Diallel Cross Analysis In Barley(*Hordeum distichum* L.), Path Coefficient and Stability under different Environmental Conditions in Kurdistan Region, Iraq

A DISSERTATION
SUBMITTED TO THE COUNCIL FACULTY OF AGRICULTURAL SCIENCES
UNIVERSITY OF SULAIMANI
AS A PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR THE DEGREE OF
DOCTOR OF FHILOSOPHY
IN
AGRICULTURE – Field Crops
(PLANT BREEDING AND GENETICS)

By

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2013 A.D. **2713 K.**

SUMMARY

Breeding barley for high yield and other desirable traits is a dire need of the day. A full diallel cross among five cultivars and pure lines of two-rowed barley (*Hordeum distichum* L.) with their twenty F1 progeny were evaluated at Kurdistan Region-Iraq at three different locations, Sulaimani- Qilyasan, Erbil-Girdarasha and Kalar during the winter season 2011-2012 using randomized complete block design with three replications. Various plant phenotypic traits were investigated. Means comparison were carried out using least significant differences (LSD) test ($P \leq 0.05$).The study revealed highly significant mean squares of locations for all studied traits. Qilyasan location exceeded significantly in all studied traits except for the traits, tillers plant^{-1} and spikes plant^{-1}. The data were genetically analyzed for general and specific combining ability (GCA and SCA), nature of gene action, heterosis and heritability using the diallel analysis of Griffing, method 1 (parents, F1 crosses and reciprocals) and model 1 (fixed) (Singh and Chaudhary,1985.) Correlation, path coefficient, stability and genotypic resultant were also estimated. Genotypes mean squares showed highly significant differences for all traits at each location. Mean squares for general, specific and reciprocal combining ability were highly significant for all traits at each location, except , peduncle diameter for SCA at Qilyasan and Erbil which was not significant, while RCA for flag leaf length; peduncle diameter and spike length were also not significant at Qilyasan, harvest index was merely significant; days to anthesis; days to maturity; peduncle diameter and awn length were not significant at Erbil and days to anthesis; days to maturity; grains spike^{-1} and 1000-grain weight were significant at Kalar.

The highest mean values were detected under Qilyasan, Erbil and Kalar conditions by parents 4, 3 and 5 for grain weight plant^{1-} and most studied traits, respectively. The maximum mean values were exhibited under Qilyasan condition by the cross 1x4, while under Erbil condition by the cross 3x4 and under Kalar condition by the cross 2x3. The reciprocal crosses 4x2, 5x2 and 4x2 gave maximum mean values for grain yield plant^{1-} and most studied traits under Qilyasan, Erbil and Kalar condition, respectively.

Heterotic patterns revealed that twelve, eight and thirteen hybrids out of twenty had positive percentage heterosis values for grain weight plant^{1-} which ranged from 1.568 to 59.372%, 4.486 to 33.102% and 6.154 to 48.734%, the hybrids 1x4, 5x2 and 4x1 were the best for grain yield plant^{-1} and most of the studied traits under Qilyasan, Erbil and Kalar conditions, respectively.

Analysis of variance revealed significant differences for GCA and SCA, indicating presence of additive as well as non-additive gene action and genetic variance analysis showed that over-dominance genetic effects were important for the expression of most traits at all locations except flag leaf length, peduncle diameter at the three locations, days to maturity at Qilyasan and Kalar, peduncle length and average spike weight at Erbil, which additive type of gene action were important.

The analysis of combining ability effects revealed that parents 4 and 5 at Qilyasan, parents 5 and 3 at Erbil and parents 2 and 3 at Kalar proved the best general combiners for most traits. These best parents can be used in hybridization program for obtaining desirable combinations. The diallel crosses 1x4, 3x5 and 1x5 at Qilyasan, 2x5 and 2x3 at Erbil and 1x4 and 1x5 at Kalar exhibited highest SCA effects which seemed to be best specific combiners for most traits. The reciprocal crosses 4x1 at Qilyasan, 4x2 at Erbil and 3x1 at Kalar exhibited highest RCA effects that seemed to be best specific combiners and these crosses may be utilized extensively in future breeding. The variance of general combining abilities effect σ^2gca revealed that parents 3 at Qilyasan, parents 5 at Erbil and parent 1 at Kalar possessed the highest values. Results of the variance of specific combining abilities effect σ^2sca revealed that parents 1 at Qilyasan, parents 2 at Erbil and parent 3 at Kalar possessed the highest values.

Results of the variance effect of RCA revealed that parents 3at Qilyasan, parents 5 at Erbil and parents 1 at Kalar possessed the highest values for grain yield plant^{-1} and most yield components. Average degree of dominance values due to the diallel crosses were less than unity for flag leaf length, peduncle diameter at the three locations, days to maturity at Qilyasan and Kalar, peduncle length and average spike weight at Erbil showing partial dominance and greater than unity showing over dominance in all rest traits at all locations. Heritability in broad - senses was found to be moderate to high in the studied traits, while it was low to moderate in narrow- senses in most cases, confirming the suitability of hybridization methods in improving these traits.

The simple correlation coefficient was calculated between grain yield plant^{1-} and its important components at each location. biological yield, tillers plant^{-1} and spikes plant^{-1} were positively and high significantly correlated with grain yield at all locations. Path analysis for grain yield showed that the biological yield and harvest index had the highest positive direct effect on grain yield at Qilyasan, Erbil and Kalar locations with values 0.744 and 0.421, 0.580 and 0.264 and 0.717 and 0.447, respectively.

The study of stability and genotypic resultant revealed the presence of highly significant effects due to genotypes x locations in all studied traits with exception of the peduncle diameter which was merely significant. Peduncle diameter had the highest stability and genotypic resultant with average values 0.951 and 0.951, respectively , while grain yield plant^{-1} manifested the lowest were 0.459 and 0.450, respectively. Better genotypic resultant were observed in two genotypes *viz.*, parent 3 and hybrid 5x2 having high grain yield plant^{-1} value with 0.602 and 0.567, respectively. These were found promising for wide adaptation over sites across environments.

ACKNOWLEDGEDGENTS

I have no words to express my deepest sense of gratitude and numerous thanks to Almighty Allah, who enabled me to complete this study.

1 wish to express my thanks and profound gratitude to my supervisor Dr Hussain A.Sadalla for his kindness, continuous guidance, inspiration during the course of my studies and reviewing the manuscript. I thank Dr Sherwan E.Tawfiqe for his generous support of my genetics research projects; I always found discussions with him very valuable. Not just the ones about my work, but certainly also those on science and life in general. I am highly thankful to Dr Aram Abbas Mohammed, Dean of Faculty of Agricultural Sciences, Dr Abdul-salam Abdul-rahman Rasool, former Head of Field Crops Department and Dr Ahmad Hama Amine, Head of Field Crops Department. We had many good meetings, and as we got along very well the cooperation has been a pleasure. I want to thank Dr Nawroz Abdul-razzak and Dr Dana Azad for their sacrifice and support in data analysis and making the write up a success.

I am deeply grateful to Mr. Khalel for their help with the experiment at Kalar. I am also grateful to Dr Ibraheem Maaroof for linguistic evaluation of my dissertation and Dr. Hussain M. Azez for summary kurdish translation.

I want to thank all colleagues and members from the Department for Field Crops. In particular, I am grateful to Miss. Ronak Ahmed , Mr. Omar A. Kareem, Dr. Araam O. Mohamad and Mr.Fawzee F.Khorshed for a nice and friendly companion.

I would especially like to take this opportunity to thank my wife for her understanding, encouragement and support during the course of this study.

I am grateful to my, brothers Salah Al-deen and Sabah and sisters Kaban and Jehaan.

Kamil Khoshnaw

DEDICATION

To my wife, for her patience and understanding.

To my daughters Vian and Jwan.

To my sons Alan, Dilshaad, Ali and Azad.

Kamil

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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
GCA	General combining ability
gi	General combining ability effect
$h^2b.s$	Heritability in broad sense
$h^2n.s$	Heritability in narrow sense
H	Hemostats
MSe	Revised mean squares of experimental error
RCA	Specific combining ability for reciprocal crosses
ri	Reciprocal combining ability effects
SCA	Specific combining ability for diallel crosses
si	Specific combining ability effects
σ^2 P	Phenotypic variance
σ^2 A	Additive variance
σ^2 D	Dominance variance
σ^2 Dr	Dominance variance for reciprocal crosses
σ^2 e	Mean squares of experimental error or (Environmental variance)
σ^2GCA (σ^2gi.)	The variance of effect of general combining ability
σ^2RCA(σ^2ri.)	The variance of effect of specific combining ability for reciprocal crosses
σ^2SCA(σ^2si.)	The variance of effect of specific combining ability for diallel crosses
σ^2G	Genetic variance

بِسمِ اللهِ الرَّحمن الرَّحيم

سُبْحَانَ الَّذِي خَلَقَ الْأَزْوَاجَ كُلَّهَا مِمَّا تُنْبِتُ الْأَرْضُ وَمِنْ أَنْفُسِهِمْ وَمِمَّا لَا يَعْلَمُونَ.

صدق الله العظيم

يس ﴿٣٦﴾

Introduction

Barley (*Hordeum vulgaer* 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). Two-row barley (*Hordeum distichum* L.) with spikelets are arrange in triplets which alternate along the rachis only the central spikelet is fertile, while other Spikelets are arranged in triplets which alternate along the rachis. Recent genetic studies have revealed a mutation in one gene, *vrs1*, is responsible for the transition from two-row to six-row barley (Komatsuda *et al.*, 2007) .

Barley is highly variable in adaptation and utilization alone have cased barley to be subjected to much physiological and genetic researches, on the other hand, the high diversity of barley phenotypes, true diploid nature, ease of hybridization and cultivation has made barley a favorite genetic organism since easily mutated, self – fertile and has large chromosomes (6-8µm) and has seven pairs of distinct chromosomes (Nilan, 1964 and Ramage, 1985). There is a long history of genetics research focused in trait inheritance and mapping in the conventional sense (Smith 1951), also more recently on molecular and physical mapping and genetic analysis (e.g., Graner *et al.*,1991; Hayes *et al.*,1993; Kleinhofs *et al.*,1993; Yu *et al.*, 2000; Kleinhofs and han, 2002; Caldwell *et al.*,2004; Druka *et al.*, 2006; Varsheny *et al*, 2007; Hamblin *et al.*, 2010 and Massman, *et al*., 2011).

Barley is most widely adapted cereal grain species with good drought, cold, and salt tolerance (Ullrich, 2011).

Barley is grown worldwide in many countries and regions with temperate and subtropical climates. Barley in recent years has been the forth most- produced cereal after maize, rice and wheat with average of 8 years (2000 – 2008) by140, 672 , 609 and 598million Mt, respectively (Ullrich, 2011). Barley has remained as a major food source in western and eastern Asia as well as in Himalayan nations and in northern and eastern Africa (Grando and Gomez, 2005).

To increase the yield of barley, certain information required regarding the nature and magnitude of gene actions involved in the expression of quantitative traits of economic importance in a hybridization program. 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 (Ullrich, 2011).

Improvement in the productivity of a crop involves multi-directional approaches including a thorough understanding of the genetics and related aspects of the crop under consideration. Productivity is the ultimate result of action and interaction of several yield related traits. Such traits have polygenic control and cannot, therefore, generally be identified individually. Identification of genetically superior parents is an important prerequisite for developing promising strains. For this, combining ability analysis provides useful information so as to select suitable parents for a hybridization program. Furthermore, combining ability analysis also provides useful information about the nature and magnitude of the various types of gene effects involved in the expression of different quantitative traits. The knowledge on nature and magnitude of gene effects controlling inheritance of traits related to crop productivity will in turn become helpful in formulating an effective and efficient breeding program. Such knowledge not merely gives an idea about the relative importance of different types of gene effects for controlling the traits, but can also elucidate the cause(s) of heterosis and inbreeding depression. Several biometrical procedures have been utilized to provide unbiased detection and precise estimation of the different components of genetic variation. The diallel analysis (Jinks and Hayman, 1953; Hayman, 1954a and b; Griffing, 1956a and b and Gardner and Eberhart, 1966) provides a unique opportunity to test a number of genotypes in all possible combinations.

Grain yield is a complex trait made up of the interaction between different yield components and the environmental effects. Several studies in recent years have identified quantitative trait loci (QTLs) for yield and its components in barley. Li *et al.* (2006) reported several QTLs for yield and its components. Additionally, study by Babb and Muehlbauer (2003) have resulted in identification of major QTL low number of tillers.

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, 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).

There is an increasing number of phenotypic stability measures used to assess the response of genotypes when grown in different environments. El-Sahookie and Al-Rawi, (2011) summarized genotype-by-environment (GxE) interaction through stability and genotypic resultant.

The main aim of the present study is to identify genetic architecture and the best combiner parents and their crosses on the bases of their general and specific combining ability of different important traits of two-row barley in different location (environments) for further improvements in grain yield and its components under condition in Kurdistan region -Iraq.

REVIEW OF LITERATURE

2.1 Diallel crosses:

A diallel cross is a mating scheme used by plant breeders, as well as geneticists, to investigate the genetic underpinnings of quantitative traits. There are four main types of diallel mating design :

1. Full diallel in which parents and reciprocal crosses are involved along with F1.
2. Half diallel with parent and without reciprocal crosses.
3. Full diallel without inclusion of parents.
4. Half diallel without parents or reciprocal crosses.

In a full diallel, all parents are crossed to make hybrids in all possible combinations. Full diallels require twice as many crosses and entries in experiments, but allow for testing for maternal and paternal effects (Crusio, 1987). If such "reciprocal" effects are assumed to be negligible, then a half diallel without reciprocals can be effective. A maternal effect, in genetics, is the phenomenon where the genotype of a mother is expressed in the phenotype of its offspring, unaltered by paternal genetic influence. The phenotype of an individual therefore reflects the genotype of its mother, rather than the genotype of the individual. This maternal effect is usually attributed to maternally-produced molecules, such as mRNAs, that are deposited in the egg cell. Maternal effect genes often affect early developmental processes. Another mechanism for the specific expression of genes from one parent is stable epigenetic modification of germ line genes in one of the sexes (Mann, 2001). This form of a parental effect is termed "genomic imprinting".

"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 inheritance the individual's phenotype reflects its own genotype, rather than the genotype of a parent. In contrast, a paternal effect is when a phenotype results from the genotype of the father, rather than the genotype of the individual (Yasuda *et* al., 1995). Common analysis methods utilize general linear models to identify heterotic groups (Griffing, 1956b), to estimate general or specific combining ability (Gardner and Eberhart, 1966 and Sparague and Tatum, 1942), to estimate interactions with testing environments and years, or estimation of additive, dominant, and epistatic genetic effects (Hayman, 1954a and 1954b) and genetic correlations (Crusio, 1993). Further advancement in yield of this important cereal species requires information regarding the nature of combining abilities in a wide array of genetic materials to be used as parents in the hybridization programmes, as well as the nature of gene action involved in the expression of quantitative traits of economic importance (Sharma *et al.*, 2002). It has become a common practice of the plant breeder working with autogamous crops to obtain genetic information from diallel cross progenies. With this information, the breeder can device the best strategy for selecting parents and the most efficient breeding method, which would guarantee better selection and identification of superior plants in the early segregating generations of a cross.

The first whom used diallel cross were (Sparague and Tatum, 1942) working on maize to determine the general and specific combining ability. (Jinks and Hayman, 1953) by laiding 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 Weises, 1958 on soybeans ; Aksel and Johnson, 1961; and Aastveit,1961 on barley; Dickson, 1967 on snap beans). Several authors have stressed the importance of determining the nature and inheritance of the components of yield in barley and other characteristics, e.g. (Riggs and Hayter, 1973) had applied untransformed data for number of grains per ear in spring barley; (Sharma *et al.,* 2003) had analyzed for the combining ability of quantitative traits in six-rowed barley for the F1 and F2 progenies of a ten-parent diallel crosses (excluding reciprocals); (Madić *et al.,* 2006) selected five divergent genotypes of two-rowed winter barley for diallel crossing in order to study the mode of inheritance, the gene effect and the components of genetic variance for the productive tillering in F1 and F2 generations; (Eshghi and Akhundova, 2009) had evaluated eight-parent diallel, involving hulless barley varieties to determine the genetic parameters contributing to plant height, days to maturity, number of tillers, number of grains per spike and grain yield per plant. Furthermore, generation mean and variance analysis were carried out on six generations (P1, P2, F1, F2, BC1 and BC2); (Aghamiri *et al.*, 2012) was evaluated seven cultivars (parents) and progeny F1 of barely, considering the significance of the variance of genotypes, (Crusio,1987) was used Hayman method to calculate the trait controlling genetic parameters including additive effect, dominance effect, average dominance degree, number of trait controlling genes, the ratio of the genes having positive and negative effects in parents, broad-sense and narrow-sense heritability and graphic analysis.

2.2 Combining ability:

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 b). Diallel analysis of self- and cross-pollinating populations is used to study the genetic control of quantitative traits (Jinks and Hayman, 1953; Hayman, 1954, 1958) to assess general and specific combining abilities (Griffing 1956a, b). Regarding cross-pollinating species, the general combining ability (GCA) effect is an indicator of the relative value of the population in terms of frequency of favorable genes and of its divergence, as compared to the other parents in the diallel. Thus, the analysis of GCA effects allows identification of superior parents, to be used in intra-population breeding programs. The specific combining ability (SCA) effect of two populations expresses the differences of gene frequencies between them and their divergence, as compared to the diallel parents. It was with such a system that the terms general and specific combining ability were originally defined by (Sprague and Tatum,1942). They defined the terms as follows: "The term 'general combining ability' is used to designate the average performance of a line in hybrid combination. The term 'specific combining ability is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved. Therefore, the GCA and SCA effects should be considered in the selection of populations for hybrid production and for reciprocal recurrent selection programs. In addition to being indicators of the divergence of each population compared to the diallel parents, the SCA effects of a population with itself allow assessment of the predominant direction of the deviations due to dominance (Cruz and Vencovsky, 1989 and Viana, 2000b).

It has become a common practice of the plant breeder working with autogamous crops to obtain genetic information from diallel cross progenies. With this information, the breeder can device the best strategy for selecting parents and the most efficient breeding method, which would guarantee better selection and identification of superior plants in the early segregating generations of a cross. It is experimentally proven that general and specific combing ability effects are very effective genetic parameters in deciding the next phase of the breeding programme for autogamous crops. According to (Arunachalam, 1976 and Baker, 1978), combining ability is a better biometrical tool than diallel cross analysis, line x tester analysis, and generation mean analysis in plant breeding. Combining ability is most helpful in determining the appropriate parents of a cross. It also indicates the appropriate breeding approaches for handling a cross to develop a cultivar. Success of any plant breeding programme depends on the choice of appropriate genotypes as parents in the hybridization programme. The combining ability studies of the parents provide information which helps in the selection of better parents for effective breeding. Combining ability analysis also provides information on additive and dominance variance. Its role is important to decide parents, crosses and appropriate breeding procedure to be followed to select segregants (Salgotra *et al*., 2009).

In a 6 x 6 half diallel study in barley was performed for yield and other quantitative traits, the GCA and SCA components were highly significant for all the traits of the study. For the traits *viz.* grain yield, plant height, spike length, tillers per plant, spikelets per spike and grains per spike, the GCA component of variance was higher than the SCA component indicating preponderance of additive gene effect. The parent RD 31 was good general combiner for grain yield per plant, spike length, tillers per plant, spikelets per spike and grains per spike. The crosses RD 103 x BL 2, RD 2052 x RD 103 and RD 2052 x RD 2433.were the best specific cross combinations for most of the traits under study (Prakash *et al.,* 2004).

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).

Combining ability effects study was conducted through line x tester analysis under normal fertile and saline sodic soil environments. The analysis of variance for combining ability showed that variances due to GCA and SCA were significant for the traits like days to maturity, plant height, length of main spike, grains per spike, seed yield per plant, 1000 seed weight, under both normal fertile and saline sodic soil conditions. Significant GCA values indicated the importance of additive or additive x additive gene effect. The component of variation due to SCA was higher than GCA for all the characters (previous and number of effective tillers/plant) in all the environments indicating the predominance of non-additive gene action (Verma *et al.,* 2007b).

10 F1 and F2 hybrids were obtained through 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 were made following the method 2, mathematical model I, for the incomplete diallel. Highly significant differences was 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).

In twenty one genotypes of six – parent half diallel were analyzed for estimating gene effects of variance, combining ability and standard heterosis for forage yield per plant, days to 50% heading, tillers per plant, plant height, ear length, spikelets per ear, biological yield per plant and grain yield per plant in barley. The analysis of variance for combining ability revealed significant mean squares due to GCA for all traits except grain yield per plant and SCA for all the traits, indicating importance of both additive and non–additive gene effects in the expression of these traits. However, the ratio of additive genetic variance to total genetic variance was less than unity, indicating the predominant role of non additive genetic components in the inheritance of all the traits except spikelets per ear (Pal and Kumar, 2009).

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 (H1and H2), 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 study (Akgun and Topal, 2011).

2.3 Genotype-by-environment interactions:

The choice of an efficient breeding program depends to a large extent on the knowledge of gene action involved in the expression of the traits. Different genetic cross designs such as generation mean, line x tester and diallel analysis were used to estimate gene action of yield and its components in barley. Among these methods, 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. Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic dependent 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. The potential of germplasm is best evaluated under a wide range of environmental conditions, so that the range of expression of important traits may be observed and genotype x environment interactions studied (Ceccarelli, 1996 and Acquaah, 2007).

In barley breeding and in many aspects of barley research, the analysis of genotype-by-environment interactions (GEIs) is of primary importance, as it is also for other crops (Ceccarelli, 1996; Annicchiarico, 2002 and Voltas *et al.,* 2002b). This issue is particularly critical in Mediterranean areas, where barley growth often progresses under the harmful influence of drought and high temperatures, and inter-annual changes in climate factors can occur (Voltas *et al.,* 1999a, b). Therefore, experimental research needs to be carried out over multiple environment trials in order to identify and analyse the major factors that are responsible for genotype adaptation (Delacy *et al.,* 1996).

It is a general agreement that germplasm diversity and genetic relatedness among elite breeding material is the fundamental element in plant breeding (Mukhtar *et al*., 2002). A genotype x environment (GE) interaction for yield has been reported in barley (Rasmusson and Lambert, 1961) and they detected a highly significant genotypic response to specific environmental conditions which was not accounted for by either year or location groupings in a 4-yr study of six barley genotypes at eight locations in Minnesota, while (May and Kozub, 1993) detected that no single genotype was superior over all locations, and the groupings of genotypes for similarity of response at locations were not consistent for year. They indicated that genotypes selected on the basis of main effect means may not be those selected from a detailed consideration of the GE interaction structure studied by them to evaluate genotype x environment interactions with respect to barley genotype selection from nine test sites and ll entries over two 3-yr spans was used. Genotype x location x year interactions .

Kaczmarek *et al*. (2002) observed that barley doubled haploids covering a wide range of malting quality, along with their parental cultivars and F2, F3 hybrids, were investigated in six environments (three locations and two years) to study the genotype-environment (G × E) interaction structure and the influence of environments on additive, dominance and epistatic gene effects. Grain and 1000-grain weight were measured. Main effects for genetic parameters were estimated to explain the interaction of gene effects with environments. The results showed that additive effects had the greatest interaction with environments for all the analyzed traits. Interaction of dominance effects was much lower and only in the case of 1000-grain weight, the results suggested that effects of heterozygous loci are more stable in contrasting environments than effects of homozygous loci.

2.4 Gene action (Genetic variance components) and average degree of dominance:

Genes are the functional units that govern the development of various traits of an individual. Gene action refers to the behavior or mode of expression of genes in a genetic populations. Genes control synthesis of proteins which in turn control expression of various traits of an organism. Knowledge of various types of gene action and their relative magnitudes in controlling various traits is basic to 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. 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).

There are four types of gene action : **additive** (when each additional gene enhances the expression of the trait by equal increments), **dominance** (is described the relationship of alleles at the same locus), **epistatic** (is described as non-allelic gene interaction), and **over-dominance** (exists when each allele at a locus produces a separate effect on the phenotype, and their combined effect exceeds the independent effect of the alleles). Because gene effects do not always fall into clear-cut categories, and quantitative traits are governed by genes with small individual effects, they are often described by their gene action rather than by the number of genes by which they are encoded. It should be pointed out that gene action is conceptually the same for major genes as well as minor genes, the essential difference being that the action of a minor gene is small and significantly influenced by the environment (Acquaah, 2007).

Additive genetic variance is of universal occurrence in plant breeding populations. Non-additive variance also exists, but is generally, smaller in magnitude than 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).

Evidence was presented that the gene for yield *per se* do not exist in barley. Hence, yield is an artifact. If there are no genes *per se* for yield, there can be no dominance effect due to yield genes, or for that matter no over dominance of yield genes or heritability of yield. F1 vigor was shown to be due to epistasis. A large share of the F1 vigor in this experiment was shown to be fixable in a true breeding form (Grafius, 1959). For grain yield, the dominance + epistatic gene effect were more importance (Sharma *et al.*, 1978; Verma and Gulati ,1976; Prakash and Sastry, 2003; Sharma *et al.*, 2002; Rohman *et al.*, 2006; Kakani *et al*., 2007; Mahmood, 2010 and Fatieh, 2012), while the additive gene effect was most important in other studies (Baier, 1978; Fejer and Fedak, 1978; Yap and Harvery, 1972; Prakash *et al*., 2004; Ali *et al*., 2007; Eshghi and Akhundova, 2009, 2010; Akgun, and Topal, 2011; and Aghamiri *et al*., 2012). In some additional studies SCA and GCA were equal importance (Nasr and Kharalla, 1976; Sharma, 1978; Gurpreet, 2005 and Verma *et al*,. 2007b). In studies evaluating the effects of environment, SCA was affected more than GCA by environmental changes (Conti, 1974 and Yap and Harvey, 1972), while in other studies the opposite was true (Singh, 1979 and Upadhaya and Rasmusion, 1976). GCA and SCA effects were equally affected in the experiments of (Sharma *et al*., 1978).

Yap and Harvey (1971) reported that the major portion of the genetic variance for the traits grain yield, yield components, 1000-kernel weight, number of kernels per head, number of heads per unit area, heading date and plant height were due to variation in general combining ability, indicating that additive gene action for the six agronomic traits was more important than non-additive gene action. Moreover, general combining ability effects were less susceptible to environment than the specific combining ability effects.

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.

Diallel analysis was applied to untransformed data for number of grains per ear in 2-row spring barley, so analysis of variance of the 2-row populations revealed complete dominance acting in the direction of greater number of grains per ear. Estimation of genetic components confirmed that a high level of dominance was operating in the inheritance of this character. Significant interactions were detected between additive and non-additive effects at F1 and years in analysis conducted over both seasons (Riggs and Hayter, 1973).

In a 6 x 6 diallel cross (excluding reciprocal) of barley (*Hordeum vulgare* L.), Rohman *et al.*, 2006 dictated that both additive and non-additive components were important but dominance components were more predominant than additive one in controlling the inheritance of the traits days to maturity, plant height, tiller/plant, grain/spike, 1000 grain weight and grain yield/plant.

Generation mean analysis was carried out in two crosses of barley, revealed that among the main effects, dominance was more important than the additive effect due to higher magnitude for days to flowering, awn length, spikelets per spike grain filling period, 1000-grain weight and grain yield per plant. Among the epistatic effects, additive x additive was more important as compared to additive x dominance and dominance x dominance components. Absolute values indicated that non-fixable gene effects were more important for the inheritance of traits studied. (Prakash *et al.,* 2005).

In a eight-parent diallel, involving hulless barley varieties. Eshghi and Akhundova (2009) noticed that the additive gene action was more important than non-additive gene action for plant height, number of tillers and days to maturity and over-dominance gene action for number of grains per spike.

In three barley crosses involving four diverse parents under three fertility environments, Prakash and Sastry (2003) reported that dominance main effect and additive x additive type of epistatic gene action were found important in controlling inheritance of effective tillers per plant, 1000- grain weight and grain yield.

In 10 x 10 half-diallel progenies (F_1) of six-row barley for grain yield and its component characters, Sharma *et al*. (2002) reported that predominance of non-additive gene effects for the traits days to heading (75%), plant height, tillers per plant, flag leaf area, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight , harvest index (%), and grain yield per plant.

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 F1 and F2 generation. The variability of the investigated trait differed. Different modes of inheritance (partial dominance, dominance and overdominance) and partial dominance were found in the F1 and F2 generation, respectively. The genetic variance components, average degree of dominance indicated partial dominance in the inheritance of tillering (Madic *et al*., 2006).

In a nine diverse parents of barley and their 36 F1 progenies, there indicated significant differences among the parents for GCA and among crosses for SCA components of variance for traits namely, days to maturity, plant height

, effective tiller per plant, biological yield ,grain yield per plant and harvest index. The GCA\SCA ratio showed preponderance of non-additive gene action for above characters. However, additive gene action was more pronounced for days to heading and test weight (Kakani *et al*., 2007).

In a six diverse parents full diallel cross of two-rowed barley and their 30 F1 progenies at Kalar. Mahmood (2010) reported the importance of non-additive effect for the characters required days to 50% anthesis, plant height, number of fertile tillers 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 and flag leaf area, while the importance of additive effect for the character 1000-grain weight was observed.

In a five diverse parents full diallel cross of six-rowed barley and their 20 F1 progenies at Qilyasan, Fatieh (2012) reported the importance of non-additive effect in the inheritance of the characters No. 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.

2. 5 Heritability:

Statistics is indispensable in plant breeding. Breeders conduct genetic analysis to understanding the inheritance of the traits they desire to manipulate. They use statistics to help identify parents to use in crossing, to evaluate the products of crossing, and to guide the selection process, as well to evaluate finished products (cultivars) for release to producers. Some of these analysis are based on the genetic structure of the plant populations. Most of the traits that plant breeders are interested in quantitatively inherited. It is important to understand the genetics that underlie the behavior of these traits in order to develop effective approaches for manipulating them (Bouzerour and Djakone, 1998 and Acquaah, 2007).

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.

Heritability is a property of the trait, the population, and the environment. Changing any of these factors will result in a different estimate of heritability. There are two different estimates of heritability. **1 Broad sense heritability**. Heritability estimated using the total genetic variance (VG) is called broad sense heritability. It is expressed mathematically as: $H = V\mathrm{G}/V\mathrm{P}$ It tends to yield a high value. Some use the symbol H^2 instead of H. **2 Narrow sense heritability**. Because the additive component of genetic variance determines the response to selection, the narrow sense heritability estimate is more useful to plant breeders than the broad sense estimate. It is estimated as: $h^2 = V\mathrm{A}/V\mathrm{P}$. The estimates are expressed as a fraction, but may also be reported as a percentage by multiplying by 100. A heritability estimate may be unity (1) or less. The magnitude of heritability estimates depends on the genetic population used, the sample size, and the method of estimation. Common methods include the variance component method and parent–offspring regression. Heritability estimates are useful for breeding quantitative traits. The major applications of heritability are: **1)** To determine whether a trait would benefit from breeding. **2)** To determine the most effective selection strategy to use in a breeding program, and **3)** To predict gain from selection (Acquaah, 2007).

