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ABSTRACT

GENETIC ANALYSIS FOR F₂ GENERATION IN BARLEY USING FULL DIALLEL CROSS SYSTEM IN SULAIMANY-IRAQ

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Five two rowed barley (*Hordeum vulgare L.*) were sown in full diallel cross including reciprocals at Qlyasan research station to produce 20 crosses.

Analysis of Variance for full diallel cross during the winter season of 2014-2015, 25 genotypes (F₂S +5 parents) were sown in a completely randomized block design (CRBD) with three replications at Qlyasan location.

The analysis of variance indicated that the mean squares for genotype and SCA were highly significant for all characters and also it was highly significant for most studied characters due to GCA and RCA mean squares.

Parent 4 and 5 recorded maximum values for most studied characters, while parent 1 and 3 recorded the lowest value for most characters.

The diallel cross 1x2 recorded the highest value for grain weight/plant with 14.640 (g) and its components number of tillers/plant and number of spike/plant with 13.67 and 10.800, while the diallel cross 3x4 gave the highest value for weight of grains/spike , average spike weight and harvest index with 1.633(g), 1.727(g) and 0.546 respectively.

The diallel crosses 1x3, 1x5 and 2x3 exhibited lowest value for most characters. The reciprocal crosses 5x2 and 5x4 gave the highest value for most studied characters. Maximum positive GCA effect values for grain weight/plant with 1.273 and some its components exhibited by parent 4, while parent 1 gave maximum negative GCA effect values for grain weight/plant with -1.136 and some its components.

The cross 2x5 produced the highest positive SCA effect values for grain weight/plant with 2.798 and some its components , and maximum negative SCA effect values for grain weight/plant with -3.196 and most its components produced by the cross 1x5. The cross 2x1 gave the highest positive RCA effect values for grain weight/plant with 2.597 and some its components, while the cross 5x4 gave the highest negative value due to grain weight/plant with -2.572 and some its components. Parent 4 gave the highest value due to the variance of effect of general combining ability for grain weight /plant with 1.61992 and some its components , while parent 2 showed the lowest value due to the

variance of effect of general combining ability for grain weight/plant with 0.00668 and some its components.

Parent 2 exhibited maximum the variance of effect of specific combining ability for diallel crosses for grain weight/plant with 6.312 and most its components, while parent 4 gave the lowest value for the variance of effect of specific combining ability for diallel crosses due to grain weight/plant with 0.390 and most its components. Parent 5 produced the highest the variance of effect of specific combining ability for reciprocal crosses for grain weight/plant with 6.464 and most its components, while parent 2 gave The ratio of the variance of general combining ability/The variance of specific combining ability values were less than unity for all studied characters, while the average degree of dominance values for almost all characters were more than unity, indicating the predominance of non-additive gene effect in the inheritance of these characters.

Heritability in broad sense was found to be high for all characters, while heritability in narrow sense was found to be low to moderate due to all characters, signifying the importance of hybridization method to improve these characters.

The grain weight/plant correlated positively and highly significantly with grain weight/spike, number of spike/plant, number of grains/spike, and biological weight/plant, while correlated positively and significantly with harvest index.

The character number of spike/plant gave the highest positive direct effect in grain weight/plant produced by grain weight/spike via biological weight/plant.

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LIST OF ABBREVIATIONS

Abbreviation	Detail
$\bar{a}$	Average degree of dominance
$\bar{a}r$	Average degree of dominance for reciprocal
G.R	Genotypic Resultant
RCA	Specific combining ability for reciprocal crosses
gi	General combining ability effect
$h^2_{b.s}$	Heritability in broad sense
$h^2_{n.s}$	Heritability in narrow sense
H	Hemostats
MSe	Revised mean squares of experimental error
σ^2_{Dr}	Dominance variance for reciprocal crosses
SCA	Specific combining ability for diallel crosses
ri	Reciprocal combining ability effects
si	Specific combining ability effects
$\sigma^2 P$	Phenotypic variance
$\sigma^2 A$	Additive variance
$\sigma^2 D$	Dominance variance
GCA	General combining ability
$\sigma^2 e$	Mean squares of experimental error or (Environmental variance)
$\sigma^2 GCA (\sigma^2 gi.)$	The variance of effect of general combining ability
$\sigma^2 RCA (\sigma^2 ri.)$	The variance of effect of specific combining ability for reciprocal crosses
$\sigma^2 SCA (\sigma^2 si.)$	The variance of effect of specific combining ability for diallel crosses
$\sigma^2 G$	Genetic variance

1. INTRODUCTION

Barley is considered as one of the first cereals domesticated for use by man as food and feed. It is an important rabi cereal crop grown through the temperate and tropical regions of the world. It occupies the fourth position in terms of acreage and third position in terms of crop production. Barley is cultivated on around 11% of the world's total area under cereal cultivation. (Anonymous, 2007).

Hordeum vulgare L. is a generally distributed genus of the public *Triticeae* by the whole of 45 grade and subspecies, consisting of as is the custom weedy regular or versed grasses adapted to the temperate zones of both the northern and southern hemispheres. Cultivated barley (*Hordeum Vulgare* L. subsp. *vulgare*) is the reality's fourth virtually important hasty pudding crop trailing wheat, rice, and maize.

A particular botanical feature of domesticated barley is that most cultivars have covered (hulled) caryopses in which the hull (outer lemma and inner palea) is firmly adherent to the pericarp epidermis at maturity but a few cultivars are of a free – threshing variant called naked (hull-less) barley. Both caryopsis types of barley have agronomic value and are used for different purposes. Covered barley is mainly used as an animal feed and for brewing whereas naked barley is preferred for human consumption. Since healthy effects of the soluble fiber rich barley products have been officially canonical and consumers, futuristic interest in nutrition might throw in one lot with the how things stack up of barley as cro magnon man food (Manjunatha, et al., 2011).

Barley (*Hordeum analyzes* L.) belongs to the genus *Hordeum* in tribe *Triticeae* of the family *Poaceae* (*Gramineae*). The basic chromosomes number is, like in all other *Triticeae* species, $x=7$ and in the genus, both diploids ($2n=14$) and polyploids ($2n=4x=28$) and ($2n = 6x = 42$) occur (Von Bothmer et al., 1995 and Kling and Hayes, 2004).

Barley is grown worldwide in many countries and regions with temperate and subtropical climates. Barley in recent years has been the fourth most- produced cereal after maize, rice and wheat with the average of 8 years (2000 – 2008) by 140, 672, 609 and 598 million Mt, respectively (Ullrich, 2011).

The choice of an efficient breeding program depends to a large extent on the knowledge of gene action involved in the expression of the character. One of the most appropriate methods of genetic analysis is the generation mean analysis. In this method, epistatic effects, as well as additive and dominance effects, can be estimated. Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic and to what extent this variation is heritable. Because the efficiency of selection mainly depends on additive genetic variance, the influence of the environment and interaction between the genotype and environment (Eshghi and Akhundova. 2010).

One of the problems inbreeding plant genotypes is the presence of relationships between pod characters. To increase the pot yield, the study of direct and indirect effects of pod traits provides the basis for its successful breeding program and hence the problem of pod yield increase can be more effectively tackled on the basis of performance of pod yield traits and selection for closely related characters (Ceyhan and Onedr, 2011).

The structure of the gene effects, i.e. the combinative ability is the indicator for assessment of the parental forms that is being carried broadly in breeding and genetical researches. It has the special important meaning of the choice of the parents who will be used in the creation of new constant and heterotic varieties. It is known that hybrids with higher yield are resaved by genotypes (sorts and lines) with high combinative ability (Turbin et al., 1974).

Different genetic cross designs such as line x tester and diallel analyses were used to estimate gene action of yield and its components in barley. Among these methods, the diallel analysis provides a unique opportunity to obtain a rapid and overall picture of genetic control of a set of parents in the early generation. Additive and dominance effects can be estimated. Beside gene effects, breeders would also like to know how much of the variation in a crop is genetic and to what extent this variation is heritable. This is due to the fact that efficiency of selection mainly depends on additive genetic variance, influence of the environment and interaction between genotype and the environment (Acquaah, 2007).

The main objective of this study is to evaluate the performance of five barley varieties their diallel, and reciprocal crosses which were appeared to be tested before at our location 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 alleles and reciprocal hybrids.

3 – Heritability in the broad and narrow sense.

4 – Average degree of dominance.

5 – Correlation coefficient and path coefficient analysis.

2. LITERATURE REVIEW

The diallel analysis is one of the biometrical techniques that have been used extensively to gain combining abilities information in various crops (Iqbal, 2004).

2.1. Diallel Analysis

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 the 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).

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). A diallel forsake is a mating step by step diagram used by tell a little white lie breeders, as lightly as geneticists, to confirm the internal underpinnings of quantitative traits.

There are four main types of diallel mating design:

Full diallel in which parents and dependent crosses are engaged along by the whole of F_1 .

Half diallel with parent and without reciprocal crosses.

Full diallel without an inclusion of parents.

Half diallel without parents or collective crosses.

In a all over but the shouting diallel, for the most part parents are crossed to the way one sees it hybrids in generally possible combinations. Full alleles change twice as large amount crosses and entries in experiments but support for mostly working for maternal and paternal effects (Crusio, 1987). "Maternal effect" should not be confused with maternal inheritance, in which some aspect of an offspring's genotype is inherited solely from the mother. This is often attributed to maternal inheritance of mitochondria or plastids, each of which contains its own genome. Maternal inheritance is distinct from maternal effect inheritance because in maternal constitution the individual's phenotype reflects its seize genotype, preferably than the genotype of a parent. In consider, a paternal chance is when a phenotype bear the genotype of the elder, preferably than the genotype of the individual (Yasuda et al., 1995).

The first who used diallel cross were (Sparague and Tatum, 1942) working on maize to determine the general and specific combining ability. (Jinks and Hayman, 1953) by leading diallel analysis methods and estimation of the general and specific combining ability and their variances. The system employing diallel crosses has been used by several authors, e. g.: (Whitehouse et al., 1958 and Aastveit and Frogner, 1963 on wheat; Leffe and Weiss, 1958 on soybeans ; Aksel and Johnson, 1961; and Aastveit, 1961 on barley; Dickson, 1967 on snap beans).

Diallel crosses have been mostly used in genetic consider to runs it up a flagpole the genetic make up of consistent traits intervening a exist of genotypes. These were devised, specially, to assess the combining privilege of the parental lines for the final cause of agape of fine and dandy parents for act with regard to in hybrid knowledge programs (Malik et al., 2004).

