31.500 kernels gave minimum number. The diallel crosses values restricted between 30.500 to 42.667 for both crosses 3×5 and 2×5 respectively.

Table 38. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character No. of kernels row^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	27.667	18.293	21.833	29.167	22.167
MSI 4279 (2)	32.167	24.300	30.283	25.667	29.167
MSI 43100 (3)	18.000	29.500	27.300	26.667	29.500
ZP 434 (4)	29.000	32.833	26.833	25.667	39.267
5012 (5)	34.967	35.167	36.167	35.000	33.367

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \le 0.05$) for genotypes*
27.660	27.201	30.963	28.798	10.741

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	33.333	36.167	38.167	31.800	39.333
MSI 4279 (2)	40.333	31.500	33.667	39.000	42.667
MSI 43100 (3)	29.167	36.000	32.667	33.000	30.500
ZP 434 (4)	34.667	36.000	38.667	37.500	33.333
5012 (5)	32.167	42.167	34.833	39.333	41.833

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \le 0.05$) for genotypes*
35.367	35.763	36.333	35.912	9.938

The reciprocal crosses values were ranged between 29.167 to 42.167 kernels for the crosses 3×1 and 5×2 respectively.

The estimation of heterosis values as the percentage of F_1s deviation from mid parental values for both diallel and reciprocal crosses for both locations were represented in Table (39). Maximum positive values were 33.032 and 31.421% for the diallel crosses 4×5 and reciprocal crosses 4×2 respectively, while maximum negative value was -29.596 % for the diallel crosses 1×2 and -34.506 % for the reciprocal crosses 3×1 in the first location .

Regarding the second location maximum positive heterosis values were 16.364 and 24.422 % for the diallel crosses 2×5 and reciprocal crosses 2×1 respectively whereas maximum negative value for the diallel crosses was -18.121 % for the cross 3×5 and -14.412 % for the reciprocal cross 5×1. Positive and negative heterosis values recorded by El-Baroudiy (1999), positive values for heterosis with (12.61 %) and (11.65 %) recorded previously by Nawar (1980) and Al-Jumaely (1996) respectively.

The estimations of reciprocal effect due to the reciprocal crosses for both locations represented in Table (40) which estimated as the percentage of F_1s diallel crosses deviation from their reciprocal crosses. Maximum positive effect values were 75.838 and 18.000 % for the crosses 2×1 and 5×4 for both locations respectively, but maximum negative effects value were -17.557 % and -23.581% for the same cross (3×1) at both locations.

Table 39. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character No. of kernels row^{-1} at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 29.596	- 20.558	9.375	- 27.362	6.254
MSI 4279 (2)	23.797		17.377	2.735	1.156	
MSI 43100 (3)	- 34.506	14.341		0.692	- 2.747	
ZP 434 (4)	8.750	31.421	1.322		33.032	
5012 (5)	14.582	21.965	19.231	18.577		
S.E	5.784					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		11.568	15.657	- 10.212	4.656	4.164
MSI 4279 (2)	24.422		4.935	13.043	16.364	
MSI 43100 (3)	- 11.616	12.208		- 5.938	- 18.121	
ZP 434 (4)	- 2.118	4.348	10.214		- 15.966	
5012 (5)	- 14.412	15.000	- 6.488	- 0.840		
S.E	3.929					

Table 40. Reciprocal effect value percentage values for the character No. of kernels row^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	75.838				
MSI 43100 (3)	- 17.557	- 2.587			
ZP 434 (4)	- 0.571	27.922	0.625		
5012 (5)	57.744	20.571	22.599	- 10.866	
S.E	9.554				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	11.521				
MSI 43100 (3)	- 23.581	6.931			
ZP 434 (4)	9.015	- 7.692	17.172		
5012 (5)	- 18.220	- 1.172	14.208	18.000	
S.E	4.670				

The estimations of general and specific combining ability effect and their variances represented in Table (41). Regarding the first location parent 5 gave maximum positive $\hat{g}ii$ which was 4.016, while parent 1 with - 2.705 showed maximum negative GCA effect. The diallel cross 4×5 with 3.541 showed maximum positive SCA effect, while maximum negative SCA effect was recorded by the diallel crosses 1×3 with -5.778, the reciprocal cross 5×4 with 2.133 showed maximum positive RCA effect, while maximum negative RCA effect value was - 6.937 exhibited by the cross 2×1. Parent 5 showed maximum variance for GCA and SCA effect with 16.125 and 17.023 respectively, whereas parent 1 with 23.785 gave maximum variance due to $\hat{r}ij$.

Some genetic parameters for the character No. of kernel row^{-1} for the first location were represented in the same table. The variance component due to GCA was larger than SCA, making the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ to be more than one

Table 41. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character No. of kernels row^{-1} at both locations.

Kanipanka Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 2.705	- 0.233	- 5.778	2.212	- 1.542	6.747	8.719	23.785
MSI 4279 (2)	- 6.937	- 0.630	3.183	0.303	- 0.017	0.397	14.596	7.349
MSI 43100 (3)	1.917	0.392	- 1.459	- 1.367	1.479	2.130	- 2.223	18.213
ZP 434 (4)	0.083	- 3.583	- 0.083	0.779	3.541	0.607	3.613	3.801
5012 (5)	- 6.400	- 3.000	- 3.333	2.133	4.016	16.125	17.023	5.702
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					
	1.689	3.379	3.777					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
14.269	5.217	3.488	1.496	10.434	5.908
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.818	0.494	0.370	1.064	0.534	0.341

Qlyasan Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 1.065	2.415	- 1.785	- 1.781	- 0.985	0.646	0.234	7.054
MSI 4279 (2)	- 2.083	0.988	- 0.088	0.432	3.629	0.976	1.747	3.169
MSI 43100 (3)	4.500	- 1.167	- 1.979	1.732	- 3.155	3.915	7.368	5.305
ZP 434 (4)	- 1.433	1.500	- 2.833	0.168	- 1.635	0.028	0.848	5.120
5012 (5)	3.583	0.250	- 2.167	- 3.000	1.888	3.565	4.712	8.920
S.E	*$\hat{g}ii$*	*$\hat{s}ij$*	*$\hat{r}ij$*					
	1.563	3.126	3.495					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
12.215	1.183	0.473	2.502	2.366	0.380
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.632	0.189	0.157	0.567	0.184	0.158

(1.496). The average degrees of dominance were 0.818 and 1.064 for both diallel and reciprocal crosses respectively confirming the importance of both additive and non-additive gene effect in the inheritance of this character.

Heritability in broad sense were 0.494 and 0.534, while in narrow sense, they were 0.370 and 0.341 for both diallel and reciprocal crosses respectively, considering that, hybridization methods were more efficient in kernels number.row^{-1} improvement.

Regarding the second location, parent 5 with 1.888 showed maximum positive GCA effect, whereas parent 3 with -1.979 produced maximum negative GCA effect. The diallel cross 2×5 with 3.629 showed maximum positive SCA effect, while maximum negative SCA value exhibited by the cross 3×5 with -3.155. The reciprocal cross 3×1 showed maximum positive RCA effect, while the cross 5×4 showed maximum negative $\hat{r}ij$ value. Parent 3 recorded maximum variance due to GCA and SCA effect with 3.915 and 7.368 respectively, while parent 5 with 8.920 recorded maximum variance due to $\hat{r}ij$.

Some genetic parameters for this character in the second location were also represented in Table (41). The variance component due to GCA was larger than SCA making $\sigma^2_{GCA} / \sigma^2_{SCA}$ to be more than one (2.502) indicating the importance of additive gene effect in controlling the inheritance of this character, while El-Baroudiy (1999) sowed that this ratio to be less than one. The average degree of dominance for diallel and reciprocal crosses was 0.632 and 0.567 respectively. Heritability in broad sense was 0.189 and 0.184, while in narrow sense, it was 0.157 and 0.158 for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method in improving this character. Heritability in broad sense estimated previously were 0.82, 0.35, 0.48, 0.97, and 0.98 that reported by Robin and Subramanian (1994); Mani and Bisht (1996); Choudhary and Chaudhari (2002), and Om prakash *et al.* (2006).

4.11. Kernel weight row^{-1} (g)

The statistical analysis as represented in Appendices (3 and 4) revealed that there were significant differences between genotypes at Kanipanka location, and highly significant differences between genotypes at Qlyasan location for the kernel weight row^{-1} as shown in Table (42). Regarding the first location parent 2 with 8.657 g showed maximum weight followed by parent 4 with 8.643 g and parent 5 with 8.617 g, while parent 3 with 7.160 g gave maximum weight. The diallel cross 1×2 recorder minimum kernel weight row^{-1} with 16.003 g, whereas the cross 1×3 with 6.397 g recorded minimum weight. Regarding the reciprocal crosses the cross 2×1 with 12.107 g showed maximum kernel weight row^{-1}, whereas the cross 3×1 with 5.830 g gave the maximum weight. Regarding the second location parent 4 with 10.287 recorded maximum kernel weights row^{-1}, and followed by parent 1 with 10.057 g. Parent 3 gave minimum weight which was 8.233 g. The diallel crosses values were ranged between 8.167 for the cross 4×5 to 11.472 g for the cross 2×4, but the reciprocal crosses value restricted between 7.743 for the cross 5×3 to 11.727 for the cross 3×2.

The estimations of heterosis value due to the character kernel weight row^{-1} as the percentage of F_1s deviation from mid-parental values at both locations represented in Table (43). Maximum positive heterosis value for the diallel cross at the first location was 89.951 % for the cross 1×2, while maximum negative value was -16.674 % for the cross 1×3 .The reciprocal cross 2×1 gave maximum positive heterosis which was 43.699 %, while the reciprocal cross 3×1 exhibited maximum negative value -24.056 %. The estimation of heterosis value at the second location represented in the same table. Maximum positive heterosis value for the diallel crosses was 22.126 % for the cross 2×4, while the cross 4×5 with -17.202 % gave maximum negative value the reciprocal cross 3×2 with 40.159 % gave maximum heterosis value, while the reciprocal cross 5×1 gave maximum negative value with -18.807 % .

Table 42. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Kernel weight row^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	8.193	16.003	6.397	7.363	7.150
MSI 4279 (2)	12.107	8.657	8.330	7.603	8.790
MSI 43100 (3)	5.830	9.133	7.160	8.950	10.463
ZP 434 (4)	6.900	9.417	9.073	8.643	8.223
5012 (5)	9.030	10.877	9.793	8.760	8.617

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
8.254	8.927	9.092	8.859	2.610

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	10.057	9.840	10.968	8.800	11.060
MSI 4279 (2)	10.195	8.500	8.913	11.472	10.695
MSI 43100 (3)	8.130	11.727	8.233	10.807	8.593
ZP 434 (4)	9.977	9.043	9.510	10.287	8.167
5012 (5)	7.915	10.013	7.743	9.373	9.440

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
9.303	9.932	9.363	9.578	2.460

Table 43. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Kernel weight row^{-1} at both locations.