Trehen *et al.* (1970) observed high estimates of heritability in broad sense as percent of mean for tillers per plant, peduncle length, ear length and grain yield per plant. Setti *et al.* (1972) working with hulled barley, reported that yield per plant, plant height, number of tillers per plant, grains per plant, days to flowering and test weight showed high heritability (h^2). Meiqin *et al*. (1991) noticed that the characters flag-leaf length, peduncle diameter and peduncle length had higher heritabilities in narrow sense. Adamski *et al.* (1996) observed that heritability coefficient appeared to be highest for 100-grain weight (80%). Fregeau *et al.* (1998) reported high heritability estimates (71- 93%) for grain number per spike in crosses between multi-rowed barley types. Mean heritability values for grain weight per spike were obtained by (Bouzerzour and Djakoune ,1998). Bichonski (2003) observed that heritability was high for 1000-grain weight. Different heritability estimates for different barley traits were also reported by (Bhantagar *et al.,* 2001 and Sharma and Sharma, 2008). Mariey (2004) found that heritability values in narrow sense were relatively high for plant height, no. of tillers per plant, number of spikes per plant, spike length and no. of seeds per spike under normal condition in barley. Al-Yassin *et al.* (2005) observed that broad-sense heritability in the individual year-location combinations varied from 0 to 0.68. Mohammadi *et al.* (2006) studied 158 double haploid barley at 2 locations for drought tolerance, highest heritability was obtained for 1000-kernal weight, followed by days to heading in both environments, indicating that these traits are controlled by additive gene effect. Ali *et al.* (2009) found that narrow sense heritability values were detected for all the studied traits which ranged between 1.40% and 72.75% under normal conditions and between 4.21% and 65.55% under stress condition. These results indicate that most of the genetic variance might be due to additive type of gene action. This is an indicator of the efficiency of selection procedure in identifying the superior genotypes; hence, selection in these characters in early generations might be effective.

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 highest heritability. In the year-I, high heritability was observed for grains per spike, grain yield plant^{-1}, length of awn, length of flag leaf, spike length, ear bearing tillers, peduncle length, number of tillers plant^{-1} and days to maturity. In year-II, more characters had high heritability. The highest heritability estimate was recorded for number of grains spike^{-1}. In the year-II, high heritability coupled with high genetic advance was observed for number of grains spike^{-1} followed by grain yield plant^{-1}, 100- grain weight, plant height, flowering days, peduncle length, length of spike, awn length, days to maturity, flag leaf length and earbearing tillers. In pooled data, heritability estimates was highest for number of grains spike^{-1}. In this study, high heritability along with high genetic advance was observed for number of grains spike^{-1} while high heritability along with low genetic advance was observed for days to maturity and grain length. El-Aty *et al.* (2011) by using the six generations (P_1, P_2 , F_1 , F_2, BC_1 and BC_2) of five barley crosses, observed that heritability estimates in narrow sense were low to moderate for the characters days to heading, days to maturity, flag leaf area, total chlorophyll content plant^{-1}, plant height, spike length, number of spikes plant^{-1}, number of grains spike^{-1}, 100-grain weight and grain yield plant^{-1}, in all crosses, ranged from 16.37% for spike length in the fifth cross to 66% for days to heading in the second cross, indicating that these characters were greatly affected by non-additive and environmental effects. By means of 9x9 half diallel (F1 and F2) progenies under four diverse environments, 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.

More recently, Aghamiri *et al*. (2012) studied the quantitative traits in seven cultivars of barley with their F1 progeny using Hayman and Jinks method, and showed that the highest and lowest values of broad sense heredity were reported to be for the traits spike length (88%), and peduncle length (70%). Moreover, the highest value of narrow-sense heredity belonged to seed yield and spike weight (72%), and the lowest value of the same to the trait awn length (35%). Madic *et al*. (2012) working in crossing multi- and two-rowed barley cultivars, and reported that the average heritability values for spike length in F1 and F2 generations were intermediate or close to those of the parent having longer spikes, with the mode of inheritance being partial dominance, dominance or over-dominance, depending on the crossing combination. The six-rowed x six-rowed and two-rowed x two-rowed crossing combinations showed dominance of increased grain number spike^{-1} and increased grain weight spike^{-1}in the inheritance of grain number spike^{-1} and grain weight spike^{-1},respectively, whereas the six-rowed x two-rowed cross was predominated by partial dominance. The high values of heritability for grain number spike^{-1} and grain weight spike^{-1} suggested significant differences in the genetic constitution between the parents and implied that their progeny will have most of the parental traits.

2. 6 Heterosis:

Heterosis is perhaps one of the greatest practical achievements of the science of plant breeding and has been extensively used in crop improvement. Therefore, an understanding of its potential genetic basis is imperative.

The phenomenon of heterosis has been a powerful force in the evolution of plants and has been exploited extensively in crop production (Birchler *et al.*, 2003). In fact, the exploitation of heterosis has been the greatest practical achievement of the science of genetics and plant breeding (Alam *et al.,* 2004).

For development of superior and heterotic hybrids in two-rowed barley, it is essential to evaluate large number of available germplasm under diverse environments. Rasmusson (1985) reported that commercial hybrid barley production depends upon the degree of heterosis, frequencies of cross pollination, availability of a practical system for inducing male sterility and /or restoring fertility, and achieving acceptable quality for product end-use.

Shull (1914) first defined this phenomenon. East (1936) also reported that heterosis was due to multiple alleles at a locus differentiating with respect to their physiological function. These explanations gave rise to the over-dominance hypothesis for heterosis. Hull (1945 and 1946) argued for over-dominance stating that additive gene action contributed to heterosis. A breeding experiment was designed to discriminate between dominance and over-dominance using the regression of the F1 on the value of one parent when the other parent is held constant. Heterosis is defined as the increased vigour of the F1 generation over the mean of the parents or over the better parent (Hayes *et al*., 1955). High parent heterosis is the comparison of hybrid performance with that of the better parent in the cross. Formula suggested by (Liang *et al.,* 1972) was used for the estimation: H (%) =(F1-HP/HP)x100. H% = percentage deviation of F1 over better parent, HP = performance of the better parent, and F1 = mean performance of hybrid formed between the i^{th} and the j^{th} parents. The terms relative heterosis and heterobeltiosis refer to the heterosis over mid and better parental values respectively. Falconer (1981) coined that heterosis or hybrid vigour when inbred lines are crossed; the progeny shows increase of characters that previously suffered reduction from inbreeding. In general terms, the fitness lost on inbreeding tends to be restored on crossing . Murfy *et al.* (1994) noticed that the product of a cross between genetically dissimilar parents (F1 generation) is called a ‘hybrid’, and hybrid vigour or heterosis is the associated phenomenon where expression of characters such as growth-related traits, flowering and grain yield fall outside the range of its parents.

The other most prevalent explanation for heterosis is the dominance hypothesis. This hypothesis is based on the idea that recessive alleles in one parent are nullified by the contribution of dominant alleles from the other parent (Xiao *et al*., 1995). The previous reports by (Yu *et al*., 1997, Graham *et al*., 1998 and Tanksley and Monforte, 2000) provide substantial evidence that heterosis is not controlled by a single locus alone, whether that locus behaves in a dominant or overdominant fashion. Linkage and epistasis among multiple loci must play a large role in the phenomenon of hybrid vigor. Budak (2002) noticed that heterosis is very likely organism dependent and population dependent. This would begin to explain the conflicting reports involving experiments designed to study the mechanism of heterosis. For example, heterosis observed in self-pollinated species like rice may be very different from heterosis observed in a naturally cross-pollinating species like maize.

If members of two inbred lines are mated, hybrid off-spring are often more vigorous in desirable traits than either of the parental lines. This phenomenon is called hybrid vigor. When this approach was used in breeding programs established for maize, crop yields increased tremendously. Unfortunately, as a consequence of segregation, the hybrid vigor extend only through the first generation (Klug and Cummings, 2005).

Much of what we know about hybrid breeding came from the discoveries and experiences of Scientists engaged in corn hybrid cultivar development. However, commercial hybrids are now available for many crops, including self-pollinating species. Heterosis, though widespread in the plant kingdom, is not uniformly manifested in all species and for all traits. It is manifested at a higher intensity in traits that have fitness value, and also more frequently among cross -pollinated species than self-pollinated species. Hybrid breeding as previously stated exploits the phenomenon of heterosis. Heterosis will be highest when one allele is fixed in one parent to be used in a cross and the other allele fixed in the other parent**.** Hybrid vigor may be defined as the increase in size, vigor, fertility, and overall productivity of a hybrid plant, over the mid-parent value (average performance of the two parents). It is calculated as the difference between the crossbred and inbred means. The two most commonly known are the dominance theory first proposed by C. G. Davenport in 1908 and later by I. M. Lerner, and the overdominance theory first proposed by Shull in1908 and later by K. Mather and J. L. Jinks. A third theory, the mechanism of epistasis (non-allelic gene interactions) has also been proposed (Acquaah, 2007).

Yield comparisons to the high-yielding parent have ranged from -26 to 47% (Suneson, 1962; Pawlisch and Van Dijk, 1965 and Gebrekidan and Rasmusson, 1970). In more divers marerial from crosses of spring and winter barleys, over 100% heterosis was reported (Fejer and Fedak, 1975). Foster and Fothergill (1981) reported that five high-yielding hybrids had a 26% yield advantage over five control varieties recommended for England and Walse. Lehman (1981) found that two-rowed hybrids yielded 86 and 119% of the control cultivars in 1979 and 1980.

Madic *et al*. (2007) in 10 F1 and F2 hybrids had obtained through diallel crossing of five divergent two-rowed barley cultivars for examination of the mode of inheritance for grain weight per barley plant. It was shown that the grain weight per plant in these investigations was dependent on genes with additive and non-additive or dominant effects. Superdominance (negative heterosis) in the inheritance of the grain weight per plant was determined to be present in the Djerdap x Jagodinac combination.

Pal and Kumar (2009) in a twenty one genotypes of six – parent half diallel were analyzed for estimating gene effects of variance, combining ability and standard heterosis for forage yield and other traits in barley, observed the predominance of non–additive components of genetic variance (H1, H2) along with positive values of additive component (D), high *per se* performance, significant SCA effects and significant standard heterosis in top ranking hybrid, HBL 276 X HBL 113. They suggested the scope of improvement for forage yield per plant, tillers per plant, ear length, biological yield per plant and grain yield per plant through bi-parental mating.

Kakani and Sharma (2010) by means of 9x9 barley half diallel (F1 and F2) progenies, observed that significant differences between parents and F1 and those between parents and F2 for most yield components under diverse environments indicating the degree of heritability was influenced by the environment and generations. They suggested the presence of heterosis.

Grain yield and its components and some growth attributes were studied during three successive seasons, to determine the type of gene effects by using the six populations (P_1, P_2 , F_1 , F_2, BC_1 and BC_2) of five barley crosses. Generation means were significantly different for all studied traits in all crosses; the mean for F_1 values exceeded the mid parent for all studied traits (days to heading, days to maturity, flag leaf area, total chlorophyll content plant^{-1}, plant height, spike length, number of spikes plant^{-1}, number of grains spike^{-1}, 100-grain weight and grain yield plant^{-1}) in the five crosses for days to heading and days to maturity, were earlier than the mid-parent, indicating partial dominance. Results, in general indicated presence of non-allelic interaction for all studied traits in all crosses under study; the additive effect was more important and greater than the dominance effect for most traits. Among the epistatic components, dominance × dominance was greater in the magnitudes than additive × additive and additive × dominance in the most studied traits. Positive heterotic effects relative to the mid-parent were found for most of the traits in the five crosses, except for heading and maturity dates that showed negative heterotic effects. Also positive heterotic effects relative to the better parent were found for the most of crosses (El-Aty *et al.*, 2011).

Aghamiri *et al*. (2012) studied the quantitative traits in seven cultivars of barley with their F1 progeny, and showed that the crossing of Nosrat and

Reyhan cultivars leads to the production of products with high values of the traits seed yield, biological yield, and hybrid awn length, since the combination of these cultivars lead to higher degree of heterosis.

Mühleisen *et al*. (2013) were studied the amount of heterosis and the potential to predict hybrid performance based on midparent values or general combining ability (GCA) effects to draw conclusions on the prospects for hybrid breeding in 124 hybrids of six-rowed winter barley, their 27 male and 38 female parental lines, as well as nine line and six hybrid varieties and one hybrid in registration was investigated in plot-based multi-environment trials. They found midparent heterosis averaged 11.3%, with a range from 0.7 to 19.9%. Better-parent heterosis was slightly lower with an average of 9.2%. Maximum commercial heterosis (i.e., the difference between the hybrid performance and the performance of the best line variety) was 7.6%, which clearly underlines the significance of hybrid barley breeding. Accuracy to predict hybrid performance was only moderate based on midparent values and GCA effects.

2.7 Correlation and path coefficient analysis:

There are two school of thoughts in explaining the cause of correlations between yield and yield components. One school of thought is that the relationships between yield and yield components are developmental (Hamid and Grafius, 1978 and Grafius, 1978). They argued that the yield components developed in a sequence and yield came at the end of this sequence. The characters set earlier had pronounced effects on the subsequent characters. For such cases, Thomas *et al*. (1971) postulated “when inter traits correlation between sequential characters exists, the more influential characters in the sequence may project their form of environmental and genetic control into the subsequent characters through the medium of this inter correlation”. This indicates some sort of developmental pleiotrophy between yield and yield components.

Alternatively, the other school of thought is that the yield components are related to yield through some genetical system rather than only developmental system. Law *et al*. (1978) proposed that relationship between yield and yield components was due to genetical linkage. Mackey (1980) also suggested the existence of morphogenetic pleiotrophy and genetic linkage between yield and yield components. 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 genetical association of yield and yield components. 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. Some studies reported that grain yield was determined by three yield components, e.g., spike number per m^2, kernel number spike^{-1} and kernel weight spike^{-1} (Grafius, 1964). Some studies concluded that spike number per m^2 was the primary determinant of grain yield in barley (Dofing and Knight, 1994). Yield was significantly correlated with number of fertile tillers, plant height, days to heading and spike length which were found to have high and positive direct effects on yield in barley. Dofing (1995) studied the relationships between patterns of phenological development and grain yield in barley grown in a subarctic environment.

Bhutta and Ibrahim (2005) in a six- rowed barley genotypes, concluded that there were significant positive correlation between grain yield with 1000-grain weight and number of spikelets spike^{-1}, grain yield was negatively 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 number of spike on yield was positive also. 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.

Studies on correlation of yield and its components in *Hordeum vulgar* L. by Drikvand *et al.* (2011) in a fifteen genotypes of hullless barley under rainfed condition revealed that grain yield had positive and significant simple correlation with number of spike per m^2, 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 m^2 (+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 m^2 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 traits affected directly or indirectly by every gene present in the plant.

2.8 Stability:

Theoretically, homozygous inbreeds and their hybrids have no genetic variance, and thus their phenotypic variance is said to be strictly environmental. Genotype-by-environment interactions (GEIs) analysis is particularly important when the rank of lines selected for breeding changes in different environments (crossover GEI). Indeed, high yielding genotypes in favorable environments can have inferior performances under poor growing conditions.So, understanding the causes of GEI would help in developing genotypes which show satisfactory performances in one to several environments (Ceccarelli, 1996)

Lin and Binns (1988) defined yield stability represents consistency of genotype performances over time, while Briggs and Knowles (1967) defined the expression of homeostasis as reduced variability of a group of plants with a single genotype grown under different environments. Most plant breeders use the term ‘‘stability’’ to characterize a genotype showing relatively constant yield across several environments. This definition of stability is in agreement with the concept of homeostasis widely used in quantitative genetics. A genotype showing constant performance in all environments does not necessarily respond to improved growing conditions with increased yield. (Becker and Leon, 1988).

Numerous methods have been extensively studied by biometricians to analyze phenotypic stability (Lin *et al.*,1986; Becker and Leon, 1988and Flores *et al.*,1998). However, no single method can adequately explain genotype performance across environments. Therefore, a comparative study among the more widely used methods seems necessary. Hussein *et al.* (2000), Yan *et al.* (2001), Mohammadi *et al.* (2005) and El-Sahookie and Al-Rawi, (2011) summarized most genotype-by-environment (GxE) interaction approaches in different crops, including analysis of variance, joint linear regression, crossover analysis, principal components analysis, principal coordinates analysis, factor analysis, cluster analysis, additive main effects, multiplicative interaction (AMMI) analysis and genotype plus genotype by- environment (GGE) biplot analyses, and stability and genotypic resultant.

Statistical methods for determining stability and adaptation of crop cultivars tested across diverse environments are used to assist breeders in selecting higher yielding and adapted genotypes (Bouzerzour and Dekhili, 1995 and Elsahookei, 1995).

May and Kuzub (1993) studied the response of barley grain yield to Canadian prairie environments to evaluate genotype x environment interactions with respect to barley genotype selection in nine test sites and ll entries over two 3-yr spans. They found that the Genotype x Location x Year interactions from analysis of variance were significant for grain yield in both data sets. No single genotype was superior over all locations, and the groupings of genotypes for similarity of response at locations were not consistent for year.

Chand *et al.* (2008b) obtained in thirty diverse elite lines of barley along with six checks assessed in three environments for three characters *i.e.* 1000-grain weight (g), harvest index (%) and grain yield per plant (g), the genotypes x environment (G x E) interactions were significant for all the traits studied. Among twenty three average yielding genotypes, only sixteen genotypes showed suitability for wide adaptation. Better phenotypic stability were observed in four genotypes having high yield mean performance. These were found promising for wide adaptation over sites across environments. Twelve genotypes had average mean performance showing stability over wider range of environments. Only two genotypes were found stable for poor environments. Thus, on the basis of mean performance and stability parameters, 16 lines were identified stable for most of the traits studied. These genotypes may be utilized as a donor in barley improvement programs .

Kadi *et al.* (2010) in 13 cultivars and breeding lines at two locations over five growing seasons under semi arid conditions to assess the magnitude of the genotype x environment (GxE) for grain yield and to determine yield stability, proposed that the set of barley genotypes had narrow adaptability as no genotype was found to have high performances in all environments.

Mohammadi, *et al*,. (2010) reported another study in three sets of cereal experiments [15 durum wheat (*Triticum turgidum* var. durum) genotypes-12 environments; 20 bread wheat (*T. aestivum* L.) genotypes-18 environments; and 13 barley (*Hordeum vulgare* L.) genotypes-18 environments] to examine phenotypic stability among nine phenotypic stability methods for grain yield per area. They examined that under these conditions, highly significant correlations were found between several of the stability measures indicating that several of the statistics probably measure similar aspects of phenotypic stability for these crop species. The AMMI stability value (ASV), variance of regression deviation (S^2 di) and Wricke’s ecovalence (W^2i) were consistently and highly correlated with each other over these crops and, therefore, could be used if selection is to be based primarily on stability. The superiority index (Pi) and geometric adaptability index (GAI), which are related to the dynamic concept of stability showed significant correlation with mean yield over these crops, suggesting that Pi and GAI would be the best methods for ranking genotypes across environments. The coefficient of variation (CV), regression coefficient (bi), yield reliability index (Ii), and environmental variance (S^2x) showed inconsistent relationships with either the static or dynamic concepts of stability over these crops .

MATERIALS AND METHODES

3.1 Plant and experiment material:

This study was conducted at three locations in Kurdistan region -Iraq, first location: 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, second location : Erbil-Grdarasha (36° 07′ 14″ N, 44° 00′ 23″ E and 419 masl), 9 Km south of Erbil city and third location: Kalar (34° 21′ 558″ N, 45° 22′ 681″ E and 178 masl) during the autumn growing seasons 2010-2011(crossing between parents at first location only) (to produce the first filial at the three locations at 2011- 2012) .

Five varieties and Pedigrees of two- rowed barley (*Hordeum distichum* L.) were used as fallows :

1. MORA/NB1054/3/MOLA/SHYRI//ARUPO*2/JET/4/…CBSS99M00293T-G-5M-1Y-1M-0Y
2. ABN-B/KA-B//RAISA/3/ALELI/4/LIMON/5/... CBSS99M00228 T-K-6M-1Y - 1M-0Y
3. Arabi aswad
4. Clipper
5. Bohoth H1

These were crossed in the season 2010-2011 in full diallel mating design to form 20 F1 hybrids (Table 1).All the F1 hybrids along with their parents were grown in the following growing season. Seeds of 20 F1s with their 5 parents (25 entries) were sown in the field experiments; they were conducted during the second half of October at Qilyasan and Erbil locations, while it was at the beginning of December 2011 in Kalar location in a randomized complete block design (RCBD) with three replication. Each treatment was one row of 2 meter length, 40 cm between rows and 20 cm between plants within a row. correlation analysis using full diallel cross analyzing technique described by (Griffing, 1956) .

Table 1. Studied breeding materials

No	Diallel, Reciprocal Crosses and Parents No.	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

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 (2a and 2b) below are shown brief descriptions of the soils and climates under study.

Table (2a): physical and chemical properties of the soil at three locations in the date of sowing season, 2011-2012*

Soil properties	Qilyasan	Erbil (Grdarasha)	Kalar
PSD	**Silty clay**	**Silty clay loam**	**Silty clay**
Sand %	**5.83**	**9.94**	**12.6**
Silt %	**42.07**	**52.06**	**45.9**
Clay %	**52.10**	**38.50**	**41.5**
PH	**7.13**	**8.22**	**7.35**
Organic matter %	**2.13**	**0.30**	**1.35**
Total Nitrogen %	**0.15**	**0.25**	**0.089**
Available phosphate (ppm)	**4.49**	**3.20**	**5.50**

***** Soil samples were analyzed at the laboratory of soil and water department, Faculty of Agricultural Science, University of Sulaimani.

Table (2b): Total rainfall, average maximum and minimum temperatures from October to May at three locations during the crop season, 2011-2012*

Period	**Qiyassan**			**Erbil (Grdarasha)**			**Kalar**		
	Temp. C°		**Rainfall mm**	**Temp. C°**		**Rainfall mm**	**Temp. C°**		**Rainfall mm**
	Max.	Min.		Max.	Min.		Max.	Min.	
Oct	**33.0**	**15.0**	**37.3**	**36.32**	**9.81**	**10.4**	**37.4**	**10.9**	**1.5**
Nov	**21.0**	**8.0**	**54.1**	**22.7**	**8.0**	**5.6**	**23.0**	**9.0**	**3.2**
Dec	**17.0**	**8.0**	**48.0**	**22.9**	**8.0**	**4.6**	**22.9**	**8.0**	**67.8**
Jan	**14.7**	**-5.7**	**94.2**	**16.3**	**-4.8**	**43.7**	**17.5**	**-1.0**	**21.2**
Feb	**15.5**	**-0.6**	**96.5**	**17.4**	**-0.4**	**33.6**	**20.9**	**2.0**	**53.5**
Mar	**21.1**	**-2.2**	**141.4**	**24.0**	**-1.7**	**56.6**	**29.5**	**8.5**	**27.3**
Apr	**30.5**	**6.1**	**34.0**	**34.1**	**10.2**	**12.7**	**36.5**	**14.8**	**11.0**
May	**35.5**	**13.7**	**36.0**	**39.5**	**15.9**	**9.4**	**41.0**	**20.8**	**5.3**
Jun	**38.6**	**16.8**	**—**	**40.2**	**18.5**	**—**	**42.1**	**24.5**	**—**
Total	**—**	**—**	**541.5**	**—**	**—**	**176.3**	**—**	**—**	**190.8**

*Metrological stations (Sulaimani, Erbil and Kalar 2011-2012)

3.3 Evaluated traits:

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

1. Number of days to 50% anthesis: were recorded as the number of days from planting date to reached 50% anthesis.
2. Flag leaf length: is the average length in centimeters from the flag leaf plant samples collected during anthesis.
3. Plant height: is the average distance in centimeters from the ground to the tip of the spike (excluding the awns) at maturity.
4. Number of days to 50% maturity : were recorded as the number of days from planting date to reached 50% field maturity
5. Biological yield plant^{-1}: 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.
6. Number of tillers plant^{-1}: is the average of total number of tillers counted from each selected plants at harvesting time.
7. Number of spikes plant^{-1}: is the average of total number of spikes counted from each selected plant at harvesting time.
8. Peduncle length: Distance from the collar (the auricle of the flag leaf) to the upper stem node in centimeters.
9. Peduncle diameter: Peduncle diameter in mm
10. Spike length: was recorded as the distance in centimeters from the lowest spikelet to the tip of the spike at maturity(without awn).
11. Average spike weight: is average weight of the spike from the spike sample collected during threshing, expressed in metric grams.

12. Awns length: is the length of the awn of spike samples in centimeter collected during threshing. The length of the awns measured from the third spikelet from the base of the spike (Sameri *et al*. 2006)
13. Number of Spikelets spike^{-1}: is the average number of spikelets spike^{-1} (two fertile rowed) in each row, harvested.
14. Number of grains spike^{-1}: is the average number of grains spike^{-1} in each row, harvested.
15. 1000- grain weight: is the weight of 1000 seeds in grams, from grains samples collected during threshing.
16. Harvest index (%): is the proportion of grain weight plant^{-1} to biological weight plant^{-1}.
17. Grain yield plant^{-1}: is the average weight of grains from the plant samples collected during threshing, expressed in metric grams.

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 Heterosis % as a deviation of F1s from their mid parents

3.4.4 Reciprocal Effect %

3.4.5 Broad Sense Heritability

3.4.6 Narrow Sense Heritability

3.4.7 Average Degree of Dominance (ā)

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)

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

Where:

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

μ : The general mean value,

τ_i : The value of the actual effect of the genotype " 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 genotype " i " in the block " j ".

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

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).

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

Where:

Y_{ijk} : observed value of the experimental unit,
μ : populations mean,
g_i : general combining ability (GCA) effect for the ith parent,
g_j : general combining ability (GCA) for the jth parent,
s_{ij} : specific combining ability (SCA) for the diallel crosses involving parent i and j,
R_{ij} : specific combining ability (RCA) for the reciprocal crosses involving parent i and j,
r_k : replication (block) effect, and
$\frac{1}{bc}\sum\sum \varepsilon_{ijk}$: means error effect.

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

$$gi = \frac{1}{2p}(Yi. + Y.j) - \frac{1}{p^2} Y..$$

$$si = \frac{1}{2}(Yij + Yji) - \frac{1}{2p}(Yi. + Y.i + Yj. + Y.j) + \frac{1}{p^2} Y..$$

$$ri = \frac{1}{2}(Yij - Yji)$$

Where : *gi* :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,*
Yij : 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 :

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

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

$$\sigma^2 ri. = \frac{1}{P-2}\sum(ri)^2 - \frac{MS'e}{2}$$

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:

$$S.E._{(gi-gi)} = \sqrt{\frac{MS'e}{p}} \quad , \quad S.E._{(sij-sik)} = \sqrt{\frac{(p-1)MS'e}{p}} \quad , \quad S.E._{(rij-rik)} = \sqrt{MS'e}$$

3.10 Estimation of heterosis:

The percent increase (+) or decrease (-) of F1 cross over mid- parent was calculated to determined hetrotic values for all characters (AGB301, 2004) .

$$\text{Heteroses (H) \%} = \left[\frac{F'1 - M.P}{M.P} \right] \text{x } 100 \qquad M.P = \frac{(P_1 + P_2)}{2}$$

Where: F′1:mean of hybrid,

P_1: parent one, and

P_2: parent two.

3.11 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 caculated by dividing additive genetic variance by total variance (Singh and Chaudhary, 1985).

$$h^2_{b.s} = \frac{\sigma^2 G}{\sigma^2 P} = \frac{\sigma^2 A + \sigma^2 D}{\sigma^2 A + \sigma^2 D + \sigma^2 e} = \frac{2\,\sigma^2 gca + \sigma^2 sca}{2\,\sigma^2 gca + \sigma^2 sca + \sigma^2 e}$$

$$h^2_{n.s} = \frac{\sigma^2 A}{\sigma^2 P} = \frac{\sigma^2 A}{\sigma^2 A + \sigma^2 D + \sigma^2 e} = \frac{2\ \sigma^2\ gca}{2\ \sigma^2 gca + \sigma^2 sca + \sigma^2 e}$$

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

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

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

σ^2_{SCA} : The variance of specific combining ability,

$\sigma^2\ e$: 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).

3.12 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: $\bar{a} = zero$ denote no dominance

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

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

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

3.13. Estimation of reciprocal effect:

$$\text{reciprocal effect (RE\%)} = \frac{(\bar{F}_{1r} - \bar{F}_1)}{\bar{F}_1} \times 100$$

Where: $\overline{\mathrm{F1}}$: the average value of diallel hybrid,

$\overline{\mathrm{F1r}}$: the average value of reciprocal hybrid

3.14. Estimation of Combined Analysis of Variance

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

$$\mu = \overline{Y}_{\ldots}$$

$$\tau_i = \overline{Y}_{i\,..} - \overline{Y}_{\ldots}$$

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

$$\gamma_k = \overline{Y}_{..k} - \overline{Y}_{\ldots}$$

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

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

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 genotype

ρ_{jk} : 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:

$$L.S.D_{Location} = t_{\alpha}\left(df_{E(a)}\right) \times \sqrt{\frac{2MS_{E(a)}}{tr}}$$

3. 15 Association Analysis

3. 15. 1 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. 15. 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 solution of the following 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 Software).