Plant breeders frequently need overall information on the average performance of individual inbred lines in crosses- known as general combining ability, for subsequent choosing the best among 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).

The mechanical procedures for making the diallel crosses will vary among crop species (self- vs. cross-pollinators) and within crop species (inbred vs. noninbred 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).

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. The 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 a future number of pollinations. Shoot bags 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).

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 an 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).

2.2. Combining Ability:

It is defined as the strain ability of superior hybrid production, through crossing with other strain in comparison with the mean of difference crosses of strain with others (Ahmed, 2003).

It is defined as the ability of a parent line in hybrid combinations. It plays an important role in selecting superior parents for hybrid combination and studying the nature of genetic variation (Kambal and Webster, 1965 and Duvick, 1999).

Combining Ability is divided in to two types:

A. General combining ability.

Is the average performance of strain in a series of cross combinations.

B. Specific combining ability.

Is the deviation in performance of cross combination from that predicted on the basis of general combining ability of the parents involved in a cross (AGB301, 2004).

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 concept 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 term of GCA is used to designate the average performance of a line in hybrid combination. The term SCA is used to designate those cases in which certain combination 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).

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).

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; the relatively higher magnitude of (GCA $\times$ Environments) interactions suggested a higher sensitivity of GCA to the environment than that of SCA (Bhathagar and Sherma, 1977).

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).

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

Analysis for GCA and SCA in barley involving nine diverse parents and their 36 F₁ and F₂ progenies indicated significant differences among the parent for GCA and among crosses for SCA for the traits days to heading (75%), days to maturity (75%), plant height, effective tillers per plant, spike length, number of grains per spike, test weight, biological yield per plant, grain yield per plant and harvest index. The GCA and SCA components of variance were significant for those traits (Kakani et al., 2007).

10 F₁ and F₂ hybrids were obtained through the diallel crossing of five divergent two-rowed barley cultivars for examination of the mode of inheritance and combining ability for grain weight per barley plant. The analysis of variance of combining abilities was made following the method 2, a mathematical model I, for the incomplete diallel. Highly significant differences were found for the general (GCA) and special (SCA) combining abilities in the F₁ generation which showed that the grain weight per plant in these investigations was dependent on genes with additive and non-additive or dominant effects. The GCA variance was higher in the F₁ generation than the SCA variance. Positive GCA values were also determined with two of the five parents, the cultivar Jagodinac in F₁ generation being the best general combiner for grain weight per plant (Madic et al., 2007).

The knowledge of inheritance mode is a permanent requirement in successful plant breeding. Grain weight per plant had been investigated in a trial consisting of 4 divergent barley varieties grown in 4x4 diallel. ANOVA of combining ability showed the crucial importance of the values for GCA and SCA. This indicates the presence of both, additive and non-additive components in the inheritance of grain weight per plant.

The value of the component of additive variance is greater than that of the dominant (H_1 and H_2), indicating that genetic variance of the mass of grains per plant depends mainly on the effects of genes with additive effects. The results were strongly influenced by parental divergence and complexity of the inheritance system for the trait in a study (Akgun and Topal, 2011).



2.3: Gene action:

The choice of an efficient breeding program depends to a large extent on the knowledge of gene action involved in the expression of the character (Eshghi and Akhundova, 2009).

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).

Knowledge of various types of gene action and their relative magnitudes in controlling various traits is basic to a maximizing efficiency of a breeding program. To increase the yield of barley requires certain information regarding the nature and magnitude of gene actions involved in the expression of quantitative traits of economic importance in a hybridization program. The diallel analysis also provides a unique opportunity to obtain a rapid and overall pictures of genetical control of a set of parents in the early generation (Acquaah, 2007).

Additive genetic variance is of universal occurrence in plant breeding populations. Non-additive variance also exists, but is general, smaller in magnitude than the additive one. In natural plant populations, additive genetic variance is predominant, which is closely followed by dominance variance. Epistatic variance is the lowest in magnitude (Falconer and Mackay, 1996 and Naryanan and Singh, 2007).

Yap and Harvey (1972) in seven-cultivar of barley diallel cross, reported that a genetic effect was found rather than an environmental effect on the expression of grain yield, tillers per plant, kernel weight, kernels per head, flag leaf area, and culm diameter. Also, additive gene action was the most important contributors to the inheritance of these traits. A five divergent genotypes of two-rowed winter barley have been selected for diallel crossing in order to study the mode of inheritance, the gene effect and the components genetic variance for the productive tillering in F_1 and F_2 generation. The variability of the investigated trait differed.

Different modes of inheritance (partial dominance, dominance, and overdominance) and partial dominance were found in the F_1 and F_2 generation, respectively. The genetic variance components, an average degree of dominance indicated partial dominance in the inheritance of tillering (Madic et al., 2006).

In a five diverse parents full diallel cross of six-rowed barley and their 20 F_1 progenies at Qilyasan, Fatieh (2012) reported the importance of non-additive effect in the inheritance of the characters number days to 50% anthesis, plant height, number of spike per plant, spike length, number of grains per spike, grains weight per spike, average spike weight, spike weight per plant, grains weight per plant, biological weight per plant, harvest index, 1000 grain weight, and flag leaf area. Dominance gene action was important in the inheritance of 1000-grain weight. In another study, (Baghizadeh, et al.), (2003), showed that dominance and additive $\times$ additive [i] interaction as well as dominance $\times$ dominance [1] epistasis were important for inheritance of this trait Wu and Takeda, (1995), opine that in general 1000-grain weight was governed by additive, dominance and not –allelic interactions. Also, Kularia and Sharma,(2005), Prakash et al., (2005) and Nakhjavan, et al., (2010), reported different types of epistasis for this trait in barley under no- stress and drought conditions.

A significant amount of genetic variation was observed for most of the plant characteristics, days took to heading and maturity, grain filling period, flag leaf area, plant height, spike length per spike, grains per spike, biomass, 1000 grain weight and harvest index (Gurmani, et al.,2006).

The role of both additive and non-additive effects to grain yield and its component characters in barley have been reported by (Choo, et al., 1988; Bhatnagar and Sharma 1995; 1998). Both additive and non-additive components were important but dominance components were more predominant than additive components in controlling the inheritance of all the characters under study (Rohman, et al., 2006).

2.4: Heritability:

The 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 (V_G/V_P) 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).

There are two conceptions for heritability, the first is broad sense heritability, and the second is narrow sense heritability that is used widely in the estimation of selection efficiency, by determining the differences resulted from additive gene action. Heritability has the variable value, changed according to the differences in character studied, genetic materials test, environmental factor that is evaluated (Eberhart, 1971).

Arnel et al. (2010) noticed, that heritability is the degree of correspondence between the phenotype and the breeding value of an individual for a particular trait.

Recently, Singh (2012) analyzed the data from 60 barley entries including varieties and genotypes conducted in two consecutive years. The estimate of heritability served as a useful guide to the breeder. In the year-I estimated broad sense heritability showed that it was high for all the characters (above 70%). Grain per spike showed the highest heritability. In the year-I, high heritability was observed for grains per spike, grain yield plant⁻¹, a length of awn, a length of flag leaf, spike length, ear bearing tillers, peduncle length, a number of tillers plant⁻¹ and days to maturity. In year-II, more characters had high heritability. The highest heritability estimate was recorded for a number of grains spike⁻¹. In the year-II, high heritability coupled with high genetic advance was observed for a number of grains spike⁻¹ followed by grain yield plant⁻¹, 1000 grain weight, plant height, flowering days, peduncle length, a length of a spike, awn length, days to maturity, flag leaf length and ear bearing tillers.

In pooled data, heritability estimates were highest for a number of grains spike⁻¹. In this study, high heritability along with high genetic advance was observed for a number of grains spike⁻¹ while high heritability along with low genetic advance was observed for days to maturity and grain length.

Kakani and Sharma (2010) noticed that narrow-sense heritability estimates obtained in component analysis ranged from low to high for different characters. The narrow sense heritability estimates were moderately high for days to heading in E₂; flag leaf area in E₁, E₃ and E₄; number of grains per spike in E₂ and test weight in E₁, while it was low for number of grains per spike in E₁ and E₄ and moderately low for test weight in E₄ for F₁, but for F₂, it was moderately low for plant height in E₁, flag leaf area in all the environments; spike length in E₁, E₃, and E₄; number of grains spike⁻¹ in E₁; test weight in E₁ and E₄ and grain yield plant⁻¹ in E₂ and low for days to heading in E₂.

Heritability estimates as would be expected were, in general, high in F₁ in comparison to F₂. The results clearly indicated that the degree of heritability was much influenced by the environment and generations. High estimates of heritability in the broad sense were recorded for plant height, the number of grains per spike and number of tillers. These traits can be used for the indirect improvement of yield. If the heritability of a trait is high, we can apply selection to improve that trait. The amount of heritability for yield was 0.55. Most probably, the high genetic variance for this trait has led to calculating its heritability become more than its actual value (Eshghi and Akhundova, 2009).

Okeno, (2001) reported significant genotypic variation, for length and width of flag leaf, plant height and yield per plant, indicated possibility of selection response in these traits in spring barley. The highest heritability was obtained for a number of grains per spike in normal condition and number of tillers in both environments, indicating that these traits are controlled by additive effects. Because of low genetic gain and heritability for grain yield compared to other characters, selection based on yield components is recommended (Eshghi, et al., 2010).

High estimates of heritability in the broad sense were recorded for 1000-grain weight and number of grains per spike followed by biological yield per plant and grain yield per plant. The characters, which showed higher estimates of genetic advance coupled with higher estimates of heritability reflecting additive gene action, were grain yield per plant and number of grains per spike followed by biological yield per plant (Chand, et al., 2008).

2.5. Correlation and Path analysis:

A. Correlation:

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).

Correlation analyzes indicated that the grain yield was positively and significantly associated with all the yield components except 1000-kernel weight. The highest correlation coefficients were found between grain yield and kernel number per spike ($r = +0.406$), and between grain yield and harvest index ($r = +0.474$) (Budaklicarpici and Celik, 2012).

The correlation analysis showed that grain yield had positive and significant simple correlation with number spike/m², harvest index, biological and straw yield, and negative correlation with spike length and awn length. The highest positive correlation was obtained between biological yield and grain yield. Using stepwise regression, 1000 kernel weight, and a number of spike/m², kernel per spike and harvest index was the most important yield component (Drikvand, et al., 2011).