Kanipanka Location						
Parents	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	S.E
MSI 4218 (1)		89.951	- 16.674	- 12.532	- 14.932	10.284
MSI 4279 (2)	43.699		5.332	- 12.100	1.775	
MSI 43100 (3)	- 24.056	15.490		13.267	32.643	
ZP 434 (4)	- 18.036	8.863	14.828		- 4.712	
5012 (5)	7.436	25.936	24.150	1.506		
S.E	6.385					

Qlyasan Location						
Parents	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	S.E
MSI 4218 (1)		6.054	19.938	- 13.485	13.455	4.451
MSI 4279 (2)	9.880		6.534	22.126	19.231	
MSI 43100 (3)	- 11.099	40.159		16.703	- 2.754	
ZP 434 (4)	- 1.917	- 3.726	2.700		- 17.202	
5012 (5)	- 18.807	11.631	- 12.373	- 4.968		
S.E	5.283					

The estimations of reciprocal effect for the character kernel weight row^{-1} as the F_1s diallel crosses deviation from their reciprocal values at both locations represented in Table (44). Maximum positive effect value was 26.294 % for the cross 5×1 and 31.563 % for the cross 3×2 at both locations respectively. Maximum negative reciprocal effect value was -24.349 % for the cross 2×1 and -25.878 % for the cross 3×1 for both locations respectively.

As shown in Appendices (3 and 4) the results in genetic analysis expressed highly mean squares of general and specific combining abilities for both diallel and reciprocal crosses in the first location, while it was significant only for specific combining ability due to the reciprocal process in the second location. The effects of general and specific combining abilities and their variances described in Table (45) at both locations.

Table 44. Reciprocal effect value percentages values for the character Kernel weight row^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 24.349				
MSI 43100 (3)	- 8.859	9.644			
ZP 434 (4)	- 6.292	23.849	1.378		
5012 (5)	26.294	23.739	- 6.403	6.526	
S.E	5.277				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	3.608				
MSI 43100 (3)	- 25.878	31.563			
ZP 434 (4)	13.371	- 21.168	- 11.999		
5012 (5)	- 28.436	- 6.374	- 9.891	14.776	
S.E	6.193				

Regarding the first location, parent 2 produced the highest positive $\hat{g}ii$ with 1.099. This value showed the good ability of parent 2 to increasing kernel weight row^{-1} in its hybrids, while parent 3 gave maximum negative value for GCA effect with -0.630, indicating the ability of this parent to reducing this character in its hybrids. Regarding the estimation of SCA effect for diallel crosses, the cross 1×2 with 4.240 gave maximum SCA effect, while the reciprocal cross 2×1 recorded maximum effect of RCA with 1.948. Parent 2 with 1.207 gave maximum variance indication the high contribution of this parent the inheritance of this character toward increasing kernel weight row^{-1} in its hybrids. Parent 1 gave maximum value for the variance $\hat{s}ij$ with 8.180 it is possible to utilize this parent to improve this character by transferring its ability to some of its hybrids. Regarding the variance $\hat{r}ij$, parent 2 with 6.682 recorded maximum value signifying the ability of this parent to transfer this character to a few number of its hybrids.

Table 45. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Kernel weight row^{-1} at both locations.

Kanipanka Location								
ĝii	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 0.142	4.240	- 2.369	- 1.084	- 0.800	- 0.014	8.180	1.183
MSI 4279 (2)	1.948	1.099	- 0.596	- 0.946	- 0.297	1.207	1.425	6.682
MSI 43100 (3)	0.283	- 0.402	- 0.630	1.284	1.726	0.396	1.336	2.028
ZP 434 (4)	0.232	- 0.907	- 0.062	- 0.501	- 0.039	0.251	0.007	1.264
5012 (5)	- 0.940	- 1.043	0.335	- 0.268	0.173	0.030	0.432	1.236
S.E	*ĝii*	*ŝij*	*r̂ij*					
	0.411	0.821	0.918					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_{D}$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{A}	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.843	0.392	5.794	0.068	0.784	0.286
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
3.845	0.886	0.106	0.854	0.559	0.410

Qlyasan Location								
ĝii	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	0.121	0.006	- 0.087	- 0.505	0.122	- 0.015	- 0.162	1.247
MSI 4279 (2)	- 0.178	0.312	0.723	0.174	0.799	0.097	0.153	1.190
MSI 43100 (3)	1.419	- 1.407	- 0.293	0.679	- 0.783	0.086	1.434	0.377
ZP 434 (4)	- 0.588	1.214	0.648	0.194	- 0.668	0.038	0.641	0.370
5012 (5)	1.573	0.341	0.425	0.603-	- 0.334	0.112	0.790	0.571
S.E	*ĝii*	*ŝij*	*r̂ij*					
	0.387	0.774	0.865					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_{D}$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{A}	$\sigma^2_{RCA} = \sigma^2_{Dr}$
0.749	0.012	0.243	0.049	0.024	0.566
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
4.532	0.262	0.023	6.919	0.440	0.018

Some genetic parameters in the first location were represented in the same table. The variance component due to SCA was larger than GCA. The ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ was less than one (0.068), suggesting that additive effects were less important than non additive effect in the inheritance of this character the average degrees of dominance were 3.845 and 0.854 for both diallel and reciprocal crosses respectively.

Heritability in broad sense were 0.886 and 0.559 and the values were 0.106 and 0.410 in narrow sense for both diallel and reciprocal crosses respectively. Considering that, hybridization methods were more efficient to improve this character.

Concerning the second location parent 2 gave maximum GCA effect value with 0.312, which means the contribution of this parent to improve this character is possible, through transferring this character to its hybrids. Regarding the value of SCA effect for diallel crosses, the maximum value was 0.799 recorded by the cross 2×5, while for the reciprocal crosses it was 1.573 for the cross 5×1. These values revealed the assurance of this character transferable with the presence of tendency to improve in the hybrids by using parents possessing this type of character. The highest variance of GCA effect was 0.112 recorded by parent 5, means the ability of this parent to improve this character in its hybrids. Parent 3 with 1.434 gave maximum variance for SCA effect, while parent 1 with 1.247 gave maximum variance $\hat{r}ij$. These results indicated the ability of this parent in transferring this character to one or a few number of their hybrids. The ratio of $\sigma^2_{GCA}/\sigma^2_{SCA}$ was 0.049 and the average degrees of dominance were 4.532 and 6.919 for both diallel and reciprocal crosses, revealing great role of non additive gene action in controlling the inheritance of this character. Heritability values in broad sense were 0.262 and 0.440, while in narrow sense were 0.023 and 0.018 for both diallel and reciprocal crosses respectively, confirming the suitability of hybridization methods to improve this character.

4.12. Kernel weight ear^{-1} (g)

Table (46), Appendices (3 and 4) showed highly significant differences between genotypes for the character kernel weight ear^{-1} at both locations. Regarding the first location maximum kernel weight ear $^{-1}$ exhibited by parent 4 with 95.300 g and followed by parent 1 with 94.260 g, while parent 3 recorded minimum weight with 64.140 g. these differences between parental values effected significantly on their diallel and reciprocal crosses .The diallel cross 4×5 with 138.627 g gave maximum kernel weight ear $^{-1}$, while the cross 1×2 with 62.957 g recorded minimum weight. Concerning the reciprocal crosses 2×1 with 139.110 g showed maximum weight, while the cross 3×1 with 68.307 exhibited minimum weight. Regarding the second location parent4 with 135.623 g gave maximum weight, while parent 5 with 93.043 g recorded minimum weight. These differences between parental value resulted in the presence of significant differences between their diallel and reciprocal crosses the diallel cross 1×5 with 189.933 g gave maximum weight, while the cross 1×4 with 79.780 g showed minimum weight. Regarding the reciprocal crosses, the cross 3×2 with 187.712 g exhibited maximum value, while the cross 2×1 with 125.067 g produced minimum value.

Estimation heterosis value as the percentage of F_1s deviation from mid parental values represented in Table (47) for both locations. Regarding the first location, it observed that most of the diallel and reciprocal crosses showed positive values. Maximum values were 49.753 and 53.504 % for both diallel cross 4×5 and reciprocal cross 2×1 respectively. In the second location, all crosses showed positive value exception of the diallel cross 1×4 with -39.497 %. Maximum values were 71.774 and 62.728 % for both diallel cross 1×5 and reciprocal cross 3×2 respectively.

Table 46. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Kernel weight ear $^{-1}$ at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	94.260	62.957	86.370	94.900	100.267
MSI 4279 (2)	139.110	86.987	81.240	95.323	120.873
MSI 43100 (3)	68.307	99.890	64.140	97.187	114.860
ZP 434 (4)	90.413	103.507	95.023	95.300	138.627
5012 (5)	116.177	117.463	94.513	105.520	89.840

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d* ($p \le 0.05$) *for genotypes*
86.105	99.260	102.992	98.122	23.824

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	128.100	159.690	157.747	79.780	189.933
MSI 4279 (2)	125.067	116.660	129.300	164.233	166.780
MSI 43100 (3)	134.520	187.712	114.047	154.330	135.463
ZP 434 (4)	135.080	134.132	135.303	135.623	120.923
5012 (5)	142.537	139.147	125.293	134.670	93.043

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d* ($p \le 0.05$) *for genotypes*
117.495	145.818	139.346	137.565	30.746

Table 47. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Kernel weight ear $^{-1}$ at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 30.529	9.053	0.127	8.926	7.761
MSI 4279 (2)	53.504		7.512	4.586	36.714	
MSI 43100 (3)	- 13.754	32.194		21.910	49.188	
ZP 434 (4)	- 4.607	13.565	19.196		49.753	
5012 (5)	26.210	32.857	22.761	13.989		
S.E	6.059					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		30.487	30.290	- 39.497	71.774	9.524
MSI 4279 (2)	2.195		12.090	30.198	59.063	
MSI 43100 (3)	11.106	62.728		23.627	30.826	
ZP 434 (4)	2.441	6.334	8.386		5.764	
5012 (5)	28.909	32.708	21.004	17.787		
S.E	5.864					

Data in Table (48) explain the reciprocal effects estimated as the F_1s diallel crosses from their reciprocal crosses for both locations. Maximum reciprocal effect values were 120.962 and 69.316 % for both 2×1 and 4×1 for both locations respectively.

The genetic analysis for the character kernel weight ear^{-1} for both locations represented in Table (49). The mean squares due to GCA and SCA were highly significant but it was not significant for RCA at the first location, while at the second location the mean squares due to SCA and RCA were highly significant, but it was not significant for GCA (Appendices 3 and 4).

Table 48. Reciprocal effect value percentages values for the character Kernel weight ear $^{-1}$ at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	120.962				
MSI 43100 (3)	- 20.914	22.957			
ZP 434 (4)	- 4.728	8.585	- 2.226		
5012 (5)	15.868	- 2.821	- 17.714	- 23.882	
S.E	13.299				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 21.682				
MSI 43100 (3)	- 14.724	45.175			
ZP 434 (4)	69.316	- 18.329	- 12.329		
5012 (5)	- 24.954	- 16.569	- 7.508	11.368	
S.E	10.052				

Regarding the first location parent 5 with 10.676 showed maximum positive GCA effect, while parent 3 with -11.555 gave maximum negative value. Maximum SCA effect for the diallel crosses was 10.287 for the cross 4×5, while it was 16.553 for the reciprocal cross 5×4. Parent 3 with 133.521 gave maximum variance for $\hat{g}ii$, while parent 2 with 492.183 recorded maximum variance for $\hat{s}ij$ and maximum variance for $\hat{r}ij$ exhibited by parent 1, which were 498.141.

Genetic parameters for kernel weight ear $^{-1}$ at the first location represented in Table (49). The variance components due to SCA were larger than GCA, and the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ was less than one (0.445). The average degree of dominance were 1.500 and 1.694 for both diallel and reciprocal crosses respectively, indicating the predominance of none additive gene effect in controlling this character.

Table 49. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Kernel weight ear^{-1} at both locations.