3.16 Stability Analysis:

$$stability\ (H)\ \% = (1 - S / \bar{X}_{i.}) \times 100$$

Where:

S: The Standard Deviation

$$S = \sqrt{S^2} = \sqrt{\frac{\sum X_i^2 - \frac{\left(\sum X_i\right)^2}{n}}{n-1}}$$ (Elsahookei,1995)

$i.$: The value of genotype

$\bar{X}_{i.}$: the average character value crossing studied environments

3.17 Estimation of Genotypic Resultant :

$$\text{Genotypic Resultant } (GR) = \left(1- \frac{S}{\bar{X}_{i.}}\right) \times \left(\frac{\bar{X}_{i.}}{\bar{X}_{..}}\right)$$

(Elsahookei,1995)

$\bar{X}_{i.}$: The average character value crossing studied environments

$\bar{X}_{.j}$: The average character value for particular environment crossing genotypes

$\bar{X}_{..}$: The general mean of particular character for all genotypes and all environments

Table (3): The average days to 50% anthesis {Diagonal, upper diagonal and sub diagonal } for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	**141.000**	**142.333**	**146.333**	**147.333**	**146.333**	723.333
2	**143.333**	**143.000**	**147.667**	**151.333**	**148.333**	733.667
3	**146.667**	**147.333**	**144.000**	**148.000**	**144.667**	730.667
4	**146.667**	**150.333**	**147.667**	**149.333**	**150.667**	744.667
5	**146.000**	**147.667**	**144.000**	**149.667**	**146.667**	734.000
Y.j	723.667	730.667	729.667	745.667	736.667	3666.333
Yi. +Y.j	1447.000	1464.333	1460.333	1490.333	1470.667	7332.667

Parental mean	Diallel	Reciprocal	General	LSD 0.05
144.800	147.300	146.933	146.653	0.826

Erbile location						
	1	2	3	4	5	Yi.
1	**135.000**	**132.000**	**131.667**	**135.667**	**134.667**	669.000
2	**132.667**	**133.667**	**136.667**	**138.667**	**136.333**	678.000
3	**132.333**	**136.333**	**135.667**	**136.667**	**131.667**	672.667
4	**135.667**	**139.333**	**136.667**	**140.000**	**135.667**	687.333
5	**134.333**	**135.667**	**132.000**	**135.333**	**134.667**	672.000
Y.j	670.000	677.000	672.667	686.333	673.000	3379.000
Yi. +Y.j	1339.000	1355.000	1345.333	1373.667	1345.000	6758.000

Parental mean	Diallel	Reciprocal	General	LSD 0.05
135.800	134.967	135.033	135.160	0.869

Kalar location						
	1	2	3	4	5	Yi.
1	**120.667**	**117.333**	**116.667**	**121.667**	**120.333**	596.667
2	**117.667**	**118.667**	**122.667**	**123.667**	**122.000**	604.667
3	**117.667**	**121.667**	**121.667**	**119.667**	**117.000**	597.667
4	**121.667**	**123.667**	**118.667**	**124.000**	**121.667**	609.667
5	**119.667**	**121.667**	**117.667**	**121.333**	**118.667**	599.000
Y.j	597.334	603.000	597.333	610.333	599.667	3007.667
Yi. +Y.j	1194.000	1207.667	1195.000	1220.000	1198.667	6015.334

Parental mean	Diallel	Reciprocal	General	LSD 0.05
120.733	120.267	120.133	120.307	0.866

Table (4): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for average days to 50% anthesis for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**0.235**	**2.690**	**1.493**	**1.738**	**0.391**
2	**0.939**		**2.904**	**3.535**	**2.417**	
3	**2.924**	**2.671**		**0.909**	**--0.459**	
4	**1.033**	**2.851**	**0.682**		**1.802**	
5	**1.506**	**1.956**	**-0.917**	**1.126**		
S.E.	**0.374**					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**-1.737**	**-2.709**	**-1.333**	**-0.124**	**0.516**
2	**-1.241**		**1.485**	**1.340**	**1.615**	
3	**-2.217**	**1.238**		**-0.846**	**-2.589**	
4	**-1.333**	**1.827**	**-0.846**		**-1.214**	
5	**-0.371**	**1.118**	**-2.343**	**-1.456**		
S.E.	**0.467**					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**-1.950**	**-3.714**	**-0.545**	**0.557**	**0.718**
2	**-1.671**		**2.080**	**1.923**	**2.809**	
3	**-2.888**	**1.248**		**-2.578**	**-2.635**	
4	**-0.545**	**1.923**	**-3.392**		**0.275**	
5	**0.000**	**2.528**	**-2.080**	**0.000**		
S.E.	**0.637**					

Table (5): Percentage values of reciprocal effect for days to 50% anthesis for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**0.703**				
3	**0.228**	**-0.226**			
4	**-0.452**	**-0.661**	**-0.225**		
5	**-0.228**	**-0.449**	**-0.461**	**-0.664**	
S.E.	**0.133**				

Erbil location					
Parents	1	2	3	4	5
1					
2	**0.505**				
3	**0.506**	**-0.244**			
4	**0.000**	**0.481**	**0.000**		
5	**-0.248**	**-0.489**	**0.253**	**-0.246**	
S.E.	**0.115**				

Kalar location					
Parents	1	2	3	4	5
1					
2	**0.284**				
3	**0.857**	**-0.815**			
4	**0.000**	**0.000**	**-0.836**		
5	**-0.554**	**-0.273**	**0.570**	**-0.274**	
S.E.	**0.178**				

Table (6) :Estimation of general and specific combining abilities effect , their variances and some genetic parameters for days to 50% anthesis for three locations.

Qilyasan Location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-1.953	-1.647	2.120	-0.080	1.053	3.812	2.745	0.097
2	-0.500	-0.220	1.687	2.020	1.153	0.048	2.806	1.033
3	-0.167	0.167	-0.620	-0.580	-2.113	0.384	1.591	2.493
4	0.333	0.500	0.167	2.380	0.720	5.664	0.274	1.558
5	0.167	0.333	0.333	0.500	0.413	0.171	0.138	2.475
S.E.	gi	si	ri					
	0.130	0.259914516	0.290593263					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
2.512	6.604	0.380	5.025	0.077	1.621	0.993	0.429	0.175	0.984	0.969

Erbil Location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-1.260	-1.907	-1.807	-0.440	1.260	1.584	2.862	0.037
2	-0.333	0.340	1.627	1.293	1.160	0.116	1.893	1.295
3	-0.333	0.167	-0.627	-0.073	-2.040	0.393	1.404	1.979
4	0.000	-0.333	0.000	2.207	-1.207	4.869	0.491	0.633
5	0.167	0.333	-0.167	0.167	-0.660	0.436	0.033	2.850
S.E.	gi	si	ri					
	0.137	0.273252	0.305505					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
841.1	4.997	0.368	3.682	0.009	1.648	0.989	0.420	0.069	0.975	0.973

Kalar Location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.907	-2.360	-2.127	0.573	1.040	0.818	3.802	0.083
2	-0.167	0.460	2.207	1.207	1.507	0.212	2.843	1.949
3	-0.500	0.500	-0.807	-2.027	-1.727	0.651	2.498	3.251
4	0.000	0.000	0.500	1.693	-0.060	2.867	0.053	1.973
5	0.333	0.167	-0.333	0.167	-0.440	0.194	0.061	2.112
S.E.	gi	si	ri					
	0.136	0.27244	0.304594					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.177	6.927	0.170	2.354	0.059	2.426	0.990	0.251	0.224	0.963	0.939

Table (7): The average flag leaf length (cm) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two- rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	**8.970**	**10.127**	**9.900**	**12.860**	**11.767**	53.623
2	**9.387**	**9.820**	**8.210**	**10.653**	**11.823**	49.893
3	**10.737**	**9.177**	**12.120**	**10.350**	**11.643**	54.027
4	**12.273**	**10.567**	**12.473**	**12.140**	**14.370**	61.823
5	**11.340**	**12.097**	**13.117**	**14.200**	**13.343**	64.097
Y.j	**52.707**	**51.787**	**55.820**	**60.203**	**62.947**	283.463
Yi. +Y.j	**106.330**	**101.680**	**109.847**	**122.027**	**127.043**	566.927
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
11.279	11.170	11.537	11.339	1.492		

Erbil location						
	1	2	3	4	5	Yi.
1	**7.287**	**8.663**	**7.990**	**9.573**	**9.460**	42.973
2	**8.060**	**6.100**	**8.547**	**8.833**	**9.003**	40.543
3	**9.440**	**8.110**	**9.723**	**8.993**	**10.110**	46.377
4	**10.087**	**8.280**	**9.963**	**9.620**	**12.430**	50.380
5	**9.867**	**9.337**	**11.613**	**11.667**	**11.750**	54.233
Y.j	**44.740**	**40.490**	**47.837**	**48.687**	**52.753**	234.507
Yi. +Y.j	**87.713**	**81.033**	**94.213**	**99.067**	**106.987**	469.013
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
8.896	9.360	9.642	9.380	0.778		

Kalar location						
	1	2	3	4	5	Yi.
1	**8.440**	**9.387**	**10.060**	**12.360**	**10.687**	50.933
2	**8.643**	**9.200**	**10.800**	**10.043**	**10.993**	49.680
3	**9.657**	**10.113**	**11.680**	**10.780**	**11.007**	53.237
4	**11.917**	**11.547**	**12.507**	**11.280**	**12.430**	59.680
5	**11.030**	**11.710**	**12.143**	**13.157**	**12.477**	60.517
Y.j	**49.687**	**51.957**	**57.190**	**57.620**	**57.593**	274.047
Yi. +Y.j	**100.620**	**101.637**	**110.427**	**117.300**	**118.110**	548.093
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
10.615	10.855	11.242	10.962	0.956		

Table (8): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for flag leaf length for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		7.778	-6.117	21.838	5.468	4.342
2	-0.089		-25.160	-2.975	2.087	
3	1.818	-16.384		-14.674	-8.548	
4	16.280	-3.764	2.830		12.780	
5	1.643	4.447	3.024	11.445		
S.E.	.2739					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		29.432	-6.055	13.249	-0.613	3.768
2	20.418		8.026	12.383	0.878	
3	10.994	2.507		-7.014	-5.837	
4	19.322	5.344	3.016		16.331	
5	3.660	4.613	8.165	9.187		
S.E.	2.055					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		6.425	0.000	25.355	2.183	2.931
2	-2.003		3.448	-1.921	1.430	
3	-4.009	-3.129		-6.098	-8.873	
4	20.859	12.760	8.943		4.644	
5	5.466	8.042	0.538	10.762		
S.E.	2.537					

Table (9): Percentage values of reciprocal effect for flag leaf length for three locations.

Qlyasan location					
Parents	1	2	3	4	5
1					
2	**-.7307**				
3	**8.451**	**11.774**			
4	**-4.562**	**-0.814**	**20.515**		
5	**-3.626**	**2.312**	**12.654**	**-1.183**	
S.E.	**.2867**				

Erbil Location					
Parents	1	2	3	4	5
1					
2	**-6.964**				
3	**18.148**	**-5.109**			
4	**5.362**	**-6.264**	**10.786**		
5	**4.299**	**3.702**	**14.870**	**-6.141**	
S.E.	**2.930**				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-7.919**				
3	**-4.009**	**-6.358**			
4	**-3.587**	**14.968**	**16.017**		
5	**3.213**	**6.519**	**10.327**	**5.846**	
S.E.	**2.756**				

Table (10) :Estimation of general and specific combining abilities effect , their variances and some genetic parameters for flag leaf length for three locations.

Qilyasan location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.706	0.294	0.453	1.070	-0.445	0.487	0.451	0.010
2	0.370	-1.171	-1.121	-0.422	0.426	1.370	0.491	0.114
3	-0.418	-0.483	-0.354	-0.437	0.030	0.125	0.107	1.044
4	0.293	0.043	-1.062	0.864	0.717	0.747	0.483	0.507
5	0.213	-0.137	-0.737	0.085	1.366	1.865	0.111	0.298
S.E.	gi	si	ri					
	0.235	0.46936403	0.524764939					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.124	0.995	1.130	2.248	0.100	0.941	0.922	0.639	0.298	0.895	0.857

Erbil location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.609	0.867	0.486	0.532	-0.426	0.368	0.459	0.204
2	0.302	-1.277	0.184	-0.073	-0.252	1.631	0.039	0.301
3	-0.725	0.218	0.041	-0.469	0.122	0.002	0.244	0.357
4	-0.257	0.277	-0.485	0.526	0.823	0.277	0.326	0.218
5	-0.203	-0.167	-0.752	0.382	1.318	1.738	0.234	0.313
S.E.	gi	si	ri					
	0.122	0.2448	0.2737					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.997	0.583	1.710	1.994	0.145	0.765	0.972	0.752	0.381	0.966	0.901

Kalar location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.900	- 0.249	0.071	1.308	-0.053	0.805	0.555	0.029
2	0.372	-0.798	0.212	-0.137	0.339	0.637	0.067	0.291
3	0.202	0.343	0.081	-0.167	-0.317	0.007	0.057	0.373
4	0.222	-0.752	-0.863	0.768	0.214	0.590	0.430	0.630
5	-0.172	-0.358	-0.568	-0.363	0.849	0.721	0.166	0.088
S.E.	gi	si	ri					
	0.150	0.3007	0.3362					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.680	0.567	1.200	1.360	0.170	0.913	0.945	0.667	0.501	0.931	0.827

Table (11): The average number of days to 50% maturity {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	**187.000**	**184.667**	**185.667**	**187.000**	**185.667**	930.000
2	**184.000**	**186.000**	**186.333**	**189.333**	**188.000**	933.667
3	**185.333**	**186.667**	**185.000**	**189.667**	**187.667**	934.333
4	**187.000**	**188.667**	**189.000**	**191.000**	**190.667**	946.333
5	**186.000**	**187.667**	**187.667**	**189.667**	**189.667**	940.667
Y.j	929.333	933.667	933.667	946.667	941.667	4685.000
Yi. +Y.j	1859.333	1867.333	1868.000	1893.000	1882.333	9370.000
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
187.733	187.467	187.167	187.400	0.740		

Erbil location						
	1	2	3	4	5	Yi.
1	**171.667**	**169.667**	**170.667**	**173.667**	**170.667**	856.333
2	**170.000**	**169.000**	**172.333**	**172.333**	**171.333**	855.000
3	**171.333**	**172.667**	**170.333**	**174.667**	**172.333**	861.333
4	**173.333**	**172.333**	**174.333**	**176.000**	**175.667**	871.667
5	**171.333**	**171.333**	**172.333**	**174.667**	**173.333**	863.000
Y.j	857.667	855.000	860.000	871.333	863.333	4307.333
Yi. +Y.j	1714.000	1710.000	1721.333	1743.000	1726.333	8614.667
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
172.067	172.333	172.367	172.293	0.902		

Kalar location						
	1	2	3	4	5	Yi.
1	**156.000**	**154.333**	**155.333**	**157.333**	**155.333**	778.333
2	**155.000**	**153.333**	**156.333**	**156.000**	**155.667**	776.333
3	**156.000**	**156.667**	**154.000**	**157.667**	**156.333**	780.667
4	**157.000**	**156.333**	**157.333**	**160.000**	**159.000**	789.667
5	**156.000**	**155.667**	**156.333**	**158.000**	**158.333**	784.333
Y.j	780.000	776.333	779.333	789.000	784.667	3909.333
Yi. +Y.j	1558.333	1552.667	1560.000	1578.667	1569.000	7818.667
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
156.333	156.333	156.433	156.373	0.711		

Table (12): The percentage values of heterosis { Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for number of days to 50% maturity for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		-0.983	-0.179	-1.058	-1.416	0.240
2	-1.340		0.449	0.442	0.089	
3	-0.358	0.629		0.887	0.178	
4	-1.058	0.088	0.532		0.175	
5	-1.239	-0.089	0.178	-0.350		
S.E.	0.224					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		-0.391	-0.195	-0.096	-1.063	0.229
2	-0.196		1.572	-0.097	0.097	
3	0.195	1.768		0.866	0.291	
4	-0.288	-0.097	0.674		0.573	
5	-0.676	0.097	0.291	0.000		
S.E.	0.210					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		-0.216	0.215	-0.422	-1.166	0.237
2	0.216		1.735	-0.426	-0.107	
3	0.645	1.952		0.425	0.107	
4	0.633-	-0.213	0.212		-0.105	
5	-0.742	-0.107	0.107	-0.733		
S.E.	0.254					

Table (13): Percentage values of reciprocal effect number of days to 50% maturity for three locations.

Qlyasan location					
Parents	1	2	3	4	5
1					
2	**-0.361**				
3	**-0.180**	**0.179**			
4	**0.000**	**-0.352**	**-0.351**		
5	**0.180**	**-0.177**	**0.000**	**-0.524**	
S.E.	**0.077**				

Erbil location					
Parents	1	2	3	4	5
1					
2	**0.196**				
3	**0.391**	**0.193**			
4	**-0.192**	**0.000**	**-0.191**		
5	**0.391**	**0.000**	**0.000**	**-0.569**	
S.E.	**0.093**				

Kalar location					
Parents	1	2	3	4	5
1					
2	**0.432**				
3	**0.429**	**0.213**			
4	**-0.212**	**0.214**	**-0.211**		
5	**0.429**	**0.000**	**0.000**	**-0.629**	
S.E.	**0.110**				

Table (14) :Estimation of general and specific combining abilities effect , their variances and some genetic parameters for number of days to 50% maturity for three locations.

Qilyasan location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-1.467	-0.933	0.233	-0.833	-0.933	2.148	0.807	0.022
2	0.333	-0.667	0.367	0.367	0.267	0.444	0.127	0.346
3	0.167	-0.167	-0.600	0.633	0.033	0.360	0.130	0.100
4	0.000	0.333	0.333	1.900	0.033	3.610	0.051	0.493
5	-0.167	0.167	0.000	0.500	0.833	0.694	0.079	0.315
S.E.	gi	si	ri					
	0.116	0.23285666	0.26034165					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.808	1.400	1.292	3.616	0.036	0.880	0.987	0.711	0.140	0.982	0.972

Erbil location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.893	-0.273	0.393	0.093	-0.740	0.794	0.228	0.042
2	-0.167	-1.293	1.660	-0.673	-0.007	1.673	1.045	0.034
3	-0.333	-0.167	-0.160	0.360	-0.140	0.026	0.062	0.979
4	0.167	0.000	0.167	2.007	0.527	4.027	0.077	0.281
5	-0.333	0.000	0.000	0.500	0.340	0.116	0.086	0.282
S.E.	gi	si	ri					
	0.142	0.283627	0.317105					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.650	1.240	1.330	3.299	0.008	0.867	0.978	0.711	0.070	0.970	0.968

Kalar location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.540	-0.060	0.640	-0.160	-0.693	0.289	0.285	0.089
2	-0.333	-1.107	1.607	-0.593	-0.127	1.225	0.999	0.020
3	-0.333	-0.167	-0.373	0.007	-0.193	0.139	0.037	1.006
4	0.167	-0.167	0.167	1.493	0.107	2.230	0.010	0.209
5	-0.333	0.000	0.000	0.500	0.527	0.277	0.099	0.182
S.E.	gi	si	ri					
	0.112	0.223772	0.250185					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.035	1.154	0.897	2.069	0.038	1.056	0.981	0.630	0.192	0.971	0.954

Table (15): The average plant height (cm) with spike {Diagonal, upper diagonal and sub diagonal } for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	92.667	102.667	101.000	114.000	104.000	514.333
2	102.000	109.000	100.333	100.333	108.667	520.333
3	105.667	105.333	89.667	102.000	102.000	504.667
4	102.000	102.333	111.333	91.000	98.000	504.667
5	107.667	105.000	110.000	98.000	94.000	514.667
Y.j	510.000	524.333	512.333	505.333	506.667	2558.667
Yi. +Y.j	1024.333	1044.667	1017.000	1010.000	1021.333	5117.333
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
95.267	103.300	104.933	102.347	6.540		

Erbil location						
	1	2	3	4	5	Yi.
1	68.333	67.333	79.667	69.000	70.667	355.000
2	74.333	66.000	68.667	64.333	68.667	342.000
3	72.667	75.000	68.000	66.333	68.000	350.000
4	66.333	62.000	68.667	52.000	61.667	310.667
5	80.000	75.667	74.667	62.333	65.333	358.000
Y.j	361.667	346.000	359.667	314.000	334.333	1715.667
Yi. +Y.j	716.667	688.000	709.667	624.667	692.333	3431.333
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
63.933	68.433	71.167	68.627	4.692		

Kalar location						
	1	2	3	4	5	Yi.
1	79.333	83.667	96.000	84.000	86.000	429.000
2	84.667	85.000	85.667	74.667	81.667	411.667
3	86.667	85.667	76.333	89.000	85.000	422.667
4	75.333	84.667	87.667	75.667	78.000	401.333
5	92.667	84.667	80.667	80.000	66.333	404.333
Y.j	418.667	423.667	426.333	403.333	397.000	2069.000
Yi. +Y.j	847.667	835.333	849.000	804.667	801.333	4138.000
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
76.533	84.367	84.267	82.760	4.402		

Table (16): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for plant height for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**1.818**	**10.786**	**24.138**	**11.429**	**2.262**
2	**1.157**		**1.007**	**0.333**	**7.061**	
3	**15.905**	**6.040**		**12.915**	**11.071**	
4	**11.071**	**2.333**	**23.247**		**5.946**	
5	**15.357**	**3.448**	**19.782**	**5.946**		
S.E.	**2.463**					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**0.248**	**16.870**	**14.681**	**5.736**	**1.748**
2	**10.670**		**2.488**	**9.040**	**4.569**	
3	**6.601**	**11.940**		**10.556**	**2.000**	
4	**10.249**	**5.085**	**14.444**		**5.114**	
5	**19.701**	**15.228**	**12.000**	**6.250**		
S.E.	**1.432**					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**1.826**	**23.340**	**8.387**	**18.078**	**2.895**
2	**3.043**		**6.198**	**-7.054**	**7.930**	
3	**11.349**	**6.198**		**17.105**	**19.159**	
4	**-2.796**	**5.394**	**15.351**		**9.859**	
5	**27.231**	**11.894**	**13.084**	**12.676**		
S.E.	**2.570**					

Table (17): Percentage values of reciprocal effect plant height for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-0.649**				
3	**4.620**	**4.983**			
4	**-10.526**	**1.993**	**9.150**		
5	**3.526**	**-3.374**	**7.843**	**0.000**	
S.E.	**1.824**				

Erbil location					
Parents	1	2	3	4	5
1					
2	**10.396**				
3	**-8.787**	**9.223**			
4	**-3.865**	**-3.627**	**3.518**		
5	**13.208**	**10.194**	**9.804**	**1.081**	
S.E.	**2.397**				

Kalar location					
Parents	1	2	3	4	5
1					
2	**1.195**				
3	**-9.722**	**0.000**			
4	**-10.317**	**13.393**	**-1.498**		
5	**7.752**	**3.673**	**-5.098**	**2.564**	
S.E.	**2.333**				

Table (18) :Estimation of general and specific combining abilities effect , their variances and some genetic parameters for plant height for three locations.

Qilyasan location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	0.087	-2.220	-0.020	6.913	3.613	-0.204	20.128	12.327
2	0.333	2.120	-0.987	-1.787	2.580	4.494	1.846	5.180
3	-2.333	-2.500	-0.647	6.313	4.513	0.418	22.176	12.917
4	1.538	-1.000	-4.667	-1.347	-2.787	1.814	20.382	30.282
5	-1.833	1.833	-4.000	0.000	-0.213	0.046	5.775	15.949
S.E.	gi	si	ri					
	1.029	2.057218547	2.30004026					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.166	61.125	0.019	2.332	6.685	7.241	0.923	0.034	2.395	0.630	0.163

Erbil location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	3.040	-1.007	2.960	2.160	3.060	9.133	7.009	14.657
2	-3.500	0.173	0.693	0.527	2.760	0.030	5.950	8.217
3	3.500	-3.167	2.340	2.693	-0.240	5.476	8.938	7.238
4	1.333	1.167	-1.167	-6.160	-1.073	37.946	0.958	4.103
5	-4.667	-3.500	-3.333	-0.333	0.607	0.368	14.158	6.064
S.E.	gi	si	ri					
	0.738	1.47578	1.64997					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
12.993	16.235	0.800	25.986	12.993	1.118	0.939	0.578	0.737	0.924	0.726

Kalar location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	2.007	-1.373	5.527	-2.807	7.193	3.931	29.869	16.107
2	-0.500	0.773	-0.007	-1.573	2.260	0.598	1.796	9.712
3	4.667	0.000	2.140	5.727	0.560	4.580	17.480	11.894
4	4.333	-5.000	0.667	-2.293	1.160	5.259	14.374	14.716
5	-3.333	-1.500	2.167	-1.000	-2.627	6.899	5.537	19.504
S.E.	gi	si	ri					
	0.692	1.38479	1.54824					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
5.101	52.390	0.097	10.202	7.332	3.205	0.963	0.157	1.199	0.880	0.512

Table (19): The average biological yield plant^{-1} (g) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	47.623	72.643	45.920	111.207	69.480	346.873
2	47.603	76.680	51.497	83.693	91.423	350.897
3	46.620	67.490	55.697	61.450	82.267	313.523
4	96.660	88.500	92.267	94.767	76.543	448.737
5	82.910	88.600	97.370	88.513	73.510	430.903
Y.j	321.417	393.913	342.750	439.630	393.223	1890.933
Yi. +Y.j	668.290	744.810	656.273	888.367	824.127	3781.867
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
69.655	74.612	79.653	75.637	8.467		

Erbil location						
	1	2	3	4	5	Yi.
1	27.027	34.407	22.850	30.390	29.760	144.433
2	25.983	24.200	26.973	22.287	31.957	131.400
3	29.047	26.153	35.700	36.897	26.333	154.130
4	32.273	20.557	28.593	24.907	26.753	133.083
5	37.797	38.507	28.390	33.767	32.657	171.117
Y.j	152.127	143.823	142.507	148.247	147.460	734.163
Yi. +Y.j	296.560	275.223	296.637	281.330	318.577	1468.327
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
28.898	28.861	30.107	29.367	3.510		

Kalar location						
	1	2	3	4	5	Yi.
1	47.723	62.147	75.600	60.897	63.880	310.247
2	46.893	52.530	78.777	57.147	68.680	304.027
3	53.787	71.037	70.553	51.290	60.823	307.490
4	64.180	70.913	75.443	47.117	59.550	317.203
5	59.197	59.153	58.130	61.817	53.613	291.910
Y.j	271.780	315.780	358.503	278.267	306.547	1530.877
Yi. +Y.j	582.027	619.807	665.993	595.470	598.457	3061.753
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
54.307	63.879	62.055	61.235	5.125		

Table (20): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for biological yield plant^{-1} for three locations.

Qilyasan l ocation						
Parents	1	2	3	4	5	S.E.
1		**16.881**	**-11.111**	**56.200**	**14.717**	7.727
2	**-23.408**		**-22.197**	**-2.368**	**21.744**	
3	**-9.756**	**1.967**		**-18.319**	**27.341**	
4	**35.768**	**3.239**	**22.643**		**-9.027**	
5	**36.890**	**17.984**	**50.720**	**5.200**		
S.E.	**7.256**					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**34.331**	**-27.144**	**17.035**	**-0.274**	6.312
2	**1.445**		**-9.939**	**-9.232**	**12.411**	
3	**-7.387**	**-12.677**		**21.758**	**-22.953**	
4	**24.288**	**-16.277**	**-5.643**		**-7.047**	
5	**26.657**	**35.452**	**-16.936**	**17.320**		
S.E.	**6.186**					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**23.979**	**27.836**	**28.420**	**26.075**	4.593
2	**-6.450**		**28.005**	**14.699**	**29.410**	
3	**-9.049**	**15.429**		**-12.824**	**-2.030**	
4	**35.344**	**42.330**	**28.229**		**18.237**	
5	**16.832**	**11.459**	**-6.368**	**22.737**		
S.E.	**5.683**					

Table (21): Percentage values of reciprocal effect biological yield plant^{-1} for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-34.470**				
3	**1.524**	**31.057**			
4	**-13.081**	**5.743**	**50.149**		
5	**19.329**	**-3.088**	**18.359**	**15.638**	
S.E.	7.459				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-24.482**				
3	**27.119**	**-3.040**			
4	**6.197**	**-7.762**	**-22.504**		
5	**27.005**	**20.497**	**7.810**	**26.215**	
S.E.	6.255				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-24.544**				
3	**-28.854**	**-9.825**			
4	**5.392**	**24.090**	**47.092**		
5	**-7.331**	**-13.871**	**-4.428**	**3.806**	
S.E.	7.174				

Table (22): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for biological yield plant^{-1} for three locations.

Qilyasan location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-8.808	-5.549	-14.286	23.905	2.591	77.232	268.004	80.522
2	12.520	-1.156	-4.978	-1.584	8.755	1.337	83.882	34.170
3	-0.350	-7.997	-10.010	-1.968	17.416	100.200	120.735	174.440
4	7.273	-2.403	-15.408	13.199	-13.084	174.222	152.744	204.551
5	-6.715	1.412	-7.552	-5.985	6.775	45.905	43.629	185.952
S.E.	gi	si	ri					
	1.332	2.66334	2.9776989					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
98.926	293.443	0.337	197.852	61.251	1.722	0.982	0.396	0.787	0.967	0.738

Erbil location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	0.289	2.383	-1.732	2.909	1.631	0.023	6.083	14.029
2	4.212	-1.844	-1.256	-4.867	5.218	3.401	22.894	5.774
3	-3.098	0.410	0.297	4.315	-4.793	0.088	16.602	7.624
4	-0.942	0.865	4.152	-1.234	-0.364	1.522	5.817	21.022
5	-4.018	-3.275	-1.028	-3.507	2.491	6.206	12.891	17.666
S.E.	gi	si	ri					
	0.552	1.104	1.2343					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
2.673	28.937	0.092	5.346	7.899	3.290	0.957	0.149	1.719	0.897	0.362

Kalar location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-3.032	-4.428	1.473	6.024	4.725	9.066	25.692	60.142
2	7.627	0.746	7.562	3.737	3.325	0.556	45.686	34.885
3	10.907	3.870	5.364	-1.545	-5.733	28.775	55.292	69.003
4	-1.642	-6.883	-12.077	-1.688	2.526	2.850	66.329	17.975
5	2.342	4.763	1.347	-1.133	-1.389	1.930	9.319	24.211
S.E.	gi	si	ri					
	0.806	1.61209	1.80237					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
10.502	67.444	0.156	21.004	40.305	2.534	0.965	0.229	1.959	0.950	0.325

Table (23): The average number of tillers plant^{-1} {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location

	1	2	3	4	5	Yi.
1	**19.333**	**29.223**	**19.887**	**34.777**	**20.777**	123.997
2	**18.443**	**30.220**	**24.443**	**30.333**	**28.557**	131.997
3	**22.000**	**25.887**	**24.443**	**24.000**	**39.223**	135.553
4	**28.333**	**33.110**	**34.777**	**32.000**	**30.223**	158.443
5	**26.553**	**30.890**	**40.443**	**29.443**	**28.663**	155.993
Y.j	114.663	149.330	143.993	150.553	147.443	705.983
Yi. +Y.j	238.660	281.327	279.547	308.997	303.437	1411.967

Parental mean	Diallel	Reciprocal	General	LSD 0.05
26.932	28.144	28.988	28.239	3.614

Erbil location

	1	2	3	4	5	Yi.
1	**17.443**	**18.540**	**15.003**	**15.667**	**14.447**	81.100
2	**16.443**	**16.447**	**17.337**	**11.557**	**17.000**	78.783
3	**17.667**	**18.670**	**25.667**	**20.337**	**14.447**	96.787
4	**15.777**	**11.777**	**16.550**	**12.667**	**15.553**	72.323
5	**18.557**	**19.663**	**15.443**	**19.777**	**15.227**	88.667
Y.j	85.887	85.097	90.000	80.003	76.673	417.660
Yi. +Y.j	166.987	163.880	186.787	152.327	165.340	835.320

Parental mean	Diallel	Reciprocal	General	LSD 0.05
17.490	15.989	17.032	16.706	2.448

Kalar location

	1	2	3	4	5	Yi.
1	**28.220**	**35.780**	**39.890**	**31.780**	**28.780**	164.450
2	**28.670**	**34.223**	**45.220**	**31.667**	**37.333**	177.113
3	**31.333**	**42.887**	**42.110**	**29.777**	**33.000**	179.107
4	**36.667**	**38.000**	**36.223**	**26.443**	**34.443**	171.777
5	**28.333**	**32.997**	**32.447**	**33.223**	**28.443**	155.443
Y.j	153.223	183.887	195.890	152.890	162.000	847.890
Yi. +Y.j	317.673	361.000	374.997	324.667	317.443	1695.780

Parental mean	Diallel	Reciprocal	General	LSD 0.05
31.888	34.767	34.078	33.916	3.791

Table (24): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for number of tillers plant^{-1}for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		17.947	-9.145	35.494	-13.425	6.872
2	-25.562		-10.568	-2.497	-3.006	
3	0.510	-5.287		-14.959	47.715	
4	10.390	6.429	23.227		-0.357	
5	10.647	4.919	52.310	-2.929		
S.E.	6.408					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		9.413	-30.395	4.063	-11.560	5.248
2	-2.961		-17.667	-20.609	7.346	
3	-18.039	-11.334		6.104	-29.345	
4	4.794	-19.098	-13.652		11.520	
5	13.601	24.163	-24.470	41.802		
S.E.	6.790					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		14.600	13.437	16.275	1.582	3.905
2	-8.173		18.480	4.396	19.149	
3	-10.896	12.367		-13.128	-6.454	
4	34.155	25.275	5.679		25.507	
5	0.006	5.309	-8.022	21.062		
S.E.	4.857					

Table (25): Percentage values of reciprocal effect number of tillers plant^{-1}for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-36.888**				
3	**10.627**	**5.905**			
4	**-18.528**	**9.154**	**44.903**		
5	**27.804**	**8.171**	**3.110**	**-2.581**	
S.E.	7.103				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-11.309**				
3	**17.752**	**7.691**			
4	**0.702**	**1.904**	**-18.620**		
5	**28.449**	**15.667**	**6.899**	**27.154**	
S.E.	4.843				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-19.871**				
3	**-21.451**	**-5.160**			
4	**15.377**	**20.000**	**21.650**		
5	**-1.552**	**-11.616**	**-1.677**	**-3.542**	
S.E.	4.869				

Table (26): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for number of tillers plant^{-1} for three locations.