Studies on correlation of yield and its components in *Hordeum vulgare L.* by Drikvand et al. (2011) in a fifteen genotypes of hulless barley under rainfed condition revealed that grain yield had positive and significant simple correlation with number of spike per m², harvest index, biological and straw yield, and negative correlation with spike length and awn length. The highest positive correlation was obtained between biological yield and grain yield.

Emine and Necmettin (2012) assessed the correlations between grain yield and yield components and to measure the direct and indirect effects of yield components on grain yield in ten two-rowed barley under the ecological conditions of the coastal zone of northwest Turkey for two years by using correlation coefficient and path analysis methods, respectively. Correlation analysis indicated that the grain yield was positively and significantly associated with all the yield components except 1000-kernel weight. The highest correlation coefficients were found between grain yield and kernel number per spike ($r = +0.406$), and between grain yield and harvest index ($r = +0.474$). Results of path analysis indicated that harvest index had the greatest direct effect (+0.7716) on grain yield followed by spike number per m² (+0.3359) and kernel number spike-1 (+0.2081). Percentages of their direct effect were 71.97%, 48.47%, and 28.22%, respectively. On the other hand, most of the indirect effects of yield components on grain yield were found to be significant and positive. Because of the significant effects of the harvest index, spike number per m² and kernel number spike-1 on grain yield, they may be regarded as criteria for barley improvement and breeding programs. Grain yield in barley is a complex trait affected directly or indirectly by every gene present in the plant.

B . Path Coefficient Analysis:

Path coefficient analysis was suggested by Wright (1921) and described by Dewey and Lu (1959) which was calculated to detect the relative importance of characters contributing to grain yield (Selvaraja and Nagarajan, 2011).

It has been applied to a vast array of complex modeling areas, including sociology and econometrics (Dodge, 2003).

Miller and Rawling (1967) suggested that intermating population breakage of coupling linkage reduced the correlation while breakage of repulsion linkage increased the correlation. All these results suggest that the linkages in both coupling and repulsion phases are operative in a genetical association of yield and yield components. A path-coefficient analysis is one of the reliable statistical techniques which allow quantifying the interrelationships of different components and their direct and indirect effects on grain yield through correlation estimates.

Bhutta and Ibrahim (2005) in a six-rowed barley genotypes, concluded that there were the significant positive correlation between grain yield with 1000-grain weight and a number of spikelets spike⁻¹, grain yield was the negative correlation with days to heading. Path coefficient analysis revealed that positive maximum association between Peduncle length and number of spikelets with grain yield, extrusion length and spike density had maximum negatively association with grain yield.

Ataei (2006) reported that grain number in spike with a direct effect on yield was the most important factor. The direct effect of 1000-kernel weight and a number of the spike on yield were positive also. The path-coefficient analysis is one of the reliable statistical techniques which allow quantifying the interrelationships of different components and their direct and indirect effects on grain yield through correlation estimates.

By means of path analysis of heritability correlation coefficients, researchers found that in barley ear length and grain weight per ear have a great direct influence on plot yield, whereas effective and ineffective grain number per ear have little direct influence on the plot yield but they have considerable indirect negative influence on plot yield through other characters. Total grain number per ear has a considerable direct negative influence on plot yield. Plant height has a considerable indirect positive influence on plot yield through other characters (ShouFu, et al., 1990).

Path analyzes indicated that harvest index had the greatest direct effect (+0.7716) on grain yield followed by spike number per m² (+0.3359) and kernel number per spike (+0.2081). Percentages of their direct effect were 71.97%, 48.47%, and 28.22%, respectively. On the other hand, most of the indirect effects of yield components on grain yield were found to be significant and positive. Because of the significant effects of the harvest index, spike number per m² and kernel number per spike on grain yield, they may be regarded as criteria for barley improvement and breeding programs (Budaklicarpici and Celik, 2012). Path coefficient analysis revealed that positive maximum association between peduncle length and number of spikelets with grain yield, extrusion length, and spike density had the maximum negative association with grain yield (Buttha et al, 2005). The direct effect of 1000- kernel weight and number of the spike on yield was also positive. A number of spike /m² had the highest positive direct effect on grain yield, This indicated that regarding the constant of other variables, an increase of this trait, grain yield has been increased (Ataei, 2006 and Drikvand, et al., 2011).

Path coefficient analysis revealed that positive maximum association was found between peduncle length and no of spikelets with grain yield. Extrusion length and spike density had the maximum negative association with grain yield (Bhutta, et al., 2005). Ganusheva, (1992) found that grain number per plant and 1000 grain weight had the greatest direct effect on grain weight per plant.



3. MATERIAL AND METHODS

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3.1. Plant and experiment material.

The present study was conducted at Kurdistan region -Iraq, Qilyasan Agricultural Research Station, Faculty of Agricultural Sciences, University of Sulaimani (35° 34' 307" N, 45° 21' 992" E and 765 masl), 2 Km North west of Sulaimani city. To evaluate the performance of 20 F₂s crosses, created by full diallel system prepared previously and their parents at 2014- 2015. Five varieties and pedigree of two – rowed barley (*Hordeum distichum* L.) were used as fallows:

1-MORA/NB1054/3/MOLA/SHYRI//ARUPO*2/JET/4/...CBSS99M00293TG-5M-1Y-1M-0Y (hybraed)

2-ABN-B/KA-B//RAISA/3/ALELI/4/LIMON/5/... CBSS99M00228 T-K-6M1Y
- 1M-0Y (hybraed)

3-Arabi award

4-Clipper

5-Booth H1

Table 3.1.1. Clasification of barley varaieties acording to some morphological characteristics of the plant during vegetative growth.

Vegetative Growth Characteristic's	Variety		
	Arabi Aswad	Clipper	Bohoth H1
Date of heading	Early	Medium	Medium
Auricle pigmentation	Strong	Weak	Strong
Plant height	Medium	Medium	Medium
Lower leaf sheath hairiness	Absent	Absent	Absent
Ear shape	Parallel	Tapering	Parallel
Awn compared to ear	Equal	Equal	Longer
Sterile spikelet lemma tip	Pointed	Rounded	Pointed
Awn denticulation	Smooth	Smooth	Rough
Ear density	Medium	Medium	Medium

Seeds of 20 F₂S with their 5 parents (25 entries) were received from PH.D student Kamil Mahmood Mustafa to completed this work the seeds were sown in the field experiment on November 15th – 2014 in a randomized complete block design (RCBD) using computer programs (Statistical Social Science, JMP, Ver-7, SAS Institute Inc.). with three replication. Each treatment was three rows of 3-meter length, 40 cm between rows and 20 cm between plants within a row. Statistical analysis using full diallel cross technique were implemented as described by (Griffing, 1956).

All cultural practices were performed normally in all treatments as recommended for barley production, at rainfed regions. The experiment was harvested on May 15th – 2015.

3. MATERIAL AND METHODS

Table 3.1.2. Studied breeding materials.

No	Diallel, Reciprocal Crosses and Parents Number	Parentage
1	1x2	MORA x ABN
2	2x1	ABN x MORA
3	1x3	MORA x Arabi aswad
4	3x1	Arabi aswad x MORA
5	1x4	MORA x Clipper
6	4x1	Clipper x MORA
7	1x5	MORA x Bohoth H1
8	5x1	Bohoth H1 x MORA
9	2x3	ABN x Arabi aswad
10	3x2	Arabi aswad x ABN
11	2x4	ABN x Clipper
12	4x2	Clipper x ABN
13	2x5	ABN x Bohoth H1
14	5x2	Bohoth H1 x ABN
15	3x4	Arabi aswad x Clipper
16	4x3	Clipper x Arabi aswad
17	3x5	Arabi aswad x Bohoth H1
18	5x3	Bohoth H1 x Arabi aswad
19	4x5	Clipper x Bohoth H1
20	5x4	Bohoth H1 x Clipper
21	1	MORA
22	2	ABN
23	3	Arabi aswad
24	4	Clipper
25	5	Bohoth H1

Table 3.1.3. Source and origin of parents.

Parents	Source	Origin
1 (pedigree line)	Center Research of Sulaimani	ICARDA
2 (pedigree line)	Center Research of Sulaimani	ICARDA
3 (cultivar)	Center Research of Kalar	ICARDA
4 (cultivar)	Center Research of Erbil	Australia
5 (pedigree line)	Center Research of Erbil	ICARDA

3.2. Climate of the studied area.

In tables (3.2.1. and 3.2.2.) below are shown brief description of the soils and climates under studied.

Table (3.2.1.) Metrological data of Qilyasan location for the season 2014 – 2015.

Data	Qiyassan Location			
	Min Temp (C°)	Max Temp (C°)	Monthly Avg. Temp (C°)	Precipitation
Oct.	9.1	34.4	20.4	4.2
NOV.	2.9	22.2	12.0	151.6
DEC.	2.2	17.9	9.2	128.6
JAN.	-3.2	16.6	6.8	100
FEB.	0.2	19.8	8.8	65
MAR.	3.2	22.0	12.0	94.8
APR.	5.0	32.2	16.7	29.4
MAY.	11.2	36.9	24.6	19.8

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Table (3.2.2.): Physical and chemical properties of the soil at Qilyasan location.

Soil properties		Qilyasan
PSD		Silty clay
Sand %		5.92
Silt %		43.28
Clay %		50.8
E.C. (ds.m ⁻¹)		0.46
PH		7.17
Organic matter %		1.8
Total Nitrogen %		0.66
Available phosphate (ppm)		5.2
CaCO ₃ (%)		26.5
Soluble Cations & Anions mmole ⁻¹	Ca ++	2.1
	Mg ⁺⁺	0.9
	K ⁺	0.17
	Na ⁺	0.63
	CO ₃ ⁻²	0.00
	HCO ₃ ⁻²	2.77
	Cl	0.13
	SO ₄ ⁻²	0.79

3.3. Evaluated traits.

Data of agronomic traits were recorded from five plants of each genotype from each replications as follows:

1. Plant height: is the average distance in centimeters from the ground to the tip of the spike (excluding the awns) at maturity.
2. Plant tillers number: is the average of total number of tillers counted from each selected plants at harvesting time.
3. Plant spikes number : is the average of total number of spikes counted from each selected plant at harvesting time.
4. Plant spikes weight : is the average weight of the spikes from the plant samples collected during threshing, expressed in metric grams.
5. Spike length: was recorded as the distance in centimeters from the lowest spikelet to the tip of the spike at maturity (without awn).
6. Spike grains number : is the average number of grains spike⁻¹ in each row, harvested.
7. Spike grains weight : is the weight of the grain harvested, expressed in metric grams per spike
8. Average spike weight: is average weight of the spike from the spike sample collected during threshing, expressed in metric grams.
9. 1000- grain weight: is the weight of 1000 seeds in grams, from grains samples collected during threshing.
10. Plant grain weight : is the average weight of grains from the plant samples collected during threshing, expressed in metric grams.
11. Plant biological yield : is the above ground biomass per plant which was recorded by weighing the whole plant including straw and grains, from the plant samples collected during threshing, expressed in metric grams.
12. Harvest index (%): is the proportion of grain weight plant⁻¹ to biological weight plant⁻¹.