Kanipanka Location								
ĝii	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^{2}\hat{g}ii$	$\sigma^{2}\hat{s}ij$	$\sigma^{2}\hat{r}ij$
MSI 4218 (1)	-3.420	5.020	-13.724	-5.033	2.844	8.889	58.451	498.141
MSI 4279 (2)	-38.077	1.312	2.686	-3.007	9.059	1.720	492.183	43.934
MSI 43100 (3)	9.032	-9.325	-11.555	6.550	7.444	133.521	65.080	100.073
ZP 434 (4)	2.243	-4.092	1.082	2.988	10.287	8.927	19.059	117.096
5012 (5)	-7.955	1.705	10.173	16.553	10.676	113.974	124.033	83.797
S.E	*ĝii*	*ŝij*	*r̂ij*					
	3.747	7.494	8.378					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_{D}$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{A}	$\sigma^2_{RCA} = \sigma^2_{Dr}$
70.197	60.440	135.961	0.445	120.881	173.402
$\bar{a}$	$h^2 b.s$	$h^2 n.s$	$\bar{a}_r$	$h^2 b.s_r$	$h^2 n.s_r$
1.500	0.785	0.370	1.694	0.807	0.332

Qlyasan Location								
ĝii	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^{2}\hat{g}ii$	$\sigma^{2}\hat{s}ij$	$\sigma^{2}\hat{r}ij$
MSI 4218 (1)	0.491	-2.050	9.270	-26.031	31.661	-4.436	550.292	528.440
MSI 4279 (2)	17.312	6.373	13.356	9.839	12.507	40.621	204.016	424.871
MSI 43100 (3)	11.613	-29.206	1.212	10.635	-4.917	1.468	335.291	126.891
ZP 434 (4)	-27.650	15.051	9.513	-4.596	-1.692	21.111	321.720	311.585
5012 (5)	23.698	13.817	5.085	-6.673	- 3.481	12.119	235.452	395.287
S.E	*ĝii*	*ŝij*	*r̂ij*					
	4.836	9.671	10.813					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_{D}$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_{A}	$\sigma^2_{RCA} = \sigma^2_{Dr}$
116.918	7.198	681.472	0.011	14.396	261.012
$\bar{a}$	$h^2 b.s$	$h^2 n.s$	$\bar{a}_r$	$h^2 b.s_r$	$h^2 n.s_r$
9.730	0.858	0.018	6.022	0.702	0.037

Heritability in broad sense were 0.785 and 0.807, while the values were 0.370 and 0.332 in narrow sense for both diallel and reciprocal crosses respectively. These results confirm suitability of hybridization method to improve this character.

The genetic analysis for the second location were represented in Table (49) also. Parent 2 gave maximum GCA effect that was 6.373, while maximum negative effect for GCA exhibited by parent 4 with - 4.596. The diallel cross 1×5 showed maximum effect for SCA. The reciprocal cross 5×1 gave maximum positive RCA effect with 23.698, parent 2 showed maximum variance for GCA effect which was 40.621, whereas parent 1 with 550.292 and 528.440 gave maximum variance for $\hat{s}ij$ and $\hat{r}ij$ respectively, the variance component due to SCA was larger than GCA and the ratio $\sigma^2_{GCA} / \sigma^2_{SCA}$ was less than one (0.011). The average degrees of dominance values were 9.730 and 6.022 showing the over dominance gene effect as controlled the inheritance of this character.

Heritability in broad sense were 0.858 and 0.702, while in narrow sense they were 0.018 and 0.037 for both diallel and reciprocal crosses respectively, confirming the importance of hybridization in improving this character.

4.13. 300-kernels weight (g)

Data in Table (50), Appendices (3 and 4) showed significant differences between genotypes for the character 300-kernels weight in both locations. Similar results were obtained previously by El-Baroudiy (1999) and Mohammad (2005). Regarding the first location, parent 1 with 86.633 gave maximum weight and followed by parent 4 and 5 with 83.150 and 82.277 g, while parent 2 with 78.373 g showed minimum 300-kernrl weight. The diallel cross 1×3 with 91.857 g recorded maximum weight, whereas the cross 1×2 with 52.240 gave minimum weight. The reciprocal cross 3×1 with 85.013 g records maximum 300-kernrl weight, while the cross 5×4 with 63.463 exhibited minimum weight.

Table 50. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character 300-kernels weight at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	86.633	52.240	91.857	76.597	74.120
MSI 4279 (2)	80.043	78.373	71.547	74.840	75.670
MSI 43100 (3)	85.013	74.907	79.870	78.250	69.630
ZP 434 (4)	77.063	73.093	79.897	83.150	81.880
5012 (5)	71.883	72.610	73.167	63.463	82.277

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \le 0.05$) for genotypes*
82.061	74.663	75.114	76.323	15.831

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	85.567	89.980	87.897	82.777	88.400
MSI 4279 (2)	74.080	70.180	79.087	90.813	69.553
MSI 43100 (3)	84.577	87.707	75.463	92.750	81.387
ZP 434 (4)	85.643	80.847	85.077	82.667	73.157
5012 (5)	73.710	74.230	74.590	75.953	74.809

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \le 0.05$) for genotypes*
77.737	83.580	79.641	80.836	14.438

Regarding the second location, the means for 300-kernel weight represented in the same table. Parent 1 recorded maximum weight with 85.567 g, while parent 2 with 70.180 showed minimum weight. The diallel cross 3×4 with 92.750 g produced maximum weight, and the cross 2×5 with 69.553 g gave minimum weight. The reciprocal cross 3×2 with 87.707 g recorded maximum weight, while the cross 5×1 with 73.710 g gave minimum weight.

Percentage of heterosis values estimated as F_1s deviation from mid parental values for both diallel and reciprocal crosses in both locations represented in Table (51). All diallel and reciprocal crosses showed negative heterosis values with the exception of the diallel cross 1×3 with 10.336 % and

Table 51. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character 300-kernels weight at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 36.681	10.336	- 9.771	- 12.237	3.771
MSI 4279 (2)	- 2.982		- 9.574	- 7.332	- 5.795	
MSI 43100 (3)	2.116	- 5.327		- 4.000	- 14.115	
ZP 434 (4)	- 9.222	- 9.495	- 1.979		- 1.007	
5012 (5)	- 14.886	- 9.605	- 9.752	- 23.273		
S.E	2.258					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		15.547	9.168	- 1.593	10.241	2.849
MSI 4279 (2)	- 4.871		8.603	18.829	- 4.057	
MSI 43100 (3)	5.045	20.440		17.309	8.319	
ZP 434 (4)	1.815	5.788	7.603		- 7.088	
5012 (5)	- 8.078	2.394	- 0.727	- 3.536		
S.E	2.536					

the reciprocal cross 3×1 with 2.116 % in the first location. Regarding the second location the diallel cross 2×4 gave maximum positive heterosis value with 18.829 % and followed by the cross 3×4 with 17.309 %. The reciprocal cross 3×2 with 20.440 % showed maximum positive heterosis value and followed by the cross 4×3 with 7.603 %. Positive and negative heterosis values confirmed by El-Baroudiy (1999); Al-Zawbaey (2001); Al-Janaby (2003), and Mohammad (2005).

Data in Table (52) explain the reciprocal effect of reciprocal crosses estimated as the F_1s diallel cross deviation from their reciprocal crosses value. Maximum positive effect was 53.222 % recorded by the cross 2×1 in the first locations, and it was 10.899 % showed by the cross 3×2 in the second location. Positive values for reciprocal effect confirm exceeding of reciprocal cross over

Table 52. Reciprocal effect value percentages for the character 300-kernels weight at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	53.222				
MSI 43100 (3)	- 7.450	4.696			
ZP 434 (4)	0.609	- 2.334	2.104		
5012 (5)	- 3.018	- 4.044	5.079	- 22.492	
S.E	6.154				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 17.671				
MSI 43100 (3)	- 3.777	10.899			
ZP 434 (4)	3.463	- 10.975	- 8.273		
5012 (5)	- 16.618	6.724	- 8.351	3.823	
S.E	3.137				

diallel cross, while negative effect values indicate to out yielding diallel cross in compare to its reciprocal cross. Similar results were recorded by Mohammad (2005).

The genetic analysis for the character 300-kernel weight for both locations represented in Table (53). The mean squares due to SCA was significant, while it was not significant for GCA and RCA in the first location (Appendix 3). In the second location, the mean squares due to GCA was highly significant while it was not significant from GCA and SCA (Appendix 4), while El-Baroudiy (1999) recorded significant mean squares due to GCA and SCA at spring season.

Table 53. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character 300-kernels weight at both locations.

Kanipanka Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	1.885	- 8.913	8.869	- 2.194	- 3.581	2.315	48.041	53.258
MSI 4279 (2)	- 13.902	- 3.153	- 2.021	- 0.018	2.596	9.943	57.487	28.458
MSI 43100 (3)	3.422	- 1.680	2.078	- 0.143	- 5.377	4.317	3.949	28.847
ZP 434 (4)	- 0.233	0.873	- 0.823	0.815	- 2.841	0.665	- 7.349	29.876
5012 (5)	1.118	1.530	- 1.768	9.208	- 1.625	2.641	19.965	18.850
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	2.490	4.980	5.567					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2 D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
30.996	2.181	33.738	0.065	4.361	14.581
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
3.933	0.551	0.063	2.586	0.379	0.087

Qlyasan Location								
$\hat{g}ii$	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	2.984	0.381	4.670	- 2.009	2.012	7.871	1.247	27.763
MSI 4279 (2)	7.950	- 2.170	3.167	4.765	- 1.998	4.710	24.545	16.341
MSI 43100 (3)	1.660	- 4.310	1.564	4.115	0.365	2.445	4.033	19.371
ZP 434 (4)	- 1.433	4.983	3.837	2.399	- 3.904	5.755	10.183	15.209
5012 (5)	7.345	- 2.338	3.398	- 1.398	- 4.776	22.812	15.541	7.803
S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$					
	2.271	4.542	5.078					

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
25.782	8.578	3.305	2.595	17.156	7.015
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
0.621	0.442	0.371	0.904	0.484	0.343

Regarding the first location parent 3 with 2.078 recorded maximum positive GCA effect , while maximum negative effect value was -3.153 recorded by parent 2. The highest effect value due to SCA was 8.869 produced by the diallel cross 1×3. Maximum positive RCA effect was 3.422 recorded by the reciprocal cross 3×1. Maximum variance for GCA effect was 9.943 and for SCA effect was 57.487 produced by parent 2, whereas maximum variance due to RCA effect was 53.258 showed by parent 1.

Some genetic parameters for 300-kernel weight in the first location were represented in the same table. The variance component due to SCA was larger than GCA, making the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ to be less than one (0.065). The average degree of dominance were more than one (3.933 and 2.586) for both diallel and reciprocal crosses respectively, indicating to the over dominance gene effect as controlled the inheritance of this character.

Heritability in broad sense were 0.551 and 0.379, while the values were 0.063 and 0.087 for both diallel and reciprocal crosses respectively. These results confirm the importance of hybridization method to improve this character.

Regarding the second location parent 1 with 2.984 recorded maximum GCA effect value and followed by parent 4 with 2.399. The diallel cross 2×4 with 4.760 gave maximum SCA effect value, while the highest RCA effect found to be 7.950 showed by the reciprocal cross 2×1. Parent 5 recorded maximum variance for $\hat{g}ii$ which was 22.812, while parent 2 with 24.545 should maximum variance for $\hat{s}ij$, and maximum variance due to $\hat{r}ij$ was 27.763 recorded by parent 1. At Qlyasan location, the variance component due to GCA was larger than SCA, making the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ to be more than one (2.595), confirming the importance of additive gene effect as controlled the inheritance of this character. Mohammad (2005) also reported that this ratio to be more than one (2.820). The average degree of dominance were 0.621 and 0.904 for both diallel and reciprocal crosses respectively.