Qilyasan location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-4.373	0.074	-2.282	5.029	-2.305	19.061	11.389	15.489
2	5.390	-0.107	-2.683	0.929	-0.514	0.011	11.910	1.272
3	-1.057	-0.722	-0.285	-1.227	9.774	0.081	32.344	13.938
4	3.222	-1.388	-5.388	2.660	-3.171	7.077	16.582	9.269
5	-2.888	-1.167	-0.610	0.390	2.104	4.428	2.860	37.056
S.E.	gi	si	ri					
	0.568	1.137	1.2712					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
7.519	32.182	0.234	15.039	7.418	2.069	0.967	0.308	0.993	0.933	0.625

Erbil location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.008	1.111	-0.536	0.497	-0.025	-0.030	0.338	1.996
2	1.048	-0.318	-0.357	-3.248	2.116	0.101	5.165	1.155
3	-1.332	-0.667	1.972	1.238	-3.561	3.890	5.226	1.416
4	-0.055	-0.110	1.893	-1.474	2.605	2.172	3.210	5.595
5	-2.055	-1.332	-0.498	-2.112	-0.172	0.030	3.316	7.982
S.E.	gi	si	ri					
	0.385	0.7699	0.8608					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.474	10.712	0.138	2.948	1.392	2.696	0.949	0.205	0.972	0.854	0.580

Kalar location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-2.148	-1.727	0.460	3.905	-1.039	4.544	5.903	11.432
2	3.555	2.184	4.369	0.182	1.236	4.772	10.492	6.357
3	4.278	1.167	3.584	-3.051	-2.605	12.846	11.315	9.923
4	-2.443	-3.167	-3.223	-1.449	3.538	2.099	12.364	8.320
5	0.223	2.168	0.277	0.610	-2.171	4.714	1.129	7.304
S.E.	gi	si	ri					
	0.596	1.1923	1.3331					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
7.084	16.121	0.439	14.168	5.501	1.509	0.945	0.442	0.881	0.917	0.661

Table (27): The average number of spikes plant^{-1}{Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location

	1	2	3	4	5	Yi.
1	19.333	28.777	19.223	34.443	20.553	122.330
2	18.443	29.887	23.780	30.000	28.000	130.110
3	22.000	25.447	23.777	23.667	39.000	133.890
4	28.000	32.777	34.223	31.890	30.000	156.890
5	26.000	30.220	39.223	29.443	28.000	152.887
Y.j	113.777	147.107	140.227	149.443	145.553	696.107
Yi. +Y.j	236.107	277.217	274.117	306.333	298.440	1392.213
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
26.577	27.744	28.578	27.844	3.293		

Erbil location

	1	2	3	4	5	Yi.
1	15.777	17.110	14.110	13.777	12.997	73.770
2	14.997	14.890	17.003	10.667	14.667	72.223
3	15.553	17.997	21.110	19.220	13.220	87.100
4	14.333	10.557	14.447	11.223	13.333	63.893
5	17.000	18.890	13.780	16.557	14.220	80.447
Y.j	77.660	79.443	80.450	71.443	68.437	377.433
Yi. +Y.j	151.430	151.667	167.550	135.337	148.883	754.867
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
15.444	14.610	15.411	15.097	2.220		

Kalar ocation

	1	2	3	4	5	Yi.
1	26.777	34.777	39.000	31.000	27.667	159.220
2	27.667	33.110	44.443	31.110	35.887	172.217
3	30.443	41.890	40.110	29.113	32.000	173.557
4	35.887	36.333	35.443	25.110	33.777	166.550
5	27.667	31.780	32.003	32.000	28.000	151.450
Y.j	148.440	177.890	191.000	148.333	157.330	822.993
Yi. +Y.j	307.660	350.107	364.557	314.883	308.780	1645.987
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
30.621	33.877	33.111	32.920	3.783		

Table (28): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for number of spikes plant^{-1}for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**16.931**	**-10.817**	**34.483**	**-13.155**	7.066
2	**-25.058**		**-11.373**	**-2.876**	**-3.259**	
3	**2.064**	**-5.162**		**-14.970**	**50.647**	
4	**9.325**	**6.113**	**22.958**		**0.184**	
5	**9.859**	**4.411**	**51.510**	**-1.675**		
S.E.	6.263					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**11.587**	**-23.495**	**2.049**	**-13.346**	4.737
2	**-2.196**		**-5.537**	**-18.305**	**0.767**	
3	**-15.670**	**-0.019**		**18.887**	**-25.163**	
4	**6.173**	**-19.147**	**-10.639**		**4.808**	
5	**13.346**	**29.784**	**-21.993**	**30.145**		
S.E.	5.978					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**16.142**	**16.615**	**19.491**	**1.016**	3.973
2	**-7.603**		**21.397**	**6.870**	**17.449**	
3	**-8.970**	**14.422**		**-10.723**	**-6.034**	
4	**38.327**	**24.814**	**8.689**		**27.195**	
5	**1.016**	**4.009**	**-6.025**	**20.505**		
S.E.	4.927					

Table (29): Percentage values of reciprocal effect number of spikes plant^{-1}for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-35.909**				
3	**14.444**	**7.009**			
4	**-18.707**	**9.256**	**44.606**		
5	**26.500**	**7.929**	**0.573**	**-1.856**	
S.E.	7.033				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-12.351**				
3	**10.229**	**5.842**			
4	**4.041**	**-1.031**	**-24.835**		
5	**30.803**	**28.795**	**4.236**	**24.175**	
S.E.	5.595				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-20.445**				
3	**-21.940**	**-5.745**			
4	**15.763**	**16.790**	**21.743**		
5	**0.000**	**-11.443**	**0.010**	**-5.260**	
S.E.	4.811				

Table (30): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for number of spikes plant^{-1} for three locations.

Qilyasan location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-4.234	0.122	-2.188	4.822	-2.334	17.870	10.711	14.802
2	5.167	-0.123	-2.676	0.878	-0.611	0.015	11.210	1.290
3	-1.388	-0.833	-0.433	-1.256	9.700	0.187	32.309	13.274
4	3.222	-1.388	-5.278	2.789	-2.911	7.779	15.759	8.559
5	-2.723	-1.110	-0.112	0.278	2.000	3.999	2.457	36.131
S.E.	gi	si	ri					
	0.518	1.0358	1.158					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
7.342	31.470	0.233	14.683	7.152	2.070	0.972	0.309	0.987	0.942	0.634

Erbil location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	0.046	0.841	-0.481	0.476	0.064	-0.022	0.183	1.603
2	1.057	0.069	0.676	-2.991	1.821	0.005	4.405	1.805
3	-0.722	-0.497	1.658	1.642	-3.046	2.748	4.040	2.154
4	-0.278	0.055	2.387	-1.564	1.620	2.445	2.594	4.823
5	-2.002	-2.112	-0.280	-1.612	-0.209	0.044	3.507	5.074
S.E.	gi	si	ri					
	0.349	0.6982	0.7806					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
1.250	6.668	0.187	2.500	1.576	2.310	0.938	0.256	1.123	0.870	0.534

Kalar location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-2.154	-1.635	0.554	4.109	-1.058	4.568	6.392	11.419
2	3.555	2.091	4.620	0.142	0.864	4.372	10.982	5.114
3	4.278	1.277	3.536	-2.746	-2.412	12.503	10.496	10.556
4	-2.443	-2.612	-3.165	-1.431	3.442	2.049	10.949	8.410
5	0.000	2.053	-0.002	0.888	-2.042	4.169	1.067	6.510
S.E.	gi	si	ri					
	0.595	1.1899	1.3303					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
6.756	16.312	0.414	13.512	5.154	1.554	0.944	0.428	0.873	0.913	0.661

Table (31): The average peduncle length(cm) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location

	1	2	3	4	5	Yi.
1	28.713	34.277	29.587	34.690	36.730	163.997
2	33.787	34.827	27.830	33.520	34.883	164.847
3	31.270	31.803	25.843	28.237	30.983	148.137
4	33.307	32.847	30.763	26.473	28.033	151.423
5	35.127	35.783	31.077	30.803	28.803	161.593
Y.j	162.203	169.537	145.100	153.723	159.433	789.997
Yi. +Y.j	326.200	334.383	293.237	305.147	321.027	1579.993

Parental mean	Diallel	Reciprocal	General	LSD 0.05
28.932	31.877	32.657	31.600	2.399

Erbil location

	1	2	3	4	5	Yi.
1	14.207	11.390	11.263	11.870	14.287	63.017
2	12.753	12.467	10.587	11.303	12.300	59.410
3	11.450	10.310	10.617	11.337	13.403	57.117
4	9.910	9.403	10.163	10.530	11.147	51.153
5	15.933	13.777	13.027	11.883	14.593	69.213
Y.j	64.253	57.347	55.657	56.923	65.730	299.910
Yi. +Y.j	127.270	116.757	112.773	108.077	134.943	599.820

Parental mean	Diallel	Reciprocal	General	LSD 0.05
12.483	11.889	11.861	11.996	1.069

Kalar location

	1	2	3	4	5	Yi.
1	20.060	22.173	18.463	20.383	23.387	104.467
2	20.433	22.497	20.400	19.507	21.853	104.690
3	18.300	21.097	16.840	17.850	21.457	95.543
4	17.307	20.250	20.280	17.313	18.343	93.493
5	23.913	20.517	19.037	19.687	19.300	102.453
Y.j	100.013	106.533	95.020	94.740	104.340	500.647
Yi. +Y.j	204.480	211.223	190.563	188.233	206.793	1001.293

Parental mean	Diallel	Reciprocal	General	LSD 0.05
19.202	20.382	20.082	20.026	1.105

Table (32): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for peduncle length(cm) for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**7.890**	**8.462**	**25.719**	**27.720**	3.316
2	**6.348**		**-8.258**	**9.364**	**9.644**	
3	**14.633**	**4.840**		**7.945**	**13.395**	
4	**20.705**	**7.167**	**17.604**		**1.429**	
5	**22.144**	**12.473**	**13.737**	**11.451**		
S.E.	1.870					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**-14.596**	**-9.252**	**-4.029**	**-0.787**	2.315
2	**-4.374**		**-8.274**	**-1.696**	**-9.091**	
3	**-7.748**	**-10.671**		**7.219**	**6.333**	
4	**-19.876**	**-18.220**	**-3.878**		**-11.264**	
5	**10.648**	**1.823**	**3.345**	**-5.400**		
S.E.	2.975					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**4.206**	**0.072**	**9.080**	**18.835**	2.313
2	**-3.971**		**3.720**	**-2.001**	**4.570**	
3	**-0.813**	**7.262**		**4.529**	**18.742**	
4	**-7.385**	**1.733**	**18.759**		**0.200**	
5	**21.511**	**-1.826**	**5.350**	**7.538**		
S.E.	2.978					

Table (33): Percentage values of reciprocal effect peduncle length(cm) for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-1.430**				
3	**5.689**	**14.277**			
4	**-3.988**	**-2.009**	**8.948**		
5	**-4.365**	**2.580**	**0.301**	**9.881**	
S.E.	2.034				

Erbil location					
Parents	1	2	3	4	5
1					
2	**11.970**				
3	**1.657**	**-2.613**			
4	**-16.512**	**-16.809**	**-10.350**		
5	**11.526**	**12.005**	**-2.810**	**6.609**	
S.E.	3.560				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-7.847**				
3	**-0.885**	**3.415**			
4	**-15.094**	**3.811**	**13.613**		
5	**2.252**	**-6.117**	**-11.279**	**7.323**	
S.E.	2.815				

Table (34): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for peduncle length(cm) for three locations.

Qilyasan location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	1.020	-0.427	-1.586	2.464	2.806	1.012	5.304	0.274
2	0.245	1.838	-1.345	0.830	1.392	3.380	1.257	1.482
3	-0.842	-1.987	-2.276	1.262	1.204	5.181	2.323	1.975
4	0.692	0.337	-1.263	-1.085	-1.599	1.178	1.340	3.423
5	0.802	-0.450	-0.047	-1.385	0.503	0.253	0.680	4.605
S.E.	gi	si	ri					
	0.377	0.7547	0.8438					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	$\bar{a}$	h^2b.s	h^2n.s	$\bar{a}$r	h^2bsr	h^2nsr
2.687	9.033	0.297	5.374	0.611	1.834	0.953	0.355	0.477	0.894	0.802

Erbil location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	0.731	-0.335	-0.881	-0.648	0.885	0.528	0.649	0.633
2	-0.682	-0.321	-0.508	-0.134	-0.135	0.103	0.205	0.526
3	-0.093	0.138	-0.719	0.661	0.440	0.517	0.171	0.471
4	0.980	0.950	0.587	-1.189	-0.791	1.413	0.896	0.337
5	-0.823	-0.738	0.188	-0.368	1.498	2.244	0.417	0.540
S.E.	gi	si	ri					
	0.168	0.3364	0.3761					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	$\bar{a}$	h^2b.s	h^2n.s	$\bar{a}$r	h^2bsr	h^2nsr
1.189	0.796	1.494	2.377	0.339	0.818	0.957	0.717	0.534	0.951	0.832

Kalar location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	0.422	-0.241	-2.011	-0.400	2.549	0.172	3.535	0.991
2	0.870	1.096	0.596	-0.041	-0.591	1.202	0.436	0.255
3	0.082	-0.348	-0.970	1.211	0.537	0.940	0.576	2.447
4	1.538	-0.372	-1.215	-1.203	-0.462	1.446	1.347	0.693
5	-0.263	0.668	1.210	-0.672	0.653	0.427	0.759	2.449
S.E.	gi	si	ri					
	0.174	0.3477	0.3887					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	$\bar{a}$	h^2b.s	h^2n.s	$\bar{a}$r	h^2bsr	h^2nsr
1.033	2.618	0.395	2.067	0.654	1.592	0.969	0.427	0.796	0.947	0.720

Table (35): The average number of peduncle diameter (mm) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	1.325	1.284	1.227	1.490	1.470	6.796
2	1.273	1.242	1.160	1.403	1.401	6.479
3	1.278	1.204	1.267	1.308	1.418	6.475
4	1.444	1.392	1.403	1.591	1.550	7.381
5	1.473	1.431	1.407	1.596	1.496	7.403
Y.j	6.793	6.553	6.465	7.388	7.335	34.534
Yi. +Y.j	13.589	13.032	12.939	14.769	14.739	69.068
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
1.384	1.371	1.390	1.381	0.114		

Erbil location						
	1	2	3	4	5	Yi.
1	1.228	1.202	1.168	1.303	1.293	6.194
2	1.157	1.161	1.150	1.298	1.273	6.039
3	1.197	1.103	1.152	1.249	1.339	6.041
4	1.355	1.242	1.291	1.453	1.404	6.745
5	1.385	1.298	1.312	1.365	1.496	6.856
Y.j	6.322	6.007	6.074	6.668	6.804	31.875
Yi. +Y.j	12.517	12.046	12.114	13.414	13.660	63.751
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
1.298	1.268	1.271	1.275	0.099		

Kalar location						
	1	2	3	4	5	Yi.
1	1.281	1.276	1.259	1.341	1.410	6.567
2	1.281	1.177	1.255	1.461	1.376	6.549
3	1.223	1.210	1.199	1.306	1.346	6.285
4	1.495	1.434	1.436	1.521	1.415	7.302
5	1.495	1.364	1.310	1.424	1.578	7.172
Y.j	6.775	6.462	6.459	7.054	7.126	33.876
Yi. +Y.j	13.342	13.011	12.745	14.356	14.298	67.752
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
1.351	1.345	1.367	1.355	0.047		

Table (36): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for peduncle diameter for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**0.052**	**-5.286**	**2.160**	**4.231**	1.422
2	**-0.805**		**-7.482**	**-0.930**	**2.362**	
3	**-1.376**	**-4.000**		**-8.491**	**2.691**	
4	**-0.994**	**-1.706**	**-1.819**		**0.443**	
5	**4.467**	**4.530**	**1.895**	**3.423**		
S.E.	0.944					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**0.670**	**-1.862**	**-2.785**	**-5.054**	0.722
2	**-3.126**		**-0.533**	**-0.663**	**-4.179**	
3	**0.574**	**-4.597**		**-4.082**	**1.108**	
4	**1.094**	**-4.923**	**-0.857**		**-4.760**	
5	**1.726**	**-2.246**	**-0.932**	**-7.383**		
S.E.	0.931					

Kalar location						
Parents	1	2	3	4	5	S.E
1		**3.865**	**1.519**	**-4.270**	**-1.399**	1.627
2	**4.218**		**5.640**	**8.302**	**-0.109**	
3	**-1.357**	**1.880**		**-3.994**	**-3.060**	
4	**6.721**	**6.326**	**5.538**		**-8.678**	
5	**4.547**	**-0.956**	**-5.652**	**-8.098**		
S.E.	1.636					

Table (37): Percentage values of reciprocal effect peduncle diameter for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-0.857**				
3	**4.128**	**3.763**			
4	**-3.088**	**-0.784**	**7.290**		
5	**0.227**	**2.118**	**-0.776**	**2.967**	
S.E.	0.982				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-3.770**				
3	**2.483**	**-4.086**			
4	**3.991**	**-4.289**	**3.362**		
5	**7.141**	**2.017**	**-2.017**	**-2.754**	
S.E.	1.287				

Kalar location					
Parents	1	2	3	4	5
1					
2	**0.340**				
3	**-2.833**	**-3.559**			
4	**11.481**	**-1.825**	**9.929**		
5	**6.030**	**-0.848**	**-2.674**	**0.636**	
S.E.	1.736				

Table (38): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for peduncle diameter for three locations.

Qilyasan location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-0.022**	**-0.002**	**-0.019**	**0.012**	**0.020**	**0.000**	**-0.0002**	**0.000**
2	**0.006**	**-0.078**	**-0.034**	**-0.001**	**0.020**	**0.006**	**-0.00002**	**0.000**
3	**-0.025**	**-0.022**	**-0.087**	**-0.034**	**0.026**	**0.008**	**0.00045**	**0.001**
4	**0.023**	**0.006**	**-0.048**	**0.096**	**0.004**	**0.009**	**0.00040**	**0.001**
5	**-0.002**	**-0.015**	**0.005**	**-0.023**	**0.093**	**0.009**	**-0.00029**	**0.001**
S.E.	**gi**	**si**	**ri**					
	0.018	**0.0359**	**0.0401**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^{2}b.s	h^{2}n.s	ār	h^{2}bsr	h^{2}nsr
0.008	**0.000**	**39.733**	**0.016**	**0.000**	**0.159**	**0.908**	**0.897**	**0.00**	**0.905**	**0.904**

Erbil location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-0.023**	**-0.002**	**-0.005**	**0.011**	**-0.004**	**0.000**	**0.000**	**0.001**
2	**0.023**	**-0.070**	**-0.014**	**-0.001**	**-0.010**	**0.005**	**0.000**	**0.000**
3	**-0.015**	**0.024**	**-0.064**	**-0.007**	**0.023**	**0.004**	**0.000**	**0.000**
4	**-0.026**	**0.028**	**-0.021**	**0.066**	**-0.048**	**0.004**	**0.001**	**0.000**
5	**-0.046**	**-0.013**	**0.014**	**0.019**	**0.091**	**0.008**	**0.001**	**0.001**
S.E.	**gi**	**si**	**ri**					
	0.016	**0.0312**	**0.0349**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^{2}b.s	h^{2}n.s	ār	h^{2}bsr	h^{2}nsr
0.005	**0.00**	**0.00**	**0.011**	**0.00**	**0.00**	**0.898**	**0.895**	**0.00**	**0.899**	**0.899**

Kalar location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-0.021**	**-0.002**	**-0.039**	**0.004**	**0.043**	**0.000**	**0.001**	**0.003**
2	**-0.002**	**-0.054**	**0.012**	**0.066**	**-0.006**	**0.003**	**0.001**	**0.000**
3	**0.018**	**0.022**	**-0.081**	**0.016**	**-0.021**	**0.006**	**0.000**	**0.002**
4	**-0.077**	**0.013**	**-0.065**	**0.081**	**-0.090**	**0.006**	**0.006**	**0.002**
5	**-0.043**	**0.006**	**0.018**	**-0.005**	**0.075**	**0.006**	**0.001**	**0.004**
S.E.	**gi**	**si**	**ri**					
	0.007	**0.0147**	**0.0165**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^{2}b.s	h^{2}n.s	ār	h^{2}bsr	h^{2}nsr
0.005	**0.004**	**1.372**	**0.011**	**0.001**	**0.854**	**0.982**	**0.720**	**0.469**	**0.978**	**0.881**

Table (39): The average spike length(cm) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	8.037	8.743	8.677	9.737	10.197	45.390
2	9.067	9.127	8.567	9.367	9.763	45.890
3	8.707	8.827	8.467	8.880	9.220	44.100
4	9.227	9.473	9.797	7.830	8.097	44.423
5	9.727	10.120	9.357	8.507	8.607	46.317
Y.j	44.763	46.290	44.863	44.320	45.883	226.120
Yi. +Y.j	90.153	92.180	88.963	88.743	92.200	452.240

Parental mean	Diallel	Reciprocal	General	LSD 0.05
8.413	9.125	9.281	9.045	0.814

Erbil location						
	1	2	3	4	5	Yi.
1	7.203	8.237	7.723	8.353	8.330	39.847
2	7.833	7.463	7.977	8.347	9.093	40.713
3	7.560	7.340	7.073	8.167	8.163	38.303
4	8.197	7.953	8.273	6.440	6.973	37.837
5	8.970	9.173	8.550	7.763	7.623	42.080
Y.j	39.763	40.167	39.597	39.070	40.183	198.780
Yi. +Y.j	79.610	80.880	77.900	76.907	82.263	397.559

Parental mean	Diallel	Reciprocal	General	LSD 0.05
7.161	8.136	8.161	7.952	0.378

Kalar ocation						
	1	2	3	4	5	Yi.
1	8.363	8.987	8.533	9.167	9.500	44.550
2	8.490	8.677	9.450	9.823	9.547	45.987
3	8.250	8.967	8.423	8.880	8.723	43.243
4	9.747	10.050	9.990	7.787	7.840	45.413
5	9.717	9.587	8.910	7.830	8.083	44.127
Y.j	44.567	46.267	45.307	43.487	43.693	223.320
Yi. +Y.j	89.117	92.253	88.550	88.900	87.820	446.640

Parental mean	Diallel	Reciprocal	General	LSD 0.05
8.267	9.045	9.154	8.933	0.366

Table (40): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for spike length for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**1.884**	**5.150**	**22.731**	**22.532**	2.758
2	**5.652**		**-2.615**	**10.478**	**10.113**	
3	**5.514**	**0.341**		**8.979**	**8.005**	
4	**16.303**	**11.736**	**20.229**		**-1.480**	
5	**16.884**	**14.135**	**9.606**	**3.508**		
S.E.	2.068					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**12.318**	**8.195**	**22.453**	**12.365**	2.317
2	**6.814**		**9.745**	**20.067**	**20.548**	
3	**5.907**	**0.986**		**20.868**	**11.091**	
4	**20.156**	**14.409**	**22.447**		**-0.830**	
5	**20.998**	**21.608**	**16.353**	**10.405**		
S.E.	2.407					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**5.477**	**1.668**	**13.519**	**15.525**	2.044
2	**-0.352**		**10.526**	**19.336**	**13.922**	
3	**-1.708**	**4.873**		**9.562**	**5.695**	
4	**20.702**	**22.089**	**23.257**		**-1.197**	
5	**18.160**	**14.399**	**7.956**	**-1.323**		
S.E.	3.195					

Table (41): Percentage values of reciprocal effect of spike length for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**3.698**				
3	**0.346**	**3.035**			
4	**-5.238**	**1.139**	**10.323**		
5	**-4.609**	**3.653**	**1.482**	**5.064**	
S.E.	1.434				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-4.901**				
3	**-2.115**	**-7.982**			
4	**-1.875**	**-4.712**	**1.306**		
5	**7.683**	**0.880**	**4.737**	**11.329**	
S.E.	1.910				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-5.527**				
3	**-3.320**	**-5.115**			
4	**6.327**	**2.307**	**12.500**		
5	**2.281**	**0.419**	**2.140**	**-0.128**	
S.E.	1.717				

Table (42): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for spike length for three locations.

Qilyasan location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-0.029**	**-0.284**	**-0.354**	**0.637**	**0.771**	**-0.002**	**0.374**	**0.008**
2	**-0.162**	**0.173**	**-0.373**	**0.372**	**0.548**	**0.030**	**0.174**	**0.044**
3	**-0.015**	**-0.130**	**-0.148**	**0.612**	**0.217**	**0.022**	**0.119**	**0.160**
4	**0.255**	**-0.053**	**-0.458**	**-0.170**	**-0.748**	**0.029**	**0.251**	**0.320**
5	**0.235**	**-0.178**	**-0.068**	**-0.205**	**0.175**	**0.031**	**0.017**	**0.501**
S.E.	**gi**	**si**	**ri**					
	0.128	**0.2559**	**0.2862**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.020	**0.696**	**0.029**	**0.040**	**0.005**	**5.902**	**0.900**	**0.049**	**0.477**	**0.352**	**0.316**

Erbil location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**0.010**	**-0.063**	**-0.399**	**0.575**	**0.414**	**-0.001**	**0.216**	**0.043**
2	**0.202**	**0.137**	**-0.268**	**0.323**	**0.770**	**0.019**	**0.264**	**0.049**
3	**0.082**	**0.318**	**-0.161**	**0.691**	**0.292**	**0.026**	**0.217**	**0.091**
4	**0.078**	**0.197**	**-0.053**	**-0.261**	**-0.597**	**0.068**	**0.129**	**0.356**
5	**-0.320**	**-0.040**	**-0.193**	**-0.395**	**0.275**	**0.076**	**0.093**	**0.402**
S.E.	**gi**	**si**	**ri**					
	0.059	**0.1189**	**0.1329**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.045	**0.749**	**0.061**	**0.091**	**0.041**	**4.064**	**0.979**	**0.106**	**0.946**	**0.881**	**0.609**

Kalar location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-0.021**	**-0.466**	**-0.717**	**0.588**	**0.847**	**0.000**	**0.592**	**0.051**
2	**0.248**	**0.293**	**0.061**	**0.754**	**0.492**	**0.086**	**0.286**	**0.096**
3	**0.142**	**0.242**	**-0.078**	**0.623**	**0.112**	**0.006**	**0.154**	**0.278**
4	**-0.290**	**-0.113**	**-0.555**	**-0.043**	**-0.904**	**0.002**	**0.402**	**0.434**
5	**-0.108**	**-0.020**	**-0.093**	**0.005**	**-0.151**	**0.023**	**0.001**	**0.597**
S.E.	**gi**	**si**	**ri**					
	0.058	**0.1151**	**0.1286**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.028	**0.939**	**0.029**	**0.055**	**0.048**	**5.842**	**0.984**	**0.054**	**1.325**	**0.862**	**0.459**

Table (43): The average spike weight (g) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	1.225	1.276	1.120	1.726	1.825	7.172
2	1.385	1.385	1.071	1.522	1.816	7.178
3	1.206	1.290	1.229	1.221	0.950	5.896
4	1.531	1.542	1.288	1.655	1.525	7.541
5	1.722	1.642	1.150	1.663	1.305	7.483
Y.j	7.069	7.135	5.858	7.787	7.421	35.269
Yi. +Y.j	14.241	14.313	11.754	15.328	14.904	70.539
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
1.360	1.405	1.442	1.411	0.081		

Erbil location						
	1	2	3	4	5	Yi.
1	0.703	0.720	0.637	0.900	0.804	3.765
2	0.664	0.724	0.629	0.866	0.873	3.756
3	0.688	0.589	0.641	0.779	0.749	3.446
4	0.893	0.749	0.883	1.028	0.865	4.417
5	0.883	0.878	0.871	0.822	0.996	4.450
Y.j	3.830	3.660	3.661	4.396	4.287	19.835
Yi. +Y.j	7.595	7.416	7.107	8.813	8.738	39.670
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
0.818	0.782	0.792	0.793	0.080		

Kalar location						
	1	2	3	4	5	Yi.
1	0.863	0.925	0.971	1.065	1.270	5.094
2	0.912	0.824	0.930	0.970	0.940	4.575
3	0.845	0.915	0.934	0.921	0.909	4.525
4	1.019	1.116	1.124	1.012	0.976	5.247
5	1.158	1.027	0.942	0.941	1.061	5.130
Y.j	4.797	4.807	4.902	4.908	5.156	24.571
Yi. +Y.j	9.892	9.382	9.427	10.155	10.286	49.141
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
0.939	0.988	1.000	0.983	0.077		

Table (44): The percentage values of heterosis { Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses of spike weight for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**-2.222**	**-8.708**	**19.838**	**44.276**	7.262
2	**6.105**		**-18.072**	**0.110**	**34.977**	
3	**-1.698**	**-1.263**		**-15.293**	**-25.046**	
4	**6.319**	**1.425**	**-10.646**		**3.029**	
5	**36.135**	**22.067**	**-9.234**	**12.352**		
S.E.	4.532					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**0.958**	**-5.135**	**4.025**	**-5.375**	1.769
2	**-6.891**		**-7.816**	**-1.104**	**1.453**	
3	**2.357**	**-13.630**		**-6.592**	**-8.450**	
4	**3.139**	**-14.536**	**5.793**		**-14.540**	
5	**3.884**	**2.034**	**6.455**	**-18.755**		
S.E.	3.010					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**9.702**	**8.086**	**13.564**	**31.994**	3.771
2	**8.081**		**5.744**	**5.628**	**-0.248**	
3	**- 5.935**	**4.114**		**-5.395**	**-8.903**	
4	**8.693**	**21.532**	**15.533**		**-5.884**	
5	**20.388**	**8.911**	**-5.562**	**-9.228**		
S.E.	3.442					

Table (45): Percentage values of reciprocal effect of spike weight for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**8.516**				
3	**7.679**	**20.517**			
4	**-11.281**	**1.314**	**5.486**		
5	**-5.643**	**-9.565**	**21.095**	**9.049**	
S.E.	3.558				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-7.774**				
3	**7.897**	**-6.306**			
4	**-0.852**	**-13.582**	**13.259**		
5	**9.784**	**0.573**	**16.281**	**-4.933**	
S.E.	3.142				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-1.477**				
3	**-12.972**	**-1.542**			
4	**-4.289**	**15.057**	**22.122**		
5	**-8.793**	**9.181**	**3.667**	**-3.553**	
S.E.	3.439				

Table (46): Estimation of general and specific combining abilities effect, their variances and some genetic parameters of spike weight for three locations.