3. MATERIAL AND METHODS

3.4. Genetic parameters.

3.4.1. General Combining Ability (GCA) variances and effects

3.4.2. Specific Combining Ability (SCA) variances and effects

3.4.3. Reciprocal Effect %

3.4.4. Broad Sense Heritability $h^2_{b.s}$

3.4.5. Narrow Sense Heritability $h^2_{n.s}$

3.4.6. Average Degree of Dominance ($\bar{a}$)

3.5. Statistical analysis.

Once all genotypes data were collected, data from 25 genotypes were utilized to perform all statistical analysis. Genotypes were considered fixed effects while replications were conceded random effects. The linear model utilized for individual analysis was as follows (Al-Mohammad and Al- Youns, 2000)

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

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”.

$$\varepsilon_{ij} \sim \text{IND} (0, \sigma^2)$$

3.6. Combining ability analysis.

The (GCA) and (SCA) were estimated using the general linear model for the analysis which takes the formula of (Singh and Chaudhary, 2007).

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

Where:

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

μ : populations mean,

g_i : general combining ability (GCA) effect for the i^{th} parent

g_j : general combining ability (GCA) for the j^{th} 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. MATERIAL AND METHODS

3.7. Estimation of general, specific combining ability and reciprocal effects.

$$g_i = \frac{1}{2P} (Y_{i.} + Y_{.j}) - \frac{1}{P^2} Y_{..}$$

$$si = \frac{1}{2} (Y_{ij} + Y_{ji}) - \frac{1}{2P} (Y_{i.} + Y_{.i} + Y_{.j} + Y_{.j}) + \frac{1}{P^2} Y_{..}$$

$$ri = \frac{1}{2} (Y_{ij} - Y_{ji})$$

Where :

g_i :Effect of expected general combining ability for parents I ,

si : Effect of expected specific combining ability for single diallel Crosses

ij when $i = j$,

ri : Effect of expected specific combining ability for single reciprocal Crosses ij when $i=j$,

Y_{ij} : F1s mean as a result of crossing parent i with parent j ,

$Y_{..}$: Sum of the means of all parents and F1s hybrids, and

P : Parents number

3.8. Estimation of components of variance for both general and specific combining ability.

$$\sigma^2 gi = (g_i)^2 - \frac{MS'e}{2p^2}$$

$$\sigma^2 si = \frac{1}{p-2} \sum si^2 - \frac{MS'e(p^2 - 2p + 2)}{2p^2}$$

$$\sigma^2 ri = \frac{1}{p-2} \sum ri^2 - \frac{MS'e}{2}$$

Where:

$\sigma^2 gi$: Variance of expected effect of general combining ability for

parent I , $\sigma^2 si$: Variance of expected effect of specific combining ability for diallel crosses of parent I ,

$\sigma^2 ri$: Variance of expected effect of specific combining ability for reciprocal crosses of parent i .

3.9. Estimation of standard error for the differences between the effects of the general combining ability of two parents, two diallel crosses and reciprocal crosses, respectively.

$$S.E._{(g_i - g_j)} = \sqrt{\frac{MS'e}{p}} \quad \text{Standard error for the differences between the effects of the general combining ability of two parents.}$$

$$S.E._{(s_{ij} - s_{ik})} = \sqrt{\frac{(p-1)MS'e}{p}} \quad \text{standard error for the differences between the effects of the specific combining ability of two diallel crosses.}$$

$$S.E._{(r_{ij} - r_{ik})} = \sqrt{MS'e} \quad \text{standard error for the differences between the effects of the specific combining ability of two reciprocal crosses.}$$

3. MATERIAL AND METHODS

3.10. Estimation of heritability.

The term heritability has been further divided into broad sense and narrow sense, broad sense heritability was calculated by dividing genotypic variance by total variance and narrow-sense heritability was calculated by dividing additive genetic variance by total variance (Singh and Chaudhary, 1985).

$$h^2_{b.s} = \frac{\sigma^2_G}{\sigma^2_P} = \frac{\sigma^2_A + \sigma^2_D}{\sigma^2_A + \sigma^2_D + \sigma^2_e} = \frac{2 \sigma^2_{gca} + \text{Variance of effect of specific combining ability for diallel crosses}}{2 \sigma^2_{gca} + \text{Variance of effect of specific combining ability for diallel crosses} + \sigma^2_e}$$

$$h^2_{n.s} = \frac{\sigma^2_A}{\sigma^2_P} = \frac{\sigma^2_A}{\sigma^2_A + \sigma^2_D + \sigma^2_e} = \frac{2 \sigma^2_{gca}}{2 \sigma^2_{gca} + \text{Variance of effect of specific combining ability for diallel crosses} + \sigma^2_e}$$

Where:

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

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

σ^2_{GCA} : The variance of general combining ability,

Variance of effect of specific combining ability for diallel crosses: The variance of specific combining ability,

σ^2_e : The variance of experimental error i.e. environmental variance,

σ^2_A : Additive genetic variance,

σ^2_D : Non-additive (dominance and epistasis) genetic variance,

σ^2_G : Total genetic variance, and

σ^2_P : Phenotypic variance (genetic and environmental variance).

3.11. Estimation of average degree of dominance.

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

If:

$\bar{a} = \text{zero}$ denote no dominance

$\bar{a} < 1$ denote partial dominance

$\bar{a} = 1$ denote complete dominance

$\bar{a} > 1$ denote over dominance

3.12. Estimation of reciprocal effect.

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

Where:

$\bar{F}_1$: the average value of diallel hybrid,

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

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3.13. Estimation of Combined Analysis of Variance.

$$S.D_{Location} = t_{\alpha} (dfE) \sqrt{\frac{2MS E(a)}{tr}}$$

$$Y_{ijk} = \mu + \tau_i + \rho_{jk} + \gamma_k + (\tau\gamma)_{ik} + \varepsilon_{ijk} \quad \begin{cases} i = 1, 2, 3, \dots, t \\ j = 1, 2, 3, \dots, r \text{ (replicates or Blocks)} \\ k = 1, 2, 3, \dots, l \text{ (locations)} \end{cases}$$

$$\mu = \bar{Y}_{...}$$

$$\tau_i = \bar{Y}_{i..} - \bar{Y}_{...}$$

$$\rho_{jk} = \bar{Y}_{.jk} - \bar{Y}_{..k}$$

$$\gamma_k = \bar{Y}_{..k} - \bar{Y}_{...}$$

$$(\tau\gamma)_{ik} = \bar{Y}_{i.k} - \bar{Y}_{i..} - \bar{Y}_{..k} + \bar{Y}_{...}$$

$$\varepsilon_{ijk} = Y_{ijk} - \bar{Y}_{i.k} - \bar{Y}_{.jk} - \bar{Y}_{i..} + \bar{Y}_{..k}$$

where :

Y_{ijk} : 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_{ijk} : effect of block (j) in location (k)

γ_k : location effect value

$(\tau\gamma)_{ik}$: interaction effect value between treatment (i) and location (k)

ε_{ijk} : experimental error for the observed value of the experimental unit (Y_{ijk})

Locations mean comparisons conducted by using Least significant difference test (L.S.D.) at 5% and 1% significant levels according to the following equation:

3.14. ASSOCIATION ANALYSIS.

3.14.1. The correlation coefficients.

The correlation coefficients were calculated to determine the degree of association of traits 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).

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

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.

3. MATERIAL AND METHODS

3.14.2. PATH COEFFICIENT ANALYSIS.

The path coefficient techniques involve partitioning of correlation coefficient to direct (unidirectional pathway 'P') and indirect effects through alternate path ways (Pathway 'P' X correlation coefficient 'r') of various variables and grain yield plant⁻¹. Grain yield was considered as the resultant variable and the others as causal variables. The path coefficient analysis was carried out through the equations as suggested by (Dewey and Lu, 1959, Soomro, 2010, Singh and Chaudhary, 1985 and Arbuckle, 2009), through (Analysis of Moment Structures, AMOS Ver. 18 Softwar).





4.RESULTS AND DISCUSSION

Data represent in Table [4.1.] indicate to the mean squares due to variance sources of the studied characters. The mean squares due to the genotype were highly significant for all studied characters, confirming the necessity of splitting this variance to its components (GCA, SCA, and RCA) according to the design of full diallel analysis for all studied characters. The mean squares of GCA for all studied characters were highly significant except the characters spike length and harvest index, which were significant and plant height which was not significant. The mean squares due to SCA were highly significant for all characters. The mean square due to RCA were highly significant for all characters except average spike weight which was significant, and the characters spike length and weight of grains/spike, which were not significant mean squares due to genotypes were observed previously by Mahmood, (2010); Mohammad, (2012) ; khoshnaw, (2013).

These results were in agreement with those reported by Ali et al (2009) and Aghamiri et al, (2012).

The significant GCA and SCA mean squares recorded previously by (Verma, A. K.; S. R. Vishwakarma and P. K. Singh 2007, Chaudhary, B. D.; R. K. singh and S. N. kakar 1974 ; Smith, E. L. and J. W. Lambert 1968 ; Schittenhelm, S.; J. A. Okeno and W. Friedt 2008).

The deference between parents and their hybrids caused a significant heterosis compared to mid – parental values, including positive and negative heterosis values. These results were in agreement with previous researchers recorded by (mahmood, 2010 ; khoshnaw, 2013 ; mohammad, 2012 ; Chaudhary, B. D.; R. K. singh and S. N. kakar 1974 ; Verma, A. K.; S. R. Vishwakarma and P. K. Singh 2007; Carleton, A. E. and W. H. Foote 1968 ; Shahnejat-Bushehri, A. A.; S. Torabi; M. Omid and M. R. Ghannadha 2005 and Crook, W. J. and J. M. Poehlman 1971).

Table (4.1.) Mean squares of the variance analysis for studied characters.