Heritability in broad sense were 0.442 and 0.484, while in narrow sense they were 0.371 and 0.343 for both diallel and reciprocal crosses respectively indication to the importance of hybridization method to improve this character. Previous workers estimated this parameter in broad sense to be 0.79, 0.52, 0.009, 0.81, 0.88, 0.97, by Robin and Subramanian (1994); Mani and Bisht (1996); Pradeep and Satyanarana (2001); Choudhary and Chaudhari (2002); Sumathi *et al.* (2005), and Om prakash *et al.* (2006).

4.14. Kernel yield plant^{-1} (g)

Data in Table (54) showed the averages of kernel yield plant^{-1} for genotypes in both locations. Regarding the first location, highly significant differences were observed between genotypes (Appendix 3).

Parent 5 with 126.720 g recorded maximum kernel yield plant^{-1} and followed by parent 2 with 125.677 g, while minimum yield produced by parent 3 with 78.583 g. The diallel cross 4×5 with 198.720 g gave maximum kernel yield and followed by the cross 2×5 with 180.703 g, whereas the cross 1×2 with 109.420 g exhibited minimum yield. The reciprocal cross 2×1 with 254.710 g produced maximum yield and followed by the cross 4×2 with 200.180 g. The reciprocal cross 3×1 with 91.710 recorded minimum yield of kernels . Plant^{-1}.

Regarding the second location it was noticed the presence of significant differences between genotypes due to these characters (Table 54 and Appendix 4), while highly significant differences between genotypes were noticed previously by Mohammad (2005). Parent 5 with 184.320 g recorded maximum yield while parent 3 with 121.373 g showed minimum yield. The diallel cross 1×2 with 230.663 g showed the highest value due to this characters which was 230.663g and followed by the cross 2×4 with 211.220 g. Concerning the reciprocal crosses, it was found that the cross 5×2 with 234.262 g exhibited maximum yield, and followed by the cross 2×1 with 226.039 g.

Table 54. Diagonal, upper diagonal, and sub diagonal values for parents, F_1 diallel crosses, and reciprocal crosses for the character Kernel yield plant^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	108.147	109.420	133.077	158.227	118.147
MSI 4279 (2)	254.710	125.677	142.370	155.547	180.703
MSI 43100 (3)	91.710	130.583	78.583	119.220	168.993
ZP 434 (4)	161.553	200.180	161.703	86.597	198.720
5012 (5)	171.170	144.507	189.193	145.883	126.720

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
105.145	148.442	165.119	146.454	68.242

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)	134.247	230.663	203.197	152.642	181.720
MSI 4279 (2)	226.039	127.187	184.307	211.220	171.522
MSI 43100 (3)	135.499	177.930	121.373	203.909	188.953
ZP 434 (4)	175.112	180.173	176.553	131.250	187.172
5012 (5)	184.247	234.262	153.521	198.627	184.320

Parental Mean	*Diallel Mean*	*Reciprocal Mean*	*General Mean*	*l.s.d ($p \leq 0.05$) for genotypes*
139.675	191.530	184.196	178.226	65.316

The estimations of heterosis values as the percentage of F_1s deviation from mid parental values represented in Table (55) for both locations. Regarded to the first location, all diallel and reciprocal crosses showed positive values with the exception of the diallel cross 1×2 and the reciprocal cross 3×1 respectively. Maximum heterosis value were 86.315 % and 117.865 % recorded by the diallel cross 4×5 and the reciprocal cross 2×1 respectively.

Concerning the second location, it was observed that all heterosis showed positive values. The diallel cross 1×2 with 76.461 % and the reciprocal cross 2×1 with 72.923 % gave maximum values. Positive heterosis values for all crosses were obtained previously by Makherijc (1971); Grogan (1972); Nawar

Table 55. Heterosis value percentages (upper diagonal and sub diagonal values) for F_1 diallel and reciprocal crosses for the character Kernel yield plant^{-1} at both locations.

Kanipanka Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100(3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		- 6.408	42.534	62.498	0.607	8.810
MSI 4279 (2)	117.865		39.401	46.553	43.190	
MSI 43100 (3)	- 1.773	27.860		44.352	64.628	
ZP 434 (4)	65.914	88.606	95.790		86.315	
5012 (5)	45.759	14.508	84.306	36.776		
S.E	12.326					

Qlyasan Location						
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100(3)*	*ZP 434 (4)*	*5012 (5)*	*S.E*
MSI 4218 (1)		76.461	58.983	14.986	14.086	7.940
MSI 4279 (2)	72.923		48.300	63.460	10.124	
MSI 43100 (3)	6.016	43.169		61.433	23.623	
ZP 434 (4)	31.913	39.433	39.775		18.625	
5012 (5)	15.672	50.406	0.441	25.884		
S.E	6.852					

(1984); Sanghi (1982); Rahman (1982); Ghandi and Hallauer (1996); Muhammad *et al.* (1988); Al- Jumaely (1996); El-Baroudiy (1999); Dawod (2001); Al-Azawy (2002), and Al-Janaby (2003) which confirming that all genes were under the controlling of over dominance effect.

Data in Table (56) explain the reciprocal effect estimated as the percentage of F_1s diallel cross deviated from their reciprocal cross, for both locations. Maximum effect value was 132.782 for the cross 2×1 and 36.578 % for the cross 5×2 for both locations respectively. Significant reciprocal effect detected previously by Mohammad (2005).

The estimation of general and specific combining abilities effect and their variances represented in Table (57). Regarding the first location, the mean squares due to SCA and RCA were highly significant. Maximum positive GCA effect was 10.622 exhibited by parent 5 and followed by parent 2 with

Table 56. Reciprocal effect value percentages for the character Kernel yield plant^{-1} at both locations.

Kanipanka Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	132.782				
MSI 43100 (3)	- 31.085	- 8.279			
ZP 434 (4)	2.102	28.694	35.634		
5012 (5)	44.879	- 20.031	11.953	- 26.588	
S.E	15.325				

Qlyasan Location					
Parents	*MSI 4218 (1)*	*MSI 4279 (2)*	*MSI 43100 (3)*	*ZP 434 (4)*	*5012 (5)*
MSI 4218 (1)					
MSI 4279 (2)	- 2.005				
MSI 43100 (3)	- 33.316	- 3.460			
ZP 434 (4)	14.721	- 14.699	- 13.416		
5012 (5)	1.390	36.578	- 18.752	6.120	
S.E	6.142				

10.484, while parent 3 with -17.052 showed maximum negative GCA effect value. The diallel cross 3×5 with 39.070showed maximum positive SCA effect, while the reciprocal cross 5×4 with 26.418 gave maximum positive RCA effect. Maximum variance due to GCA effect was 290.768 exhibited by parent 3, while parent 2 with 1708.082 showed maximum variance for SCA effect, and parent 1 with 1848.923 gave maximum variance due to RCA effect.

The variance component due to SCA was larger than GCA making the ratio $\sigma^2_{GCA}/\sigma^2_{SCA}$ to be less than one (0.072), and the average degree of dominance be more than one (3.734) and (2.701) for both diallel and reciprocal crosses respectively, indicating the importance of non additive gene effect in controlling the inheritance of this character.

Table 57. Estimation of general and specific combining abilities effects, their variances, and some genetic parameters for the character Kernel yield plant^{-1} at both locations.

Kanipanka Location								
$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 5.023	30.151	- 38.997	17.490	- 7.394	2.191	733.788	1848.923
MSI 4279 (2)	- 72.645	10.484	- 3.409	19.957	- 4.954	109.909	1708.082	589.791
MSI 43100(3)	20.683	5.893	- 17.052	10.091	39.070	290.768	501.099	694.683
ZP 434 (4)	- 1.663	- 22.317	- 21.242	0.969	14.257	0.939	189.258	501.315
5012 (5)	- 26.512	18.098	- 10.100	26.418	10.622	112.828	414.287	602.972

S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$
	10.733	21.466	23.999

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
575.975	77.321	1077.803	0.072	154.642	564.232
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
3.734	0.682	0.086	2.701	0.555	0.119

Qlyasan Location								
$\hat{g}ii$	MSI 4218 (1)	MSI 4279 (2)	MSI 43100 (3)	ZP 434 (4)	5012 (5)	$\sigma^2\hat{g}ii$	$\sigma^2\hat{s}ij$	$\sigma^2\hat{r}ij$
MSI 4218 (1)	- 2.465	43.767	- 4.110	- 8.449	- 1.418	- 15.032	489.205	162.484
MSI 4279 (2)	2.312	8.823	5.634	12.083	7.202	77.849	-101.083	1050.245
MSI 43100 (3)	33.849	3.188	- 11.546	27.004	- 4.065	133.733	454.491	183.194
ZP 434 (4)	- 11.235	15.523	13.678	- 3.435	9.468	11.799	35.243	326.470
5012 (5)	- 1.263	- 31.370	17.716	- 5.727	8.641	74.661	264.713	53.351

S.E	$\hat{g}ii$	$\hat{s}ij$	$\hat{r}ij$
	10.273	20.546	22.971

Mse´	σ^2_{GCA}	$\sigma^2_{SCA} = \sigma^2_D$	$\sigma^2_{GCA}/\sigma^2_{SCA}$	σ^2_A	$\sigma^2_{RCA} = \sigma^2_{Dr}$
527.647	23.264	999.793	0.023	46.529	40.966
$\bar{a}$	$h^2b.s$	$h^2n.s$	$\bar{a}_r$	$h^2b.s_r$	$h^2n.s_r$
6.556	0.665	0.030	1.327	0.142	0.076

Heritability in broad sense were 0.682 and 0.555 while in narrow sense, it was 0.086 and 0.119 for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character. Regarding the second location, the mean square due to SCA effect was highly significant while it was not significant for GCA and RCA effect (Appendix 4). Maximum positive GCA effect was 8.823 exhibited by parent 2 and followed by parent 5 with 8.641 while parent 3 with -11.546 produced maximum negative GCA effect. The diallel cross 1×2 with 43.767 gave maximum positive SCA effect, while the reciprocal cross 3×1 with 33.849 showed maximum positive RCA effect. Parent 3 with 133.733 produced the highest value due to the variance of GCA effect, while parent 1 with 489.205 showed maximum variance for SCA effect, and parent 2 with 1050.245 produced maximum value for the variance of RCA effect. El-Baroudiy (1999) and Mohammad (2005) showed significant mean squares due to GCA and SCA previously. Some genetic parameters due to this character represented in the same table. The variance component due to SCA was larger than GCA and the ratio of $\sigma^2_{GCA} / \sigma^2_{SCA}$ was found to be less than one (0.023) and the average degree of dominance was larger than one (6.556) and (1.327) for both dialed and reciprocal crosses respectively, indicating the impotence of non additive gene effect in controlling this character. Similar results were recorded previously by El-Baroudiy (1999) and Mohammad (2005).

Heritability in broad sense were 0.665 and 0.142 while they were 0.030 and 0.076 in narrow sense for both diallel and reciprocal crosses respectively, confirming the importance of hybridization method to improve this character. High estimation of heritability in broad sense were reported by Robin and Subramanian (1994); Mani and Bisht (1996); Choudhary and Chaudhari (2002); Sumathi *et al.* (2005), and Akbar *et al.* (2008), which were 0.64, 0.67, 0.73, 0.99, 0.82 respectively.