Qilyasan location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**0.013**	**-0.114**	**-0.154**	**0.082**	**0.270**	**0.000**	**0.039**	**0.005**
2	**-0.054**	**0.020**	**-0.015**	**-0.022**	**0.218**	**0.000**	**0.017**	**0.011**
3	**-0.043**	**-0.110**	**-0.235**	**-0.043**	**-0.205**	**0.055**	**0.019**	**0.012**
4	**0.097**	**-0.010**	**-0.033**	**0.122**	**-0.018**	**0.015**	**0.003**	**0.005**
5	**0.052**	**0.087**	**-0.100**	**-0.069**	**0.080**	**0.006**	**0.008**	**0.054**
S.E.	**gi**	**si**	**ri**					
	0.013	**0.025404**	**0.028402**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.019	**0.057**	**0.339**	**0.038**	**0.005**	**1.717**	**0.992**	**0.401**	**0.502**	**0.982**	**0.872**

Erbil location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-0.034**	**-0.015**	**-0.045**	**0.049**	**0.003**	**0.001**	**0.001**	**0.001**
2	**0.028**	**-0.052**	**-0.050**	**-0.022**	**0.053**	**0.003**	**0.002**	**0.001**
3	**-0.025**	**0.020**	**-0.083**	**0.032**	**0.019**	**0.007**	**0.001**	**0.004**
4	**0.004**	**0.059**	**-0.052**	**0.088**	**-0.118**	**0.008**	**0.006**	**0.001**
5	**-0.039**	**-0.003**	**-0.061**	**0.021**	**0.080**	**0.006**	**0.002**	**0.006**
S.E.	**gi**	**si**	**ri**					
	0.013	**0.025**	**0.028**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.006	**0.005**	**1.299**	**0.012**	**0.001**	**0.878**	**0.956**	**0.690**	**0.399**	**0.944**	**0.875**

Kalar location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**0.006**	**-0.026**	**-0.046**	**0.020**	**0.179**	**0.00001**	**0.012**	**0.002**
2	**0.007**	**-0.045**	**0.024**	**0.072**	**-0.001**	**0.00199**	**0.002**	**0.003**
3	**0.063**	**0.007**	**-0.040**	**0.047**	**-0.063**	**0.00161**	**0.003**	**0.004**
4	**0.023**	**-0.073**	**-0.102**	**0.033**	**-0.103**	**0.00107**	**0.009**	**0.003**
5	**0.056**	**-0.043**	**-0.017**	**0.017**	**0.046**	**0.00210**	**0.002**	**0.016**
S.E.	**gi**	**si**	**ri**					
	0.012	**0.0243**	**0.0272**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.002	**0.013**	**0.123**	**0.003**	**0.002**	**2.851**	**0.957**	**0.189**	**1.167**	**0.881**	**0.524**

Table (47): The average awn length (cm) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location

	1	2	3	4	5	Yi.
1	15.210	15.777	15.597	17.853	16.693	81.130
2	15.387	15.373	16.263	17.237	16.150	80.410
3	15.010	15.340	13.720	16.570	15.680	76.320
4	17.143	17.297	18.117	16.373	16.890	85.820
5	16.740	17.093	15.530	17.183	16.447	82.993
Y.j	79.490	80.880	79.227	85.217	81.860	406.673
Yi. +Y.j	160.620	161.290	155.547	171.037	164.853	813.347

Parental mean	Diallel	Reciprocal	General	LSD 0.05
15.425	16.471	16.484	16.267	0.369

Erbil location

	1	2	3	4	5	Yi.
1	13.577	13.837	13.127	15.210	14.423	70.173
2	13.493	12.163	13.633	14.330	14.127	67.747
3	13.590	13.683	11.987	14.507	14.473	68.240
4	15.170	14.063	15.167	14.643	14.887	73.930
5	14.430	13.983	14.437	15.120	13.827	71.797
Y.j	70.260	67.730	68.350	73.810	71.737	351.887
Yi. +Y.j	140.433	135.477	136.590	147.740	143.533	703.773

Parental mean	Diallel	Reciprocal	General	LSD 0.05
13.239	14.255	14.314	14.075	0.801

Kalar location

	1	2	3	4	5	Yi.
1	13.483	13.697	12.950	14.987	14.193	69.310
2	13.087	13.330	14.173	15.263	15.140	70.993
3	14.340	15.073	12.847	14.543	14.207	71.010
4	15.170	14.770	15.330	15.660	15.243	76.173
5	14.597	14.643	14.043	14.733	14.703	72.720
Y.j	70.677	71.513	69.343	75.187	73.487	360.207
Yi. +Y.j	139.987	142.507	140.353	151.360	146.207	720.413

Parental mean	Diallel	Reciprocal	General	LSD 0.05
14.005	14.440	14.579	14.408	0.580

Table (48): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses of awn length for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		3.172	7.823	13.055	5.465	1.271
2	0.621		11.801	8.589	1.508	
3	3.768	5.454		10.124	3.956	
4	8.559	8.967	20.403		2.925	
5	5.760	7.438	2.961	4.713		
S.E.	1.708					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		7.511	2.699	7.796	5.267	1.004
2	4.843		12.905	6.914	8.708	
3	6.324	13.320		8.950	12.138	
4	7.512	4.924	13.907		4.578	
5	5.316	7.605	11.854	6.217		
S.E.	1.109					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		2.163	-1.633	2.848	0.710	1.019
2	-2.387		8.290	5.301	8.014	
3	8.925	15.166		2.035	3.134	
4	4.106	1.897	7.554		0.406	
5	3.571	4.471	1.948	-2.953		
S.E.	1.697					

Table (49): Percentage values of reciprocal effect awn length for three locations.

Qilyasan ocation

Parents	1	2	3	4	5
1					
2	**-2.472**				
3	**-3.761**	**-5.677**			
4	**-3.977**	**0.348**	**9.334**		
5	**0.280**	**5.841**	**-0.957**	**1.737**	
S.E.	1.467				

Erbil location

Parents	1	2	3	4	5
1					
2	**-2.481**				
3	**3.530**	**0.367**			
4	**-0.263**	**-1.861**	**4.550**		
5	**0.046**	**-1.015**	**-0.253**	**1.567**	
S.E.	0.705				

Kalar location

Parents	1	2	3	4	5
1					
2	**-4.454**				
3	**10.734**	**6.350**			
4	**1.223**	**-3.232**	**5.409**		
5	**2.842**	**-3.280**	**-1.150**	**-3.346**	
S.E.	1.618				

Table (50): Estimation of general and specific combining abilities effect, their variances and some genetic parameters of awn length for three locations.

Qilyasan location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.205	-0.342	-0.455	0.600	0.436	0.041	0.286	0.075
2	0.195	-0.138	0.385	0.301	0.274	0.019	0.112	0.185
3	0.293	0.462	-0.712	0.952	-0.168	0.507	0.405	0.320
4	0.355	-0.030	-0.773	0.837	-0.285	0.700	0.263	0.459
5	-0.023	-0.472	0.075	-0.147	0.218	0.048	0.078	0.125
S.E.	gi	si	ri					
	0.058	0.1161	0.1298					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.327	0.841	0.389	0.655	0.123	1.603	0.989	0.433	0.613	0.979	0.824

Erbil location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.032	0.149	-0.219	0.448	0.105	-0.002	0.067	-0.012
2	0.172	-0.528	0.527	-0.050	0.229	0.279	0.094	0.015
3	-0.232	-0.025	-0.416	0.479	0.518	0.173	0.157	0.145
4	0.020	0.133	-0.330	0.699	-0.049	0.488	0.016	0.149
5	-0.003	0.072	0.018	-0.117	0.278	0.077	-0.021	0.112
S.E.	gi	si	ri					
	0.126	0.252	0.2817					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.247	0.532	0.464	0.493	0.017-	1.469	0.928	0.447	0.00	0.857	0.837

Kalar location

gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.410	-0.449	0.021	0.352	0.184	0.166	0.106	0.188
2	0.305	-0.158	0.746	0.038	0.429	0.025	0.264	0.176
3	-0.695	-0.450	-0.373	0.174	-0.123	0.139	0.229	0.239
4	-0.092	0.247	-0.393	0.728	-0.360	0.530	0.104	0.073
5	-0.202	0.248	0.082	0.255	0.212	0.045	0.044	0.121
S.E.	gi	si	ri					
	0.091	0.1826	0.2041					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.222	0.345	0.644	0.445	0.097	1.246	0.950	0.535	0.660	0.929	0.763

Table (51): The average number of spikelets spike⁻¹{Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	28.867	29.967	30.067	31.533	32.233	152.667
2	29.767	28.633	27.800	29.767	31.100	147.067
3	29.767	29.300	27.000	28.767	29.300	144.133
4	31.400	30.167	30.867	29.067	27.467	148.967
5	32.467	31.600	29.667	29.067	29.467	152.267
Y.j	152.267	149.667	145.400	148.200	149.567	745.100
Yi. +Y.j	304.933	296.733	289.533	297.167	301.833	1490.200
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
28.607	29.800	30.407	29.804	1.005		

Erbil location						
	1	2	3	4	5	Yi.
1	27.667	29.133	28.833	29.133	28.200	142.967
2	27.600	24.367	26.467	27.933	29.933	136.300
3	27.400	24.833	22.767	26.967	25.367	127.333
4	29.000	26.833	28.000	26.167	25.533	135.533
5	29.800	28.733	27.167	25.767	27.367	138.833
Y.j	141.467	133.900	133.233	135.967	136.400	680.967
Yi. +Y.j	284.433	270.200	260.567	271.500	275.233	1361.933
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
25.667	27.750	27.513	27.239	1.282		

Kalar location						
	1	2	3	4	5	Yi.
1	27.600	28.400	28.467	29.200	30.400	144.067
2	29.500	26.633	29.100	29.567	29.567	144.367
3	27.033	27.633	25.100	26.733	26.967	133.467
4	30.533	30.700	30.433	27.467	25.500	144.633
5	31.267	29.933	26.533	26.167	28.000	141.900
Y.j	145.933	143.300	139.633	139.133	140.433	708.433
Yi. +Y.j	290.000	287.667	273.100	283.767	282.333	1416.867
Parental mean	27.600	28.400	28.467	29.200		
26.960	28.390	28.973	28.337	0.691		

Table (52): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for number of spikelets spike^{-1}for three locations.

Qilyasan location

Parents	1	2	3	4	5	S.E.
1		**4.232**	**7.637**	**8.861**	**10.514**	1.530
2	**3.536**		**-0.060**	**3.177**	**7.057**	
3	**6.563**	**5.333**		**2.616**	**3.778**	
4	**8.400**	**4.564**	**10.107**		**-6.150**	
5	**11.314**	**8.778**	**5.077**	**-0.683**		
S.E.	1.116					

Erbil location

Parents	1	2	3	4	5	S.E.
1		**11.980**	**14.342**	**8.235**	**2.483**	2.057
2	**6.086**		**12.306**	**10.554**	**15.722**	
3	**8.658**	**5.375**		**10.218**	**1.197**	
4	**7.740**	**6.201**	**14.441**		**-4.608**	
5	**8.298**	**11.082**	**8.378**	**-3.736**		
S.E.	1.482					

Kalar location

Parents	1	2	3	4	5	S.E.
1		**4.733**	**8.033**	**6.053**	**9.353**	1.845
2	**8.789**		**12.500**	**9.304**	**8.237**	
3	**2.593**	**6.830**		**1.712**	**1.569**	
4	**10.896**	**13.494**	**15.789**		**-8.053**	
5	**12.470**	**9.579**	**-0.063**	**-5.649**		
S.E.	2.112					

Table (53): Percentage values of reciprocal effect number of spikelets spike^{-1}for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-0.667**				
3	**-0.998**	**5.396**			
4	**-0.423**	**1.344**	**7.300**		
5	**0.724**	**1.608**	**1.251**	**5.825**	
S.E.	0.936				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-5.263**				
3	**-4.971**	**-6.171**			
4	**-0.458**	**-3.938**	**3.832**		
5	**5.674**	**-4.009**	**7.096**	**0.914**	
S.E.	1.546				

Kalar location					
Parents	1	2	3	4	5
1					
2	**3.873**				
3	**-5.035**	**-5.040**			
4	**4.566**	**3.833**	**13.840**		
5	**2.851**	**1.240**	**-1.607**	**2.614**	
S.E.	1.723				

Table (54): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for number of spikelets spike^{-1}for three locations.

Qilyasan location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	0.689	-0.496	-0.019	1.061	1.477	0.470	1.142	-0.046
2	0.100	-0.131	-0.273	0.381	1.297	0.017	0.595	0.304
3	0.150	-0.750	-0.851	0.951	0.151	0.724	0.461	0.404
4	0.067	-0.200	-1.050	-0.087	-1.829	0.008	1.455	0.938
5	-0.117	-0.250	-0.183	0.800-	0.379	0.144	0.207	2.412
S.E.	**gi**	**si**	**ri**					
	0.158	0.316	0.3533					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.329	2.728	0.121	0.659	0.187	2.878	0.964	0.188	0.753	0.871	0.679

Erbil location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	1.205	0.142	-0.041	0.712	0.272	1.443	0.132	0.480
2	0.767	-0.219	-0.188	0.452	2.029	0.048	1.579	0.450
3	0.717	0.817	-1.182	1.515	-0.075	1.397	1.092	0.371
4	0.067	0.550	-0.517	-0.089	-1.785	0.008	1.184	1.007
5	-0.800	0.600	-0.900	-0.117	0.285	0.081	0.539	2.460
S.E.	**gi**	**si**	**ri**					
	0.202	0.4032	0.4508					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.726	3.561	0.204	1.452	0.315	2.215	0.961	0.278	0.659	0.897	0.737

Kalar location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	0.663	-0.479	-1.313	0.827	1.937	0.437	2.110	0.453
2	-0.550	0.429	0.627	1.327	1.087	0.184	1.193	0.374
3	0.717	0.733	-1.027	1.234	-0.456	1.055	0.907	1.862
4	-0.667	-0.567	-1.850	0.039	-2.439	0.002	3.359	1.360
5	-0.433	-0.183	0.217	-0.333	-0.104	0.011	0.106	3.698
S.E.	**gi**	**si**	**ri**					
	0.109	0.2175	0.2431					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.417	4.402	0.095	0.834	0.563	3.249	0.989	0.157	1.162	0.959	0.573

Table (55): The average number of grains spike^{-1}{Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	25.100	25.333	18.623	27.267	29.133	125.457
2	27.167	25.333	13.800	25.867	28.967	121.133
3	17.900	18.100	22.233	15.933	12.867	87.033
4	25.933	26.833	17.167	26.267	22.900	119.100
5	27.600	27.200	13.933	24.200	22.233	115.167
Y.j	123.700	122.800	85.757	119.533	116.100	567.890
Yi. +Y.j	249.157	243.933	172.790	238.633	231.267	1135.780
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
24.233	22.069	22.603	22.716	1.518		

Erbil location						
	1	2	3	4	5	Yi.
1	22.033	21.233	14.500	22.467	23.133	103.367
2	20.767	20.567	13.533	21.233	24.067	100.167
3	14.567	14.000	18.233	14.000	13.333	74.133
4	21.033	18.833	17.100	22.567	20.767	100.300
5	22.067	23.133	13.633	22.100	21.200	102.133
Y.j	100.467	97.767	77.000	102.367	102.500	480.100
Yi. +Y.j	203.833	197.933	151.133	202.667	204.633	960.200
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
20.920	18.827	18.723	19.204	1.653		

Kalar location						
	1	2	3	4	5	Yi.
1	25.233	23.667	16.500	25.600	26.900	117.900
2	24.300	21.467	15.933	23.967	22.200	107.867
3	16.167	15.000	20.833	14.600	13.667	80.267
4	25.267	24.200	16.467	22.400	21.633	109.967
5	26.100	24.733	14.367	21.300	25.700	112.200
Y.j	117.067	109.067	84.100	107.867	110.100	528.200
Yi. +Y.j	234.967	216.933	164.367	217.833	222.300	1056.400
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
23.127	20.467	20.790	21.128	1.551		

Table (56): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for number of grains spike^{-1}for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**0.463**	**-21.310**	**6.165**	**23.099**	7.725
2	**7.733**		**-41.976**	**0.258**	**21.794**	
3	**-24.366**	**-23.896**		**-34.296**	**-42.129**	
4	**0.973**	**4.005**	**-29.210**		**-5.567**	
5	**16.620**	**14.366**	**-37.331**	**-0.206**		
S.E.	6.203					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**-0.313**	**-27.980**	**0.747**	**7.016**	5.695
2	**-2.504**		**-30.241**	**-1.546**	**15.243**	
3	**-27.649**	**-27.835**		**-31.373**	**-32.375**	
4	**-5.680**	**-12.674**	**-16.176**		**-5.103**	
5	**2.082**	**10.774**	**-30.854**	**0.990**		
S.E.	4.563					

Kalar Location						
Parents	1	2	3	4	5	S.E.
1		**1.356**	**-28.365**	**7.488**	**5.628**	5.836
2	**4.069**		**-24.665**	**9.271**	**-5.866**	
3	**-29.812**	**-29.078**		**-32.460**	**-41.261**	
4	**6.088**	**10.334**	**-23.824**		**-10.049**	
5	**2.487**	**4.876**	**-38.252**	**-11.435**		
S.E.	5.767					

Table (57): Percentage values of reciprocal effect number of grains spike^{-1}for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**7.237**				
3	**-3.884**	**31.159**			
4	**-4.890**	**3.737**	**7.741**		
5	**-5.263**	**-6.099**	**8.290**	**5.677**	
S.E.	3.513				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-2.198**				
3	**0.460**	**3.448**			
4	**-6.380**	**-11.303**	**22.143**		
5	**-4.611**	**-3.878**	**2.250**	**6.421**	
S.E.	2.895				

Kalar location					
Parents	1	2	3	4	5
1					
2	**2.676**				
3	**-2.020**	**-5.858**			
4	**-1.302**	**0.974**	**12.785**		
5	**-2.974**	**11.411**	**5.122**	**-1.541**	
S.E.	1.950				

Table (58): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for number of grains spike^{-1}for three locations.

Qilyasan location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	2.200	-0.343	-4.627	0.537	3.040	4.829	10.256	0.525
2	-0.917	1.678	-3.007	0.809	3.279	2.815	6.999	1.918
3	0.362	-2.150	-5.437	-1.877	-4.290	29.557	8.796	10.373
4	0.667	-0.483	-0.617	1.148	-0.724	1.317	0.431	1.629
5	0.767	0.883	-0.533	-0.650	0.411	0.169	0.595	12.974
S.E.	gi	si	ri					
	0.239	0.4775	0.5339					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
9.646	22.106	0.436	19.292	0.730	1.514	0.993	0.463	0.275	0.986	0.950

Erbil location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	1.179	0.027	-4.363	0.304	0.957	1.377	6.566	0.115
2	0.233	0.589	-1.936	-0.823	2.547	0.347	3.541	0.571
3	-0.033	-0.233	-4.091	-0.626	-2.889	16.734	2.817	8.402
4	0.717	1.200	-1.550	1.063	-0.093	1.129	1.340	0.535
5	0.533	0.467	-0.150	-0.667	1.259	1.586	0.208	5.254
S.E.	gi	si	ri					
	0.260	0.5201	0.5815					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
5.263	9.821	0.536	10.526	0.374	1.366	0.984	0.509	0.267	0.970	0.937

Kalar location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	2.369	-0.079	-5.232	1.281	1.901	5.599	10.778	0.043-
2	-0.317	0.565	-1.535	1.735	0.671	0.320	1.871	0.614
3	0.167	0.467	-4.691	-1.559	-3.522	22.009	4.925	10.242
4	0.167	-0.117	-0.933	0.655	-1.419	0.429	0.874	2.369
5	0.400	-1.267	-0.350	0.167	1.102	1.214	0.537	6.161
S.E.	gi	si	ri					
	0.244	0.4878	0.5454					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
7.366	15.433	0.477	14.732	0.169	1.447	0.990	0.484	0.151	0.980	0.969

Table (59): The average 1000-grain weight {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location

	1	2	3	4	5	Yi.
1	42.177	45.537	46.543	54.517	53.060	241.833
2	43.843	47.940	52.637	49.953	51.380	245.753
3	50.763	50.200	46.993	54.927	53.760	256.643
4	51.970	49.283	53.783	52.197	53.727	260.960
5	53.250	51.007	56.003	54.937	51.417	266.613
Y.j	242.003	243.967	255.960	266.530	263.343	1271.803
Yi. +Y.j	483.837	489.720	512.603	527.490	529.957	2543.607
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
48.145	51.604	51.504	50.872	1.722		

Erbil location

	1	2	3	4	5	Yi.
1	26.153	27.950	35.130	32.640	28.353	150.227
2	26.520	27.020	36.050	33.737	28.673	152.000
3	36.860	33.997	32.553	43.210	41.053	187.673
4	34.213	32.837	39.920	36.970	34.500	178.440
5	30.440	30.363	42.340	30.573	35.787	169.503
Y.j	154.187	152.167	185.993	177.130	168.367	837.843
Yi. +Y.j	304.413	304.167	373.667	355.570	337.870	1675.687
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
31.697	34.130	33.806	33.514	2.265		

Kalar ocation

	1	2	3	4	5	Yi.
1	29.753	34.897	45.430	35.263	38.607	183.950
2	32.820	33.530	45.673	35.027	34.373	181.423
3	42.397	45.987	38.863	47.320	47.953	222.520
4	34.597	37.553	50.050	36.343	37.387	195.930
5	36.730	34.340	47.797	33.940	36.373	189.180
Y.j	176.297	186.307	227.813	187.893	194.693	973.003
Yi. +Y.j	360.247	367.730	450.333	383.823	383.873	1946.007
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
34.973	40.193	39.621	38.920	2.656		

Table (60): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for 1000 grain weight for three locations.

Qilyasan ocation

Parents	1	2	3	4	5	S.E.
1		**1.062**	**4.392**	**15.534**	**13.384**	1.717
2	**-2.697**		**10.892**	**-0.230**	**3.425**	
3	**13.857**	**5.758**		**10.750**	**9.257**	
4	**10.137**	**-1.568**	**8.445**		**3.706**	
5	**13.790**	**2.674**	**13.816**	**6.042**		
S.E.	1.944					

Erbil location

Parents	1	2	3	4	5	S.E.
1		**5.128**	**19.680**	**3.417**	**-8.449**	4.051
2	**-0.251**		**21.027**	**5.444**	**-8.693**	
3	**25.573**	**14.134**		**24.304**	**20.144**	
4	**8.402**	**2.631**	**14.839**		**-5.163**	
5	**-1.711**	**-3.312**	**23.910**	**-15.957**		
S.E.	4.118					

Kalar location

Parents	1	2	3	4	5	S.E.
1		**10.287**	**32.417**	**6.702**	**16.766**	3.997
2	**3.724**		**26.181**	**0.258**	**-1.655**	
3	**23.575**	**27.047**		**25.840**	**27.473**	
4	**4.685**	**7.490**	**33.100**		**2.828**	
5	**11.090**	**-1.750**	**27.057**	**-6.651**		
S.E.	4.351					

Table (61): Percentage values of reciprocal effect 1000 grain weight for three locations.

Qilyasan ocation					
Parents	1	2	3	4	5
1					
2	**-3.719**				
3	**9.067**	**-4.629**			
4	**-4.671**	**-1.341**	**-2.082**		
5	**0.358**	**-0.727**	**4.173**	**2.252**	
S.E.	1.368				

Erbil location					
Parents	1	2	3	4	5
1					
2	**-5.116**				
3	**4.925**	**-5.696**			
4	**4.820**	**-2.668**	**-7.614**		
5	**7.360**	**5.894**	**3.134**	**-11.382**	
S.E.	2.096				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-5.951**				
3	**-6.677**	**0.686**			
4	**-1.891**	**7.214**	**5.769**		
5	**-4.861**	**-0.097**	**-0.327**	**-9.219**	
S.E.	1.682				

Table (62): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for 1000 grain weight for three locations.

Qilyasan location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-2.488**	**-1.794**	**0.970**	**2.983**	**2.648**	**6.178**	**6.564**	**2.083**
2	**0.847**	**-1.900**	**2.058**	**-1.231**	**0.098**	**3.611**	**2.034**	**1.616**
3	**-2.110**	**1.218**	**0.388**	**1.218**	**1.498**	**0.151**	**3.096**	**2.254**
4	**1.273**	**0.335**	**0.572**	**1.877**	**-0.541**	**3.523**	**0.660**	**4.087**
5	**-0.095**	**0.187**	**-1.122**	**-0.605**	**2.124**	**4.509**	**0.431**	**3.185**
S.E.	**gi**	**si**	**ri**					
	0.271	**0.541603**	**0.605531**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
4.460	**11.003**	**0.405**	**8.920**	**0.855**	**1.571**	**0.982**	**0.440**	**0.438**	**0.964**	**0.880**

Erbil location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-3.072**	**- 0.109**	**5.268**	**0.942**	**-1.318**	**9.414**	**9.914**	**0.672**
2	**0.715**	**-3.097**	**0.754**	**0.827**	**-1.172**	**9.592**	**0.829**	**0.661**
3	**-0.865**	**1.027**	**3.853**	**2.155**	**4.057**	**14.845**	**7.419**	**10.480**
4	**-0.787**	**0.450**	**1.645**	**2.043**	**-3.294**	**4.175**	**4.576**	**3.357**
5	**-1.043**	**-0.845**	**-0.643**	**1.963**	**0.273**	**0.075**	**1.808**	**10.138**
S.E.	**gi**	**si**	**ri**					
	0.356	**0.7124**	**0.7965**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
9.468	**15.391**	**0.615**	**18.936**	**0.874**	**1.275**	**0.982**	**0.542**	**0.304**	**0.969**	**0.926**

Kalar location								
gi	**1**	**2**	**3**	**4**	**5**	**σ^2gi.**	**σ^2si.**	**σ^2ri.**
1	**-2.895**	**-0.019**	**5.885**	**-0.557**	**2.176**	**8.349**	**12.931**	**1.020**
2	**1.038**	**-2.147**	**2.944**	**0.055**	**-1.884**	**4.610**	**4.135**	**0.540**
3	**1.517**	**-0.157**	**6.113**	**4.189**	**3.374**	**37.371**	**10.125**	**15.057**
4	**0.333**	**-1.263**	**-1.365**	**-0.538**	**-2.186**	**0.289**	**2.487**	**6.945**
5	**0.938**	**0.017**	**0.078**	**1.723**	**-0.533**	**0.284**	**0.989**	**8.150**
S.E.	**gi**	**si**	**ri**					
	0.418	**0.8355**	**0.9341**					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
12.647	**26.747**	**0.473**	**25.295**	**0.647**	**1.454**	**0.984**	**0.478**	**0.226**	**0.967**	**0.943**

Table (63): The average harvest index {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	0.430	0.448	0.362	0.450	0.452	2.143
2	0.465	0.467	0.306	0.462	0.463	2.162
3	0.419	0.379	0.441	0.334	0.303	1.876
4	0.380	0.480	0.338	0.447	0.477	2.122
5	0.453	0.464	0.312	0.438	0.399	2.065
Y.j	2.146	2.238	1.759	2.131	2.095	10.368
Yi. +Y.j	4.289	4.399	3.635	4.253	4.159	20.735
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
0.437	0.406	0.413	0.415	0.023		

Erbil location						
	1	2	3	4	5	Yi.
1	0.330	0.294	0.313	0.331	0.285	1.552
2	0.313	0.346	0.306	0.340	0.314	1.619
3	0.284	0.327	0.350	0.315	0.279	1.555
4	0.318	0.297	0.341	0.376	0.349	1.681
5	0.300	0.332	0.297	0.326	0.332	1.587
Y.j	1.545	1.596	1.608	1.686	1.559	7.995
Yi. +Y.j	3.097	3.215	3.164	3.367	3.146	15.989
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
0.347	0.313	0.314	0.320	0.033		

Kalar location						
	1	2	3	4	5	Yi.
1	0.416	0.448	0.393	0.439	0.447	2.143
2	0.457	0.442	0.394	0.442	0.385	2.121
3	0.369	0.381	0.442	0.371	0.334	1.897
4	0.462	0.451	0.375	0.424	0.445	2.158
5	0.439	0.442	0.366	0.371	0.487	2.106
Y.j	2.144	2.164	1.971	2.048	2.098	10.425
Yi. +Y.j	4.286	4.285	3.868	4.206	4.204	20.849
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
0.442	0.410	0.411	0.417	0.024		

Table (64): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for harvesit index for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**0.023**	**-16.784**	**2.535**	**9.124**	5.320
2	**3.680**		**-32.654**	**1.052**	**6.934**	
3	**-3.710**	**-16.497**		**-24.781**	**-27.790**	
4	**-13.449**	**4.971**	**-23.794**		**12.629**	
5	**9.154**	**7.157**	**-25.823**	**3.408**		
S.E.	4.194					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**-13.049**	**-7.812**	**-6.241**	**-13.803**	1.586
2	**-7.302**		**-12.009**	**-5.752**	**-7.232**	
3	**-16.514**	**-5.998**		**-13.286**	**-18.233**	
4	**-9.723**	**-17.551**	**-6.130**		**-1.316**	
5	**-9.128**	**-1.906**	**-12.855**	**-7.950**		
S.E.	1.542					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**4.311**	**-8.350**	**4.362**	**-1.107**	3.359
2	**6.485**		**-10.860**	**2.116**	**-17.043**	
3	**-13.942**	**-13.801**		**-14.275**	**-28.166**	
4	**9.913**	**4.194**	**-13.351**		**-2.268**	
5	**-2.804**	**-4.772**	**-21.134**	**-18.581**		
S.E.	3.470					

Table (65): Percentage values of reciprocal effect harvesit index for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**3.657**				
3	**15.711**	**23.992**			
4	**-15.589**	**3.878**	**1.312**		
5	**0.028**	**0.208**	**2.725**	**-8.187**	
S.E.	3.485				

Erbil location					
Parents	1	2	3	4	5
1					
2	**6.609**				
3	**-9.439**	**6.832**			
4	**-3.714**	**-12.519**	**8.252**		
5	**5.425**	**5.742**	**6.578**	**-6.723**	
S.E.	2.503				

Kalar location					
Parents	1	2	3	4	5
1					
2	**2.085**				
3	**-6.102**	**-3.299**			
4	**5.319**	**2.035**	**1.077**		
5	**-1.716**	**14.792**	**9.790**	**-16.692**	
S.E.	2.743				

Table (66): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for harvesit index for three locations.