Mean Squears													
S.O.V	D.F	plant hight (cm)	number of tillers /plant	number of spike /plant	Weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
Blocks	2	0.08	5.26	3.85	3.57	1.89	0.607	0.01	0.04	10.973	9.85	16.30	0.003
Genotypes	24	176.56**	10.564 **	6.601 **	22.058 **	5.067 **	12.660 **	0.087 **	0.152 **	88.103 **	20.092 **	160.789 **	0.014 **
GCA	4	24.635 n.s	3.3503 **	2.131 **	17.831 **	1.665 *	3.844 **	0.047 **	0.039 **	14.991 **	11.930 **	103.436 **	0.003 *
SCA	10	85.137 **	4.522 **	2.595 **	6.739 **	2.837 **	6.310 **	0.037 **	0.084 **	48.663 **	6.511 **	53.130 **	0.004 **
RCA	10	46.257 **	2.588 **	1.833 **	3.774 **	0.55 n.s	2.279 **	0.014 n.s	0.021 *	15.822 **	4.790 **	34.126 **	0.005 **
Error	48	45.80	2.05	1.28	1.00	1.52	2.20	0.03	0.03	7.765	5.24	7.67	0.004
Mse'		15.268	0.682	0.426	0.332	0.507	0.733	0.011	0.009	2.588	1.748	2.556	0.001

SOV : source of variance

D.F : Degree of Freedom

Mse' : Revised mean squares of experimental

GCA : General combining ability

SCA : Spicific combining ability of deallil crosses

RCA :Spicific combining ability of reciprocal crosses

The average of studied characters represent in Table [4.2.] for both diallel and reciprocal crosses and their parents. Regarding to the diallel crosses the cross 1x2 produced maximum values for the characters number of tillers/plant, number of spike/plant and grain weight plant with 13.067, 10.800, and 14.640 g. respectively. The cross 1x3 gave the lowest value for the characters plant height, number of tillers/plant, weight of grain/spike, grain weight/plant and harvest index with 93.933, 8.533, 1.093, 7.259, and 0.224 cm. respectively. While the lowest due to the characters number of spike/plant, spike length and number of grains/spike exhibited by the cross 1x5 with 6.033, 14.033, and 20.833 respectively. The highest value for the character plant height was 115.767 produced by the cross 2x3 and produced the lowest value due to the characters weight of spike/plant, average spike weight and 1000 grain weight with 6.200, 1.000, and 46.33 respectively. The highest value for the characters number of grain/spike and 1000 grain weight recorded by the cross 2x4 with 26.833, and 54.667 respectively. And for the characters weight of spikes/plant and biological weight/plant recorded by the cross 2x5 with 13.00, and 44.467 respectively, while the cross 3x4 exhibited the highest value for the characters weight of grains/spike, average spike weight and harvest index with 1.633, 1.727, and 0.546 respectively. And produced the lowest value for the characters biological weight with 24.333. The maximum spike length was 19.200 recorded by the cross 3x5. Regarding to the reciprocal crosses, the cross 4x1 gave the highest value for plant height with 127.833, and maximum number of tillers recorded by the cross 3x2 with 14.667, while it produced the lowest value for the characters number of spike/plant, weight of spike/plant, number of grains spike, weight of grains/spike, average spike weight, 1000 grain weight, grain weight/plant and harvest index. The cross 5x2 exhibited the highest value for the characters plant height, number of grains/spike, weight of grains/spike, average spike weight, 1000 grain weight and biological weight with 127.833, 27.733, 1.700, 1.900, 55.333, and 48.733 respectively. The cross 5x3 recorded maximum value due to spike length with 19.333, and 5x4 gave maximum value due to number of spike/plant, weight of spike/plant and grain weight/plant with 10.733, 14.067, and 15.978 respectively.

Concerning to parental values, parent 1 recorded the lowest value for the characters number of tillers/plant, number of spike/plant, biological weight/plant and harvest index. Parent 2 recorded maximum value for 1000 grain weight with 50.000 g and the lowest value for spike length and grain weight/plant. Parent 3 showed the lowest value for plant height, weight of spike/plant, number of grain/spike and weight of grains/spike. The highest value for the characters plant height, number of tillers/plant, number of spike/plant, weight of spike plant, grain weight/plant and harvest index recorded by parent 4 with 119.400, 13.667, 11.733, 14.267, 13.407, and 0.298 respectively, while recorded the lowest value for average spike weight and 1000 grain weight. Parent 5 recorded maximum value for spike length, number of grains/spike, weight of grains/spike, average spike weight and biological weight/plant with 17.333, 25.833, 1.467, 1.567, and 45.600 respectively.

These results were in a good agreement with those found by privation researchers, whom revealed significant differences among genotype, indicating the genetic variability in the material and possibility of selection for these traits, Rohman et al. 2006 ;Madic et al. 2009, Mahmood 2012 and Khoshnaw 2013.

Table (4.2.) Averages of studied characters for parents and their F2 crosse

	Crosses & Parents	plant height (cm)	number of tillers /plant	Number of spike /plant	weight of spikes /plant (g)	spike length (cm)	Number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 Grain Weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest index (%)
DIALLEL CROSSES	1 x 2	99.067	13.067	10.800	12.600	17.167	25.667	1.367	1.500	49.333	14.640	41.000	0.358
	1 x 3	93.933	8.533	6.667	8.333	16.933	24.700	1.093	1.167	49.000	7.259	32.467	0.224
	1 x 4	109.767	11.400	9.100	7.867	16.233	24.367	1.400	1.533	46.667	12.740	35.000	0.367
	1 x 5	110.633	8.867	6.033	6.800	14.033	20.833	1.227	1.333	53.000	7.465	26.000	0.285
	2 x 3	115.767	10.200	8.233	6.200	14.567	23.767	1.200	1.000	46.333	9.757	26.600	0.367
	2 x 4	113.667	10.200	7.767	9.800	17.667	26.833	1.533	1.467	54.667	12.057	37.467	0.318
	2 x 5	108.367	12.133	10.667	13.000	16.300	25.800	1.367	1.500	48.667	14.633	44.467	0.328
	3 x 4	104.367	10.533	8.133	8.933	15.967	23.467	1.633	1.727	48.667	13.193	24.333	0.546
	3 x 5	112.667	12.133	9.467	7.000	19.200	24.967	1.400	1.533	52.000	13.207	44.133	0.301
	4 x 5	113.500	11.533	8.333	8.133	16.167	23.167	1.300	1.467	49.333	10.833	37.067	0.291
RECIPROCAL CROSSES	2 x 1	109.733	12.933	7.600	6.733	16.600	23.767	1.233	1.567	45.667	9.447	23.533	0.403
	3 x 1	100.333	10.933	9.367	7.500	16.333	24.200	1.133	1.500	46.333	10.623	30.933	0.347
	4 x 1	127.833	13.733	8.567	8.933	16.733	26.200	1.340	1.700	54.667	11.542	32.400	0.356
	5 x 1	127.433	9.200	6.600	7.067	14.900	24.200	1.233	1.100	44.333	8.159	27.400	0.299
	3 x 2	109.733	14.667	5.967	4.600	16.233	20.300	1.000	0.967	36.000	5.960	37.267	0.160
	4 x 2	100.333	10.733	8.733	10.800	16.533	26.233	1.453	1.567	53.000	12.528	34.933	0.359
	5 x 2	127.833	10.800	9.000	12.900	16.200	27.733	1.700	1.900	55.333	15.413	48.733	0.319
	4 x 3	127.433	8.400	7.067	8.133	18.233	24.300	1.367	1.533	46.667	10.007	28.267	0.346
	5 x 3	108.433	9.533	7.800	6.267	19.333	27.433	1.440	1.667	52.667	11.272	34.533	0.328
	5 x 4	101.333	14.200	10.733	14.067	16.467	25.200	1.477	1.533	47.333	15.978	48.333	0.332
PARENTS	1	110.533	10.600	7.667	8.867	15.333	25.633	1.293	1.467	45.333	9.864	34.400	0.105
	2	110.533	14.333	8.333	7.733	14.433	22.967	1.167	1.267	50.000	9.673	36.600	0.213
	3	109.667	13.267	9.333	7.467	15.600	20.600	1.133	1.300	43.333	10.513	38.800	0.233
	4	119.400	13.667	11.733	14.267	16.233	21.167	1.143	1.233	32.333	13.407	42.533	0.298
	5	114.767	11.333	8.333	12.733	17.333	25.833	1.467	1.567	43.333	12.240	45.600	0.268
	L.S.D (P≤0.05)	11.111	2.348	1.856	1.638	2.025	2.435	0.298	0.265	4.575	3.759	4.546	0.118

Data in table [4.3.] signify positive and negative value due to reciprocal effect for studied characters, estimated as the percentage of F_2S reciprocal crosses deviated from their diallel crosses. The reciprocal cross 2x1 recorded maximum negative effect for the characters number of spike/plant, weight of spikes/plant and biological weight/plant with -29.630, -46.561 and -42.602 % respectively. The cross 3x1 gave maximum positive reciprocal effect values for the characters number of tillers/plant, number of spike/plant, average spike weight and harvest index with 28.125, 40.500, 28.571 and 55.038 % respectively. The cross 4x1 recorded maximum positive effect value for the characters plant height and 1000 grain weight with 16.459 and 17.143 % respectively. The cross 5x1 recorded maximum positive effect value for the characters number of grains/spike with 16.160 % and maximum negative value for characters average spike weight and 1000 grain weight with -17.500 and -15.723 % respectively. The cross 4x2 recorded the highest positive effect for the character biological weight/plant with 39.348 % and maximum negative reciprocal effect for number of grains/spike, weight of grains/spike, grain weight/plant and harvest index with -14.586, -16.667, -38.914 and -56.323 % respectively. The cross 4x2 exhibited maximum negative effect for the characters spike length with -6.415 %, while maximum effect for the character weight of grains/spike and spike length recorded by the crosses 5x2 and 4x3 with 24.390 and 14.196 % respectively. The cross 5x3 showed maximum negative reciprocal effect for the characters plant height and number of tillers/plant with -10.059 and -21.429 % respectively. Maximum positive reciprocal effect for the characters weight of spikes/plant and grain weight/plant recorded by the cross 5x4 with 72.131 and 47.489 % respectively. The positive values due to reciprocal effect confirm the superiority of reciprocal crosses values in compare to their diallel crosses, while the negative effect values indicate to the diallel cross values compare to their reciprocal cross values. Previous workers signified to positive and negative reciprocal effect, indicating to the presence of maternal effect (mahmood, 2010 ; mohammed,2012;Khoshnaw,2013).