4.15. Correlation Among Traits

Data in Table (58) show the correlation among all pairs of traits at Kanipanka location, highly significant and positive correlation (0.693**) was observed between days to 50 % tasseling and days to 50 % silking, while days to 50 % tasseling has negative and highly significant correlation (- 0.569**) with cob weight and negative, but significant correlation (-0.404*) with cob length. Previously Molhotra and Khehra (1986), and Debnath and Khan (1991) recorded positive correlation between this character and kernels yield plant^{-1}.

Ear height has a highly significant and positive correlation (0.530**) with No. of rows ear^{-1}, while previously Molhotra and Khehra (1986), and Boraneog and Duara (1993) recorded positive correlation between this character and kernels yield plant^{-1}.

Cob width has highly significant positive correlations (0.529** and 0.562**) with No. of rows ear^{-1} and kernels weight ear^{-1} respectively.

Highly significant and positive correlation (0.529**) was observed between No. of ears plant^{-1} and kernels weight row^{-1}.

No. of rows ear^{-1} has positive and highly significant correlations (0.620** and 0.533**) with No. of kernels row^{-1} and kernels weight ear^{-1} respectively.

No. of kernels row^{-1} has highly significant positive correlations (0.671** and 0.610**) with kernels weight ear^{-1} and kernels yield plant^{-1} successively. This result is in accordance with the previous result of Appadurai and Nagarajan (1975).

A positive and highly significant correlation (0.682**) was observed between kernel weight row^{-1} and 300-kernels weight.

Highly significant and positive correlation (0.758**) was observed between kernel weight row^{-1} and kernels yield plant^{-1}.

Kernels yield plant^{-1} has no significant correlation with most of the characters under study, but it has significant and positive correlation with No. of kernels row^{-1}, and kernels weight row^{-1}. In contrary to our results, previous workers recorded that kernels yield plant^{-1} has significant and positive correlation with days to 50 % silking, plant height, ear height, cob weight, cob length, No. of rows ear^{-1}, No. of kernels row^{-1}, and 300-kernels weight (Sharma *et al.*, 1982; Ei-Nagouly *et al.*, 1983; Saha and Mukherjee, 1985; Malhotra and Khehra, 1986; Tyagi *et al.*, 1988; Maharajan *et al.*, 1990; Singh *et al.*, 1991; Debnath and Khan, 1991; Boraneog and Duara, 1993; Saha and Mukherjee, 1993; Satyanarayana, 1996; Kumar and Kumar, 1997; Basheeruddin *et al.*, 1999; Bello *et al.*, 2010; Kashiani *et al.*, 2010; Wannows *et al.*, 2010, and Selvaraja and Nagarajan, 2011).

Table 58. Correlation among all pairs of traits at Kanipanka location

Traits	Days to 50 % Tasseling	Days to 50 % silking	Plant height (cm)	Ear height (cm)	Cob weight (g)	Cob length (cm)	Cob width (cm)	No. of ears plant^{-1}	No. of rows ear^{-1}	No. of kernels row^{-1}	Kernels weight row^{-1} (g)	Kernels weight ear^{-1} (g)	300-kernels weight (g)
Days to 50 % silking	0.693**												
Plant height (cm)	-0.060	0.230											
Ear height (cm)	0.050	0.120	0.100										
Cob weight (g)	-0.569**	-0.390	0.240	-0.140									
Cob length (cm)	-0.404*	-0.130	-0.070	-0.020	0.120								
Cob width (cm)	-0.050	0.110	0.400	0.340	-0.080	0.240							
No. of ears plant^{-1}	-0.060	0.170	0.260	-0.060	0.320	-0.090	-0.050						
No. of rows ear^{-1}	-0.060	-0.060	0.190	0.530**	-0.010	-0.020	0.529**	-0.280					
No. of kernels row^{-1}	-0.240	-0.030	0.300	0.478*	0.150	0.360	0.370	-0.060	0.620**				
Kernels weight row^{-1} (g)	-0.060	0.210	0.290	0.200	0.050	0.290	0.170	0.529**	-0.060	0.070			
Kernels weight ear^{-1} (g)	-0.320	-0.350	0.140	0.230	0.110	0.390	0.562**	0.030	0.533**	0.671**	0.140		
300-kernels weight (g)	-0.070	-0.210	-0.300	-0.180	-0.070	0.010	-0.040	-0.360	-0.080	-0.070	-0.682**	0.060	
Kernels yield plant^{-1} (g)	-0.300	-0.210	0.070	0.350	0.180	0.350	0.390	**0.350**	**0.370**	**0.610****	**0.260**	**0.758****	**-0.102**

***. Correlation is significant at the 0.01 level (2-tailed) ,* $t_{0.01}(23)=2.807$

**. Correlation is significant at the 0.05 level (2-tailed) ,* $t_{0.05}(23)=2.068$

Table (59) shows correlation among all pairs of traits at Qlyasan location, days to 50 % Tasseling was correlated high significantly and positively (0.861**) with days to 50 % silking, while has negative and highly significant correlation (- 0.586**) with cob weight and negative and significant correlations (-0.402* and -0.483*) with cob length and No. of kernels row^{-1} alternatively.

Concerning Days to 50 % silking, highly significant and negative correlation (- 0.642**) was observed with cob weight, while has negative and significant correlation (- 0.503*) with cob width, while Rather *et al.* (1999) estimated positive correlation between Days to 50 % silking with ear height and kernels yield plant^{-1}.

Plant height has a positive and significant correlation (0.426*) with ear height only. Rather *et al.* (1999) found that plant height has no significant correlation with kernels yield plant^{-1} also. Whereas, Kumar and Kumar (2000) put an emphasis on plant height with greater ear height, No. of row.ear^{-1}, and No. of kernels row^{-1} for better kernels yield plant^{-1}.

Highly significant and positive correlation (0.576**) was observed between cob weight and cob width, while cob weight has positive and significant correlations (0.492* and 0.431*) with cob length and kernels yield plant^{-1} successively.

Cob width has significant positive correlation (0.497*) with No. of rows ear^{-1}.

No. of rows ear^{-1} has no significant correlation with other traits under study, while previous workers recorded significant correlation between No. of row ear^{-1} and kernels yield plant^{-1} (Trifunovic, 1988; Ivakhnenko and Klimov, 1991; Singh and Singh, 1993; Singh *et al.*, 1995, and Kumar and Kumar, 2000).

Highly significant and positive correlation (0.583**) was observed between No. of kernels row^{-1} and kernels weight row^{-1}, while has significant and positive correlation (0.505**) with kernels yield plant^{-1}

Kernels weight row^{-1} has positive and highly significant correlations (0.669** and 0.553**) with kernel weight ear^{-1} and 300-kernels weight respectively, while has a positive and significant correlation (0.399*) with kernels yield plant^{-1}. This is agreeing with a previous work of Annapurna *et al.* (1998) , Khatun *et al.*(1999) and Mani *et al.* (1999), while disagree with Gautam *et al.* (1999a).

A positive and significant correlation (0.462*) was observed between kernel weight ear^{-1} and 300-kernels weight.

Kernels yield plant^{-1} has no significant correlation with most of the characters under study, but it has significant and positive correlation with cob weight, No. of kernels row^{-1}, and kernels weight row^{-1}. But previous workers recorded that kernels yield plant^{-1} has significant and positive correlation with No. of kernel row^{-1} (Mahajan *et al.*,1990; Singh and Singh, 1993; Kumar and Mishra, 1995; Singh *et al.*, 1995; Agrama, 1996; Annapurna *et al.*, 1998; Arias *et al.*, 1999; Gautam *et al.*,1999 b; Khatun *et al.*, 1999; Mani *et al.*, 1999; Geetha and Jayaraman, 2000, and Kumar and Kumar, 2000).

Table 59. Correlation among all pairs of traits at Qlyasan location

Traits	Days to 50 % Tasseling	Days to 50 % silking	Plant height (cm)	Ear height (cm)	Cob weight (g)	Cob length (cm)	Cob width (cm)	No. of ears plant^{-1}	No. of rows ear^{-1}	No. of kernels row^{-1}	Kernels weight row^{-1} (g)	Kernels weight ear^{-1} (g)	300-kernels weight (g)
Days to 50 % silking	0.861**												
Plant height (cm)	0.180	0.240											
Ear height (cm)	0.130	0.150	0.426*										
Cob weight (g)	-0.586**	-0.642**	-0.040	0.130									
Cob length (cm)	-0.402*	-0.240	-0.090	0.250	0.492*								
Cob width (cm)	-0.090	-0.110	0.130	0.070	0.170	0.000							
No. of ears plant^{-1}	-0.320	-0.503*	-0.200	-0.030	0.576**	0.090	-0.030						
No. of rows ear^{-1}	-0.100	-0.130	0.170	0.200	-0.010	-0.040	0.497*	-0.190					
No. of kernels row^{-1}	-0.483*	-0.300	0.250	0.190	0.260	0.310	0.180	-0.030	0.090				
Kernels weight row^{-1} (g)	-0.250	-0.310	-0.030	0.060	0.250	0.250	0.060	-0.030	-0.170	0.583**			
Kernels weight ear^{-1} (g)	0.020	-0.130	0.100	0.140	0.220	0.120	0.260	0.010	0.070	0.290	0.669**		
300-kernels weight (g)	0.070	-0.150	-0.150	0.180	0.170	0.280	-0.170	-0.020	-0.360	-0.120	0.553**	0.462*	
Kernels yield plant^{-1} (g)	-0.130	-0.260	0.040	0.120	0.431*	0.390	0.160	**0.260**	**-0.060**	**0.505***	**0.399***	**0.350**	**0.180**

***. Correlation is significant at the 0.01 level (2-tailed) ,* $t_{0.01}(23)=2.807$

**. Correlation is significant at the 0.05 level (2-tailed) ,* $t_{0.05}(23)=2.068$

Path Coefficient Analysis For Some Yield Related Traits

Table (60) shows the path coefficient analysis confirming direct and indirect effects on kernels yield plant^{-1} at Kanipanka location. The maximum positive direct effect on kernels yield plant^{-1} was obtained by the traits kernels weight ear^{-1} (0.606) confirm the positive contribution of this traits on kernel yield plant^{-1} , followed by No. of ears plant^{-1} with (0.366) and No. of kernels row^{-1} with (0.223), while kernels weight row^{-1} and 300-kernels weight recorded negative direct effect on kernels yield plant^{-1} with -0.059 and -0.030 respectively.

No. of kernels row^{-1} had the maximum positive indirect effect on kernels yield plant^{-1} via kernels weight ear^{-1} with (0.407), while have negative indirect effect via No. of ears plant^{-1} (-0.020) and kernels weight row^{-1} (-0.004).

No. of rows ear^{-1} recorded positive indirect effect on kernels yield plant^{-1} via kernels weight ear^{-1} (0.323), while the negative indirect effect of this traits was via No. of ears plant^{-1} (-0.101).

Kernels weight row^{-1} recorded positive indirect effect on kernels yield plant^{-1} via No. of ears plant^{-1} with (0.194) and kernels weight ear^{-1} possessed positive indirect effect on kernels yield plant^{-1} via No. of kernels row^{-1} (0.150).

300-kernels weight showed highest negative indirect effect on kernels yield plant^{-1} via No. of ears plant^{-1} (-0.132).

Table 60. Path coefficient analysis confirming direct (diagonal values) and indirect on Kernels yield plant^{-1} at Kanipanka location.