Qilyasan location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	0.014	0.002	-0.015	-0.025	0.022	0.000	0.000	0.001
2	-0.008	0.025	-0.046	0.020	0.022	0.001	0.001	0.000
3	-0.028	-0.037	-0.051	-0.038	-0.057	0.003	0.002	0.001
4	0.035	-0.009	-0.002	0.011	0.031	0.000	0.001	0.001
5	0.000	0.000	-0.004	0.020	0.001	0.000	0.000	0.002
S.E.	gi	si	ri					
	0.004	0.0072	0.008					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.001	0.004	0.243	0.002	0.000	2.028	0.988	0.323	0.638	0.971	0.807

Erbil location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.010	-0.008	-0.014	-0.002	-0.012	0.00010	0.00009	0.00007
2	-0.010	0.002	-0.001	-0.020	0.007	0.000003	0.00013	0.00024
3	0.015	-0.010	-0.003	-0.006	-0.023	0.00001	0.00025	0.00015
4	0.006	0.021	-0.013	0.017	0.006	0.00029	0.00018	0.00019
5	-0.008	-0.009	-0.009	0.012	-0.005	0.00003	0.00007	0.00025
S.E.	gi	si	ri					
	0.005	0.0104216	0.0116517					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.00009	0.00050	0.186	0.00019	0.00008	2.320	0.836	0.227	0.904	0.660	0.469

Kalar location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	0.0116	0.012	-0.039	0.018	0.011	0.00013	0.00069	0.00007
2	-0.005	0.0115	-0.011	0.015	-0.018	0.00013	0.00020	0.00034
3	0.012	0.006	-0.030	-0.017	-0.040	0.00091	0.00068	0.00165
4	-0.012	-0.005	-0.002	0.004	-0.016	0.00001	0.00011	0.00174
5	0.004	-0.029	-0.016	0.037	0.003	0.00001	0.00080	0.00077
S.E.	gi	si	ri					
	0.004	0.00743	0.008312					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.00029	0.00186	0.158	0.00059	0.00025	2.516	0.973	0.234	0.922	0.924	0.648

Table (67): The average grains yield plant^{-1} (g) {Diagonal, upper diagonal and sub diagonal} for parents, F1 diallel crosses and reciprocal crosses of two-rowed barley for three locations.

Qilyasan location						
	1	2	3	4	5	Yi.
1	20.460	32.587	16.657	50.093	31.437	151.233
2	22.120	35.753	15.760	38.670	42.270	154.573
3	19.517	25.567	24.557	20.533	24.930	115.103
4	36.723	42.407	31.240	42.403	36.473	189.247
5	37.517	41.040	30.333	38.693	29.353	176.937
Y.j	136.337	177.353	118.547	190.393	164.463	787.093
Yi. +Y.j	287.570	331.927	233.650	379.640	341.400	1574.187
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
30.505	30.941	32.516	31.484	3.727		

Erbil location						
	1	2	3	4	5	Yi.
1	8.930	10.103	7.130	10.033	8.490	44.687
2	8.140	8.407	8.287	7.597	10.053	42.483
3	8.253	8.487	12.533	11.613	7.373	48.260
4	10.237	6.087	9.740	9.363	9.400	44.827
5	11.363	12.807	8.453	11.017	10.837	54.477
Y.j	46.923	45.890	46.143	49.623	46.153	234.733
Yi. +Y.j	91.610	88.373	94.403	94.450	100.630	469.467
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
10.014	9.008	9.458	9.389	1.530		

Kalar location						
	1	2	3	4	5	Yi.
1	19.907	27.843	29.747	26.690	28.547	132.733
2	21.450	23.187	31.020	25.280	26.480	127.417
3	19.867	27.057	31.177	19.063	20.300	117.463
4	29.660	31.967	28.330	19.977	26.513	136.447
5	26.000	26.163	21.300	22.940	26.107	122.510
Y.j	116.883	136.217	141.573	113.950	127.947	636.570
Yi. +Y.j	249.617	263.633	259.037	250.397	250.457	1273.140
Parental mean	Diallel	Reciprocal	General	LSD 0.05		
24.071	26.148	25.473	25.463	2.663		

Table (68): The percentage values of heterosis {Upper diagonal and sub diagonal} for F1 diallel crosses and reciprocal crosses for grains yield plant^{-1}for three locations.

Qilyasan location						
Parents	1	2	3	4	5	S.E.
1		**15.939**	**-25.998**	**59.372**	**26.218**	10.463
2	**-21.300**		**-47.737**	**-1.045**	**29.848**	
3	**-13.291**	**-15.216**		**-38.670**	**-7.513**	
4	**16.835**	**8.517**	**-6.691**		**1.658**	
5	**50.629**	**26.070**	**12.533**	**7.846**		
S.E.	6.904					

Erbil location						
Parents	1	2	3	4	5	S.E.
1		**16.555**	**-33.561**	**9.694**	**-14.098**	5.768
2	**-6.095**		**-20.853**	**-14.500**	**4.486**	
3	**-23.094**	**-18.943**		**6.074**	**-36.899**	
4	**11.917**	**-31.495**	**-11.037**		**-6.931**	
5	**14.975**	**33.102**	**-27.657**	**9.076**		
S.E.	6.758					

Kalar location						
Parents	1	2	3	4	5	S.E.
1		**29.223**	**16.463**	**33.840**	**24.080**	6.721
2	**-0.449**		**14.121**	**17.136**	**7.438**	
3	**-22.219**	**-0.460**		**-25.466**	**-29.124**	
4	**48.734**	**48.120**	**10.765**		**15.067**	
5	**13.011**	**6.154**	**-25.633**	**-0.441**		
S.E.	7.862					

Table (69): Percentage values of reciprocal effect grains yield plant^{-1}for three locations.

Qilyasan location					
Parents	1	2	3	4	5
1					
2	**-32.119**				
3	**17.170**	**62.225**			
4	**-26.690**	**9.663**	**52.143**		
5	**19.340**	**-2.910**	**21.674**	**6.087**	
S.E.	9.434				

Erbil Location					
Parents	1	2	3	4	5
1					
2	**-19.433**				
3	**15.755**	**2.414**			
4	**2.027**	**-19.877**	**-16.131**		
5	**33.844**	**27.387**	**14.647**	**17.199**	
S.E	6.112				

Kalar location					
Parents	1	2	3	4	5
1					
2	**-22.962**				
3	**-33.214**	**-12.777**			
4	**11.128**	**26.450**	**48.610**		
5	**-8.921**	**-1.196**	**4.926**	**-13.477**	
S.E.	7.650				

Table (70): Estimation of general and specific combining abilities effect, their variances and some genetic parameters for grains yield $plant^{-1}$ for three locations.

Qilyasan location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-2.727	-3.113	-6.499	8.171	3.063	7.366	42.106	26.929
2	5.233	1.709	-4.411	0.865	5.806	2.920	26.516	12.533
3	-1.430	-4.903	-8.119	-3.959	1.610	65.914	14.200	32.547
4	6.685	-1.868	-5.353	6.480	-3.037	41.994	28.103	28.139
5	-3.040	0.615	-2.702	-1.110	2.656	7.056	5.466	18.304
S.E.	gi	si	ri					
	0.586	1.1723	1.3107					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
31.158	50.832	0.613	62.316	13.987	1.277	0.985	0.543	0.670	0.978	0.799

Erbil location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.228	0.513	-0.943	0.918	0.092	0.041	0.569	0.973
2	0.982	-0.552	-0.502	-2.051	1.919	0.305	2.937	0.913
3	-0.562	-0.100	0.051	1.181	-2.201	0.003	2.089	0.770
4	-0.102	0.755	0.937	0.056	0.090	0.003	0.390	2.366
5	-1.437	-1.377	-0.540	-0.808	0.674	0.454	1.536	2.847
S.E.	gi	si	ri					
	0.241	0.4812	0.538					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.175	4.203	0.042	0.350	0.620	4.899	0.940	0.072	1.882	0.770	0.278

Kalar location								
gi	1	2	3	4	5	σ^2gi.	σ^2si.	σ^2ri.
1	-0.501	-1.216	-1.591	3.636	2.729	0.216	7.928	12.378
2	3.197	0.901	2.234	2.683	0.375	0.811	7.219	5.536
3	4.940	1.982	0.441	-1.784	-4.687	0.194	17.527	9.747
4	-1.485	-3.343	-4.633	-0.423	0.104	0.179	11.322	8.932
5	1.273	0.158	-0.500	1.787	-0.417	0.174	1.398	9.854
S.E.	gi	si	ri					
	0.419	0.8376	0.9364					

σ^2gca	σ^2sca = σ^2D	σ^2gca / σ^2sca	σ^2A	σ^2Dr	ā	h^2b.s	h^2n.s	ār	h^2bsr	h^2nsr
0.315	19.564	0.016	0.629	7.410	7.885	0.958	0.030	4.853	0.902	0.071

Table (71): Correlation coefficients among each pair of traits at Qilyasan location.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)	(16)	(17)
Biological yield (1)	1.00																
Grains yield /plant (2)	0.87^{**}	1.00															
1000 grains weight (3)	0.60^{**}	0.33	1.00														
Spikes/plant (4)	0.82^{**}	0.57^{**}	0.57^{**}	1.00													
Spike weight (5)	0.54^{**}	0.80^{**}	0.22	0.04	1.00												
Days to maturity (6)	0.50^{*}	0.41^{*}	0.54^{**}	0.49^{*}	0.22	1.00											
Days to anthesis (7)	0.39	0.44^{*}	0.55^{**}	0.24	0.44^{*}	0.69^{**}	1.00										
Grains/spike (8)	0.27	0.65^{**}	-0.30	-0.18	0.84^{**}	-0.06	0.08	1.00									
Harvest index (9)	0.12	0.58^{**}	-0.36	-0.18	0.72^{**}	-0.04	0.14	0.89^{**}	1.00								
Peduncle diameter (10)	0.69^{**}	0.69^{**}	0.54^{**}	0.47^{*}	0.63^{**}	0.66^{**}	0.46^{*}	0.39	0.30	1.00							
Peduncle length (11)	0.35	0.46^{*}	0.00	0.08	0.53^{**}	-0.36	-0.07	0.54^{**}	0.39	0.07	1.00						
Spikeletes /spike (12)	0.44^{*}	0.44^{*}	0.19	0.08	0.56^{**}	-0.16	0.06	0.45^{*}	0.17	0.30	0.79^{**}	1.00					
Plant height (13)	0.41^{*}	0.28	0.36	0.33	0.18	-0.22	0.00	-0.04	-0.11	-0.09	0.69^{**}	0.59^{**}	1.00				
Tellers/ plant (14)	0.82^{**}	0.56^{**}	0.57^{**}	1.00^{**}	0.03	0.48^{*}	0.23	-0.20	-0.20	0.45^{*}	0.08	0.08	0.34	1.00			
Spike length (15)	0.44^{*}	0.39	0.30	0.25	0.41^{*}	-0.19	0.08	0.25	0.07	0.09	0.81^{**}	0.79^{**}	0.74^{**}	0.26	1.00		
Awn length (16)	0.66^{**}	0.61^{**}	0.54^{**}	0.40^{*}	0.53^{**}	0.55^{**}	0.64^{**}	0.25	0.08	0.59^{**}	0.32	0.51^{**}	0.36	0.39	0.44^{*}	1.00	
Flag leaf length (17)	0.63^{**}	0.55^{**}	0.61^{**}	0.53^{**}	0.40^{*}	0.54^{**}	0.37	0.14	0.13	0.83^{**}	-0.05	0.13	0.00	0.53^{**}	0.10	0.40^{*}	1.00

Table (72): Correlation coefficients among each pair of traits at Erbil location.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)	(16)	(17)
Biological yield (1)	1.00																
Grains yield /plant (2)	0.97**	1.00															
1000 grains weight (3)	-0.05	-0.07	1.00														
Spikes/plant (4)	0.71**	0.69**	-0.09	1.00													
Spike weight (5)	0.23	0.34	0.19	-0.42*	1.00												
Days to maturity (6)	-0.01	0.15	0.56**	-0.25	0.56**	1.00											
Days to anthesis (7)	-0.14	0.08	0.06	-0.22	0.35	0.54**	0.00										
Grains/spike (8)	0.24	0.36	-0.71**	-0.18	0.53**	-0.03	0.28	1.00									
Harvest index (9)	-0.07	0.33	-0.07	0.00	0.34	0.40*	0.55**	0.35	1.00								
Peduncle diameter (10)	0.22	0.28	0.24	-0.41*	0.91**	0.62**	0.22	0.42*	0.21	1.00							
Peduncle length (11)	0.37	0.24	-0.29	0.10	0.22	-0.31	-0.44*	0.32	-0.26	0.32	1.00						
Spikeletes /spike (12)	0.22	0.05	-0.18	-0.21	0.36	-0.09	-0.10	0.36	-0.34	0.22	0.29	1.00					
Plant height (13)	0.23	0.02	-0.10	0.40*	-0.41*	-0.56**	-0.61**	-0.28	-0.50*	-0.43*	0.41*	0.35	1.00				
Tellers/ plant (14)	0.72**	0.72**	-0.12	0.96**	-0.37	-0.21	-0.21	-0.10	0.07	-0.35	0.05	-0.28	0.30	1.00			
Spike length (15)	0.42*	0.19	-0.04	0.08	0.20	-0.26	-0.16	0.13	-0.50*	0.05	0.36	0.68**	0.51**	0.00	1.00		
Awn length (16)	0.12	0.07	0.33	-0.38	0.64**	0.73**	0.27	0.18	-0.06	0.64**	-0.04	0.44*	-0.25	-0.37	0.30	1.00	
Flag leaf length (17)	0.35	0.35	0.44*	-0.09	0.57**	0.60**	-0.02	0.04	0.03	0.73**	0.11	-0.02	-0.19	0.02	0.04	0.58**	1.00

Table (73): Correlation coefficients among each pair of traits at Kalar location.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)	(16)	(17)
Biological yield (1)	1.00																
Grains yield /plant (2)	0.81**	1.00															
1000 grains weight (3)	0.46*	0.02	1.00														
Spikes/plant (4)	0.86**	0.68**	0.39	1.00													
Spike weight (5)	0.26	0.47*	0.01	-0.20	1.00												
Days to maturity (6)	-0.17	-0.22	0.13	-0.27	0.23	1.00											
Days to anthesis (7)	0.13	0.30	-0.34	0.14	0.22	0.35	1.00										
Grains/spike (8)	-0.30	0.23	-0.87**	-0.44*	0.46*	-0.06	0.35	1.00									
Harvest index (9)	-0.21	0.39	-0.68**	-0.21	0.37	-0.10	0.27	0.85**	1.00								
Peduncle diameter (10)	-0.13	0.08	-0.22	-0.43*	0.65**	0.64**	0.33	0.48*	0.34	1.00							
Peduncle length (11)	0.09	0.09	-0.14	-0.09	0.28	-0.42*	-0.19	0.25	0.04	-0.04	1.00						
Spikeletes /spike (12)	0.25	0.42*	-0.15	-0.05	0.65**	-0.11	0.17	0.45*	0.32	0.42*	0.46*	1.00					
Plant height (13)	0.32	0.05	0.42*	0.19	0.06	-0.35	-0.38	-0.36	-0.43*	-0.44*	0.40*	0.26	1.00				
Tellers/ plant (14)	0.85**	0.68**	0.36	1.00**	-0.20	-0.29	0.16	-0.41*	-0.20	-0.45*	-0.09	-0.06	0.19	1.00			
Spike length (15)	0.47*	0.51*	0.13	0.27	0.48*	-0.30	0.22	0.14	0.09	0.16	0.41*	0.80**	0.30	0.26	1.00		
Awn length (16)	0.03	0.00	0.04	-0.12	0.37	0.74**	0.56**	0.09	-0.04	0.68**	-0.07	0.27	-0.28	-0.14	0.24	1.00	
Flag leaf length (17)	0.31	0.28	0.19	0.10	0.46*	0.58**	0.28	-0.01	-0.03	0.55**	-0.27	-0.04	-0.30	0.09	0.04	0.54**	1.00

4.18 Correlation among traits:

Simple correlation coefficients between the grain yield plant^{-1} and its components were represented in tables (71, 72 and 73).

Qilyasan location:

The correlation among grain yield plant^{-1} and other traits revealed highly positive significant correlation recorded with biological yield plant^{-1}, number of spikes plant^{-1}, spike weight, number of grains spike^{-1}, harvest index, peduncle diameter, number of tillers plant^{-1}, awn length and flag leaf length. While, days to 50% anthesis, days to 50% maturity, peduncle length and number of spikelets spike^{-1} had positive significant correlation.

The highest correlation with grain yield plant^{-1} recorded by biological yield plant^{-1} (0.87), spike weight (0.80), peduncle diameter (0.69), number of grains spike^{-1} (0.65) and awn length (0.61).

Erbil location:

Only three traits, biological yield plant^{-1} (0.92), number of tillers plant^{-1} (0.72) and number of spikes plant^{-1} (0.69) had highly positive significant correlation with grain yield plant^{-1}.

Kalar location:

Grain weight plant^{-1} had highly significant correlations with biological yield plant^{-1}, number of tillers plant^{-1} and number of spikes plant^{-1}, and three traits spike weight, number of spikelets spike^{-1}, and spike length, showed significant correlations. A negative correlation was recorded between grain yield plant^{-1} and days to 50% maturity.

The correlation among grain yield plant^{-1} and other traits at three locations revealed that, there were three traits, biological yield plant^{-1}, number of spikes plant^{-1} and number of tillers plant^{-1} had positive highly significant correlations with grain weight plant^{-1}. This mean, the three traits were less affected by different environments. These results are in agreement with those obtained by

Kole ,2006 who noticed that grain yield plant^{-1} had positive and highly significant correlations with tiller number at both genotypic and phenotypic levels; Ali *et al.,* 2009, who recorded that significant and highly significant positive correlations were found between grain yield and both number of spikes plant^{-1} and biological yield, respectively under both normal and drought environment; Mahmood, 2010, at Kalar; Sharief *et al*., 2011, whom obtained that over four locations number of spikes/m² were positively and highly significantly correlated with grain yield $^{-h}$; Fatieh, 2012, at Qilyasan and Khaiti, 2012, whom showed that grain yield plant^{-1} had highly significant positive correlation with number of tillers under two environments, normal and drought conditions. Therefore, to develop a wide adaptable variety for these locations, the breeder can work with these three traits to increase yield plant^{-1} because there were highly significant correlation among these traits and grains weight plant^{-1}, as well as these traits were stabile in three locations and had low to moderate heritability in narrow-sense (biological yield plant^{-1} 0.396, 0.149, 0.229; spikes plant^{-1} 0.309, 0.256, 0.428; tillers plant^{-1} 0.308, 0.205, 0.442, at Qilyasan, Erbil and Kalar, respectively) suggesting an ample scope for heterosis breeding to improve these traits in two-rowed barley.

Only at Qilyasan location most traits had highly positive significant (9 traits) and significant (4 traits) correlations with grain yield plant^{-1}. It is due to different environment in Qilyasan, more moisture and lower temperature than other locations, causing the development of these traits and had high contributions in grain yield plant^{-1}.

Previous workers confirmed positive and highly significant correlation coefficients between grain yield and the traits spikes plant^{-1}, spike length, grain spike^{-1}, biological yield, and1000-grains weight (Mahmood, 2010 and Fatieh 2012). Some researchers have already shown that spike weight, has highly significant correlation coefficients with yield (Kole, 2006; Mahmood , 2010 and Tas and Çelik, 2011), while (Sharief *et al.,* 2011; Babaiy *et al.,* 2011 and

Hosseinpour, 2012) noticed positive relations. Positive correlation of peduncle length with grain yield was recorded by (Bhutta *et al.,* 2005; Babaiy *et al.,* 2011; and Hosseinpour, 2012). Highly significant correlation coefficients between grain yield and plant height recorded by (Budakli and Celik 2012 and Niazi-Fard *et al.,* 2012), while (Bhutta *et al.,* 2005) obtained significant correlation and (Dyulgerova, 2012) showed merely positive relations, however (Tas and Çelik, 2011) noticed negative relations. Niazi-Fard *et al.* (2012) recorded that highly significant positive correlations were found between grain yield and days to 50% maturity, days to 50% anthesis and harvest index.

4.19 Path coefficient analysis for grain yield plant^{-1} and its related traits:

The correlation coefficient illustrates the correlation among traits without estimation of the direct and indirect effects of each trait independently. Therefore, path analysis which divided the correlation to direct and indirect effects between any two variables. Through this method, the breeder can Inference to gate the selection index which is useful in selection or hybridization programs (Samonta *et al.,* 1998).

Qilyasan location:

Table (74) shows that the traits biological yield and harvest index had high positive direct effects on the grain yield plant^{-1} (Degrees of Path coefficient analysis were determined according to Link and Mishra, 1973). That means any improvement in these traits will have direct contribution in yield improvement

Two traits, peduncle length and peduncle diameter had negative direct effects on the weight plant^{-1}, although they had significant positive correlations with grain yield plant^{-1}. Tyagi and Khan (2010) found positive genetic correlation and negative direct effect on the yield or vice versa therefore, the breeder in his program must utilize the positive indirect effect through these traits. The traits peduncle length and peduncle diameter showed negative indirect effect on the yield, also it had negative indirect effect through some traits. Previous study at Qilyasan by Fatieh (2012) showed highly positive direct effect of the traits biological yield plant^{-1} and number of spikes plant^{-1} and merely positive direct effect of the traits number of grains spike^{-1} and 1000-grain weight on the grain yield plant^{-1}.

Erbil location:

Table (75) represents high positive direct effects of the traits biological yield plant^{-1}, number of grains spike^{-1}, and moderate positive direct effects for number of spikes plant^{-1}, harvest index and 1000-grain weight on the grain yield plant^{-1}. That means any improvement in these traits will have direct contribution in yield improvement under this environment.

Kalar location:

Table (76) represents the positive direct effects of the traits biological yield plant^{-1}, number of tillers, harvest index, number of grains spike^{-1}, 1000-grain weight, spike weight, peduncle diameter and number of spikes plant^{-1}, while both traits days to 50% maturity and peduncle length had negative direct effects on the grain yield plant^{-1}.

Plant breeder usually looking for the high correlated and high positive direct effect of the trait of the yield .Path coefficient for these three location revealed that some traits recorded high positive direct effect on the grain yield plant^{-1} at all locations as biological weight plant^{-1} and harvest index. So that the selection for these traits lead to improve the adaptation of promising varieties and directly increased the yield. Similar results were reported by other researchers who conducted studies on different barely genotypes and determined the high direct effects of different yield components on grain yield: Ilker, 2006; Akdeniz, *et al.*, 2004; Ataei, 2006 and Srivastava *et al.*, 2012 for number of grains spike^{-1} and number of spikes m^{-2} ; Madic *et al.*, 2005 for biological yield, harvest index and number of spikes plant^{-1}; Drikvand *et al.*, 2011 for number of spikes m^{-2} and harvest index and Budakli Carpici and Celik, 2012 for number of grains spike^{-1}, number of spikes m^{-2} and harvest index. However, Srivastava *et al.*, 2012 noticed that harvest index, tillers running meter^{-1}, 1000-grain weight, peduncle length, spikelets spike^{-1}, days to 50% heading and days to maturity exhibited high positive and direct influence on grain yield plant^{-1}.

Table (74): Path coefficient analysis conforming direct (diagonal values) and indirect on grains yield plant⁻¹ at Qilyasan location.

Traits	No .of days to maturity	No .of spikes plant ⁻¹	No .of grains spike ⁻¹	Peduncle length	Peduncle diameter	Spike weight	1000-Grain weight	Harvest index	Biological yield plant ⁻¹	No .of tillers plant ⁻¹	Grains weight Plant ⁻¹ ***(Correlation)***
No .of days to maturity	**0,053**	**0.122**	-0.010	0.015	-0.089	0.006	0.054	-0.017	**0.368**	-0.097	**0.406***
No .of spikes plant ⁻¹	0.026	**0.250**	-0.030	-0.003	-0.063	0.001	0.057	-0.077	**0.611**	-0.202	**0.570****
No .of grains spike ⁻¹	-0.003	-0.046	**0.165**	-0.022	-0.053	0.023	-0.030	**0.375**	**0.203**	0.040	**0.653****
Peduncle length	-0.019	**0.020**	0.089	**-0.041**	-0.009	0.015	0.000	**0.166**	**0.259**	-0.016	**0.464***
Peduncle diameter	0.035	**0.117**	0.064	-0.003	**-0.138**	0.017	0.054	**0.125**	**0.511**	-0.091	**0.693****
Spike weight	0.012	**0.010**	0.139	-0.022	-0.085	**0.028**	0.022	**0.302**	**0.401**	-0.005	**0.801****
1000-Grain weight	0.029	**0.142**	-0.049	0.000	-0.073	0.006	**0.101**	-0.151	**0.444**	-0.115	**0.334**
Harvest index	-0.002	-0.046	0.147	-0.016	-0.040	0.020	-0.036	**0.421**	**0.087**	0.040	**0.575****
Biological yield plant ⁻¹	0.026	**0.205**	0.045	-0.014	-0.093	0.015	0.060	**0.049**	**0.744**	-0.165	**0.873****
No .of Tillers plant ⁻¹	0.026	**0.250**	-0.032	-0.003	-0.061	0.001	0.057	-0.084	**0.608**	**-0.202**	**0.599****

Table (75): Path coefficient analysis conforming direct (diagonal values) and indirect on grains yield plant^{-1} at Erbil location.

Traits	No .of days to maturity	No .of spikes plant $^{-1}$	No .of grains spike $^{-1}$	Peduncle length	Peduncle diameter	Spike weight	1000-Grain weight	Harvest index	Biological yield plant $^{-1}$	No .of tillers plant $^{-1}$	Grains weight Plant $^{-1}$ ***(Correlation)***
No .of days to maturity	**-0.056**	-0.071	-0.009	0.007	0.050	0.013	0.132	0.107	-0.004	-0.019	**0.150**
No .of spikes plant $^{-1}$	0.014	**0.286**	-0.056	-0.002	-0.033	-0.010	-0.021	0.001	**0.420**	**0.086**	**0.685****
No .of grains spike $^{-1}$	0.002	-0.052	**0.309**	-0.007	0.034	0.012	-0.168	0.093	**0.142**	-0.009	**0.335**
Peduncle length	0.017	**0.027**	0.099	**-0.022**	0.025	0.005	-0.069	-0.069	**0.217**	0.005	**0.236**
Peduncle diameter	-0.035	-0.118	0.130	-0.007	**0.080**	0.021	0.056	0.057	**0.128**	-0.032	**0.279**
Spike weight	-0.031	-0.121	0.163	-0.005	0.073	**0.023**	0.044	0.090	**0.136**	-0.033	**0.338**
1000-Grain weight	-0.031	-0.026	-0.220	0.006	0.019	0.004	**0.235**	-0.018	-0.030	-0.011	**-0.071**
Harvest index	-0.023	0.001	0.109	0.006	0.017	0.008	-0.016	**0.264**	-0.040	0.007	**0.332**
Biological yield plant $^{-1}$	0.000	**0.204**	0.074	-0/008	0.017	0.005	-0.012	-0.018	**0.589**	**0.064**	**0.916****
No .of Tillers plant $^{-1}$	0.012	**0.275**	-0.030	-0.001	-0.028	-0.008	-0.028	0.019	**0.422**	**0.090**	**0.721****

Table (76): Path coefficient analysis conforming direct (diagonal values) and indirect on grains yield plant^{-1} at Kalar location.

Traits	No .of days to maturity	No .of spikes plant $^{-1}$	No .of grains spike $^{-1}$	Peduncle length	Peduncle diameter	Spike weight	1000-Grain weight	Harvest index	Biological yield plant $^{-1}$	No .of tillers plant $^{-1}$	Grains weight Plant $^{-1}$ ***(Correlation)***
No .of days to maturity	**-0.043**	-0.019	-0.007	0.022	0.001	0.020	0.006	-0.050	-0.127	-0.026	**-0.223**
No .of spikes plant $^{-1}$	0.012	**0.070**	-0.058	0.005	0.000	-0.017	0.019	-0.098	**0.656**	**0.090**	**0.679^{**}**
No .of grains spike $^{-1}$	0.002	-0.031	**0.132**	-0.013	0.000	0.040	-0.043	0.403	-0.227	-0.037	**0.228**
Peduncle length	0.018	-0.006	0.033	**-0.051**	0.000	0.025	-0.007	0.021	**0.067**	-0.008	**0.092**
Peduncle diameter	-0.027	-0.030	0.063	0.002	**0.001**	0.057	-0.011	0.163	-0.098	-0.040	**0.078**
Spike weight	-0.010	-0.014	0.061	-0.014	0.001	**0.087**	0.000	0.175	**0.201**	-0.018	**0.469^{*}**
1000-Grain weight	-0.006	0.028	-0.115	0.007	0.000	0.001	**0.049**	-0.326	**0.351**	**0.033**	**0.022**
Harvest index	0.004	-0.014	0.112	-0.002	0.000	0.032	-0.034	**0.447**	-0.163	-0.018	**0.394**
Biological yield plant $^{-1}$	0.007	0.060	-0.039	-0.004	0.000	0.023	0.022	-0.101	**0.767**	**0.077**	**0.812^{**}**
No .of Tillers plant $^{-1}$	0.012	0.070	-0.055	0.005	0.000	-0.017	0.018	-0.094	**0.654**	**0.090**	**0.683^{**}**

4.20 Genotype-by-environment interactions:

In barley breeding and in many aspects of barley research, the analysis of genotype-by-environment interactions is of primary importance, as it is also for other crops (Ceccarelli, 1996; Annicchiarico 2002;Voltas *et al.*,2002a and Rodriguez, *et al.*, 2008). Genotype-by-environment interactions can affect breeding progress because they often complicate the evaluation and selection of superior genotypes. The genetic resources are a determinant instrument for improvements in crop productivity (Haussmann *et al.*, 2004). Generally, heterozygous individuals (e.g., F1 hybrids) are more stable in their performance than their homozygous inbred parents (Acquaah, 2007).

The data in table (77) and Appendix (4) confirm the presence of highly significant effect due to locations for all studied traits. Qilyasan location exceeded the rest significantly for all studied traits with the exception of the traits number of tillers plant^{-1} and number of spikes plant^{-1}, in which Kalar location outyielded the rest in these two traits. It was observed the exceeding of Erbil location compared to Kalar location due to the traits, days to 50% anthesis and days to 50% maturity. Kalar location predominated Erbil location in the traits flag leaf length, plant height, biological yield plant^{-1}, no. of tillers plant^{-1}, no. of Spikes plant^{-1}, peduncle length, peduncle diameter, spike length, spike weight, awn length, No.of Spikelets spike^{-1}, no. of grains spike^{-1}, 1000 grains weight, harvest Index and grains yield plant^{-1}, while the lowest value for almost all studied characters exhibited by Erbil location with exception of the characters days to 50% anthesis and days to 50% maturity compared with these recorded at Kalar location. Appendex (4) also indicated that there were highly significant interaction between the locations and genotypes in regard to all the studied traits except the trait peduncle diameter in which shows only significant interaction.

Many studies carried out across diverse environments have reported for barley. By means of 9 x 9 half diallel, F1 progenies under four diverse environments, the environmental effect was found significant for the traits days to heading, days to maturity, plant height, flag leaf area, effective tillers plant^{-1}, spike length, number of grains spike^{-1}, test weight , biological yield plant^{-1}, grain yield plant^{-1} and harvest index (Kanaki and Sharma., 2010). Rodriguez *et al.*, 2008 across six Mediterranean environments for 24 barley genotypes, obtained that the environment significantly affected of the recorded traits like grain yield m^{-2}, number of kernels m^{-2}, number of spikes m^{-2}, number of kernels spike^{-1}, 1000-kernel weight (g), plant height and degree days to maturity.