Table (4.3.) the estimates of % reciprocal effect values for reciprocal crosses.

Reciprocal Crosses	plant height (cm)	number of tillers /plant	number of spike /plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
2 x 1	10.767	-1.020	-29.630	-46.561	-3.301	-7.403	-9.756	4.444	-7.432	-35.474	-42.602	12.703
3 x 1	6.813	28.125	40.500	-10.000	-3.543	-2.024	3.659	28.571	-5.442	46.354	-5.544	55.038
4 x 1	16.459	20.468	-5.861	13.559	3.080	7.524	-4.286	10.870	17.143	-9.403	-7.429	-3.223
5 x 1	15.185	3.759	9.392	3.922	6.176	16.160	0.543	-17.500	-15.723	9.297	5.385	4.944
3 x 2	-0.288	43.791	-27.530	-25.806	11.442	-14.586	-16.667	-3.333	-22.302	-38.914	39.348	-56.323
4 x 2	0.411	5.229	12.446	10.204	-6.415	-2.236	-5.217	6.818	-3.049	3.909	-6.762	12.786
5 x 2	2.553	-10.989	-15.625	-0.769	-0.613	7.494	24.390	26.667	13.699	5.330	8.696	-2.924
4 x 3	3.897	-20.253	-13.115	-8.955	14.196	3.551	-16.327	-11.197	-4.110	-24.154	16.164	-36.623
5 x 3	-10.059	-21.429	-17.606	-10.476	0.694	9.880	2.857	8.696	1.282	-14.649	-21.752	8.823
5 x 4	-2.614	23.121	28.800	72.131	1.856	8.777	13.590	4.545	-4.054	47.489	30.396	13.966
Standard of error	2.599	6.826	7.510	9.792	2.091	2.914	4.057	4.604	3.750	9.535	7.625	9.531

Data in table [4.4.] explain the GCA effect values for the parents. Parent 1 recorded the highest negative GCA effect value for the characters number of tillers/plant, number of spike/plant, spike length, grain weight/plant and biological weight/plant with -0.491, -0.475, -0.469, -1.136 and -3.951 respectively. The highest positive GCA effect for the characters number of tillers/plant and 1000 grain weight recorded by the parent 2 with 0.863 and 1.127 respectively. Maximum negative GCA effect value for the characters plant height, weight of spikes/plant, number of grains/spike, weight of grains/spike, average spike weight and 1000 grain weight recorded by parent 3 with -1.756, -1.877, -0.951, -0.071, -0.074 and -1.340 respectively, and recorded maximum positive GCA effect for the character spike length with 0.371. Parent 4 recorded maximum positive GCA effect values for the characters plant height, number of spike/plant, weight of spike/plant, grain weight/plant and harvest index with 2.314, 0.709, 1.447, 1.273 and 0.032 respectively. Parent 5 gave the highest positive GCA effect value for the characters number of grains/spike, weight of grains/spike, average spike weight and biological weight/plant with 0.729, 0.084, 0.073 and 4.469 respectively, while recorded maximum negative GCA effect value for the character harvest index with - 0.020. The positive GCA effect values indicate clearly a high contribution of these parents to increase the value of these character in their parents, while the negative values indicate to the contribution of these parents in reducing these characters in their parents. These result were in agood agreement with the result of previous workers (mahmood, 2010 ; mohammed, 2012 ; Khoshnaw, 2013 ;Tawfiq,S.I.,2004).

Table (4.4.) Estimation of GCA effect values for the parents.

Parents	plant height (cm)	number of tillers /plant	number of spike plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
1	-0.989	-0.491	-0.475	-0.710	-0.469	0.149	-0.063	-0.010	0.227	-1.136	-3.951	0.000
2	-0.199	0.863	0.062	0.143	-0.416	0.233	-0.005	-0.044	1.127	0.082	0.983	-0.008
3	-1.756	-0.331	-0.345	-1.877	0.371	-0.951	-0.071	-0.074	-1.340	-1.066	-2.111	-0.005
4	2.314	0.329	0.709	1.447	0.217	-0.161	0.055	0.056	-1.207	1.273	0.609	0.032
5	0.631	-0.371	0.049	0.997	0.297	0.729	0.084	0.073	1.193	0.848	4.469	-0.020
Standard of Error	1.747	0.369	0.292	0.258	0.318	0.383	0.047	0.042	0.719	0.591	0.715	0.017

The estimation of SCA effect for diallel crosses represent in table [4.5.], indicating that the cross 1x2 gave the highest negative effect value for the character plant height recording -11.484. The cross 1x5 gave the highest positive SCA effect value for plant height recording 8.529, while it recorded the lowest value for SCA effect due the characters number of spike/plant, weight of spikes/plant, spike length, number of grains/spike, grain weight/plant and biological weight/plant with -1.739,-2.420,-1.791, -2.733, -3.196 and -9.496 respectively. The cross 2x3 recorded the highest negative SCA effect value for the characters weight of grains/spike, average spike weight, 1000 grain weight and harvest index with -0.148, -0.342, -6.393 and -0.045 respectively. The 2x4 exhibited maximum negative SCA effect value for the character number of tillers/plant recording -2.203, and also recorded maximum positive SCA value for number of grains/spike and 1000 grain weight with 2.091 and 6.140 respectively. The 2x5 exhibited maximum positive SCA effect value for the characters number of spike/plant, weight of spikes/plant, average spike weight, grain weight/plant and biological weight/plant recording 1.241, 2.743, 0.227, 2.798 and 5.271 respectively. The cross 3x4 gave maximum positive SCA value for weight of grains/spike and harvest index with 0.192 and 0.097 respectively. The cross 3x5 showed the highest positive SCA effect value for the character spike length recording 2.169 and the cross 4x5 exhibited the highest value for the character number of tillers/plant recording 1.431. The cross with positive SCA effect value confirm the high value for this cross compare to it is parental values, while the negative effect of SCA value indicate the decrease in the character value in compare to their parents.

Similar result were recorded previously by (mahmood, 2010 ; mohammed, 2012 ; Khoshnaw, 2013 ; Tawfiq, S. I., 2004 ; Sharma, 2002 ; Pandey, R. M. 2007 ; Chaudhary, 1974 ; Smith, E. L. and J. W. Lambert 1968 ; Schittenhelm, S.; J. A. Okeno and W. Friedt 2008).

Table (4.5.) Estimation of SCA effect values for diallel crosses.

Diallel	plant height (cm)	number of tillers /plant	number of spike plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
1 x 2	-5.274	1.151	1.131	1.167	1.339	-0.036	0.044	0.144	-1.627	1.801	-0.443	0.066
1 x 3	-11.484	-0.749	0.321	0.640	0.679	-0.086	-0.097	-0.003	-0.893	-0.360	2.584	-0.037
1 x 4	6.613	1.251	0.118	-1.403	0.306	0.924	0.054	0.128	3.873	0.708	1.364	0.007
1 x 5	8.529	-1.583	-1.739	-2.420	-1.791	-2.733	-0.115	-0.290	-0.360	-3.196	-9.496	-0.010
2 x 3	6.693	0.424	-1.099	-1.933	-0.984	-1.619	-0.148	-0.342	-6.393	-2.454	-2.716	-0.045
2 x 4	0.923	-2.203	-1.002	-0.357	0.869	2.091	0.120	0.061	6.140	-0.359	-1.069	-0.008
2 x 5	-1.544	-0.503	1.241	2.743	-0.061	1.434	0.131	0.227	1.907	2.798	5.271	0.029
3 x 4	-5.021	-2.009	-1.245	-0.103	0.083	0.624	0.192	0.205	2.440	0.097	-7.876	0.097
3 x 5	-2.737	0.057	0.448	-1.553	2.169	2.051	0.083	0.158	4.707	1.161	1.297	0.018
4 x 5	-1.791	1.431	0.295	-0.443	-0.627	-0.756	-0.074	-0.072	0.573	-0.011	1.944	-0.023
Standard of error	3.495	0.738	0.584	0.515	0.637	0.766	0.094	0.083	1.439	1.182	1.430	0.033

The estimation of RCA effect values represent in table [4.6.]. The reciprocal cross 2x1 recorded maximum positive RCA effect values for the characters number of spike/plant, weight of spikes/plant, grain weight/plant and biological weight/plant with 1.600, 2.933, 2.597 and 8.733 respectively. The cross 3x1 recorded maximum negative RCA effect values for the characters number of spike/plant and harvest index with -1.350 and -0.062 respectively. The cross 4x1 gave the highest negative effect value for RCA effect due to the characters plant height and 1000 grain weight recording -9.033, -4.000 respectively. The cross 5x1 gave the highest negative effect value for the character number of grains/spike with -1.683 and also recorded maximum positive RCA effect value for the character average spike weight with 0.117. The cross 3x2 recorded the highest positive RCA effect value due to the characters number of grains/spike, 1000 grain weight and harvest index with 1.733, 5.167 and 0.103 respectively. The cross 5x2 gave the maximum negative RCA value for the characters weight of grains/spike and average spike weight recording -0.167 and -0.200 respectively. The cross 4x3 gave maximum negative RCA effect value for the character spike length with -1.133 and maximum positive RCA value for the character weight of grains/spike with 0.133. The reciprocal cross 5x3 recorded the highest positive RCA effect value for the characters plant height and number of tillers/plant with 5.667 and 1.300 respectively. The cross 5x4 recorded maximum negative RCA effect value for the characters number of tillers/ plant, weight of spikes/plant, grain weight/plant and biological weight/plant with -1.333, -2.933, -2.572 and -5.633 respectively. Positive and negative estimation of RCA effect were recorded for all studied characters due to reciprocal crosses similar result were noticed previously by (mahmood, 2010 ; mohammed, 2012 ; Khoshnaw, 2013).

Table (4.6.) Estimation of RCA effect values for reciprocal cross.