Traits	No. of ears plant^{-1}	No. of rows ear^{-1}	No. of kernels row^{-1}	Kernels weight row^{-1} (g)	Kernels weight ear^{-1} (g)	300-kernels weight (g)	Kernels yield plant^{-1} (g) *Correlation*
No. of ears plant^{-1}	**0.366**	-0.001	-0.012	-0.031	0.017	0.011	0.350 $^{n.s}$
No. of rows ear^{-1}	-0.101	**0.004**	0.138	0.003	0.323	0.002	0.370 $^{n.s}$
No. of kernels row^{-1}	-0.020	0.002	**0.223**	-0.004	0.407	0.002	0.610 **
Kernels weight row^{-1} (g)	0.194	-0.0002	0.016	**- 0.059**	0.087	0.020	0.258 $^{n.s}$
Kernels weight ear^{-1} (g)	0.010	0.002	0.150	-0.008	**0.606**	0.002	0.758 **
300-kernels weight (g)	-0.132	-0.0003	-0.015	0.040	0.035	**- 0.030**	- 0.102 $^{n.s}$

Table (61) shows the path coefficient analysis showing direct and indirect effects on kernels yield plant^{-1} at Qlyasan location. The maximum positive direct effect on kernels yield plant^{-1} was obtained by the traits No. of kernels row^{-1} (0.686) confirm the positive contribution of this traits on kernel yield plant^{-1}, followed by 300-kernels weight (0.340), No. of ears plant-1 (0.268), and kernel weight ear-1 (0.218) while kernels weight row^{-1} has maximum negative direct effect (-0.330) on kernels yield plant^{-1} . Parh *et al.* (1986); Dash *et al.* (1992); Han *et al.* (1994); Rahman *et al.* (1995); Packiaraj (1995); Gautam *et al.* (1999b); Arias *et al.* (1999); Khatun *et al.* (1999); Geetha and Jayaraman (2000); Venugopal *et al.* (2003); Bao Heping *et al.* (2004); Kumar *et al.* (2006); Sofi and Rather (2007); Xie Zhen Jiang *et al.* (2007); Abirami *et al.* (2007), and Akbar *et al.* (2008) reported previously that maize yield was mainly influenced positively by No. of kernels row^{-1}, No. of rows ear^{-1}, and 300-kernels weight has appositive direct effect on kernels yield plant^{-1}.

Kernels weight row^{-1} possessed the maximum positive indirect effect on kernels yield plant^{-1} via No. of kernels row^{-1} (0.400), while negative indirect effect was via No. of ears plant^{-1} (-0.008).

Kernels weight ear^{-1} recorded positive indirect effect on kernels yield plant^{-1} via No. of kernels row^{-1} with (0.196) and No. kernels row^{-1} possessed positive indirect effect on kernels yield plant^{-1} via kernels weight row^{-1} (0.192).

In contrary to these results, Trifunovic (1988); Ivakhnenko and Klimov (1991); Singh and Singh (1993); Han *et al.* (1994); Singh *et al.* (1995), and Kumar and Kumar (2000) suggested previously that indirect selection for kernel yield through No. of rows ear^{-1} would be effective.

Table 61. Path coefficient analysis confirming direct (diagonal values) and indirect effects on Kernels yield plant^{-1} at Qlyasan location.

Traits	No. of ears plant^{-1}	No. of rows ear^{-1}	No. of kernels row^{-1}	Kernels weight row^{-1} (g)	Kernels weight ear^{-1} (g)	300-kernels weight (g)	Kernels yield plant^{-1} (g) ***Correlation***
No. of ears plant^{-1}	**0.268**	0.004	-0.019	0.010	0.002	-0.007	0.260 $^{n.s}$
No. of rows ear^{-1}	-0.051	**-0.020**	0.063	0.057	0.015	-0.122	- 0.060 $^{n.s}$
No. of kernels row^{-1}	-0.008	-0.002	**0.686**	0.192	0.062	-0.041	0.505 *
Kernels weight row^{-1} (g)	-0.008	0.003	0.400	**-0.330**	0.146	0.188	0.399 *
Kernels weight ear^{-1} (g)	0.003	-0.001	0.196	-0.221	**0.218**	0.157	0.350 $^{n.s}$
300-kernels weight (g)	-0.006	0.007	-0.084	-0.182	0.101	**0.340**	0.180 $^{n.s}$

CONCLUSIONS

The following conclusions can be drawn from the present study:

- Analysis of variance confirmed highly significant differences among genotypes for kernel yield and most of its components.
- Parents (*MIS 4279*) and (*ZP 434*) possessed the best values for kernel yield and most of its components.
- The best yield values and some of its components were obtained by the diallel cross (*ZP 434* x *5012*).
- Maximum kernel yield and some of the most important components exhibited by the reciprocal cross (*MIS 4279*x *MIS 4218*).
- Parents (*MIS 4279*) and (*5012*) possessed the best general combiner for kernel yield and all of its components.
- The diallel crosses participated with parent (*5012*) showed the best reciprocal combiner towards increasing kernel yield and most of its components.
- The reciprocal cross (*5012*x *ZP 434*) possessed the best specific combiner for kernel yield and almost all of its components.
- The percentages of maternal effects for all studied characters were obviously noticed positively or negatively in reciprocal crosses.
- The controlling of non-additive gene action was observed obviously in almost all of the studied characters in their inheritance.
- Kernel yield plant^{-1} revealed positive and significant correlation with No. of kernels row^{-1} and kernel weight row^{-1} at Kanipanka location, and with cob weight, No. of kernels row^{-1}, and kernel weight row^{-1} at Qlyasan location.
- Path coefficient analysis indicated that the characters kernel weight ear^{-1}, No. of ears plant^{-1}, and No. of kernels row^{-1} at Kanipanka location, and the characters No. of kernels row^{-1}, 300-kernels weight, No. of ears plant^{-1}, and kernel weight ear^{-1} at Qlyasan location, exerted high positive direct effect on kernel yield plant^{-1}.

RECOMMENDATIONS

According to our results in this study, the following recommendations can be laid:

- Further and complementary breeding programs are needs for this crop to produce some suitable hybrids for Kurdistan region, and progress in genetic improvement of the yielding ability of maize hybrids may be attempt through such yield related characters.
- Attempting to obtain new genetic materials through inbred lines and varieties from different sources and introducing them to breeding programs in order to improving maize productivity in our region.
- It recommends that Qlyasan location is better than Kanipanka to grow during spring season because of the suitability of the environmental condition of this location to produce a desirable yield.
- Results obtained showed that most of the created crosses possess a good yield ability, survival to climatical conditions prevailing in Qlyasan location.

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Appendix 1. The meteorological data of both locations

Kanipanka Location

Year	*Months*	*Air temperature °C*			*RH %*	*Precipitation Depth (mm)*	*Average Sunshine Duration (Hours)*	*ETo (mm)*
		avg.	*max.*	*Min.*				
2009	*Oct.*	23.7	30.3	17.2	30.3	80.2	7.8	5.7
	Nov.	13.1	17.2	9.0	58.8	145.6	5.5	1.8
	Dec.	9.7	13.2	6.3	62.4	97.1	4.1	1.0
2010	*Jan.*	10.3	14.3	6.2	55.3	71.8	5.1	1.4
	Feb.	*10.0*	14.0	5.6	58.7	91.2	5.0	1.6
	Mar.	*15.1*	19.9	10.2	50.4	125.9	5.3	3.3
	Apr.	*17.3*	23.0	11.9	51.3	146.3	6.7	4.3
	May	*24.2*	30.5	17.9	37.4	99.1	7.5	7.1
	Jun.	*32.8*	40.1	25.4	24.8	3.8	10.3	12.6

Qlyasan Location

Year	*Months*	*Air temperature °C*			*RH %*	*Precipitation Depth (mm)*	*Average Sunshine Duration (Hours)*	*ETo (mm)*
		avg.	*max.*	*Min.*				
2009	*Oct.*	22.5	28.9	16.1	38.6	72.9	7.6	4.2
	Nov.	13.2	17.5	8.8	68.3	136.4	5.2	2.4
	Dec.	9.9	13.4	6.3	76.0	98.3	3.3	1.3
2010	*Jan.*	10.3	14.3	6.3	69.0	69.0	4.1	1.7
	Feb.	10.3	14.4	6.1	69.0	161.9	4.0	1.6
	Mar.	14.8	19.5	10.0	58.0	93.2	4.5	2.5
	Apr.	17.5	22.6	12.4	62.0	77.1	5.9	3.5
	May	23.0	28.7	17.6	46.0	80.8	7.1	6.0
	Jun.	31.0	37.0	25.2	26.0	0.0	9.9	9.3

* Total precipitation = (861.0 and 789.6) for Kanipanka and Qlyasan respectively.

* Total ET_O = (38.8 and 32.5) for Kanipanka and Qlyasan respectively.

Appendix 2. Physical & chemical properties of soil at both locations

Soil Properties		Kanipanka	Qlyasan
P.S.D		Clay	Silty loam
Sand (gm Kg^{-1})		41.6	116.3
Silt (gm Kg^{-1})		429.2	640.9
Clay (gm Kg^{-1})		529.2	240.8
E.C. (dS m^{-1})		0.54	0.41
pH		7.64	7.63
Organic Matter (gm Kg^{-1})		27.8	19.18
Total Nitrogen (mg Kg^{-1})		1.03	1.02
Available Phosphate (mg Kg^{-1}) Soil		5.45	4.49
$CaCO_3$ (gm Kg^{-1})		119.4	273.5
Soluble Cations & Anions mmole L^{-1}	Calcium (Ca^{+2})	1.72	1.62
	Potassium (K^{+})	0.16	0.39
	Sodium (Na^{+})	0.46	0.44
	Carbonate ($CO_3^{=}$)	0.00	0.00
	Bicarbonate ($HCO_3^{=}$)	2.99	2.88
	Chloride (Cl^{-})	0.48	0.45
	Sulphate ($SO_4^{=}$)	0.83	0.81

These analyses were carried out at Soil and Water Sciences Department, Faculty of Agricultural Science, University of Sulaimani.

Appendix 3. Mean squares of variance analysis for genotypes, general and specific combining ability and of the parents for the studied characters at Kanipanka location

Source of Variation	***Replication***	***Genotypes***	***GCA***	***SCA***	***RCA***	***σ^2e***	***GCA / SCA***	***GCA / RCA***	***MSé***
d.f ***Characters***	2	24	4	10	10	48			
Days to 50 % tasseling	1.453	1.981**	1.797**	0.261 $^{n.s}$	0.606*	0.689	6.893	2.967	0.230
Days to 50 % silking	6.653	4.514**	4.563**	0.758 $^{n.s}$	1.028*	1.514	6.017	4.440	0.505
Plant height (cm)	1575.093	812.998**	279.258 $^{n.s}$	305.623**	233.072*	327.496	0.914	1.198	109.165
Ear height (cm)	23.480	187.302**	131.207**	54.903*	42.456 $^{n.s}$	64.387	2.390	3.090	21.462
Stem diameter (cm)	0.147	0.157*	0.049 $^{n.s}$	0.073**	0.033 $^{n.s}$	0.077	0.675	1.503	0.026
Cob Weight (g)	69.367	254.146**	131.154**	92.206**	58.649*	65.071	1.422	2.236	21.690
Cob Length (cm)	4.060	3.868 $^{n.s}$	1.794 $^{n.s}$	1.340 $^{n.s}$	1.037 $^{n.s}$	2.749	1.339	1.730	0.916
Cob Width (cm)	0.051	0.049*	0.042**	0.009 $^{n.s}$	0.013 $^{n.s}$	0.023	4.838	3.148	0.008
No. of ears plant $^{-1}$	0.153	0.330**	0.253**	0.109*	0.054 $^{n.s}$	0.139	2.321	4.693	0.046
No. of rows ear $^{-1}$	2.732	10.654**	11.660**	1.273 $^{n.s}$	2.586**	2.446	9.161	4.509	0.815
No. of kernels row $^{-1}$	85.860	88.021*	66.440**	17.757 $^{n.s}$	26.084 $^{n.s}$	42.807	3.742	2.547	14.269
Kernel weight row $^{-1}$(g)	5.387	12.445**	4.762**	6.637**	1.415 $^{n.s}$	2.528	0.718	3.366	0.843
Kernel weight ear $^{-1}$ (g)	407.97	1116.248**	674.600**	206.158**	417.000**	210.590	3.272	1.618	70.197
300 – kernels weight (g)	72.787	182.517*	52.803 $^{n.s}$	64.734*	60.159 $^{n.s}$	92.988	0.816	0.878	30.996
Kernel yield plant $^{-1}$ (g)	440.536	4872.363**	1349.186 $^{n.s}$	1653.778**	1704.439**	1727.925	0.816	0.792	575.975