Table (77): Effect of locations on two-rowed barley genotypes traits.

Locations	Days to 50% anthesis	Flag leaf length (cm)	Days to 50% maturity	Plant height (cm)	Biological yield plant^{-1} (g)	No. of Tillers plant^{-1}	No. of Spikes plant^{-1}	Peduncle length (cm)	Peduncle diameter (mm)
Qilyasan	**146.653**	**11.339**	**187.400**	**102.347**	**75.637**	**28.239**	**27.844**	**31.600**	**1.381**
Erbil	**135.160**	**9.380**	**172.293**	**68.627**	**29.367**	**16.706**	**15.097**	**11.996**	**1.275**
Kalar	**120.307**	**10.962**	**156.373**	**82.760**	**61.235**	**33.916**	**32.920**	**20.026**	**1.355**
LSD (P≤0.05)	**0.251**	**0.330**	**0.194**	**1.623**	**2.265**	**1.665**	**1.672**	**0.808**	**0.033**

Locations	spike length (cm)	spike weight (g)	awn length (cm)	No. of Spikelets spike^{-1}	No. of Grains spike^{-1}	1000 grains weight (g)	Harvest Index	grains yield plant^{-1} (g)
Qilyasan	**9.045**	**1.411**	**16.267**	**29.804**	**22.716**	**50.872**	**0.415**	**31.484**
Erbil	**7.952**	**0.793**	**14.075**	**27.239**	**19.204**	**33.514**	**0.320**	**9.389**
Kalar	**8.933**	**0.983**	**14.408**	**28.337**	**21.128**	**38.920**	**0.417**	**25.463**
LSD (P≤0.05)	**0.176**	**0.023**	**0.187**	**0.273**	**0.416**	**0.930**	**0.007**	**1.042**

4. 21 Stability and Genotypic resultant:

Genotype-by-environment interactions (GEIs) can affect breeding progress because they often complicate the evaluation and selection of superior genotypes. So we can be reduced by gaining insights into GEI processes and genotype adaptation. Yield and other quantitative traits of crop plants, are among the most important in studying genotypes grown in multi-environments . In these kinds of studies, it is important to differentiate the best genotype in term of performance and stability across environments. For the minor and multi-genes controlling quantitative traits, the traits of genotypes will be different from an environment to another. Modern agriculture requires determining the stable genotypes and high performance (Becker and Leon, 1988; Ceccarelli, 1996 and Elsahookie and Al-Rawi, 2011).

Appendix (4) confirms the presence of highly significant interaction due to genotypes × locations for all studied traits with exception peduncle diameter which was merely significant. This is in agreement with (Sinebo, 2005) who obtained highly significant GE interaction by Sixteen barley genotypes in three sowing date with three seasons for the traits spike number meter^{-2}, harvest index, kernels spike^{-1}, kernel weight, mature plant height, vegetative duration, time to maturity and flag leaf length;**(** Bleidere, 2008) for 1000-grain weight; . Rodriguez *et al*., 2008 for 1000 grain weight, number of grains spike, plant hight and days to maturity; (Jalata *et al*., 2011) for grain yield plant^{-1}, 1000-grain weight, number of spikelets spike^{-1} and number of grains spike^{-1}.

Table (78) confirms variant values of stability and genotypic resultant for the studied traits. In general, the traits peduncle diameter, number of spikelets per spike, spike length, awn length, days to 50% maturity, number of grains spike^{-1} and days to 50% anthesis should be stable and close to high genotypic resultant with average values 0.951 and 0.95, 0.949 and 0.950, 0.925 and 0.926, 0.918 and 0.918, 0.910 and 0.910, 0.906 and 0.903, 0.901 and 0.901 respectively, while the trait flag leaf length had stability value 0.890, the rest traits showed unstable and low genotypic resultant average values . However the traits grain yield plant^{-1}, peduncle length and biological yield plant^{-1} showed the lowest unstable and genotypic resultant average values 0.459 and 0.450, 0.534 and 0.534 and 0.550 and 0.543 respectively. Elsahookie (1995) and Elsahookie and Al-Rawi (2011) noticed the highest stability is manifested as S_i=1and if stability value was less than 0.85, it should be not stable, while genotypic resultant value more than 1.00 meaning the genotype had high yield and high stability.

According to the grain yield plant^{-1} and their components (number of spikes plant^{-1}, 1000-grain weight and number of grains spike^{-1}) traits, should be not stable and had low genotypic resultant values. For the trait grain weight plant^{-1} were observed among the genotypes. The hybrid 3x4 versus all hybrids and parent (1) versus all parents had the greatest stability values with 0.720 and 0.604 respectively indicating that these two genotypes more stabile for yield performance among divers environments than others, while parent (3) versus all parents and hybrid 5x2 versus all hybrids had the greatest genotypic resultant values of 0.602 and 0.567, respectively, indicating these genotypes having the highest stable yield performances among divers environments. Experimental studies comparing hybrids and lines showed higher (Jordaan, 1996 and Koekemoer *et al.*, 2011) or similar yield stability (Bruns and Peterson, 1998and Koemel et al. 2004).

There were low stability and genotypic resultant values for the trait number of spikes plant^{-1}. The hybrid 3x4 versus all hybrids and parent (1) versus all parents had the greatest stability values with 0.794 and 0.728 respectively indicating these genotypes having more stabile spiking performance among divers environments than others, while hybrid 5x2 versus all hybrids and parent (3) versus all parents had the greatest genotypic resultant values with 0.788 and 0.714 respectively indicating these genotypes having the highest stable spiking performance among divers environments.

For the trait 1000-grain weight. The hybrid 3x4 versus all hybrids and parent (3) versus all parents had the greatest stability values with 0.877 and 0.817, respectively indicating these genotypes having more stability grain weighting performances among divers environments than others, while hybrid 3x4 versus all hybrids and parent (4) versus all parents had the highest genotypic resultant values with 1.035 and 0.799, respectively indicating these genotypes having the highest stable grain weighing performances among divers environments. Kaczmarek *et al.* (2002) for 1000-grain weight in six environments (three locations, two years) suggested that effects of heterozygous loci are more stable in contrasting environments than effects of homozygous loci.

Regarding yield and the three yield components, number of grains spike^{-1} demonstrated the greatest performance stability and genotypic resultant values across diverse environmental conditions. The hybrid 4x3 versus all hybrids and parent (1) versus all parents had the highest stability values with 0.977 and 0.925 respectively indicating that these two genotypes more stabile for spike graining performance among divers environments than others, while hybrid 1x5 versus all hybrids and parent (1) versus all parents had the highest genotypic resultant values with 1.111 and 1.062 respectively indicating that these two genotypes having the highest stable spike graining performance among divers environments. The stability and genotypic for grain yield is strong for genotypes with extreme number of grains spike^{-1} values. Hallauer *et al.* (1988) noticed that the main advantages of hybrid versus line varieties are larger yield stability especially in marginal environments. Rodriguez *et al*. (2008) in set of 24 barley genotypes that were grown across six environments (location-by-year combinations) from using the additive main effects and multiplicative interaction (AMMI) model, obtained the stability and performance for the traits 1000-grain weight (0.82), number of grains spike^{-1} (0.62), plant height (0.55), days to maturity (0.56) and grains yield m^{-2} (0.64).

Very high genotypic resultant values were obtained in the present study for the characters flag leaf length (1.132 by the hybrid 4x5), peduncle diameter (1.103 by the parent 5 and 1.042 by the hybrid 5x1), spike length (1.059 by the hybrid 5x2), and number of spikelets spike^{-1} (1.049 by the hybrid 5x1). Indicating these genotypes having high performances among divers environments and should be not ignored in future studies.

In particular, the data of Table (78) revealed that the best genotypes indicated to the genotype parent 3 was the overall ‘‘winner’’ in this trial which had the highest genotypic resultant values for five traits days to 50% anthesis (0.914), number of tillers plant^{-1} (0.794), number of spikes plant^{-1} (0.714) , biological yield plant^{-1} (0.659) and grain yield plant^{-1} (0.602), while the hybrid 5x2 was over all hybrids which had the highest genotypic resultant values for four traits spike length (1.059), number of spikes plant^{-1} (0.788), number of tillers plant^{-1} (0.787) and grain yield plant^{-1} (0.567) . So the stability of these genotypes needs to be better evaluated in a set of environments tested across different years.

Table (78): Stability (H%) and genotypic resultant(GR) of traits for tow-rowed barley genotypes , a crossing locations.

characters	Days to anthesis		Flag leaf length		Days to maturity		Plant height		Biological yield plant^{-1}		Tillers plant^{-1}		Spikes plant^{-1}		Peduncle length		Peduncle diameter	
Crosses	H	G.R	H	G.R	H	G.R	H	G.R	H	G.R	H	G.R	H	G.R	H	G.R	H	G.R
1 x 2	0.904	0.880	0.922	0.820	0.911	0.897	0.791	0.791	0.650	0.661	0.688	0.728	0.666	0.708	0.494	0.526	0.964	0.904
2 x 1	0.902	0.883	0.924	0.761	0.915	0.902	0.839	0.863	0.694	0.503	0.690	0.556	0.678	0.546	0.523	0.551	0.944	0.873
1 x 3	0.887	0.871	0.876	0.773	0.911	0.903	0.879	0.958	0.450	0.391	0.471	0.447	0.455	0.434	0.533	0.497	0.962	0.876
3 x 1	0.890	0.878	0.930	0.876	0.914	0.908	0.812	0.849	0.705	0.549	0.705	0.635	0.671	0.601	0.505	0.484	0.966	0.891
1 x 4	0.905	0.910	0.847	0.931	0.914	0.917	0.743	0.781	0.395	0.482	0.625	0.652	0.581	0.606	0.483	0.508	0.928	0.957
4 x 1	0.907	0.911	0.897	0.971	0.913	0.915	0.772	0.741	0.500	0.581	0.609	0.624	0.582	0.600	0.407	0.387	0.950	1.017
1 x 5	0.903	0.901	0.892	0.898	0.911	0.903	0.808	0.830	0.605	0.593	0.663	0.538	0.640	0.517	0.545	0.637	0.935	0.973
5 x 1	0.901	0.896	0.928	0.944	0.912	0.907	0.852	0.941	0.624	0.675	0.787	0.733	0.756	0.705	0.614	0.724	0.960	1.042
2 x 3	0.908	0.919	0.847	0.736	0.913	0.911	0.813	0.816	0.506	0.478	0.500	0.552	0.497	0.558	0.559	0.517	0.951	0.846
3 x 2	0.905	0.912	0.890	0.770	0.913	0.913	0.826	0.866	0.545	0.540	0.573	0.636	0.570	0.641	0.490	0.487	0.949	0.832
2 x 4	0.900	0.925	0.906	0.844	0.903	0.906	0.768	0.724	0.434	0.426	0.541	0.505	0.520	0.492	0.476	0.481	0.940	0.976
4 x 2	0.903	0.928	0.835	0.801	0.906	0.908	0.756	0.742	0.412	0.446	0.495	0.521	0.474	0.498	0.437	0.429	0.926	0.939
2 x 5	0.903	0.913	0.863	0.867	0.906	0.904	0.764	0.780	0.531	0.614	0.631	0.663	0.590	0.611	0.507	0.551	0.950	0.959
5 x 2	0.904	0.910	0.865	0.905	0.907	0.904	0.830	0.868	0.595	0.666	0.743	0.787	0.739	0.788	0.517	0.570	0.952	0.971
3 x 4	0.894	0.899	0.907	0.863	0.908	0.918	0.790	0.801	0.753	0.677	0.807	0.759	0.794	0.753	0.555	0.501	0.974	0.938
4 x 3	0.891	0.893	0.875	0.965	0.909	0.917	0.760	0.802	0.496	0.585	0.624	0.693	0.580	0.643	0.495	0.476	0.945	0.973
3 x 5	0.894	0.875	0.929	0.961	0.909	0.909	0.800	0.804	0.500	0.510	0.554	0.609	0.525	0.583	0.599	0.620	0.968	0.990
5 x 3	0.900	0.881	0.938	1.092	0.909	0.909	0.786	0.822	0.436	0.482	0.566	0.634	0.537	0.602	0.563	0.559	0.959	0.963
4 x 5	0.893	0.906	0.914	1.132	0.910	0.926	0.770	0.722	0.534	0.523	0.629	0.640	0.577	0.586	0.558	0.505	0.944	1.028
5 x 4	0.895	0.905	0.902	1.111	0.909	0.920	0.777	0.736	0.554	0.613	0.748	0.782	0.682	0.701	0.543	0.532	0.918	1.004
1 x 1	0.921	0.908	0.895	0.698	0.910	0.907	0.848	0.803	0.708	0.521	0.734	0.605	0.728	0.594	0.652	0.646	0.962	0.919
2 x 2	0.907	0.892	0.762	0.604	0.904	0.890	0.751	0.770	0.486	0.449	0.654	0.671	0.625	0.642	0.519	0.569	0.964	0.860
3 x 3	0.916	0.914	0.886	0.937	0.909	0.897	0.860	0.793	0.676	0.659	0.679	0.794	0.637	0.714	0.569	0.477	0.952	0.859
4 x 4	0.907	0.932	0.884	0.922	0.912	0.931	0.730	0.629	0.358	0.359	0.580	0.523	0.537	0.483	0.558	0.476	0.954	1.086
5 x 5	0.895	0.890	0.936	1.110	0.910	0.919	0.784	0.697	0.616	0.592	0.681	0.624	0.660	0.611	0.654	0.644	0.969	1.103
mean	0.901	0.901	0.890	0.892	0.910	0.910	0.796	0.797	0.550	0.543	0.639	0.636	0.612	0.609	0.534	0.534	0.951	0.951

- Continued-

Table (78): Complement

Characters crosses	Spike length		Spike weight		Awn length		Spikeletes spike^{-1}		Grains spike^{-1}		1000-grain weight		Harvest index		Grains yield plant^{-1}	
	H	GR	H	GR	H	GR	H	GR	H	GR	H	GR	H	GR	H	GR
1 x 2	0.956	0.957	0.711	0.652	0.919	0.890	0.973	0.997	0.912	1.016	0.755	0.663	0.775	0.801	0.496	0.527
2 x 1	0.928	0.909	0.629	0.584	0.912	0.856	0.959	0.976	0.867	0.993	0.745	0.623	0.792	0.850	0.543	0.423
1 x 3	0.938	0.902	0.728	0.623	0.893	0.832	0.971	0.994	0.875	0.689	0.851	0.878	0.887	0.824	0.364	0.293
3 x 1	0.929	0.879	0.709	0.609	0.950	0.912	0.947	0.934	0.897	0.692	0.838	0.884	0.808	0.753	0.584	0.419
1 x 4	0.923	0.971	0.645	0.747	0.900	0.967	0.954	1.005	0.903	1.079	0.707	0.702	0.838	0.887	0.305	0.399
4 x 1	0.913	0.957	0.705	0.762	0.928	0.985	0.960	1.022	0.890	1.019	0.748	0.733	0.813	0.819	0.463	0.535
1 x 5	0.899	0.972	0.607	0.742	0.909	0.920	0.933	0.993	0.885	1.111	0.690	0.671	0.759	0.781	0.452	0.467
5 x 1	0.954	1.046	0.659	0.778	0.916	0.936	0.957	1.049	0.887	1.066	0.706	0.690	0.788	0.816	0.475	0.536
2 x 3	0.914	0.917	0.743	0.613	0.905	0.892	0.953	0.930	0.909	0.624	0.814	0.887	0.848	0.741	0.369	0.306
3 x 2	0.892	0.865	0.623	0.547	0.939	0.926	0.917	0.878	0.864	0.645	0.806	0.851	0.916	0.865	0.493	0.455
2 x 4	0.918	0.975	0.685	0.722	0.905	0.947	0.965	0.987	0.902	1.016	0.772	0.743	0.842	0.910	0.346	0.374
4 x 2	0.882	0.934	0.650	0.695	0.889	0.917	0.928	0.954	0.825	0.914	0.788	0.764	0.760	0.811	0.303	0.367
2 x 5	0.964	1.056	0.565	0.643	0.933	0.947	0.973	1.033	0.861	1.027	0.690	0.641	0.808	0.816	0.387	0.459
5 x 2	0.951	1.059	0.657	0.731	0.892	0.912	0.952	1.007	0.918	1.093	0.716	0.672	0.829	0.892	0.470	0.567
3 x 4	0.952	0.952	0.768	0.704	0.922	0.940	0.960	0.927	0.933	0.659	0.877	1.035	0.915	0.811	0.720	0.556
4 x 3	0.899	0.973	0.814	0.842	0.898	0.975	0.948	0.992	0.977	0.786	0.850	0.991	0.941	0.862	0.495	0.517
3 x 5	0.939	0.946	0.878	0.719	0.947	0.939	0.927	0.887	0.970	0.613	0.866	1.003	0.910	0.724	0.481	0.381
5 x 3	0.955	0.987	0.853	0.794	0.947	0.932	0.940	0.918	0.974	0.648	0.859	1.018	0.888	0.752	0.451	0.409
4 x 5	0.923	0.815	0.685	0.723	0.932	0.979	0.957	0.880	0.951	0.985	0.752	0.766	0.843	0.930	0.432	0.472
5 x 4	0.949	0.882	0.602	0.647	0.916	0.963	0.933	0.885	0.934	1.001	0.668	0.648	0.851	0.838	0.427	0.467
1 x 1	0.924	0.841	0.713	0.624	0.931	0.879	0.975	0.960	0.925	1.062	0.743	0.591	0.861	0.879	0.604	0.449
2 x 2	0.898	0.875	0.636	0.585	0.881	0.804	0.920	0.858	0.887	0.948	0.704	0.619	0.847	0.923	0.390	0.396
3 x 3	0.901	0.833	0.685	0.603	0.933	0.803	0.915	0.802	0.901	0.876	0.817	0.784	0.872	0.934	0.585	0.602
4 x 4	0.893	0.759	0.702	0.814	0.944	0.985	0.947	0.918	0.908	1.026	0.785	0.799	0.911	0.988	0.295	0.319
5 x 5	0.939	0.881	0.855	0.902	0.911	0.916	0.962	0.956	0.898	0.984	0.785	0.787	0.808	0.855	0.553	0.552
mean	0.925	0.926	0.700	0.696	0.918	0.918	0.949	0.950	0.906	0.903	0.773	0.778	0.845	0.842	0.459	0.450

CONCLUSIONS AND RECOMMENDATIONS

A. Conclusions

Our results obtained from 25 two-rowed barley genotypes at 3 locations showed that**:**

1. Highly significant mean squares of locations for studied traits. Qilyasan location exceeded significantly in fifteen out of seventeen studied traits. A very strong genotype x environment interaction for all traits were seen. Moreover, there were negative crossovers between traits levels of genotypes grown in different environments.
2. Analysis of variance showed that mean squares for general, specific and reciprocal combining ability were highly significant for most traits at each location. suggesting that the traits were determined by genes with additive and non-additive or dominant effects.
3. The analysis of genetic variance components showed that the dominant gene effect was the most contributing factor to the inheritance of grain yield plant^{-1} and most traits for the three locations. Meaning the stableness of gene action type among divers locations. Thus, it is suggested that hybridization method and selection in the segregating generations to be used which can be more efficient.
4. Additive effect genes prevailed in the inheritance of peduncle diameter and flag leaf length at divers locations. In conclusion, it is recommended that in case the main part of genetic variance of any trait is due to the additive effects of the gene, selection can play a great role in breeding method of that traits.
5. Both additive and dominant gene effects played an important role in the inheritance of 50% days to maturity, peduncle length and average spike weight according to the environments change. Therefore, some forms of recurrent selection like diallel selective mating or bi-parental mating in early segregating generation might proved to be effective alternative approach.

6. In the crosses with the dominance effects which had greater shares, since narrow-sense heritability of this trait was low like grain yield plant^{-1}. It can therefore be concluded that some forms of recurrent selection might proved to be effective alternative approach for improvement in two-rowed barley.

7. Additive effects formed major part of variability for peduncle diameter, flag leaf length and somewhat average spike weight. Thus, genetic improvement in grain weight plant^{-1} would be easier through indirect selection for those traits rather than direct selection for grain yield plant^{-1}.

8. The degree of dominance ranging from partial to overdominance. Overdominance mostly occurred in the inheritance of the studied traits

9. The estimate of heritability serves as a useful guide to the breeder. The breeder is able to appreciate the proportion of variation due to Genotypic (Broad sense heritability) or additive (Narrow sense heritability) effect that is the heritable portion of variation in the first case and the portion of genetic variation that is pure line in the later case. Heritability in broad -senses was found to be moderate to high in the studied traits. Narrow-sense heritability estimates obtained in component analysis ranged from low to high for different traits. The results indicated that the degree of heritability was much influenced by the environment for most traits. However, some traits showed stable degrees of Narrow-sense heritability like flag leaf length, 50% days to maturity, peduncle diameter, number of spikelets spike^{-1}and awn length among variable environments.

10. Path coefficient analysis indicated that the direct effects of biological yield plant^{-1} and harvest index on grain yield were strongly positive at each location. Therefore, those traits can be used as the most important selection criteria to increase grain yield in two-rowed barley in the region, it is advisable that other yield components should be taken into account.

11. The presence of the genotype x environment interaction was indicated by changes in relative rankings over environments. The stability pattern revealed by the analysis indicated that the tested barley genotypes are narrowly adapted, and no genotype was found to have high grain yield plant^{-1} performances in all environments.

B. Recommendations:

1. The cultivars, Clipper (P4) at Qilyasan and Arabi aswad (P3) at Erbil and Kalar locations could be used in future breeding programs to increase yield ability under normal and drought stress conditions, respectively.

2. High *per se* performance, significant SC*A* effects and high positive heterosis values in top ranking hybrids, 1x4 at Qilyasan, 5x2 at Erbil and 4x2 at Kalar, suggested the scope of improvement for most traits including grain yield plant^{-1} and their components through bi-parental mating in future breeding programs to increase yield ability under specific conditions.

3. Clipper (P4) at Qilyasan, Bohoth H1 (P5) at Erbil and ABN (P2) at Kalar were the best general combiners for grain yield plant^{-1}. These parents could be used in crossing programs for enhancing favorable genes in later generations.

4. The reciprocal crosses 3x2, 5x1 and 4x3 had the highest positive reciprocal effects for grain yield plant^{-1} and most of the studied traits under Qlyasan, Erbil and Kalar conditions, respectively.

5. The both parent 1 and the hybrid 5X2 were the best in adaptability and genotypic resultant at all environments for grain yield plant^{-1}.

6. More researches are needed to screen tow-rowed barley genotypes for their agronomic performance under specific and major environments.

7. The next future needs, high hybrids yield with flowering and maturing date for earliness association to option elite line$_{(s)}$ for normal, moderate and or drought environments.

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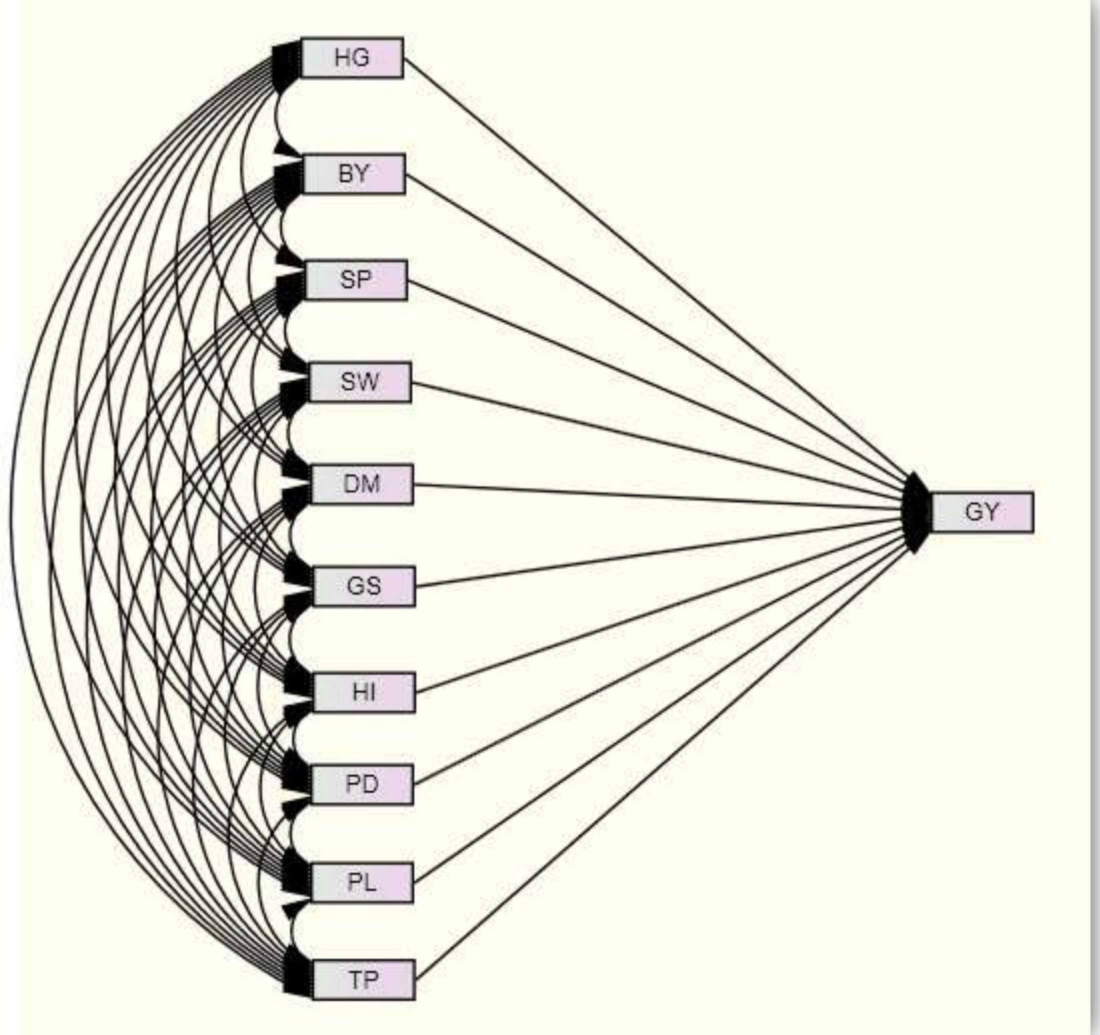
Appendix (4): ANOVA TABILE FOR COMBINE ANALYSIS for studied traits at three locations.

Traits	Locations	Blocks/ locations= E(a)	Genotypes / locations	Genotypes	Genotypes x Locations	Error / Location = E(b)
Days to 50% anthesis	13085.813**	0.396	17.329**	42.360**	4.813**	0.271
Flag leaf length (cm)	80.977**	0.681	6.370**	16.887**	1.112**	0.463
Days to 50% maturity	18053.898**	0.236	9.367**	25.509**	1.296**	0.231
Plant height (cm)	21505.338**	16.502	114.142**	237.028**	52.699**	10.410
Biological yield plant^{-1} (g)	42050.195**	32.144	454.112**	479.042**	441.647**	13.639
No. of Tillers plant^{-1}	5767.314**	17.362	67.444**	65.127**	68.603**	4.134
No. of Spikes plant^{-1}	6323.533**	17.515	63.555**	59.589**	65.538**	3.720
Peduncle length (cm)	7284.071**	4.087	15.708**	30.696**	8.214**	1.005
Peduncle diameter (mm	0.230**	0.007	0.037**	0.100**	0.005*	0.003
spike length (cm)	27.130**	0.194	1.342**	3.447**	0.289**	0.116
spike weight (g)	7.502**	0.003	0.085**	0.157**	0.049**	0.002
awn length (cm)	104.599**	0.219	2.350**	5.872**	0.589**	0.138
No. of Spikelets spike^{-1}	124.239**	0.466	8.182**	20.728**	1.910**	0.378
No. of Grains spike^{-1}	231.920**	1.083	58.839**	164.427**	6.045**	0.921
1000 grains weight (g)	5917.419**	5.412	70.287**	156.972**	26.945**	1.874
Harvest Index	0.231**	0.000	0.005**	0.010**	0.003**	0.000
grains yield plant^{-1}(g)	9784.631**	6.803	105.062**	122.389**	96.398**	2.884



Fiure (1): Path diagram

GY: grain yield plant^{-1}, **BY**: biologic yield plant^{-1}, **DM:**50% days to maturity, **HG:**1000-grain weight, **PL:** peduncle length, **PD:** peduncle diameter, **HI:** harvest index, **TP:** number of tellers plant^{-1}, **SP:** number of spikes plant^{-1}, **GS:** number of grains spike^{-1} and **SW**: average spike weight

Appendix 1. Mean Squares of variance analysis for genotypes, general and specific combining ability for the Parents, and F1 diallel crosses, and reciprocal crosses of the studied traits at Qilyasan location.

Source of Variation	Replications	Genotypes	Gca	Sca	Rca	σ^2e	Gca / Sca	Gca / Rca	MSe*
d.f Characters	**2**	**24**	**4**	**10**	**10**	**48**			
Days to 50% anthesis	0.253	21.263**	25.209**	6.688**	0.239**	0.253	3.769	105.526	0.084
Flag leaf length (cm)	0.912	7.938**	11.513**	1.270**	0.475$^{n.s}$	0.826	9.064	24.242	0.275
Days to 50% maturity	0.120	11.083**	18.150**	1.468**	0.139*	0.203	12.366	130.680	0.068
Plant height (cm)	6.773	114.819**	16.948**	66.415**	18.661**	15.871	0.255	0.908	5.290
Biological yield plant^{-1} (g)	0.429	1041.162**	998.129**	302.309**	131.369**	26.600	3.302	7.598	8.867
No. of Tillers plant^{-1}	0.362	101.217**	76.810**	33.798**	16.452**	4.848	2.273	4.669	1.616
No. of Spikes plant^{-1}	0.038	97.949**	74.758**	32.811**	15.644**	4.023	2.278	4.779	1.341
Peduncle length (cm)	8.555	28.389**	27.580**	9.745**	1.934**	2.136	2.830	14.263	0.712
Peduncle diameter (mm)	0.008	0.043**	0.080**	0.002$^{n.s}$	0.001$^{n.s}$	0.005	44.251	83.844	0.002
spike length (cm)	0.410	1.227**	0.282*	0.778**	0.091$^{n.s}$	0.246	0.362	3.096	0.082
spike weight (gm)	0.004	0.182**	0.193**	0.057**	0.011**	0.002	3.359	18.372	0.001
awn length (cm)	0.002	3.046**	3.290**	0.858**	0.262**	0.051	3.835	12.537	0.017
No. of Spikelets spike^{-1}	0.322	5.899**	3.419**	2.853**	0.498**	0.375	1.198	6.860	0.125
No. of Grains spike^{-1}	0.423	78.543**	96.745**	22.391**	1.745**	0.855	4.321	55.429	0.285
1000 grains weight (gm)	6.477	39.290**	44.964**	11.370**	2.076**	1.100	3.955	21.655	0.367
Harvest Index	0.000	0.010**	0.009**	0.004**	0.001**	0.000	2.406	11.370	0.000
grains yield plant^{-1}	2.234	259.452**	313.297**	52.550**	29.693**	5.154	5.962	10.551	1.718

$F_{0.05}(4,48) = 2.565$, $F_{0.05}(10.48) = 2.035$, $F_{0.05}(24,48) = 1.746$

$F_{0.01}(4,48) = 3.737$, $F_{0.01}(10.48) = 2.715$, $F_{0.01}(24,48) = 2.201$

Appendix 2 . Mean Squares of variance analysis for genotypes, general and specific combining ability for the Parents, and F1 diallel crosses, and reciprocal crosses of the studied traits at Erbil location.