Reciprocal crosses	plant height (cm)	number of tillers /plant	number of spike plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
2 x 1	-5.333	0.067	1.600	2.933	0.283	0.950	0.067	-0.033	1.833	2.597	8.733	-0.023
3 x 1	-3.200	-1.200	-1.350	0.417	0.300	0.250	-0.020	-0.167	1.333	-1.682	0.900	-0.062
4 x 1	-9.033	-1.167	0.267	-0.533	-0.250	-0.917	0.030	-0.083	-4.000	0.599	1.300	0.006
5 x 1	-8.400	-0.167	-0.283	-0.133	-0.433	-1.683	-0.003	0.117	4.167	-0.347	-0.700	-0.007
3 x 2	0.167	-2.233	1.133	0.800	-0.833	1.733	0.100	0.017	5.167	1.898	-5.233	0.103
4 x 2	-0.233	-0.267	-0.483	-0.500	0.567	0.300	0.040	-0.050	0.833	-0.236	1.267	-0.020
5 x 2	-1.383	0.667	0.833	0.050	0.050	-0.967	-0.167	-0.200	-3.333	-0.390	-1.933	0.005
4 x 3	-2.033	1.067	0.533	0.400	-1.133	-0.417	0.133	0.097	1.000	1.593	-1.967	0.100
5 x 3	5.667	1.300	0.833	0.367	-0.067	-1.233	-0.020	-0.067	-0.333	0.967	4.800	-0.013
5 x 4	1.483	-1.333	-1.200	-2.933	-0.150	-1.017	-0.088	-0.033	1.000	-2.572	-5.633	-0.020
Standard error	3.907	0.826	0.653	0.576	0.712	0.856	0.105	0.093	1.609	1.322	1.599	0.037

Table [4.7.] represent the estimation of The variance of general combining ability effect The variance of general combining ability effect effect for the parents. Parent 1 recorded maximum variance due to The variance of general combining ability effect The variance of general combining ability effect effect for the character spike length recording 0.19999, while it recorded the lowest value for The variance of general combining ability effect The variance of general combining ability effect due to the characters number of grains/spike, average spike weight, 1000 grain weight and harvest index. Parent 2 gave the highest value for The variance of general combining ability effect The variance of general combining ability effect due to the character number of tillers/plant recording 0.74419, while it recorded the lowest The variance of general combining ability effect The variance of general combining ability effect value for the characters weight of spikes/ plant, weight of grains/spike and grain weight/plant. The parent 3 exhibited the highest value for The variance of general combining ability effect The variance of general combining ability effect regards to the characters weight of spikes/plant, number of grains/spike, average spike weight and 1000 grain weight recording 3.52188, 0.90377, 0.00554 and 1.79560 respectively. Maximum value due to The variance of general combining ability effect The variance of general combining ability effect effect for the characters plant height, number of spike/plant, grain weight/plant and harvest index recorded by parent 4 with 5.35460, 0.50221, 1.61992 and 0.00105 respectively, in which it recorded lowest value due to The variance of general combining ability effect The variance of general combining ability effect for the characters number of tillers/plant, spike length and biological weight/plant. Parent 5 exhibited the highest value for The variance of general combining ability effect The variance of general combining ability effect effect due to the characters weight of grains/spike and biological weight/plant recorded 0.00700 and 19.97494 respectively, and it recorded the lowest value for the variance of general combining ability effect.

The variance of general combining ability effect due to the character number of spike/plant Parents recorded the high value for the variance of GCA indicate to there contribution in increasing the value of the characters in their hybrids, while the low value of The variance of general combining ability effect The variance of general combining ability effect recorded by the parents indicate to their contribution in the reeducation of the value of these characters in their hybrids. Similar results were recorded previously by (mahmood, 2010 ; mohammed, 2012 ; Khoshnaw, 2013 ; Smith, E. L. and J. W. Lambert 1968 ; Marcial, L. and A. Sarrafi 1996).

Table (4.7.) Estimation of the variance due to GCA effect for the parents.

parents	plant height (cm)	number of tillers /plant	number of spike plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
1	0.36806	0.21349	0.20826	0.49082	0.19999	-0.00702	0.00349	-0.00024	-0.05216	1.22099	15.50553	-0.00005
2	0.03973	0.74419	0.00384	0.02054	0.17306	0.05413	0.00003	0.00191	1.26938	0.00668	0.96563	0.00006
3	3.08354	0.10934	0.11880	3.52188	0.13739	0.90377	0.00499	0.00554	1.79560	1.13630	4.45491	0.00003
4	5.35460	0.10846	0.50221	2.09284	0.04723	0.02581	0.00302	0.00309	1.45604	1.61992	0.37129	0.00105
5	0.39774	0.13739	0.00237	0.99334	0.08841	0.53193	0.00700	0.00532	1.42404	0.71847	19.97494	0.00039

The estimation of the variance due to SCA effect Variance of effect of specific combining ability for diallel crosses for the parents represent in table [4.8.]. Parent 1 recorded maximum value for Variance of effect of specific combining ability for diallel crosses for the characters plant height and spike length with 86.867 and 1.679. Maximum Variance of effect of specific combining ability for diallel crosses value for the characters number of spike/plant, weight of spikes/plant, number of grains/spike, weight of grains/spike, average spike weight, 1000 grain weight, grain weight/plant and biological weight/plant recorded by parent 2 with 1.959, 6.552, 3.068, 0.016, 0.055, 27.644, 6.312 and 36.655 respectively. The highest Variance of effect of specific combining ability for diallel crosses value for the character number of tillers/plant and harvest index recorded by parent 3 with 3.258 and 0.008 respectively. Parent 4 recorded the lowest value for Variance of effect of specific combining ability for diallel crosses for most studied characters which were number of spike/plant, weight of spikes/plant, number of grains/spike, weight of grains/spike, average spike weight, 1000 grain weight, grain weight/plant and biological weight/plant with 0.080, 0.184, 0.309, 0.005, 0.005, 5.128, 0.390 and 2.778 respectively. Parents with the high values due to Variance of effect of specific combining ability for diallel crosses indicate to their contribution in transferring these characters to a few number of their hybrids, while the low value of Variance of effect of specific combining ability for diallel crosses recorded by parents indicate to their contribution to transfer these characters to most of their hybrid. Similar results were obtained previously by (mahmood, 2010 ; mohammed, 2012 ; Khoshnaw, 2013 ; Rohman et. al, 2006 ; Budak, 2000, singh et.al, 1999).

Table (4.8.) Estimation of the variance due to SCA effect for the parents.

parents	plant height (cm)	number of tillers /plant	number of spike plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biologica l weight /plant (g)	Harvest Index (%)
1	86.867	1.753	1.328	3.086	1.679	2.527	0.005	0.037	5.312	4.103	32.100	0.001
2	20.299	1.531	1.959	6.552	0.430	3.068	0.016	0.055	27.644	6.312	36.655	0.001
3	9.132	3.258	1.475	0.966	1.660	2.305	0.014	0.029	17.979	2.003	29.768	0.008
4	24.474	1.307	0.080	0.184	0.515	0.309	0.005	0.005	5.128	0.390	2.778	0.003
5	30.404	1.082	0.825	2.807	-0.100	1.858	0.008	0.017	8.981	2.014	18.798	0.001

The estimation of the variance of specific combining ability for reciprocal crosses for the studied parents represented in table [4.9.] indicating that the parent number 1 exhibited the lowest value the characters number of tillers/plant, spike length, number of grains/spike, weight of grains/spike, average spike weight and harvest index, while the lowest value due to σ^2_{rca} for the characters plant height, weight of spikes/plant, grain weight/plant and biological weight/plant recorded by parent 2. Parent 3 gave the highest value for σ^2_{rca} due to the characters plant height and harvest index with 70.973 and 0.005 respectively, and recorded the lowest value for the character number of spike/plant. Parent 4 gave the highest σ^2_{rca} for the characters number of tillers/plant, number of spike/plant, weight of grains/ spike and 1000 grain weight recording 4.077, 1.336, 0.021 and 19.885 respectively. Parent 5 produced the maximum value for the characters weight of spikes/plant, spike length, number of grains/spike, average spike weight, grain weight/plant and biological weight/plant due to σ^2_{rca} with 5.331, 2.770, 4.767, 0.055, 6.464 and 41.339 respectively, while the lowest value for σ^2_{rca} due to the character 1000 grain weight exhibited by the same parent. Similar result were recorded previously by (mahmood, 2010 ; mohammed, 2012 ; Khoshnaw, 2013).

Table (4.9.) Estimation of the variance due to RCA effect for the parents.

parents	plant height (cm)	number of tillers /plant	number of spike plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
1	55.981	0.604	1.298	2.861	-0.113	1.180	-0.004	0.012	11.539	2.477	25.142	0.001
2	9.937	2.276	1.164	0.751	0.937	1.343	0.014	0.021	13.715	2.352	10.975	0.005
3	70.973	1.190	0.763	1.481	0.906	1.441	0.017	0.044	14.261	3.208	13.654	0.005
4	23.995	4.077	1.336	3.571	0.293	2.216	0.021	0.021	19.885	2.419	32.257	0.003
5	28.611	1.603	1.617	5.331	2.770	4.767	0.014	0.055	8.749	6.464	41.139	0.001

Data in table [4.10.] explain the estimation of some genetic parameters for all studied characters the ratio of σ^2_{gca} /Variance of effect of specific combining ability for diallel crosses was found to be less than unity for all characters, while the value of the average degree of dominance for the diallel crosses were more than unity for all characters and ranged between 1.913 to 8.636 for the characters weight of spikes/plant and plant height, indicating the large contribution of non additive gene effect in the inheritance of these characters. The average degree of dominance for reciprocal crosses was more than unity due to most characters such as plant height, number of tillers/plant, number of spike/plant, number of grains/spike, average spike weight, 1000 grain weight, grain weight/plant, biological weight/plant and harvest index confirming the additive gene effect in the inheritance of these characters, while the value of the average degree of dominance due to reciprocal crosses for the characters weight of spikes/plant, spike length and weight of grains/spike were found to be less than unity indicating the importance of both additive and non additive gene effect in controlling the inheritance of these characters. Heritability in broad sense for diallel crosses were found to be high for all characters, and restricted between 0.737 to 0.968 for the characters harvest index and weight of spike/plant respectively. Heritability in narrow sense for diallel crosses was found to be low for all studied characters and restricted between 0.022 to 0.342 for the characters plant height and weight of spikes/plant respectively. Heritability in broad sense for the reciprocal cross was found to be high for the characters number of spike/plant, weight of spikes/plant, 1000 grain weight and biological weight/plant recording 0.710, 0.940, 0.779 and 0.934 respectively and it was moderate for plant height number of tillers/plant, number of grains/spike, average spike weight, grain weight/plant and harvest index with 0.532, 0.686, 0.656, 0.592, 0.671 and 0.640 respectively, while it was low for the characters spike length and weight of grains/spike with 0.333 and 0.448 respectively. Heritability in narrow sense for reciprocal crosses was found to be low for all characters except the characters weight of spikes/plant and biological weight/plant which were found to be moderate recording 0.630 and 0.524 respectively. Using selection was found to be the best method to improve the characters recording the high value due to the parameter of heritability in narrow sense, while the hybridization method was found to be the best method to improve the characters recording the low to moderate value for heritability in

Narrow sense The non-additive type of gene action was controlled the inheritance of most studied characters, which was similar to the previous works recorded by (Rohman et. al, 2006 ; Budak, 2000, singh et.al, 1999).