$F_{0.05}(4,48) = 2.565$, $F_{0.05}(10,48) = 2.035$, $F_{0.05}(24,48) = 1.746$
$F_{0.01}(4,48) = 3.737$, $F_{0.01}(10,48) = 2.715$, $F_{0.01}(24,48) = 2.201$

Appendix 4. Mean squares of variance analysis for genotypes, general and specific combining ability and of the parents for the studied characters at Qlyasan location

Source of Variation	***Replication***	***Genotypes***	***GCA***	***SCA***	***RCA***	***σ^2e***	***GCA / SCA***	***GCA / RCA***	***MSé***
d.f ***Characters***	2	24	4	10	10	48			
Days to 50 % tasseling	2.253	7.861**	10.356**	0.736 $^{n.s}$	1.411*	1.698	14.079	7.339	0.566
Days to 50 % silking	2.520	6.500**	8.094**	0.551 $^{n.s}$	1.411**	1.437	14.688	5.736	0.479
Plant height (cm)	386.893	196.103**	103.213*	39.720 $^{n.s}$	75.878*	87.893	2.599	1.360	29.298
Ear height (cm)	618.059	183.385**	105.484**	47.038 $^{n.s}$	57.476*	71.345	2.243	1.835	23.782
Stem diameter (cm)	0.190	0.110**	0.035*	0.041**	0.033**	0.035	0.858	1.087	0.012
Cob Weight (g)	1559.560	124.785*	54.621*	45.355*	32.625 $^{n.s}$	63.145	1.204	1.674	21.048
Cob Length (cm)	6.955	6.754$^{n.s}$	1.795 $^{n.s}$	1.941 $^{n.s}$	2.744 $^{n.s}$	5.457	0.925	0.654	1.819
Cob Width (cm)	0.018	0.045 $^{n.s}$	0.035*	0.011 $^{n.s}$	0.011 $^{n.s}$	0.029	3.090	3.178	0.010
No. of ears plant $^{-1}$	1.636	0.085 $^{n.s}$	0.030 $^{n.s}$	0.024 $^{n.s}$	0.033 $^{n.s}$	0.069	1.254	0.905	0.023
No. of rows ear $^{-1}$	2.145	5.984**	4.100**	2.359**	0.789 $^{n.s}$	2.254	1.738	5.197	0.751
No. of kernels row $^{-1}$	49.875	44.104 $^{n.s}$	24.047 $^{n.s}$	12.688 $^{n.s}$	12.976 $^{n.s}$	36.646	1.895	1.853	12.215
Kernel weight row $^{-1}$(g)	13.785	4.022*	0.867 $^{n.s}$	0.991 $^{n.s}$	1.880*	2.246	0.874	0.461	0.749
Kernel weight ear $^{-1}$ (g)	928.177	1891.116 **	188.900 $^{n.s}$	798.391**	638.942**	350.755	0.237	0.296	116.918
300 – kernels weight (g)	372.399	141.907*	111.564**	29.087 $^{n.s}$	39.813 $^{n.s}$	77.345	3.836	2.802	25.782
Kernel yield plant $^{-1}$ (g)	19079.167	3051.418*	760.290 $^{n.s}$	1527.440**	609.578 $^{n.s}$	1582.941	0.498	1.247	527.647

$F_{0.05}(4,48) = 2.565$, $F_{0.05}(10,48) = 2.035$, $F_{0.05}(24,48) = 1.746$
$F_{0.01}(4,48) = 3.737$, $F_{0.01}(10,48) = 2.715$, $F_{0.01}(24,48) = 2.201$

تحليل التهجينات التبادلية الكاملة للذرة الصفراء
(*Zea mays* L.)

إطروحة مقدمة الى مجلس فاكلتي العلوم الزراعية في جامعة السليمانية
كجزء من متطلبات نيل درجة دكتوراه فلسفة
في العلوم الزراعية / *المحاصيل الحقلية*
(تربية النبات و الوراثة)

تقدم بها
دانا ئازاد عبدالخالق بشدەري
بكالوريوس في المحاصيل الحقلية/ كلية الزراعة/ جامعة السليمانية (1997).
ماجستير في المحاصيل الصناعية/ كلية الزراعة/ جامعة السليمانية (2006).

بإشراف
الأستاذ المساعد د. شيروان إسماعيل توفيق

27 **ذي الحجة** 1432 **هـ**
2 **سەرماوەرز** 2711 **ك**
November 23rd, 2011

الخلاصة

أُجريت تصميم التضريب التبادلي من ضمنها التهجينات المتعاكسة خلال الموسم الربيعي 2009 لأنتاج 20 هجيناً من الذرة الصفراء بإستخدام نظام (5X5) جميع الهجن التبادلية و المتعاكسة و آبائها أُدخلت في تجربة مقارنة في الموسم الخريفي 2010 في موقعين من محافظة السليمانية هما كاني بانكة و قلياسان بإستخدام تصميم القطاعات العشوائية الكاملة CRBD و بثلاث مكررات.

ظهرت فروقات معنوية بين التراكيب الوراثية (الآباء و الهجن) لجميع الصفات عدا صفة طوا العرنوص في منطقة كاني بانكة و الصفات طول العرنوص، عرض العرنوص، عدد العرنيص / نبات، و عدد الحبوب / خط في منطقة قلياسان.

في منطقة كاني بانكة، أضهرت التحليلات الوراثية بأن القابلية العامة على الأئتلاف (GCA) قد كانت معنوية لمعظم الصفات عدا الصفات إرتفاع النبات، طول العرنوص، وزن 300 حبة، و وزن الحبوب/ نبات و التي ظهرت عدم معنويتها. مجموع المربعات للقابلية الخاصة على الأئتلاف (SCA) كانت معنوية للصفات إرتفاع النبات، وزن العرنوص، عدد العرانيص / نبات، وزن الحبوب / خط، وزن الحبوب / عرنوص، وزن 300 حبة، و حاصل الحبوب / نبات. القابلية المتعاكسة على الأئتلاف (RCA) كانت معنوية للصفات الأيام اللازمة حتى 50٪ تزهير ذكري، الأيام اللازمة حتى 50٪ تزهير أنثوي ،إرتفاع النبات، وزن العرنوص، سمك العرنوص، عدد الخطوط / عرنوص، و وزن 300 حبة.

بالنسبة لمنطقة قلياسان، مجموع مربعات القابلية العامة على الإئتلاف (GCA) كانت معنوية للصفات الأيام اللازمة حتى 50٪ تزهير ذكري، الأيام اللازمة حتى 50٪ تزهير إنثوي، إرتفاع النبات، إرتفاع العرنوص، وزن العرنوص، سمك العرنوص،عدد الخطوط/عرنوص، و وزن 300 حبة. والفروقات أظهرت عدم معنويتها بالنسبة للصفات طول العرنوص، عدد العرانيص/نبات، عدد الحبوب/خط، وزن الحبوب/عرنوص، وزن الحبوب/خط، حاصل الحبوب/نبات. قدرة الإئتلاف الخاصة (SCA) كانت معنوية للصفات وزن العرنوص، عدد الخطوط/عرنوص، وزن الحبوب/عرنوص، حاصل الحبوب/نبات. ظهرت مجموع مربعات معنوية لقدرة الإئتلاف المتعاكسة (RCA) للصفات الأيام اللازمة حتى 50٪ تزهير ذكري، إرتفاع النبات، إرتفاع العرنوص، وزن الحبوب/خط، و وزن الحبوب/عرنوص، ولم تكن معنوية للصفات الأخرى.

في منطقة كانى بانكة، أعطى التضريب (ZP434 x MIS43100) أحسن قيمة بالنسبة للصفات الأيام اللازمة حتى 50٪ تزهير ذكري، طول العرنوص، والتضريب (ZP 434 x 5012) للصفات الأيام اللازمة حتى 50٪ تزهير إنثوي، عدد الحبوب/خط، والتضريب MSI43100 x MSI4279) للصفات إرتفاع النبات و وزن العرنوص، والتضريب (5012 x MIS43100) لصفة إرتفاع العرنوص، والتضريب (5012 x MIS4279) لصفة سمك العرنوص، والتضريب (MIS4218 x MIS4279) لصفة وزن الحبوب/خط، التضريب (ZP434 x MIS4279) لصفة عدد الخطوط/عرنوص، التضريب (MIS4279 x MIS4218) للصفات عدد العرانيص/نبات، وزن الحبوب/عرنوص، وحاصل الحبوب/نبات، التضريب (MIS4218 x MIS43100) لصفة وزن 300 حبة.

في منطقة قلياسان، أعطى التضريب (ZP434 x MIS43100) أحسن قيمة بالنسبة للصفات الأيام اللازمة حتى 50٪ تزهير ذكري، وزن العرنوص، طول العرنوص. التضريب (MIS4279 x ZP434) لصفة الأيام اللازمة حتى 50٪ تزهير إنثوي، التضريب (MIS43100 x 5012) لصفة إرتفاع النبات، التضريب

(MIS4218 x MIS43100) لصفة إرتفاع العرنوص، التضريب (5012 x MIS4279) لصفات سمك العرنوص وحاصل الحبوب/نبات، التضريب (5012 x ZP434) لصفة عدد العرانيص/نبات، والتضريب (5012 x MIS4218) لصفة عدد الخطوط/عرنوص، والتضريب (5012 x MIS4279) لصفة عدد الحبوب/خط، والتضريب (MIS43100 x MIS4279) لصفة وزن الحبوب/خط، والتضريب (MIS4218 x 5012) لصفة وزن الحبوب/عرنوص، التضريب (MIS43100 x ZP434) لصفة وزن 300 حبة.

النسبة بين إختلاف القدرة العامة على الإئتلاف وإختلاف القدرة الخاصة على الإئتلاف ($\sigma^2_{GCA}/\sigma^2_{SCA}$) كانت أقل لمعضم الصفات ولكلا الموقعين من واحد مما يدل على تأثير فعل الجين غير الإضافية على توريث هذه الصفات. وكان معدل درجة السيادة لهذه الصفات أكبر من واحد عدا الصفات الأيام اللازمة حتى 50٪ تزهير ذكري، الأيام اللازمة حتى 50٪ تزهير إنثوي، سمك العرنوص، عدد الحبوب/خط في كلا الموقعين، عدد الخطوط/عرنوص في منطقة كاني بانكة، وعدد العرانيص/نبات، و وزن 300 حبة في منطقة قلياسان.

كانت نسبة التوريث بمداه الواسع ذو نتائج متوسطة الى مرتفعة مما يدل على أن نسبة كبيرة من الصفات المظهرية يرجع الى التأثيرات الوراثية. لكن نسبة التوريث بمداه الضيق كانت ذو نتائج منخفضة الى متوسطة لحوالي معضم الصفات في كلا المنطقتين.