Source of Variation	Replications	Genotypes	Gca	Sca	Rca	σ^2e	Gca / Sca	Gca / Rca	MSe*
d.f Characters	**2**	**24**	**4**	**10**	**10**	**48**			
Days to 50% anthesis	0.280	15.753**	18.502**	5.091**	$0.111^{n.s}$	0.280	3.635	166.520	0.093
Flag leaf length (cm)	0.817	6.301**	10.046**	0.658**	0.364**	0.225	15.268	27.572	0.075
Days to 50% maturity	0.093	10.120**	16.597**	1.341**	$0.117^{n.s}$	0.302	12.379	142.257	0.101
Plant height (cm)	25.653	111.092**	132.652**	18.957**	16.856**	8.167	6.997	7.870	2.722
Biological yield plant^{-1} (g)	69.004	73.852**	28.251**	30.460**	17.321**	4.570	0.927	1.631	1.523
No. of Tillers plant^{-1}	38.263	26.463**	15.482**	11.453**	3.524**	2.223	1.352	4.393	0.741
No. of Spikes plant^{-1}	35.682	20.352**	13.109**	7.278**	3.760**	1.828	1.801	3.486	0.609
Peduncle length (cm)	2.798	8.208**	12.026**	0.937**	0.819**	0.424	12.835	14.689	0.141
Peduncle diameter (mm)	0.011	0.031**	0.056**	$0.001^{n.s}$	$0.001^{n.s}$	0.004	51.136	46.174	0.001
spike length (cm)	0.045	1.317**	0.471**	0.766**	0.099**	0.053	0.614	4.768	0.018
spike weight (gm)	0.003	0.041**	0.062**	0.006**	0.003**	0.002	11.282	22.699	0.001
awn length (cm)	0.615	2.094**	2.546**	0.611**	$0.046^{n.s}$	0.238	4.163	55.353	0.079
No. of Spikelets spike^{-1}	0.492	9.478**	7.463**	3.764**	0.833**	0.610	1.983	8.957	0.203
No. of Grains spike^{-1}	0.340	40.541**	52.967**	10.159**	1.087**	1.014	5.214	48.725	0.338
1000 grains weight (gm)	5.223	70.667**	95.315**	16.025**	2.382**	1.903	5.948	40.008	0.634
Harvest Index	0.000	0.002**	0.001**	0.001**	0.000*	0.000	1.676	3.716	0.000
grains yield plant^{-1}	10.298	8.549**	2.041**	4.492**	1.530**	0.868	0.454	1.334	0.289

$F_{0.05}(4,48) = 2.565$, $F_{0.05}(10.48) = 2.035$, $F_{0.05}(24,48) = 1.746$

$F_{0.01}(4,48) = 3.737$, $F_{0.01}(10.48) = 2.715$, $F_{0.01}(24,48) = 2.201$

Appendix 3 . Mean Squares of variance analysis for genotypes, general and specific combining ability for the parents, and F1 diallel crosses, and reciprocal crosses of the studied traits at Kalar location.

Source of Variation	Replications	Genotypes	Gca	Sca	Rca	$\sigma^2 e$	Gca / Sca	Gca / Rca	MSe*
d.f Characters	**2**	**24**	**4**	**10**	**10**	**48**			
Days to 50% anthesis	0.653	14.970**	11.863**	7.020**	0.211*	0.278	1.690	56.185	0.093
Flag leaf length (cm)	0.313	4.872**	6.911**	0.680**	0.454**	0.339	10.170	15.229	0.113
Days to 50% maturity	0.493	6.898**	10.408**	1.216**	0.139*	0.188	8.557	74.936	0.063
Plant height (cm)	17.080	116.514**	53.408**	54.787**	17.061**	7.191	0.975	3.130	2.397
Biological yield plant^{-1} (g)	27.000	247.321**	108.267**	70.692**	83.858**	9.746	1.532	1.291	3.249
No. of Tillers plant^{-1}	13.460	74.653**	72.615**	17.899**	12.778**	5.331	4.057	5.683	1.777
No. of Spikes plant^{-1}	16.824	72.363**	69.327**	18.082**	12.077**	5.309	3.834	5.740	1.770
Peduncle length (cm)	0.908	10.528**	10.484**	2.770**	1.459**	0.453	3.785	7.184	0.151
Peduncle diameter (mm)	0.002	0.036**	0.055**	0.004**	0.003**	0.001	12.907	20.562	0.000
spike length (cm)	0.129	1.482**	0.292**	0.955**	0.113**	0.050	0.305	2.576	0.017
spike weight (gm)	0.003	0.032**	0.017**	0.014**	0.005**	0.002	1.218	3.290	0.001
awn length (cm)	0.042	1.911**	2.266**	0.387**	0.235**	0.125	5.857	9.630	0.042
No. of Spikelets spike^{-1}	0.584	9.171**	4.228**	4.461**	1.184**	0.177	0.948	3.570	0.059
No. of Grains spike^{-1}	2.487	57.434**	73.957**	15.730**	0.635*	0.892	4.702	116.539	0.297
1000 grains weight (gm)	4.536	100.904**	127.346**	27.619**	2.166*	2.618	4.611	58.793	0.873
Harvest Index	0.000	0.005**	0.003**	0.002**	0.001**	0.000	1.559	5.284	0.000
grains yield plant^{-1}	7.876	47.185**	4.024**	20.441**	15.698**	2.631	0.197	0.256	0.877

$F_{0.05}(4,48) = 2.565$, $F_{0.05}(10.48) = 2.035$, $F_{0.05}(24,48) = 1.746$

$F_{0.01}(4,48) = 3.737$, $F_{0.01}(10.48) = 2.715$, $F_{0.01}(24,48) = 2.201$

Appendix (5): Analysis of Variance for Full Diallel Cross According to Griffing 1956, Method I, Model I (Parents, Diallel Crosses and Reciprocal Crosses) (Singh and Chaudhary, 1985).

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

شیکاری لێگدانی تاکی گوراو بۆ جۆی (*Hordeum distichum* **L.**) و شیکردنەوەی ئاراستەی جێگیربوون لە ژێر جیاوازی ژینگە لە هەرێمی کوردستانی عێراق

ئەم تێزی دکتۆرایە

پێشکەشە کراوە بە ئەنجومەنی فاکەڵتی زانستە کشتوکاڵیەکان - زانکۆی
سلێمانی وەك بەشێك لە پێداویستیەکانی بە دەستهینانی پلەی دکتۆرا لە
بەرووبوومی کێلگەیی د ا

(پەروەردەکردنی ڕووەك و بۆماوەزانی)

لەلایەن

کامل محمود مستەفا خووشناو

بەکالۆریۆس لە بەرهەمی ڕووەکی / 1979

ماستەر لە بەرووبوومی کێلگەیی / 2000

بەسەرپەرشتی

د.حسین احمد سعدالله

سەرۆکی تو ێژینەوەرانی زانستی

2713 ك

تحليل التهجين التبادلي في الشعير (.*Hordeum distichum* L) و معامل المسار و الأستقرارية تحت ظروف بيئية مختلفة في اقليم كوردستان العراق

أطروحة مقدمة الى مجلس فاكلتي العلوم الزراعية في جامعة السليمانية

كجزء من متطلبات نيل درجة دكتوراه فلسفة

في العلوم الزراعية / المحاصيل الحقلية

(تربية النبات والوراثة)

تقدم بها

كامل محمود مصطفى خوشناو

بكالوريوس في الأنتاج النباتي (1979).

ماجستير في المحاصيل الحقلية (2000).

بأشراف

رئيس باحثين علمي د. حسين أحمد سعد الله

28 شوال 1434 هـ   5 أيلول 2013 م

الخلاصة

زرعت خمسة تراكيب وراثية نقية من الشعير ذو الصفين (*Hordeum distichum* L.) وفق نظام التضريبات التبادلية الكاملة خلال الموسم الشتوي 2010- 2011 لأنتاج 20 هجينا من الأباء التالية: MORA/NB1054/3/MOLA/SHYRI//ARUPO*2/JET/4/…CBSS99M002 9TG-5M-1Y-1M-0Y; ABN-B/KAB//RAISA/3/ALELI/4/LIMON/5/.CBSS99M00228 T-K 6M-1Y- 1M-0Y; Arabi aswade; Clipper; Bohoth H1.

زرعت العشرون هجينا مع الأباء الخمسة في الموسم الشتوي 2011-2012 في ثلاثة مواقع مختلفة بيئيا وهي محطة ابحاث قلياسان- السليمانية، محطة ابحاث كرده ره ش - اربيل و محطة ابحاث كلار في اقليم كوردستان العراق وفق تصميم القطاعات العشوائية الكاملة و بثلاثة مكررات. تم دراسة مختلف الصفات المظهرية للنبات. تمت مقارنة المتوسطات بطريقة اقل فرق معنوي عند مستوى معنوية 5% واظهرت النتائج وجود اختلافات معنوية بين المواقع للصفات جميعها، وكان موقع قلياسان قد اختلف معنويا للصفات جميعها ما عدا صفتي عدد الأشطاء\ نبات وعدد السنابل\ نبات. تم اجراء التحليل الوراثي للبيانات للقدرتين العامة والخاصة على التآلف، وتحديد طبيعة الفعل الجيني، وقوة الهجين والتوارث بأستخدام نظام التهجينات التبادلية لـ Griffing الطريقة الأولى (الأباء، الهجن والهجن العكسية للجيل الأول) وباعتماد الأنموذج الثابت وبالطريقه التي شرحها Singh and Chaudhary,1985. كما تم دراسة الأرتباط و تحليل المسار والأستقرارية والمحصلة الوراثية. اشارت نتائج التحليل الأحصائي الى وجود فروقات عالية المعنوية بين التراكيب الوراثية ولجميع الصفات المدروسة في كل موقع، مما يدل على وجود تباين وراثي بين التراكيب الوراثية. وكان متوسط مربعات القدرتين العامة والخاصة للتآلف والتأثير العكسي معنويا عاليا للصفات جميعها المدروسة في كل موقع، ماعدا قطرحامل السنبلة للقدرة الخاصة في قلياسان واربيل حيث كانت معنوية، بينما كان التأثير العكسي لـطول ورقة العلم و قطرحامل السنبلة وطول السنبلة غير معنويا في قلياسان، وكان دليل الحصاد معنوي فقط و عدد الأيام اللازمة لـ 50% للتزهير وعدد الأيام اللازمة لـ 50% للنضج وطول السفا وقطرحامل السنبلة كانت غير معنوية في اربيل، فيما عدد الأيام اللازمة لـ 50% للتزهير وعدد الأيام اللازمة لـ 50% للنضج ووزن 1000 حبة و عدد الحبوب\ سنبلة كانت معنوية في كلار.

تشير النتائج الى ان اعلى المتوسطات للصفات كانت تحت ظروف قلياسان، اربيل وكلار بواسطة الأباء 3 و 4 و 5 لوزن حبوب\ نبات ومعظم الصفات المدروسة على التوالي ،بينما القيم الادنى كانت للأباء 2 و 1 و1 على التوالي واعطت الهجن 4 x1 في موقع قلياسان و 4x3 في موقع اربيل و 3x2 في موقع كلار اعلى المتوسطات. تميزت الهجن العكسية 2x4 في موقع اربيل و 2x4 اما في موقع كلار بالقيم الاعلى لصفة حاصل حبوب\ نبات ومعظم الصفات المدروسة .

ظهرت قوة الهجين في اثناعشر و ثمانية و ثلاثةعشر من مجموع عشرون هجين (التبادلية والعكسية) موجبة لصفة وزن حبوب\ نبات بمدى 1.568 الى 59.372% و 4.486 الى 33.102% و 6.154 الى 48.734 وكانت الهجن 4x1 و 2x5 و 1x4 الأفضل لصفة حاصل حبوب\ نبات ومعظم الصفات المدروسة تحت ظروف قلياسان و اربيل وكلار على التوالي. اوضحت نتائج التأثيرات العكسية للهجن العكسية ان سبعة، ثمانية و اربعة من عشرة هجن عكسية امتلكت اعلى تأثيرات عكسية ذات قيم موجبة لصفة وزن حبوب\ نبات بمدى 6.087 الى 62.225% و 2.027 الى % 33.844% و 4.926 الى 48.610% ، وكانت الهجن العكسية 2x3، 1x5 و 3x4 هي الاحسن لصفة حاصل حبوب\ نبات ومعظم الصفات المدروسة تحت ظروف قلياسان، اربيل وكلار على التوالي.

اظهرت نتائج تحليل التباين ان متوسط المربعات للقدرتين العامة والخاصة للتآلف كان معنويا دلالة على وجود تأثيرات اضافية وغير اضافية للفعل الجيني، وان التحليل الوراثي للتباين اظهر اهمية تأثيرات السيادة الفائقة للفعل الجيني في التعبير عن التوريث لمعظم الصفات المدروسة ولكل المواقع فيما عدا طول ورقة العلم و قطر حامل السنبلة في المواقع الثلاثة، عدد الأيام اللازمة لـ 50% للنضج في قلياسان وكلار، طول حامل السنبلة في اربيل و معدل وزن السنبلة في كلار حيث كان النوع الاضافي من الفعل الجيني هو المهم. وأظهر تحليل تأثير القدرة على التآلف ان الأباء 4 و 5 في قلياسان و5 و3 في اربيل و 2 و3 في كلار هي الواهب العام الأحسن لأغلب الصفات المدروسة، و أمكانية استخدامها في برامج التهجين للحصول على التوافقات المرغوبة. في حين اظهرت الهجن التبادلية 1×4 و 3×5 و 1×5 في قلياسان و 2×5 و 2×3 في اربيل و 1×4 في كلار القيم الأعلى لتأثير القدرة الخاصة للتآلف ومن ثم امكانية استخدامها في التربية المستقبلية. وبخصوص معدل درجة السيادة في الهجن التبادلية فقد كان اقل من واحد صحيح لصفتي طول ورقة العلم و قطر حامل السنبلة في المواقع الثلاثة، عدد الأيام اللازمة لـ 50% للنضج في اربيل ومعدل وزن السنبلة في كلار مبينا تأثير السيادة الجزئية للفعل الجيني المسيطرة على هذه الصفات، فيما كانت اكبر من واحد صحيح للصفات الأخرى ولكل المواقع مؤكدا، تأثيرات السيادة الفائقة للفعل الجيني في توريث هذه الصفات. اما بالنسبة للهجن العكسية فأن قيمة معدل درجة السيادة كانت اقل من واحد صحيح لاغلب الصفات فيما عدا طول النبات في قلياسان والحاصل البايولوجي\ نبات و عدد السنابل\ نبات و حاصل حبوب\ نبات في اربيل و طول النبات و الحاصل لبايولوجي\ نبات و طول السنبلة و عدد السنيبلات\ سنبلة و وزن حبوب\ نبات و معدل وزن السنبلة في كلار والتي كانت اعلى من واحد صحيح. كانت درجةالتوريث بالمعنى العام متوسطة الى عالية لاغلب الصفات ولكل المواقع بينما كانت منخفظة الى متوسطة في معناها الخاص مشيرا الى اتباع طرق التهجين لتحسين تلك الصفات. تم تقدير معامل الارتباط البسيط بين وزن حبوب\ نبات والصفات المهمة لكل موقع مبينا وجود ارتباطات عالية المعنوية وموجبة بين حاصل حبوب\ نبات والحاصل البايولوجي\ نبات و عدد الحبوب\ سنبلة و عدد الأشطاء\ نبات لكل المواقع. و اشارت نتائج تحليل المسار ان الحاصل البايولوجي\

نبات ودليل الحصاد اظهرا اعلى قيمة موجبة للتأثير المباشر على حاصل حبوب\ نبات لكل المواقع قلياسان واربيل و كلار وكانت 0،744 و 0.421، 0.580 و 0.264 و 0.717 و0.447 على التوالي.

أوضحت الدراسة للأستقرارية والمحصلة الوراثية وجود تداخل عالي المعنوية بين التراكيب الوراثية و المواقع وللصفات جميعها فيما عدا قطر حامل السنبلة الذي كان معنوي فقط. ان قطر حامل السنبلة امتلك الأستقرارية والمحصلة الوراثية الأعلى بمعدل قيمة 0.951 لكلاهما، فيما صفة حاصل الحبوب\ نبات كانت الأدنى بمعدل قيمة 0.459 و 0.567 على التوالي. و حقق الأب 1 و الهجين 2 x5 القيمة الأعلى لصفة حاصل الحبوب\ نبات بـ 0.567 و 0.602 على التوالي وهما الأكثر كفاءة خلال مختلف الظروف البيئية المدروسة. ان الهدف الرئيسي من الدراسة الحالية هو التعرف على البنية والهيكلية الوراثية و احسن الأباء للتآلف وهجنها على اساس القدرة العامة والخاصة للتآلف للصفات المهمة للشعير ذو الصفين تحت ظروف بيئية مختلفة لزيادة تحسين الحاصل الحبوبي ومكوناته تحت الظروف الأعتيادية، السائدة لأقليم كوردستان العراق.

پوختەی كار و ئه نجامەكان

چاندنی پێنج پێكهاتەی بۆماوەیی پوخت جۆری دوو ڕیز (*Hordeum distichum L.*) به بەكارهێنانی ڕێی لێكدانی دووانه ئەلیلی تەواو، له وەرزی زستانی (2010–2011) بۆ وەبەرهێنانی (20) دووڕەگ له ئەم باوكانەی خوارەوە:

MORA/NB1054/3/MOLA/SHYRI//ARUPO*2/JET/4/…CBSS99M002 9TG- 5M-1Y-1M-0Y; ABN-B/KA-B//RAISA/3/ALELI/4/LIMON/5/..CBSS99M00228 T-K 6M-1Y- 1M-0Y; Arabi aswade; Clipper; Bohoth H1

(20) ڕەگی گوڵ و پێنج له باوكەكانیان، له وەرزی زستانی (2011–2012)، له سێ شوێنی كەشوهەوای جیاواز، له ئێستگەی توێژینەوەی (قلیاسان) له (سوله یمانیی)، ئێستگەی توێژینەوەی (گردەڕەش) له (هەولێر) و ئێستگەی توێژینەوەی (كەلار) چێنرا. دیزایینی بلۆكه هەرەمییه تەواوەكان به سێ دووبارەبوونەوە پێڕەوكرا. توێژینەوە لەسەر جیاواز خەسڵەتی شێوەكانی ڕووەك كرا.

نێوەندی بەهای خەسڵەتەكان بەراوردكران، كەمترین جیاوازیی واتادار لەسەر ئاستی (5٪) بەكارهێنرا. توێژینەوەكان، كارتێكردنی واتاداری باڵای شوێن له خەسڵەتەكانی دەرخست و دەركەوت: (قلیاسان) به شێوەیەكی واتادار، جگه له خەسڵەتی ژمارەی لق/ڕووەك و ژمارەی گوڵ/ڕووەك له هەموو خەسڵەتەكانی دیكەدا باشتربوو.

شیكردنەوەی بۆماوەیی داتاكان، بۆ دیارییكردنی توانای گشتیی و تایبەتی بەرگرتن، سرووشتی كاری جینیی، لێكدان و بۆماوەیی كرا. ڕێی لێكدانی دووانەی (Griffing) بەكارهێنرا. ڕێی یەكەم: (باوكەكان، لێكدراو و لێكدراوی پێچەوانەیی نەوەی یەكەم) و شێوەی یەكەم (جێگیر) بوو. (Singh and Chaudhary,**1985**) هەروەها له پێوەندیی شیكردنەوەی ئاراستەی جێگیربوون و ئه نجامی بۆماوەیی توێژرایەوە.

ئه نجامەكانی شیكردنەوەی بۆماوەیی دەریخست: له نێوان پێكهاته بۆماوەییەكانی هەموو خەسڵەته لێتوێژراوەكان و هەموو شوێنەكان، جیاوازییەكی واتاداری بەرز هەبوو. ئەمەش ئەوە دەگەیەنێ: جیاوازیی بۆماوەیی له نێوان پێكهاته بۆماوەییەكاندا هەبوو. هەروەها، دووجای نێوەندەكانی توانای گشتیی وتایبەتی یەكگرتن و توانای تایبەتی یەكگرتنی لێكدراوه پێچەوانەكان، بۆ هەموو خەسڵەته لێتوێژراوەكان و هەموو شوێنەكان، واتادارێكی بەرزیان هەبوو،

جگە لە تیرەی گوڵهەڵگری توانای تایبەتی لە (قلیاسان) و (هەولێر)، تەنیا واتاداربوون. بەڵام توانای تایبەتی لێکدانی پێچەوانەیی درێژیی گەڵای ئاڵا، تیرەی گوڵهەڵگر و درێژیی گوڵ لە (قلیاسان) واتادارنەبوون. تەنیا ڕێبەری دروێنە واتاداربوو. ژمارەی ڕۆژە پێویستەکانی لە (50٪)ی گوڵکردن، ژمارەی ڕۆژە پێویستەکانی لە (50٪)ی پێگەشتن، درێژیی سەفا و تیرەی گوڵهەڵگر، لە (هەولێر) واتادار نەبوون. بەڵام ژمارەی ڕۆژە پێویستەکانی لە (50٪)ی گوڵکردن و ژمارەی ڕۆژە پێویستەکانی لە (50٪)ی پێگەشتن، کێشی (1000) دەنك و ژمارەی دەنك/گوڵ لە (کەلار) واتاداربوون.

ئە نجامەکان دەریا نخست: خەسڵەتەکان لە ڕەوشی (قلیاسان، هەولێر و کەلار)، بە هۆی باوکەکانی (3,4,5) بۆ کێشی دەنك/ڕووەك و زۆربەی خەسڵەتەکان یەك لە دوای یەك، بەرزترین بەهایان هەبوو. بەڵام کەمترین بەها لە باوکەکانی (1,2,1) یەك لە دوای یەك بوون. لێکدراوەکانی 1× لە (قلیاسان)، 3×4 لە (هەولێر) و 2×3 لە (کەلار)، بەرزترین بەهایان داوە. بۆ خەسڵەتی کێشی دەنك/ڕووەك و زۆربەی خەسڵەتە لێتوێژراوەکان، کەمترین بەهایان هەبوو.

لێکدراوە پێچەوانەییەکانی 2x4. لە (قلیاسان)، . 2x5 لە (هەولێر) و 2x4 لە (کەلار)، هەر لێکدراوە پێچەوانەکەی بەرزترین بەهایان هەبوولە خەسڵەتی کێشی دەنك/ڕووەك و زۆربەی خەسڵەتەکاندا.

ئەوەش دەرکەوت: لە شێوە لێکدانی (12، 8 و 13) لە نێوان (20) لێکدراودا: (لێکدراوی تەواو و پێچەوانە)، توانای لێکدانی خەسڵەتەکانـــــــی کێشی دەنك/ڕووەك لە نێوان (1.568 – 59. 372 ٪)، (4. 486 - 33.102 ٪) و (6. 154 - 48.734٪) بەهای پۆزەتیڤیان هەبوو. لە هەمان کاتیشدا، لێکدراوەکانی (4x1، 2x5 و 1x4)، لە خەسڵەتەکانی کێشی دەنك/ڕووەك و زۆربەی خەسڵەتەکان لە (قلیاسان، هەولێر و کەلار) یەك لە دوای یەك، باشترین بوون.

لە ئەم ئە نجامانەوە دەردەکەوێ: کارتێکردنی پێچەوانەیی لێکدانی پێچەوانە لە (7، 8 و 4) لە (10) لێکداراوی پێچەوانەدا، بەرزترین کارتێکردنە پێچەوانەکەی بەهای پۆزەتیف لە خەسڵەتی کێشی دەنك/ڕووەك لەنێوان (6.087 - 62.225 ٪، 2.027٪ - 33.844٪ و 4.926٪ - 48.610٪) بوون. لەگەڵ ئەوەی لێکدراوی پێچەوانەی (3×2، 5×1 و 4×3) لە خەسڵەتەکانی کێشی دەنك/ڕووەك و زۆربەی خەسڵەتەکانی دیکە لە (قلیاسان، هەولێر و کەلار) یەك لە دوای یەك، باشترین بوون.

ئه نجامەکانی شیکردنەوە جیاوازەکان دەریا نخست: جیاوازییەکی واتادار لە توانای گشتیی و تایبەتی یەکگرتندا هەیە، ئەمەش نیشانەی ئەوەیە: کارتێکردنی زیادکراو و زیادنەکراو، لە کاری جینیی و شیکردنەوەی جیاوازیی بۆماوەیی دەریخست: بایەخی کارتێکردنی زاڵبوونی سەرکەوتووی کاری جینیی، لە گوزارە و زۆربەی خەسڵەتە لێتوێژراوەکان لە هەموو شوێنەکاندا هەیە، جگە لە درێژیی گەڵای ئاڵا، تیرەی گوڵهەڵگر لە هەر سێ شوێنەکەدا، ژمارەی ڕۆژە پێویستەکانی لە (50٪)ی پێگەیشتن لە (قلیاسان) و (کەلار)، درێژیی گوڵهەڵگر لە (هەولێر) و تێکڕای کێشی گوڵ لە (کەلار)، جۆرێکی زیادەی لە کاری جینی گرنگ بوو. بە تێکڕای زاڵبوون لە لێکدراوی دووانیدا، لە یەکی تەواوی خەسڵەتەکانی درێژیی گەڵای ئاڵا و تیرەی گوڵهەڵگر، لە هەر سێ شوێنەکەدا، ژمارەی ڕۆژە پێویستەکانی لە (50٪)ی پێگەیشتن لە (هەولێر) و تێکڕای کێشی گوڵ لە (کەلار)، کارتێکردنی کەمتربوو. زاڵبوونی بەشێ کە کاری جینیی زاڵ لە ئەم خەسڵەتەدا دەردەکەوێ. دەر کەوت دەرئە نجامی شیکردنەوەی کاریگەریلەسەر بەرگرتن باوکەکان 4و5 لە قلیسان و 5و3 لە هەولیر و2 و3 کەلار دا ویەتی بەگشتی باشترین بۆ زۆربەی خەسلەتەکان . توانای بەکارهێنا نی لە پرۆگرامی لێکدانی بەدەستهێنانی گونجاندنی باوەڕپێکراو. لە کاتێکدا دەرکەوت لێگدانی تاك گوراو 1× 4 و 3×5 و 1× 5 لە قلیسان و 2×5 و 2×3 لە هەولیر و1×4 لە کەلار بەرزترین ڕێژە بۆ کاریگەری توانای تایبەتی بەرگرتن وە لەگەڵ توانای بەکاهێنانی لە پەروەردەی ئاینده . بەڵام خەسڵەتەکانی دیکە و هەموو شوێنەکانی دیکەش، کارتێکردنی زاڵبوونی باڵای کاری جینیی لە بۆماوەیی ئەم خەسڵەتەدا، لە یەکی تەواو گەورەتربوو.

سەبارەت بە لێکدراوی پێچەوانە، تێکڕای بەهای زاڵبوون لە زۆربەی خەسڵەتەکاندا، لە یەکی تەواو کەمتر بوو. جگە لە درێژیی ڕووەك لە (هەولێر) و (قلیاسان)، کێشی بایۆلۆجی/ڕوەك، ژمارەی گوڵ/ڕوەك، کێشی دەنك/ڕوەك، لە (هەولێر)، درێژیی ڕووەك، کێشی بایۆلۆجی/ڕوەك، درێژیی گوڵ، ژمارەی گوڵۆچکە/گوڵ، کێشی دەنك/ڕووەك و تێکڕای کێشی گوڵ لە (کەلار)، لە یەکی تەواو بەرزتربوون. کارتێکردنی پلەی بۆماوەیی بە واتای گشتیی، لە زۆربەی خەسڵەتەکان و زۆربەی شوێنەکان، مامناوەندیی – بەرز بوون. بەڵام نێوەندی واتای تایبەت، بۆ پێڕەوکردنی ڕێیەکانی لێکدان و بۆ باشترکردنی ئەو خەسڵەتانە نزمبوو. لە هەمان کاتدا، لە واتای تایبەتدا، نزم – مامناوەندیی بوو. ئەمەش نیشانەی ئەوە بوو، بۆ چاککردنی ئەو خەسڵەتانە، ڕێی لێکدان پێڕەوکراوە.

هۆکاری پێوەندیی ساکار لە نێوان کێشی دەنك/ڕووەك و خەسڵەتە گرنگەکانی هەر شوێنێ ئەژمارکرا و دەرکەوت: پێوەندیی واتاداری بەرز و پۆزەتیڤ، لە نێوان کێشی دەنك/ڕووەك و کێشی بایۆلۆجی/ڕووەك، ژمارەی دەنك/گوڵ و ژمارەی برالەکان {Tillers}/ڕووەك لە هەموو شوێنەکان هەبوو.

ئەنجامەکانی شیکردنەوەی تاقیکردنەوەی کێشی بایۆلۆجی/ڕووەك وەرێ پشاندەری بەرهەم بەرزترین بەهای پۆزێتیڤی کارتێکردنی ڕاستەوخۆی، لە هەر سێ شوێنەکەی: (قلیاسان، هەولێر و کەلار)، لە کێشی دەنك/ڕووەك کردووە و ئەنجامەکەشی، یەك لە دوای یەك (0.744، 0.421 و 0.580 0.264، و 0 .717 0 .447 0) بوون.

توێژینەوەی جێگیربوون و ئەنجامی بۆماوەیی ڕوونیکردەوە: کارتێکردنی واتاداری بەرزی بەیەکداچوونی پێکهاتە بۆماوەییەکان، لەگەڵ شوێنەکان و هەموو خەسڵەتە لێتوێژراوەکان هەبوو. جگە لە تیرەی گوڵهەڵگر، تەنیا واتادار بوو. تیرەی گوڵهەڵگر، جێگیربوون و ئەنجامێکی بۆماوەیی بەرزی هەبوو، تێکڕای بەهای هەردووکیان (0.951) بوو. بەڵام خەسڵەتی کێشی دەنك/ڕووەك، نزمترین بوو، تێکڕای بەهاکەیان یەك لە دوای یەك، (0.459 و 0.567) بوو.

باوکی ژمارە (1) و لێکدراوی (5×2)، بەرزترین بەهای خەسڵەتی کێشی دەنك/ڕووەکیان بەدەسهێنا و یەك لە دوای یەك، (0.567 و 0.602) بوون. لە ڕەوشی ژینگە جیاوازەکانی لێتوێژینەوەکانیشدا، بەرزترین توانایان هەبوو.

ئامانجی سەرەکیی ئەم توێژینەوەیە ئەوەیە: پێکهاتە و پەیکەری بۆماوەیی و باشترین باوکەکانی پێکەوەلکان بناسرێن، لەبەر ڕۆشنایی توانای گشتیی و تایبەتی پێکەوەلکانی، خەسڵەتە گرنگەکانی جۆی دوو ڕیز، لە ڕەوشی ژینگەی جیاوازدا لێکدرێن، بۆ ئەوەی لە ڕەوشی ئاسایی، مامناوەندیی و ووشکی هەرێمی کوردستانی عێراق، بەرهەمی دەنك و پێکهاتەکانی چاککرێن.

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