High heritability in broad sense were recorded previously by (mahmood, 2010 ; mohammed, 2012 ; Khoshnaw, 2013 ; Chand, N.; S. R. Vishwakarma; O. P. Verma and M. Kumar 2008 ; Boukerrou, L. and D. D. Rasmusson 1990), while heritability in narrow sense was found to be low to moderate for most characters similar results recorded by (mahmood, 2010 ; mohammed, 2012) confirming the suitability of hybridization method to improve these characters.



Table (4.10.) Estimation of some genetic parameters.

Genetic parameters	plant height (cm)	number of tillers /plant	number of spike plant	weight of spikes /plant (g)	spike length (cm)	number of grains /spike	weight of grains /spike (g)	average spike weight (g)	1000 grain weight (g)	Grain weight /plant (g)	Biological weight /plant (g)	Harvest Index (%)
$\sigma^2_{gca} / \sigma^2_{sca}$	0.013	0.069	0.079	0.273	0.050	0.056	0.140	0.041	0.027	0.214	0.199	0.074
σ^2_A	1.874	0.534	0.341	3.500	0.232	0.622	0.007	0.006	2.481	2.037	20.176	0.000
σ^2_{Dr}	15.495	0.953	0.703	1.721	0.022	0.773	0.002	0.006	6.617	1.522	15.785	0.002
σ^2_D	69.870	3.841	2.170	6.408	2.331	5.578	0.026	0.076	46.076	4.764	50.575	0.003
$\bar{a}$	8.636	3.794	3.567	1.913	4.485	4.234	2.677	4.931	6.095	2.163	2.239	3.674
$\bar{a}r$	4.067	1.890	2.031	0.992	0.431	1.576	0.666	1.428	2.310	1.222	1.251	2.796
$h^2_{b.s}$	0.825	0.865	0.855	0.968	0.835	0.894	0.753	0.904	0.949	0.796	0.965	0.737
$h^2_{n.s}$	0.022	0.106	0.116	0.342	0.076	0.090	0.164	0.069	0.049	0.238	0.275	0.095
h^2_{bsr}	0.532	0.686	0.710	0.940	0.333	0.656	0.448	0.592	0.779	0.671	0.934	0.640
h^2_{nsr}	0.057	0.246	0.232	0.630	0.305	0.292	0.366	0.293	0.212	0.384	0.524	0.130
σ^2_G	71.743	4.375	2.511	9.907	2.563	6.200	0.033	0.082	48.556	6.800	70.751	0.004
Mse'	15.268	0.682	0.426	0.332	0.507	0.733	0.011	0.009	2.588	1.748	2.556	0.001

$\sigma^2_{gca} / \sigma^2_{sca}$: The ratio of the variance of general combining ability / The variance of specific combining ability.

σ^2_A : Additive variance.

σ^2_{Dr} :Dominance variance for reciprocal crosses.

σ^2_D : Dominance variance .

$\bar{a}$: Average degree of dominance.

$\bar{a}r$: Average degree of dominance for reciprocal.

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

h^2_{bsr} : Heritability in broad sense of reciprocal crosses.

h^2_{nsr} : Heritability in narrow sense of reciprocal crosses.

σ^2_G : Genetic variance.

Mse' : Revised mean squares of experimental.

The simple correlation coefficient among studied characters represent in table [4.11.]. Highly significant and positive correlation was present between grain weight/plant and the characters grain weight/spike, number of spike/plant, number of grains/spike and biological weight/plant with 0.722, 0.830, 0.519 and 0.640, while it recorded significantly and positively with harvest index recording 0.467. The character 1000 grain weight correlated high significantly and positively with the character grain weight /spike and number of grains/spike recording 0.574 and 0.633 respectively. Grain weight /spike recorded highly significant and positive correlation with number of grains/spike and harvest index with 0.700 and 0.550 respectively. The character number of spike/ plant correlated high significantly and positively with biological weight/plant reaching 0.623. Number of grains/spike gave significant and positive correlation with spike length recording 0.504. Previous researchers confirmed positive and significant correlation coefficients between grain weight and spike length, grain number/spike, grain weight/spike, spike number/plant (Buaklicarpici, and Celik 2012; Bhutta, et al., 2005; Kisana et al., 1999; Samarra, et al., 1987).

Akdeniz, et al., (2004) observed positive and significant correlations between grain yield and plant height, spike length and spike number per m², while they found negative and non significant correlations between grain yield and kernel number per spike.

Positive and significant correlations of grain yield with spike number per m² and 1000-kernel weight were reported by (Ataei, 2006). While Buhtta, et al., (2005), found no significant correlation between grain yield and 1000 grain weight. (Mohammad, 2012) confirmed the presence of highly significant and positive correlation between grain weight/plant, and all its components namely number of spikes/plant, spike length, number of grains/spike, grain weight/spike, 1000 grain weight and biological weight/plant.

Previous workers indicate to the importance of non additive gene effect in the inheritance of grain yield in barely, (Madic, 1995a; Madic et al., 2000; Sharma et al., 2002; Prakash and Sastry, 2003; Rohman et al., 2006; Pal and Kumar, 2009; Kakani et al., 2010; Kakani and Sharma, 2010; Eshghi et al., 2010; and Mahmood, 2010).

However, a preponderance of additive effects were reported by (Prakash et al., 2004; Ali et al., 2007; Eshghi and Akhundova, 2009; Eshghi and Akhundova, 2010; Akgun and Topal, 2011 and Aghamiri et al., 2012), while (Verma et al., 2007b) obtained that additive and non-additive gene action controlling the inheritance of number of grain yield under two divers environments, in barley. However grains yield was determined by genes with additive and non-additive or dominant effects in two-rowed barley (Madic et al., 2007).



Table (4.11.) : Correlation Coefficient.

	Grain Weight / Plant	1000-Grain weight	Grain weight / Spike	No. of Spike / Plant	No. of grains / Spike	Spike length	Biological Weight / Plant	Harvest Index
Grain weight / Plant	1.000							
1000 -Grain weight	0.240	1.000						
Grain weight / Spike	0.722**	0.574**	1.000					
No. of spike / Plant	0.830**	-0.123	0.222	1.000				
No. of grains / Spike	0.519**	0.633**	0.700**	0.166	1.000			
Spike length	0.319	0.191	0.359	0.153	0.504*	1.000		
Biological weight / Plant	0.640**	-0.036	0.291	0.623**	0.278	0.294	1.000	
Harvest Index	0.467*	0.263	0.550**	0.269	0.254	0.049	-0.364	1.000

The path correlation analysis between grain weight/plant and its components was present in table [4.12.], indicating the direct effect and indirect effect in grain weight/plant. Maximum positive direct effect in grain weight/plant recorded by number of spike/plant with (0.532) and followed by the character grain weight/spike with (0.403). The highest positive indirect effect in grain weight/plant recorded by number of spike/plant via biological weight/plant recording 0.331 and followed by grain weight /spike via number of grains/spike recording 0.282. Regards to path coefficient analysis.

Mohammad, 2012 revealed that biological weight showed maximum positive direct effect in grain weight/plant followed by grain weight/spike with values 0.588 and 0.362 respectively. Maximum positive indirect effect value recorded by number of spikes /plant, via biological weight/plant followed by grain weight/spike also via biological weight/plant were 0.498 and 0.437 respectively.

Path analysis for grain yield showed that the biological yield and harvest index had the highest positive direct effect on grain yield at Qilyasan, location with values 0.744 and 0.421, 0.580 and 0.264 and 0.717 and 0.447, respectively. (khoshnaw, 2013).

Table (4.12): Path coefficient.

	1000 -Grain weight	Grain weight / Spike	No. of Spike / Plant	No. of grains / Spike	Spike length	Biological Weight / Plant	Harvest Index	Grain weight / Plant correlation
1000 -Grain weight	0.024	0.232	-0.065	0.011	-0.001	-0.009	0.048	0.240
Grain weight / Spike	0.014	0.403	0.118	0.012	-0.002	0.074	0.101	0.722**
No. of spike / Plant	-0.003	0.090	0.532	0.003	-0.001	0.159	0.050	0.830**
No. of grains / Spike	0.015	0.282	0.088	0.018	-0.002	0.071	0.047	0.519**
Spike length	0.005	0.145	0.082	0.009	-0.005	0.075	0.009	0.319
Biological weight / Plant	-0.001	0.117	0.331	0.005	-0.001	0.255	-0.067	0.640**
Harvest Index	0.006	0.222	0.143	0.004	0.000	-0.093	0.184	0.467*



5. CONCLUSION AND RECOMMENDATIONS

- 1 – The non-additive type of gene effect is considered to be the major source of the genetic variance for the inheritance of all the studied characters, indicating that selection of superior plants should be postponed to later generation.
- 2 – The highly significant mean squares due to genotypes of all characters confirm the necessity of genotypes analysis to know the significance of general and specific combining abilities of each characters.
- 3- Parents 4 and 5 possessed the best combination and superiority for most characters indicating their ability to be concluded in breeding program.
- 4- The crosses 5x2 and 5x4 possessed the best values for most studied characters.
- 5- The differences between diallel and reciprocal crosses, confirm the presence of maternal effect for all characters.
- 6- The large value for average degree of dominance for almost all characters, which were more than unity, confirm the superiority of non-additive gene effect in the inheritance of these characters, makes the hybridization method was most suitable to improve these characters.
- 7- The grain weight/plant correlated positively and high significantly with grain weight/spike, number of spike/plant, number of grains/spike, biological weight/plant. The character number of spike/plant recorded maximum positive direct effect in grain weight/plant, while it has also the maximum positive indirect effect in grain weight/plant via biological weight/plant.

As a recommendation ;

- 1-Continues breeding program required to completion this work, and more investigation are required for the parent 4 and 5 in the region.
- 2-Further works is recommended to fix the desirable genes.
- 3-Hybridization method is recommended to improve the characters measured under the present study.

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