كانت هنالك علاقة موجبة ومعنوية بين صفة حاصل الحبوب/نبات والصفات عدد الحبوب/خط و وزن الحبوب/عرنوص في كلا المنطقتين ومع وزن العرنوص في منطقة كاني بانكة فقط، كما لم يوجد أي إرتباط معنوي مع باقي الصفات المدروسة.

أضهرت نتائج تحليل المسار بأن وزن الحبوب / عرنوص، عدد العرانيص/نبات و عددالحبوب/خط كانت لهم تاثير مباشر و عالي على حاصل الحبوب/ نبات في منطقة كاني بانكة ،بينما في منطقة قلياسان عدد الحبوب/خط، وزن 300 حبة ،عدد العرانيص/ نبات و وزن الحبوب/ عرنوص أضهرت تاثيراً عالياً و مباشراً على حاصل الحبوب/ نبات ، و عليه بالامكان إستخدام هذه الصفات كمعايير انتخابية و التي تعتبر كمكونات اساسية للحاصل ولتحسين حاصل الحبوب.

شیکردنەوەی لێکدانی دووانە ئەلیلی تەواو لە گەنمەشامیدا (*Zea mays* L.)

ئەم تێزەیە پێشکەش کراوە بە ئە نجوومەنی فاکەڵتی زانستە کشتوکاڵیەکان لە
زانکۆی سلێمانی وەك بەشێك لە پێداویستییەکانی بەدەستهێنانی
پلەی دکتورا فەلسەفە
لە زانستە کشتوکاڵیەکاندا / بەروبوومی کێڵگەیی
(پەروەردەکردنی رووەك و بۆماوەزانی)

لەلایەن

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بەکالۆریۆس لە بەروبوومی کێڵگەیی/ کۆلێجی کشتوکاڵ/ زانکۆی سلێمانی (1997).
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بە سەرپەرشتی

پرۆفیسۆری یاریدەدەر د. شیروان ئیسماعیل توفیق

November 23rd, 2011 2 **سەرماوەرز** 2711 **ك** 27 **ذي الحجة** 1432 **هـ**

کورتە

بەرنامەی لێکدانی دووانە ئەلیلی تەواو ئە نجامدرا لەماوەی وەرزی بەهاری 2009 بۆ بەرهەمهێنانی 20 دوو ڕەگ لە گە نمەشامی بەبەکارهێنانی سستمی (5X5) هەریەك لە دووڕەگە دوانە ئەلیلەکان و دوو ڕەگە پێچەوانەییەکان و باوکەکانیان هەڵسەنگێندران لەوەرزی پایزی 2010 دا لە دووشوێنی ناوچەی سلێمانی کەئەوانیش کانی پانکەو قلیاسانن بەبەکارهێنانی دیزاینی بلۆکە هەڕەمەکییە تەواوەکان CRBD بە سێ دووبارە بوونەوە.

جیاوازی واتادار دەرکەوت لەنێوان پێکهاتە بۆماوەییەکان دا (باوکەکان و دووڕەگەکانیان) بۆ هەموو سیفەتەکان جگە لە سیفەتی درێژی کۆز لەناوچەی کانی پانکە و سیفەتەکانی درێژی کۆز , پانی کۆز , ژمارەی کۆز / رووەك، و ژمارەی تۆو / ریز دا لەناوچەی قلیاسان. لەناوچەی کانی پانکە، شیکارە بۆماوەییەکان دەریا نخست کە توانای یەکگرتنی گشتی(GCA) واتادار بوو بۆ زۆربەی سیفەتەکان جگە لە بەرزی رووەك، درێژی کۆز، کێشی 300 تۆو، کێشی تۆو/ رووەك دا کە دەرکەوتن واتادار نین. دوجای ناوەندەکان بۆ توانای یەکگرتنی تایبەت (SCA) واتاداربوون بۆ سیفەتەکانی بەرزی رووەك، کێشی کۆز، ژمارەی کۆز/ رووەك، کێشی تۆو/ ریز، کێشی تۆو/ کۆز، کێشی 300 تۆو،و بەرهەمی تۆو / رووەك. تێکرای توانای یەکگرتنی پێچەوانەیی (RCA) واتاداربوو بۆ سیفەتەکانی رۆژ بۆ 50٪ گوڵی نێرە، رۆژ بۆ 50٪ گوڵی مێیە، بەرزی رووەك، کێشی کۆز، پانی کۆز، ژمارەی ریزە / کۆز، و کێشی 300 تۆو.

سەبارەت بەناوچەی قلیاسان ، دوجای ناوەندەکان بۆ توانای یەکگرتنی گشتی (GCA) واتاداربوو بۆ سیفەتەکانی رۆژ بۆ 50٪ گوڵی نێرە، رۆژ بۆ 50٪ گوڵی مێیە، بەرزی رووەك، بەرزی کۆز، کێشی کۆز ، پانی کۆز ، ژمارەی ریز/ کۆز، کێشی 300 تۆو . بەڵام سیفەتەکانی درێژی کۆز ، ژمارەی کۆز / رووەك ، ژمارەی تۆو/ ریز، کێشی تۆو/کۆز ، کێشی تۆو/ ریز، و بەرهەمی تۆو/ رووەك، جیاوازی واتادارنەبوونیان پیشاندا. توانای یەکگرتنی تایبەت (SCA) واتاداربوو بۆ سیفەتەکانی کێشی کۆز ، ژمارەی ریز/ کۆز، کێشی تۆو/کۆز، و بەرهەمی تۆو/ رووەك. دووجای ناوەندی واتادار بۆ توانای یەکگرتنی پێچەوانەیی (RCA) دەرکەوت بۆ سیفەتەکانی رۆژ بۆ 50٪ گوڵی نێرە، بەرزی رووەك، بەرزی کۆز، کێشی تۆو/ریز، کێشی تۆو/ کۆز بەڵام واتادارنەبوو بۆ سیفەتەکانی تر.

لەناوچەی کانی پانکە، دووڕەگی (ZP434 x MIS43100) باشترین بەهای بەدەستهێناوە بۆ سیفەتەکانی رۆژ بۆ 50٪ گوڵی نێرە، درێژی کۆز ، دووڕەگی (ZP 434 x 5012) بۆ سیفەتەکانی رۆژ بۆ 50٪ گوڵی مێیە، ژمارەی تۆو/ ریز، دورەگی (MSI43100 x MSI4279) بۆ سیفەتەکانی بەرزی رووەك و کێشی کۆز. دووڕەگی (5012 x MIS43100) بۆ سیفەتی بەرزی کۆز، دوورەگی (5012 x MIS4279) بۆ سیفەتی پانی کۆز، دوورەگی (MIS4218 x MIS4279) بۆ سیفەتی کێشی تۆو/ ریز، دووڕەگی (ZP434 x MIS4279) بۆ سیفەتی ژمارەی ریز/کۆز، دوورەگی (MIS4279 x MIS4218) بۆ سیفەتەکانی ژمارەی کۆز / رووەك، کێشی تۆو/ کۆز، و بەرهەمی تۆو/ رووەك، دووڕەگی (MIS4218 x MIS43100) بۆ سیفەتی کێشی 300 تۆو.

لە ناوچەی قلیاسان، باشترین بەها بەدەست هات لەنێوان دوورەگی (ZP434 x MIS43100) بۆ سیفەتەکانی رۆژ بۆ 50٪ گوڵی نێرە، کێشی کۆز ، درێژی کۆز. هەروەها دوورەگی (MIS4279 x ZP434) بۆ سیفەتی رۆژ بۆ 50٪ گوڵی مێیە، دوورەگی (5012 x MIS43100) بۆ سیفەتی بەرزی رووەك، دوورەگی (MIS4218 x MIS43100) بۆ سیفەتی بەرزی کۆز، دوورەگی (5012 x MIS4279) بۆ سیفەتەکانی پانی کۆز و بەرهەمی تۆو/ رووەك، دوورەگی (ZP434 x 5012) بۆ سیفەتی ژمارەی کۆز/ رووەك ، دوورەگی (5012 x MIS4218) بۆ سیفەتی ژمارەی ریز / کۆز، دوورەگی (MIS4279 x 5012) بۆ سیفەتی ژمارەی تۆو/ ریز، دوورەگی (MIS43100 x MIS4279) بۆ سیفەتی کێشی تۆو / ریز، دوورەگی (MIS4218 x 5012) بۆ سیفەتی کێشی تۆو/کۆز، دوورەگی (MIS43100 x ZP434) بۆ سیفەتی کێشی 300 تۆو.

رێژەی جیاوازی توانای یەکگرتنی گشتی بۆ جیاوازی توانای یەکگرتنی تایبەت ($\sigma^2_{GCA}/\sigma^2_{SCA}$) کەمتر بووە لە یەك بۆ نزیکەی زۆربەی سیفەتەکان لەهەردوو ناوچەکەدا کەئەمەش نیشانەیە بۆ گرنگی کاریگەری جینە کەڵەکەنەبووەکان لەبۆماوەیی ئەم سیفەتانە. هەروەها پلەی زاڵبوونی ئەم سیفەتانە لە یەك زۆرتر بووە جگە لەسیفەتەکانی رۆژ بۆ 50٪ گوڵی نێرە، رۆژ بۆ 50٪ گوڵی مێیە، پانی کۆز، ژمارەی تۆو/ ریز لەهەردوو ناوچەکە دا، ژمارەی ریز/ کۆز لەناوچەی کانی پانکە، و ژمارەی کۆز/ رووەك و کێشی 300 تۆو لەناوچەی قلیاسان.

رێژەی بۆماوەیی بەمانی فراوان ئەنجامێکی ناوەند بۆ بەرزی هەبووە، ئەمەش نیشانەی ئەوەیە کە رێژەیەکی گەورە لەبەها روخسارییەکان دەگەڕێتەوە بۆ کاریگەرە بۆماوەییەکان. بەڵام رێژەی بۆماوەیی بەمانی تەسك ئەنجامێکی کەم بۆ ناوەندی هەبووە بۆ نزیکەی زۆربەی سیفەتەکان لەهەردوو ناوچەکەدا.

بەرهەمی تۆو / رووەك پەیوەندییەکی واتادارو پۆزەتیڤی هەبووە بەسیفەتەکانی ژمارەی تۆو/ ریز، کێشی تۆو/ کۆز لەهەردوو ناوچەکە دا و لەگەڵ کێشی کۆز لەناوچەی کانی پانکە بەتەنها، هیچ پەیوەندییەکی واتاداری نەبووە بە سیفەتەکانی ترەوە.

ئەنجامەکانی شیکردنەوەی رێڕەو (Path Analysis) دەریخست کە سیفەتەکانی کێشی تۆو/ کۆز، ژمارەی کۆز/ رووەك ، و ژمارەی تۆو / ریز کاریگەری راستەوخۆ و بەرزیان هەبووە لەسەر بەرهەمی تۆو/ رووەك لە ناوچەی کانی پانکە، بەڵام لە ناوچەی قلیاسان سیفەتەکانی ژمارەی تۆو / ریز، کێشی 300 تۆو، ژمارەی کۆز/ رووەك، و کێشی تۆو / کۆز کاریگەری بەرز و راستەوخۆیان هەبووە لەسەر بەرهەمی تۆو/ رووەك. هەربۆیە دەتوانرێت ئەم سیفەتانە وەك پێوەرێك بۆ هەڵبژاردن بەکاربهێنرێت کە بە پێکهێنەری سەرەکی بەرهەم و چاککردنی بەرهەمی تۆو دادەنرێن.